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(19) **United States**(12) **Patent Application Publication**
Houghton et al.(10) **Pub. No.: US 2006/0069054 A1**(43) **Pub. Date: Mar. 30, 2006**(54) **COMPOSITIONS AND METHODS FOR THE
THERAPY AND DIAGNOSIS OF BREAST
CANCER**(75) Inventors: **Raymond L. Houghton**, Bothell, WA
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SEATTLE, WA 98104-7092 (US)**(73) Assignee: **Corixa Corporation**, Seattle, WA(21) Appl. No.: **11/226,869**(22) Filed: **Sep. 13, 2005****Related U.S. Application Data**

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which is a continuation-in-part of application No. 09/551,621, filed on Apr. 17, 2000, now Pat. No. 6,844,325, which is a continuation-in-part of application No. 09/433,826, filed on Nov. 3, 1999, now Pat. No. 6,579,973, which is a continuation-in-part of application No. 09/389,681, filed on Sep. 2, 1999, now Pat. No. 6,518,237, which is a continuation-in-part of application No. 09/339,338, filed on Jun. 23, 1999, now Pat. No. 6,573,368, which is a continuation-in-part of application No. 09/285,480, filed on Apr. 2, 1999, now Pat. No. 6,590,076, which is a continuation-in-part of application No. 09/222,575, filed on Dec. 28, 1998, now Pat. No. 6,387,697.

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435/325; 530/350; 530/388.8;
536/23.5

(57)

ABSTRACT

Compositions and methods for the therapy and diagnosis of cancer, particularly breast cancer, are disclosed. Illustrative compositions comprise one or more breast tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly breast cancer.

SYN18C6 NORTHERN BLOT

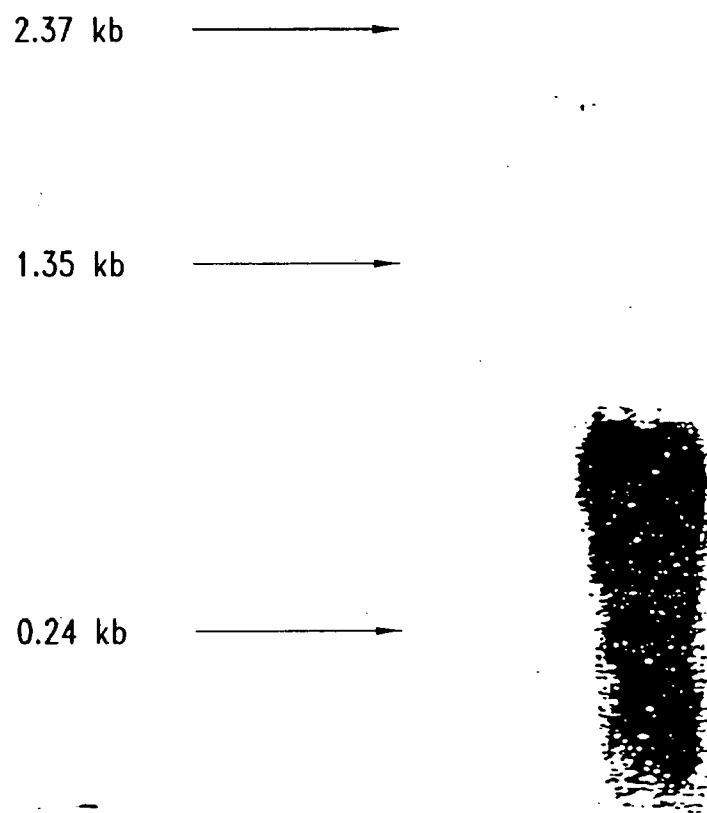


Fig. 1

D207 B726P-specific CTL Clone 1-9A recognize HTB 21
a breast tumor cell line that expresses HLA-B*1501 and B726P

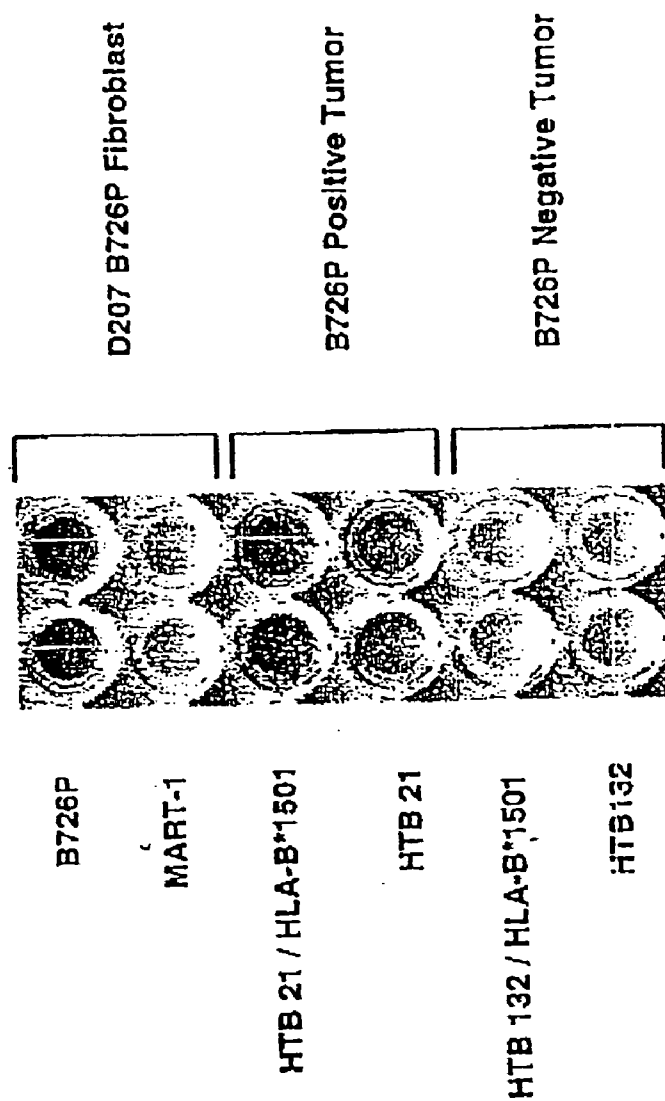


FIG. 2

COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF BREAST CANCER

TECHNICAL FIELD OF THE INVENTION

[0001] The present invention relates generally to therapy and diagnosis of cancer, such as breast cancer. The invention is more specifically related to polypeptides, comprising at least a portion of a breast tumor protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides are useful in pharmaceutical compositions, e.g., vaccines, and other compositions for the diagnosis and treatment of breast cancer.

BACKGROUND OF THE INVENTION

[0002] 1. Field of the Invention

[0003] Breast cancer is a significant health problem for women in the United States and throughout the world. Although advances have been made in detection and treatment of the disease, breast cancer remains the second leading cause of cancer-related deaths in women, affecting more than 180,000 women in the United States each year. For women in North America, the life-time odds of getting breast cancer are one in eight.

[0004] 2. Description of the Related Art

[0005] No vaccine or other universally successful method for the prevention or treatment of breast cancer is currently available. Management of the disease currently relies on a combination of early diagnosis (through routine breast screening procedures) and aggressive treatment, which may include one or more of a variety of treatments such as surgery, radiotherapy, chemotherapy and hormone therapy. The course of treatment for a particular breast cancer is often selected based on a variety of prognostic parameters, including an analysis of specific tumor markers. See, e.g., Porter-Jordan and Lippman, *Breast Cancer* 8:73-100 (1994). However, the use of established markers often leads to a result that is difficult to interpret, and the high mortality observed in breast cancer patients indicates that improvements are needed in the treatment, diagnosis and prevention of the disease.

[0006] Accordingly, there is a need in the art for improved methods for the treatment and diagnosis of breast cancer. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

[0007] In one aspect, the present invention provides polynucleotide compositions comprising a sequence selected from the group consisting of:

[0008] (a) sequences provided in SEQ ID NO:1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576;

[0009] (b) complements of the sequences provided in SEQ ID NO:1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576;

[0010] (c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO:1-61,

63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576;

[0011] (d) sequences that hybridize to a sequence provided in SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576, under moderately stringent conditions;

[0012] (e) sequences having at least 75% identity to a sequence of SEQ ID NO:1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576;

[0013] (f) sequences having at least 90% identity to a sequence of SEQ ID NO:1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576; and

[0014] (g) degenerate variants of a sequence provided in SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576.

[0015] In one preferred embodiment, the polynucleotide compositions of the invention are expressed in at least about 20%, more preferably in at least about 30%, and most preferably in at least about 50% of breast tumors samples tested, at a level that is at least about 2-fold, preferably at least about 5-fold, and most preferably at least about 10-fold higher than that for normal tissues.

[0016] The present invention, in another aspect, provides polypeptide compositions comprising an amino acid sequence that is encoded by a polynucleotide sequence described above.

[0017] The present invention further provides polypeptide compositions comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO:62, 176, 179, 181, 469-473, 475, 478, 483, 485, 487, 488, 493-503, 507-509, 514-519, 534-547, 551-553, 565, 570-573, and 577-627.

[0018] In certain preferred embodiments, the polypeptides and/or polynucleotides of the present invention are immunogenic, i.e., they are capable of eliciting an immune response, particularly a humoral and/or cellular immune response, as further described herein.

[0019] The present invention further provides fragments, variants and/or derivatives of the disclosed polypeptide and/or polynucleotide sequences, wherein the fragments, variants and/or derivatives preferably have a level of immunogenic activity of at least about 50%, preferably at least about 70% and more preferably at least about 90% of the level of immunogenic activity of a polypeptide sequence set forth in SEQ ID NO: 62, 176, 179, 181, 469-473, 475, 478, 483, 485, 487, 488, 493-503, 507-509, 514-519, 534-547, 551-553, 565, 570-573, and 577-627 or a polypeptide sequence encoded by a polynucleotide sequence set forth in SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576.

[0020] The present invention further provides polynucleotides that encode a polypeptide described above, expres-

sion vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

[0021] Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

[0022] Within a related aspect of the present invention, the pharmaceutical compositions, e.g., vaccine compositions, are provided for prophylactic or therapeutic applications. Such compositions generally comprise an immunogenic polypeptide or polynucleotide of the invention and an immunostimulant, such as an adjuvant.

[0023] The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a polypeptide of the present invention, or a fragment thereof; and (b) a physiologically acceptable carrier.

[0024] Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Illustrative antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

[0025] Within related aspects, pharmaceutical compositions are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

[0026] The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins, typically in the form of pharmaceutical compositions, e.g., vaccine compositions, comprising a physiologically acceptable carrier and/or an immunostimulant. The fusions proteins may comprise multiple immunogenic polypeptides or portions/variants thereof, as described herein, and may further comprise one or more polypeptide segments for facilitating the expression, purification and/or immunogenicity of the polypeptide(s).

[0027] The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins. Exemplary fusion proteins according to the present invention comprise a first amino acid portion and a second amino acid portion wherein the first amino acid portion includes 9 or more contiguous amino acids from mammaglobin as depicted by amino acids 1-93 of SEQ ID NO:493 (SEQ ID NO:503); wherein the second amino acid portion includes 9 or more contiguous amino acids from B726P as depicted by SEQ ID NO:475, SEQ ID NO:469, or SEQ ID NO:176; and wherein the first amino acid portion is connected to either the amino terminal or carboxy-terminal end of the second amino acid portion.

[0028] Still further embodiments of the present invention provide fusion proteins wherein said first amino acid portion is selected from the group consisting of: IDELKECFLNQTDETLSNVE (SEQ ID NO:496; amino acids 59-78 of SEQ ID NO:493); TFNAIDELKECFLNQ (SEQ ID NO:497; amino acids 55-69 of SEQ ID NO:493); SQHCY-AGSGCPLLENVISKTI (SEQ ID NO:498; amino acids

13-33 of SEQ ID NO:493); EYKELLQEFIDDNATTNAID (SEQ ID NO:499; amino acids 41-60 of SEQ ID NO:493); KLLMVLMLA (SEQ ID NO:500; amino acids 2-10 of SEQ ID NO:493); QEFIDDNATTNAI (SEQ ID NO:501; amino acids 47-59 of SEQ ID NO:493); LKECFLNQTDETL (SEQ ID NO:502; amino acids 62-74 of SEQ ID NO:493), and any one of the amino acid sequences set forth in SEQ ID NO:578-593.

[0029] Alternative embodiments provide fusion proteins wherein the second amino acid portion includes 9 or more contiguous amino acids encoded by (1) the combined upstream and downstream open reading frame (ORF) of B726P as depicted in SEQ ID NO:475; (2) the upstream ORF of B726P as depicted in SEQ ID NO:469; and (3) the downstream ORF of B726P as depicted in SEQ ID NO:176. Fusion proteins according to the present invention may also comprise a second amino acid portion that includes 9 or more contiguous amino acids from the amino acid sequence depicted by amino acids 1-129 of SEQ ID NO:475. Still additional exemplary fusion proteins are depicted herein by SEQ ID NO:493, SEQ ID NO:494, and SEQ ID NO:495.

[0030] Fusion proteins are provided wherein the mammaglobin amino acid portion is connected to the amino-terminus of the B726P amino acid portion while other fusion proteins are provided wherein the mammaglobin amino acid portion is connected to the carboxy-terminus of the B726P amino acid portion. The connection between the mammaglobin amino acid portion and the B726P portion may be a covalent bond. Additionally, a stretch of amino acids either unrelated or related to either mammaglobin and/or B726P may be incorporated between or either amino- or carboxy-terminal to either the mammaglobin and/or B726P amino acid portion.

[0031] The present invention also provides isolated polynucleotides that encode any of the fusion proteins that are specifically disclosed herein as well as those fusion proteins that may be accomplished with routine experimentation by the ordinarily skilled artisan.

[0032] Within further aspects, the present invention provides methods for stimulating an immune response in a patient, preferably a T cell response in a human patient, comprising administering a pharmaceutical composition described herein. The patient may be afflicted with breast cancer, in which case the methods provide treatment for the disease, or patient considered at risk for such a disease may be treated prophylactically.

[0033] Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition as recited above. The patient may be afflicted with breast cancer, in which case the methods provide treatment for the disease, or patient considered at risk for such a disease may be treated prophylactically.

[0034] The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a polypeptide of the present invention, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

[0035] Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

[0036] Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a polypeptide of the present invention, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

[0037] Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

[0038] The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of polypeptide disclosed herein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

[0039] Within further aspects, the present invention provides methods for determining the presence or absence of a cancer, preferably a breast cancer, in a patient comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody.

[0040] The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

[0041] The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a polypeptide of the present invention; (b) detecting in the sample a level of a polynucleotide, preferably mRNA,

that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

[0042] In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a polypeptide of the present invention; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

[0043] Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

[0044] 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.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

[0045] FIG. 1 shows the results of a Northern blot of the clone SYN18C6 (SEQ ID NO:40).

[0046] FIG. 2 shows the results of an IFN-gamma ELISPOT assay demonstrating that the B726P-specific CTL clone recognizes and lyses breast tumor cell lines expressing B726P.

[0047] SEQ ID NO:1 is the determined cDNA sequence of JBT2.

[0048] SEQ ID NO:2 is the determined cDNA sequence of JBT6.

[0049] SEQ ID NO:3 is the determined cDNA sequence of JBT7.

[0050] SEQ ID NO:4 is the determined cDNA sequence of JBT10.

[0051] SEQ ID NO:5 is the determined cDNA sequence of JBT13.

[0052] SEQ ID NO:6 is the determined cDNA sequence of JBT14.

- [0053] SEQ ID NO:7 is the determined cDNA sequence of JBT15.
- [0054] SEQ ID NO:8 is the determined cDNA sequence of JBT16.
- [0055] SEQ ID NO:9 is the determined cDNA sequence of JBT17.
- [0056] SEQ ID NO:10 is the determined cDNA sequence of JBT22.
- [0057] SEQ ID NO:11 is the determined cDNA sequence of JBT25.
- [0058] SEQ ID NO:12 is the determined cDNA sequence of JBT28.
- [0059] SEQ ID NO:13 is the determined cDNA sequence of JBT32.
- [0060] SEQ ID NO:14 is the determined cDNA sequence of JBT33.
- [0061] SEQ ID NO:15 is the determined cDNA sequence of JBT34.
- [0062] SEQ ID NO:16 is the determined cDNA sequence of JBT36.
- [0063] SEQ ID NO:17 is the determined cDNA sequence of JBT37.
- [0064] SEQ ID NO:18 is the determined cDNA sequence of JBT51.
- [0065] SEQ ID NO:19 is the determined cDNA sequence of JBTT1.
- [0066] SEQ ID NO:20 is the determined cDNA sequence of JBTT7.
- [0067] SEQ ID NO:21 is the determined cDNA sequence of JBTT11.
- [0068] SEQ ID NO:22 is the determined cDNA sequence of JBTT14.
- [0069] SEQ ID NO:23 is the determined cDNA sequence of JBTT18.
- [0070] SEQ ID NO:24 is the determined cDNA sequence of JBTT19.
- [0071] SEQ ID NO:25 is the determined cDNA sequence of JBTT20.
- [0072] SEQ ID NO:26 is the determined cDNA sequence of JBTT21.
- [0073] SEQ ID NO:27 is the determined cDNA sequence of JBTT22.
- [0074] SEQ ID NO:28 is the determined cDNA sequence of JBTT28.
- [0075] SEQ ID NO:29 is the determined cDNA sequence of JBTT29.
- [0076] SEQ ID NO:30 is the determined cDNA sequence of JBTT33.
- [0077] SEQ ID NO:31 is the determined cDNA sequence of JBTT37.
- [0078] SEQ ID NO:32 is the determined cDNA sequence of JBTT38.
- [0079] SEQ ID NO:33 is the determined cDNA sequence of JBTT47.
- [0080] SEQ ID NO:34 is the determined cDNA sequence of JBTT48.
- [0081] SEQ ID NO:35 is the determined cDNA sequence of JBTT50.
- [0082] SEQ ID NO:36 is the determined cDNA sequence of JBTT51.
- [0083] SEQ ID NO:37 is the determined cDNA sequence of JBTT52.
- [0084] SEQ ID NO:38 is the determined cDNA sequence of JBTT54.
- [0085] SEQ ID NO:39 is the determined cDNA sequence of SYN17F4.
- [0086] SEQ ID NO:40 is the determined cDNA sequence of SYN18C6 (also known as B709P).
- [0087] SEQ ID NO:41 is the determined cDNA sequence of SYN19A2.
- [0088] SEQ ID NO:42 is the determined cDNA sequence of SYN19C8.
- [0089] SEQ ID NO:43 is the determined cDNA sequence of SYN20A12.
- [0090] SEQ ID NO:44 is the determined cDNA sequence of SYN20G6.
- [0091] SEQ ID NO:45 is the determined cDNA sequence of SYN20G6-2.
- [0092] SEQ ID NO:46 is the determined cDNA sequence of SYN21B9.
- [0093] SEQ ID NO:47 is the determined cDNA sequence of SYN21B9-2.
- [0094] SEQ ID NO:48 is the determined cDNA sequence of SYN21C10.
- [0095] SEQ ID NO:49 is the determined cDNA sequence of SYN21G10.
- [0096] SEQ ID NO:50 is the determined cDNA sequence of SYN21G10-2.
- [0097] SEQ ID NO:51 is the determined cDNA sequence of SYN21G11.
- [0098] SEQ ID NO:52 is the determined cDNA sequence of SYN21G11-2.
- [0099] SEQ ID NO:53 is the determined cDNA sequence of SYN21H8.
- [0100] SEQ ID NO:54 is the determined cDNA sequence of SYN22A10.
- [0101] SEQ ID NO:55 is the determined cDNA sequence of SYN22A10-2.
- [0102] SEQ ID NO:56 is the determined cDNA sequence of SYN22A12.
- [0103] SEQ ID NO:57 is the determined cDNA sequence of SYN22A2 (also referred to as B718P).
- [0104] SEQ ID NO:58 is the determined cDNA sequence of SYN22B4.

[0105] SEQ ID NO:59 is the determined cDNA sequence of SYN22C2.

[0106] SEQ ID NO:60 is the determined cDNA sequence of SYN22E10.

[0107] SEQ ID NO:61 is the determined cDNA sequence of SYN22F2.

[0108] SEQ ID NO:62 is a predicted amino acid sequence for SYN18C6 (also known as B709P).

[0109] SEQ ID NO:63 is the determined cDNA sequence of B723P.

[0110] SEQ ID NO:64 is the determined cDNA sequence for B724P.

[0111] SEQ ID NO:65 is the determined cDNA sequence of B770P.

[0112] SEQ ID NO:66 is the determined cDNA sequence of B716P.

[0113] SEQ ID NO:67 is the determined cDNA sequence of B725P.

[0114] SEQ ID NO:68 is the determined cDNA sequence of B717P.

[0115] SEQ ID NO:69 is the determined cDNA sequence of B771P.

[0116] SEQ ID NO:70 is the determined cDNA sequence of B722P.

[0117] SEQ ID NO:71 is the determined cDNA sequence of B726P.

[0118] SEQ ID NO:72 is the determined cDNA sequence of B727P.

[0119] SEQ ID NO:73 is the determined cDNA sequence of B728P.

[0120] SEQ ID NO:74-87 are the determined cDNA sequences of isolated clones which show homology to known sequences.

[0121] SEQ ID NO:88 is the determined cDNA sequence of 13053.

[0122] SEQ ID NO:89 is the determined cDNA sequence of 13057.

[0123] SEQ ID NO:90 is the determined cDNA sequence of 13059.

[0124] SEQ ID NO:91 is the determined cDNA sequence of 13065.

[0125] SEQ ID NO:92 is the determined cDNA sequence of 13067.

[0126] SEQ ID NO:93 is the determined cDNA sequence of 13068.

[0127] SEQ ID NO:94 is the determined cDNA sequence of 13071.

[0128] SEQ ID NO:95 is the determined cDNA sequence of 13072.

[0129] SEQ ID NO:96 is the determined cDNA sequence of 13073.

[0130] SEQ ID NO:97 is the determined cDNA sequence of 13075.

[0131] SEQ ID NO:98 is the determined cDNA sequence of 13078.

[0132] SEQ ID NO:99 is the determined cDNA sequence of 13079.

[0133] SEQ ID NO:100 is the determined cDNA sequence of 13081.

[0134] SEQ ID NO:101 is the determined cDNA sequence of 13082.

[0135] SEQ ID NO:102 is the determined cDNA sequence of 13092.

[0136] SEQ ID NO:103 is the determined cDNA sequence of 13097.

[0137] SEQ ID NO:104 is the determined cDNA sequence of 13101.

[0138] SEQ ID NO:105 is the determined cDNA sequence of 13102.

[0139] SEQ ID NO:106 is the determined cDNA sequence of 13119.

[0140] SEQ ID NO:107 is the determined cDNA sequence of 13131.

[0141] SEQ ID NO:108 is the determined cDNA sequence of 13133.

[0142] SEQ ID NO:109 is the determined cDNA sequence of 13135.

[0143] SEQ ID NO:110 is the determined cDNA sequence of 13139.

[0144] SEQ ID NO:111 is the determined cDNA sequence of 13140.

[0145] SEQ ID NO:112 is the determined cDNA sequence of 13146.

[0146] SEQ ID NO:113 is the determined cDNA sequence of 13147.

[0147] SEQ ID NO:114 is the determined cDNA sequence of 13148.

[0148] SEQ ID NO:115 is the determined cDNA sequence of 13149.

[0149] SEQ ID NO:116 is the determined cDNA sequence of 13151.

[0150] SEQ ID NO:117 is the determined cDNA sequence of 13051

[0151] SEQ ID NO:118 is the determined cDNA sequence of 13052

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[0153] SEQ ID NO:120 is the determined cDNA sequence of 13058

[0154] SEQ ID NO:121 is the determined cDNA sequence of 13062

[0155] SEQ ID NO:122 is the determined cDNA sequence of 13064

[0156] SEQ ID NO:123 is the determined cDNA sequence of 13080

[0157] SEQ ID NO:124 is the determined cDNA sequence of 13093

[0158] SEQ ID NO:125 is the determined cDNA sequence of 13094

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[0160] SEQ ID NO:127 is the determined cDNA sequence of 13096

[0161] SEQ ID NO:128 is the determined cDNA sequence of 13099

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[0164] SEQ ID NO:131 is the determined cDNA sequence of 13106

[0165] SEQ ID NO:132 is the determined cDNA sequence of 13107

[0166] SEQ ID NO:133 is the determined cDNA sequence of 13108

[0167] SEQ ID NO:134 is the determined cDNA sequence of 13121

[0168] SEQ ID NO:135 is the determined cDNA sequence of 13126

[0169] SEQ ID NO:136 is the determined cDNA sequence of 13129

[0170] SEQ ID NO:137 is the determined cDNA sequence of 13130

[0171] SEQ ID NO:138 is the determined cDNA sequence of 13134

[0172] SEQ ID NO:139 is the determined cDNA sequence of 13141

[0173] SEQ ID NO:140 is the determined cDNA sequence of 13142

[0174] SEQ ID NO:141 is the determined cDNA sequence of 14376

[0175] SEQ ID NO:142 is the determined cDNA sequence of 14377

[0176] SEQ ID NO:143 is the determined cDNA sequence of 14383

[0177] SEQ ID NO:144 is the determined cDNA sequence of 14384

[0178] SEQ ID NO:145 is the determined cDNA sequence of 14387

[0179] SEQ ID NO:146 is the determined cDNA sequence of 14392

[0180] SEQ ID NO:147 is the determined cDNA sequence of 14394

[0181] SEQ ID NO:148 is the determined cDNA sequence of 14398

[0182] SEQ ID NO:149 is the determined cDNA sequence of 14401

[0183] SEQ ID NO:150 is the determined cDNA sequence of 14402

[0184] SEQ ID NO:151 is the determined cDNA sequence of 14405

[0185] SEQ ID NO:152 is the determined cDNA sequence of 14409

[0186] SEQ ID NO:153 is the determined cDNA sequence of 14412

[0187] SEQ ID NO:154 is the determined cDNA sequence of 14414

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[0200] SEQ ID NO:167 is the determined cDNA sequence of 14399

[0201] SEQ ID NO:168 is the determined cDNA sequence of 14406

[0202] SEQ ID NO:169 is the determined cDNA sequence of 14407

[0203] SEQ ID NO:170 is the determined cDNA sequence of 14408

[0204] SEQ ID NO:171 is the determined cDNA sequence of 14417

[0205] SEQ ID NO:172 is the determined cDNA sequence of 14418

[0206] SEQ ID NO:173 is the determined cDNA sequence of 14423

[0207] SEQ ID NO:174 is the determined cDNA sequence of 14424

[0208] SEQ ID NO:175 is the determined cDNA sequence of B726P-20

[0209] SEQ ID NO:176 is the predicted amino acid sequence of B726P-20 (also referred to as B726P downstream ORF)

[0210] SEQ ID NO:177 is a PCR primer

[0211] SEQ ID NO:178 is the determined cDNA sequence of B726P-74

[0212] SEQ ID NO:179 is the predicted amino acid sequence of B726P-74

[0213] SEQ ID NO:180 is the determined cDNA sequence of B726P-79

[0214] SEQ ID NO:181 is the predicted amino acid sequence of B726P-79

[0215] SEQ ID NO:182 is the determined cDNA sequence of 19439.1, showing homology to the mammaglobin gene

[0216] SEQ ID NO:183 is the determined cDNA sequence of 19407.1, showing homology to the human keratin gene

[0217] SEQ ID NO:184 is the determined cDNA sequence of 19428.1, showing homology to human chromosome 17 clone

[0218] SEQ ID NO:185 is the determined cDNA sequence of B808P (19408), showing no significant homology to any known gene

[0219] SEQ ID NO:186 is the determined cDNA sequence of 19460.1, showing no significant homology to any known gene

[0220] SEQ ID NO:187 is the determined cDNA sequence of 19419.1, showing homology to Ig kappa light chain

[0221] SEQ ID NO:188 is the determined cDNA sequence of 19411.1, showing homology to human alpha-1 collagen

[0222] SEQ ID NO:189 is the determined cDNA sequence of 19420.1, showing homology to mus musculus proteinase-3

[0223] SEQ ID NO:190 is the determined cDNA sequence of 19432.1, showing homology to human high motility group box

[0224] SEQ ID NO:191 is the determined cDNA sequence of 19412.1, showing homology to the human plasminogen activator gene

[0225] SEQ ID NO:192 is the determined cDNA sequence of 19415.1, showing homology to mitogen activated protein kinase

[0226] SEQ ID NO:193 is the determined cDNA sequence of 19409.1, showing homology to the chondroitin sulfate proteoglycan protein

[0227] SEQ ID NO:194 is the determined cDNA sequence of 19406.1, showing no significant homology to any known gene

[0228] SEQ ID NO:195 is the determined cDNA sequence of 19421.1, showing homology to human fibronectin

[0229] SEQ ID NO:196 is the determined cDNA sequence of 19426.1, showing homology to the retinoic acid receptor responder 3

[0230] SEQ ID NO:197 is the determined cDNA sequence of 19425.1, showing homology to MyD88 mRNA

[0231] SEQ ID NO:198 is the determined cDNA sequence of 19424.1, showing homology to peptide transporter (TAP-1) mRNA

[0232] SEQ ID NO:199 is the determined cDNA sequence of 19429.1, showing no significant homology to any known gene

[0233] SEQ ID NO:200 is the determined cDNA sequence of 19435.1, showing homology to human polymorphic epithelial mucin

[0234] SEQ ID NO:201 is the determined cDNA sequence of B813P (19434.1), showing homology to human GATA-3 transcription factor

[0235] SEQ ID NO:202 is the determined cDNA sequence of 19461.1, showing homology to the human AP-2 gene

[0236] SEQ ID NO:203 is the determined cDNA sequence of 19450.1, showing homology to DNA binding regulatory factor

[0237] SEQ ID NO:204 is the determined cDNA sequence of 19451.1, showing homology to Na/H exchange regulatory co-factor

[0238] SEQ ID NO:205 is the determined cDNA sequence of 19462.1, showing no significant homology to any known gene

[0239] SEQ ID NO:206 is the determined cDNA sequence of 19455.1, showing homology to human mRNA for histone HAS.Z

[0240] SEQ ID NO:207 is the determined cDNA sequence of 19459.1, showing homology to PAC clone 179N16

[0241] SEQ ID NO:208 is the determined cDNA sequence of 19464.1, showing no significant homology to any known gene

[0242] SEQ ID NO:209 is the determined cDNA sequence of 19414.1, showing homology to lipophilin B

[0243] SEQ ID NO:210 is the determined cDNA sequence of 19413.1, showing homology to chromosome 17 clone hRPK.209_J_20

[0244] SEQ ID NO:211 is the determined cDNA sequence of 19416.1, showing no significant homology to any known gene

[0245] SEQ ID NO:212 is the determined cDNA sequence of 19437.1, showing homology to human clone 24976 mRNA

[0246] SEQ ID NO:213 is the determined cDNA sequence of 19449.1, showing homology to mouse DNA for PG-M core protein

[0247] SEQ ID NO:214 is the determined cDNA sequence of 19446.1, showing no significant homology to any known gene

[0248] SEQ ID NO:215 is the determined cDNA sequence of 19452.1, showing no significant homology to any known gene

[0249] SEQ ID NO:216 is the determined cDNA sequence of 19483.1, showing no significant homology to any known gene

[0250] SEQ ID NO:217 is the determined cDNA sequence of 19526.1, showing homology to human lipophilin C

[0251] SEQ ID NO:218 is the determined cDNA sequence of 19484.1, showing homology to the secreted cement gland protein XAG-2

[0252] SEQ ID NO:219 is the determined cDNA sequence of 19470.1, showing no significant homology to any known gene

[0253] SEQ ID NO:220 is the determined cDNA sequence of 19469.1, showing homology to the human HLA-DM gene

[0254] SEQ ID NO:221 is the determined cDNA sequence of 19482.1, showing homology to the human pS2 protein gene

[0255] SEQ ID NO:222 is the determined cDNA sequence of B805P (19468.1), showing no significant homology to any known gene

[0256] SEQ ID NO:223 is the determined cDNA sequence of 19467.1, showing homology to human thrombospondin mRNA

[0257] SEQ ID NO:224 is the determined cDNA sequence of 19498.1, showing homology to the CDC2 gene involved in cell cycle control

[0258] SEQ ID NO:225 is the determined cDNA sequence of 19506.1, showing homology to human cDNA for TREB protein

[0259] SEQ ID NO:226 is the determined cDNA sequence of B806P (19505.1), showing no significant homology to any known gene

[0260] SEQ ID NO:227 is the determined cDNA sequence of 19486.1, showing homology to type I epidermal keratin

[0261] SEQ ID NO:228 is the determined cDNA sequence of 19510.1, showing homology to glucose transporter for glycoprotein

[0262] SEQ ID NO:229 is the determined cDNA sequence of 19512.1, showing homology to the human lysyl hydroxylase gene

[0263] SEQ ID NO:230 is the determined cDNA sequence of 19511.1, showing homology to human palmitoyl-protein thioesterase

[0264] SEQ ID NO:231 is the determined cDNA sequence of 19508.1, showing homology to human alpha enolase

[0265] SEQ ID NO:232 is the determined cDNA sequence of B807P (19509.1), showing no significant homology to any known gene

[0266] SEQ ID NO:233 is the determined cDNA sequence of B809P (19520.1), showing homology to clone 102D24 on chromosome 11q13.31

[0267] SEQ ID NO:234 is the determined cDNA sequence of 19507.1, showing homology to topoisomerase beta-subunit

[0268] SEQ ID NO:235 is the determined cDNA sequence of 19525.1, showing homology to human pro-urokinase precursor

[0269] SEQ ID NO:236 is the determined cDNA sequence of 19513.1, showing no significant homology to any known gene

[0270] SEQ ID NO:237 is the determined cDNA sequence of 19517.1, showing homology to human PAC 128M19 clone

[0271] SEQ ID NO:238 is the determined cDNA sequence of 19564.1, showing homology to human cytochrome P450-IIB

[0272] SEQ ID NO:239 is the determined cDNA sequence of 19553.1, showing homology to human GABA-A receptor pi subunit

[0273] SEQ ID NO:240 is the determined cDNA sequence of B811P (19575.1), showing no significant homology to any known gene

[0274] SEQ ID NO:241 is the determined cDNA sequence of B810P (19560.1), showing no significant homology to any known gene

[0275] SEQ ID NO:242 is the determined cDNA sequence of 19588.1, showing homology to aortic carboxypeptidase-like protein

[0276] SEQ ID NO:243 is the determined cDNA sequence of 19551.1, showing homology to human BCL-1 gene

[0277] SEQ ID NO:244 is the determined cDNA sequence of 19567.1, showing homology to human proteasome-related mRNA

[0278] SEQ ID NO:245 is the determined cDNA sequence of B803P (19583.1), showing no significant homology to any known gene

[0279] SEQ ID NO:246 is the determined cDNA sequence of B812P (19587.1), showing no significant homology to any known gene

[0280] SEQ ID NO:247 is the determined cDNA sequence of B802P (19392.2), showing homology to human chromosome 17

[0281] SEQ ID NO:248 is the determined cDNA sequence of 19393.2, showing homology to human nicein B2 chain

[0282] SEQ ID NO:249 is the determined cDNA sequence of 19398.2, human MHC class II DQ alpha mRNA

[0283] SEQ ID NO:250 is the determined cDNA sequence of B804P (19399.2), showing homology to human Xp22 BAC GSHB-184P14

[0284] SEQ ID NO:251 is the determined cDNA sequence of 19401.2, showing homology to human ikB kinase-b gene

[0285] SEQ ID NO:252 is the determined cDNA sequence of 20266, showing no significant homology to any known gene

[0286] SEQ ID NO:253 is the determined cDNA sequence of B826P (20270), showing no significant homology to any known gene

[0287] SEQ ID NO:254 is the determined cDNA sequence of 20274, showing no significant homology to any known gene

[0288] SEQ ID NO:255 is the determined cDNA sequence of 20276, showing no significant homology to any known gene

[0289] SEQ ID NO:256 is the determined cDNA sequence of 20277, showing no significant homology to any known gene

[0290] SEQ ID NO:257 is the determined cDNA sequence of B823P (20280), showing no significant homology to any known gene

[0291] SEQ ID NO:258 is the determined cDNA sequence of B821P (20281), showing no significant homology to any known gene

[0292] SEQ ID NO:259 is the determined cDNA sequence of B824P (20294), showing no significant homology to any known gene

[0293] SEQ ID NO:260 is the determined cDNA sequence of 20303, showing no significant homology to any known gene

[0294] SEQ ID NO:261 is the determined cDNA sequence of B820P (20310), showing no significant homology to any known gene

[0295] SEQ ID NO:262 is the determined cDNA sequence of B825P (20336), showing no significant homology to any known gene

[0296] SEQ ID NO:263 is the determined cDNA sequence of B827P (20341), showing no significant homology to any known gene

[0297] SEQ ID NO:264 is the determined cDNA sequence of 20941, showing no significant homology to any known gene

[0298] SEQ ID NO:265 is the determined cDNA sequence of 20954, showing no significant homology to any known gene

[0299] SEQ ID NO:266 is the determined cDNA sequence of 20961, showing no significant homology to any known gene

[0300] SEQ ID NO:267 is the determined cDNA sequence of 20965, showing no significant homology to any known gene

[0301] SEQ ID NO:268 is the determined cDNA sequence of 20975, showing no significant homology to any known gene

[0302] SEQ ID NO:269 is the determined cDNA sequence of 20261, showing homology to Human p120 catenin

[0303] SEQ. ID NO:270 is the determined cDNA sequence of B822P (20262), showing homology to Human membrane glycoprotein 4F2

[0304] SEQ ID NO:271 is the determined cDNA sequence of 20265, showing homology to Human Na, K-ATPase Alpha 1

[0305] SEQ ID NO:272 is the determined cDNA sequence of 20267, showing homology to Human heart HS 90, partial cds

[0306] SEQ ID NO:273 is the determined cDNA sequence of 20268, showing homology to Human mRNA GPI-anchored protein p137

[0307] SEQ ID NO:274 is the determined cDNA sequence of 20271, showing homology to Human cleavage stimulation factor 77 kDa subunit

[0308] SEQ ID NO:275 is the determined cDNA sequence of 20272, showing homology to Human p190-B

[0309] SEQ ID NO:276 is the determined cDNA sequence of 20273, showing homology to Human ribophorin

[0310] SEQ ID NO:277 is the determined cDNA sequence of 20278, showing homology to Human ornithine amino transferase

[0311] SEQ ID NO:278 is the determined cDNA sequence of 20279, showing homology to Human S-adenosylmethionine synthetase

[0312] SEQ ID NO:279 is the determined cDNA sequence of 20293, showing homology to Human x inactivation transcript

[0313] SEQ ID NO:280 is the determined cDNA sequence of 20300, showing homology to Human cytochrome p450

[0314] SEQ ID NO:281 is the determined cDNA sequence of 20305, showing homology to Human elongation factor-1 alpha

[0315] SEQ ID NO:282 is the determined cDNA sequence of 20306, showing homology to Human epithelial ets protein

[0316] SEQ ID NO:283 is the determined cDNA sequence of 20307, showing homology to Human signal transducer mRNA

[0317] SEQ ID NO:284 is the determined cDNA sequence of 20313, showing homology to Human GABA-A receptor pi subunit mRNA

[0318] SEQ ID NO:285 is the determined cDNA sequence of 20317, showing homology to Human tyrosine phosphatase

[0319] SEQ ID NO:286 is the determined cDNA sequence of 20318, showing homology to Human cathepsin B proteinase

[0320] SEQ ID NO:287 is the determined cDNA sequence of 20320, showing homology to Human 2-phosphopyruvate-hydratase-alpha-enolase

[0321] SEQ ID NO:288 is the determined cDNA sequence of 20321, showing homology to Human E-cadherin

[0322] SEQ ID NO:289 is the determined cDNA sequence of 20322, showing homology to Human hsp86

[0323] SEQ ID NO:290 is the determined cDNA sequence of B828P (20326), showing homology to Human x inactivation transcript

[0324] SEQ ID NO:291 is the determined cDNA sequence of 20333, showing homology to Human chromatin regulator, SMARCA5

[0325] SEQ ID NO:292 is the determined cDNA sequence of 20335, showing homology to Human sphingolipid activator protein 1

[0326] SEQ ID NO:293 is the determined cDNA sequence of 20337, showing homology to Human hepatocyte growth factor activator inhibitor type 2

[0327] SEQ ID NO:294 is the determined cDNA sequence of 20338, showing homology to Human cell adhesion molecule CD44

[0328] SEQ ID NO:295 is the determined cDNA sequence of 20340, showing homology to Human nuclear factor (erythroid-derived)-like 1

[0329] SEQ ID NO:296 is the determined cDNA sequence of 20938, showing homology to Human vinculin mRNA

[0330] SEQ ID NO:297 is the determined cDNA sequence of 20939, showing homology to Human elongation factor EF-1-alpha

[0331] SEQ ID NO:298 is the determined cDNA sequence of 20940, showing homology to Human nestin gene

[0332] SEQ ID NO:299 is the determined cDNA sequence of 20942, showing homology to Human pancreatic ribonuclease

[0333] SEQ ID NO:300 is the determined cDNA sequence of 20943, showing homology to Human transcobalamin I

[0334] SEQ ID NO:301 is the determined cDNA sequence of 20944, showing homology to Human beta-tubulin

[0335] SEQ ID NO:302 is the determined cDNA sequence of 20946, showing homology to Human HS1 protein

[0336] SEQ ID NO:303 is the determined cDNA sequence of 20947, showing homology to Human cathepsin B

[0337] SEQ ID NO:304 is the determined cDNA sequence of 20948, showing homology to Human testis enhanced gene transcript

[0338] SEQ ID NO:305 is the determined cDNA sequence of 20949, showing homology to Human elongation factor EF-1-alpha

[0339] SEQ ID NO:306 is the determined cDNA sequence of 20950, showing homology to Human ADP-ribosylation factor 3

[0340] SEQ ID NO:307 is the determined cDNA sequence of 20951, showing homology to Human IFP53 or WRS for tryptophanyl-tRNA synthetase

[0341] SEQ ID NO:308 is the determined cDNA sequence of 20952, showing homology to Human cyclin-dependent protein kinase

[0342] SEQ ID NO:309 is the determined cDNA sequence of 20957, showing homology to Human alpha-tubulin isoform 1

[0343] SEQ ID NO:310 is the determined cDNA sequence of 20959, showing homology to Human tyrosine phosphatase-61 bp deletion

[0344] SEQ ID NO:311 is the determined cDNA sequence of 20966, showing homology to Human tyrosine phosphatase

[0345] SEQ ID NO:312 is the determined cDNA sequence of B830P (20976), showing homology to Human nuclear factor NF 45

[0346] SEQ ID NO:313 is the determined cDNA sequence of B829P (20977), showing homology to Human delta-6 fatty acid desaturase

[0347] SEQ ID NO:314 is the determined cDNA sequence of 20978, showing homology to Human nuclear aconitase

[0348] SEQ ID NO:315 is the determined cDNA sequence of clone 23176.

[0349] SEQ ID NO:316 is the determined cDNA sequence of clone 23140.

[0350] SEQ ID NO:317 is the determined cDNA sequence of clone 23166.

[0351] SEQ ID NO:318 is the determined cDNA sequence of clone 23167.

[0352] SEQ ID NO:319 is the determined cDNA sequence of clone 23177.

[0353] SEQ ID NO:320 is the determined cDNA sequence of clone 23217.

[0354] SEQ ID NO:321 is the determined cDNA sequence of clone 23169.

[0355] SEQ ID NO:322 is the determined cDNA sequence of clone 23160.

[0356] SEQ ID NO:323 is the determined cDNA sequence of clone 23182.

[0357] SEQ ID NO:324 is the determined cDNA sequence of clone 23232.

[0358] SEQ ID NO:325 is the determined cDNA sequence of clone 23203.

[0359] SEQ ID NO:326 is the determined cDNA sequence of clone 23198.

[0360] SEQ ID NO:327 is the determined cDNA sequence of clone 23224.

[0361] SEQ ID NO:328 is the determined cDNA sequence of clone 23142.

[0362] SEQ ID NO:329 is the determined cDNA sequence of clone 23138.

[0363] SEQ ID NO:330 is the determined cDNA sequence of clone 23147.

[0364] SEQ ID NO:331 is the determined cDNA sequence of clone 23148.

[0365] SEQ ID NO:332 is the determined cDNA sequence of clone 23149.

[0366] SEQ ID NO:333 is the determined cDNA sequence of clone 23172.

[0367] SEQ ID NO:334 is the determined cDNA sequence of clone 23158.

[0368] SEQ ID NO:335 is the determined cDNA sequence of clone 23156.

[0369] SEQ ID NO:336 is the determined cDNA sequence of clone 23221.

[0370] SEQ ID NO:337 is the determined cDNA sequence of clone 23223.

[0371] SEQ ID NO:338 is the determined cDNA sequence of clone 23155.

[0372] SEQ ID NO:339 is the determined cDNA sequence of clone 23225.

[0373] SEQ ID NO:340 is the determined cDNA sequence of clone 23226.

[0374] SEQ ID NO:341 is the determined cDNA sequence of clone 23228.

[0375] SEQ ID NO:342 is the determined cDNA sequence of clone 23229.

[0376] SEQ ID NO:343 is the determined cDNA sequence of clone 23231.

[0377] SEQ ID NO:344 is the determined cDNA sequence of clone 23154.

[0378] SEQ ID NO:345 is the determined cDNA sequence of clone 23157.

[0379] SEQ ID NO:346 is the determined cDNA sequence of clone 23153.

[0380] SEQ ID NO:347 is the determined cDNA sequence of clone 23159.

[0381] SEQ ID NO:348 is the determined cDNA sequence of clone 23152.

[0382] SEQ ID NO:349 is the determined cDNA sequence of clone 23161.

[0383] SEQ ID NO:350 is the determined cDNA sequence of clone 23162.

[0384] SEQ ID NO:351 is the determined cDNA sequence of clone 23163.

[0385] SEQ ID NO:352 is the determined cDNA sequence of clone 23164.

[0386] SEQ ID NO:353 is the determined cDNA sequence of clone 23165.

[0387] SEQ ID NO:354 is the determined cDNA sequence of clone 23151.

[0388] SEQ ID NO:355 is the determined cDNA sequence of clone 23150.

[0389] SEQ ID NO:356 is the determined cDNA sequence of clone 23168.

[0390] SEQ ID NO:357 is the determined cDNA sequence of clone 23146.

[0391] SEQ ID NO:358 is the determined cDNA sequence of clone 23170.

[0392] SEQ ID NO:359 is the determined cDNA sequence of clone 23171.

[0393] SEQ ID NO:360 is the determined cDNA sequence of clone 23145.

[0394] SEQ ID NO:361 is the determined cDNA sequence of clone 23174.

[0395] SEQ ID NO:362 is the determined cDNA sequence of clone 23175.

[0396] SEQ ID NO:363 is the determined cDNA sequence of clone 23144.

[0397] SEQ ID NO:364 is the determined cDNA sequence of clone 23178.

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[0399] SEQ ID NO:366 is the determined cDNA sequence of clone 23180.

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[0401] SEQ ID NO:368 is the determined cDNA sequence of clone 23143.

[0402] SEQ ID NO:369 is the determined cDNA sequence of clone 23183.

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[0404] SEQ ID NO:371 is the determined cDNA sequence of clone 23185.

[0405] SEQ ID NO:372 is the determined cDNA sequence of clone 23186.

[0406] SEQ ID NO:373 is the determined cDNA sequence of clone 23187.

[0407] SEQ ID NO:374 is the determined cDNA sequence of clone 23190.

[0408] SEQ ID NO:375 is the determined cDNA sequence of clone 23189.

[0409] SEQ ID NO:376 is the determined cDNA sequence of clone 23202.

[0410] SEQ ID NO:378 is the determined cDNA sequence of clone 23191.

[0411] SEQ ID NO:379 is the determined cDNA sequence of clone 23188.

[0412] SEQ ID NO:380 is the determined cDNA sequence of clone 23194.

[0413] SEQ ID NO:381 is the determined cDNA sequence of clone 23196.

[0414] SEQ ID NO:382 is the determined cDNA sequence of clone 23195.

[0415] SEQ ID NO:383 is the determined cDNA sequence of clone 23193.

[0416] SEQ ID NO:384 is the determined cDNA sequence of clone 23199.

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[0418] SEQ ID NO:386 is the determined cDNA sequence of clone 23192.

[0419] SEQ ID NO:387 is the determined cDNA sequence of clone 23201.

[0420] SEQ ID NO:388 is the determined cDNA sequence of clone 23141.

[0421] SEQ ID NO:389 is the determined cDNA sequence of clone 23139.

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[0423] SEQ ID NO:391 is the determined cDNA sequence of clone 23205.

[0424] SEQ ID NO:392 is the determined cDNA sequence of clone 23206.

[0425] SEQ ID NO:393 is the determined cDNA sequence of clone 23207.

[0426] SEQ ID NO:394 is the determined cDNA sequence of clone 23208.

[0427] SEQ ID NO:395 is the determined cDNA sequence of clone 23209.

[0428] SEQ ID NO:396 is the determined cDNA sequence of clone 23210.

[0429] SEQ ID NO:397 is the determined cDNA sequence of clone 23211.

[0430] SEQ ID NO:398 is the determined cDNA sequence of clone 23212.

[0431] SEQ ID NO:399 is the determined cDNA sequence of clone 23214.

[0432] SEQ ID NO:400 is the determined cDNA sequence of clone 23215.

[0433] SEQ ID NO:401 is the determined cDNA sequence of clone 23216.

[0434] SEQ ID NO:402 is the determined cDNA sequence of clone 23137.

[0435] SEQ ID NO:403 is the determined cDNA sequence of clone 23218.

[0436] SEQ ID NO:404 is the determined cDNA sequence of clone 23220.

[0437] SEQ ID NO:405 is the determined cDNA sequence of clone 19462.

[0438] SEQ ID NO:406 is the determined cDNA sequence of clone 19430.

[0439] SEQ ID NO:407 is the determined cDNA sequence of clone 19407.

[0440] SEQ ID NO:408 is the determined cDNA sequence of clone 19448.

[0441] SEQ ID NO:409 is the determined cDNA sequence of clone 19447.

[0442] SEQ ID NO:410 is the determined cDNA sequence of clone 19426.

[0443] SEQ ID NO:411 is the determined cDNA sequence of clone 19441.

[0444] SEQ ID NO:412 is the determined cDNA sequence of clone 19454.

[0445] SEQ ID NO:413 is the determined cDNA sequence of clone 19463.

[0446] SEQ ID NO:414 is the determined cDNA sequence of clone 19419.

[0447] SEQ ID NO:415 is the determined cDNA sequence of clone 19434.

[0448] SEQ ID NO:416 is the determined extended cDNA sequence of B820P.

[0449] SEQ ID NO:417 is the determined extended cDNA sequence of B821P.

[0450] SEQ ID NO:418 is the determined extended cDNA sequence of B822P.

[0451] SEQ ID NO:419 is the determined extended cDNA sequence of B823P.

[0452] SEQ ID NO:420 is the determined extended cDNA sequence of B824P.

[0453] SEQ ID NO:421 is the determined extended cDNA sequence of B825P.

[0454] SEQ ID NO:422 is the determined extended cDNA sequence of B826P.

[0455] SEQ ID NO:423 is the determined extended cDNA sequence of B827P.

[0456] SEQ ID NO:424 is the determined extended cDNA sequence of B828P.

[0457] SEQ ID NO:425 is the determined extended cDNA sequence of B829P.

[0458] SEQ ID NO:426 is the determined extended cDNA sequence of B830P.

[0459] SEQ ID NO:427 is the determined cDNA sequence of clone 266B4.

[0460] SEQ ID NO:428 is the determined cDNA sequence of clone 22892.

[0461] SEQ ID NO:429 is the determined cDNA sequence of clone 266G3.

[0462] SEQ ID NO:430 is the determined cDNA sequence of clone 22890.

[0463] SEQ ID NO:431 is the determined cDNA sequence of clone 264B4.

[0464] SEQ ID NO:432 is the determined cDNA sequence of clone 22883.

[0465] SEQ ID NO:433 is the determined cDNA sequence of clone 22882.

[0466] SEQ ID NO:434 is the determined cDNA sequence of clone 22880.

[0467] SEQ ID NO:435 is the determined cDNA sequence of clone 263G1.

[0468] SEQ ID NO:436 is the determined cDNA sequence of clone 263G6.

[0469] SEQ ID NO:437 is the determined cDNA sequence of clone 262B2.

[0470] SEQ ID NO:438 is the determined cDNA sequence of clone 262B6.

[0471] SEQ ID NO:439 is the determined cDNA sequence of clone 22869.

[0472] SEQ ID NO:440 is the determined cDNA sequence of clone 21374.

[0473] SEQ ID NO:441 is the determined cDNA sequence of clone 21362.

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[0476] SEQ ID NO:444 is the determined cDNA sequence of clone 21097.

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[0479] SEQ ID NO:447 is the determined cDNA sequence of clone 21093.

[0480] SEQ ID NO:448 is the determined cDNA sequence of clone 21091.

[0481] SEQ ID NO:449 is the determined cDNA sequence of clone 21089.

[0482] SEQ ID NO:450 is the determined cDNA sequence of clone 21087.

[0483] SEQ ID NO:451 is the determined cDNA sequence of clone 21085.

[0484] SEQ ID NO:452 is the determined cDNA sequence of clone 21084.

[0485] SEQ ID NO:453 is a first partial cDNA sequence of clone 2BT1-40.

[0486] SEQ ID NO:454 is a second partial cDNA sequence of clone 2BT1-40.

[0487] SEQ ID NO:455 is the determined cDNA sequence of clone 21063.

[0488] SEQ ID NO:456 is the determined cDNA sequence of clone 21062.

[0489] SEQ ID NO:457 is the determined cDNA sequence of clone 21060.

[0490] SEQ ID NO:458 is the determined cDNA sequence of clone 21053.

[0491] SEQ ID NO:459 is the determined cDNA sequence of clone 21050.

[0492] SEQ ID NO:460 is the determined cDNA sequence of clone 21036.

[0493] SEQ ID NO:461 is the determined cDNA sequence of clone 21037.

[0494] SEQ ID NO:462 is the determined cDNA sequence of clone 21048.

[0495] SEQ ID NO:463 is a consensus DNA sequence of B726P (referred to as B726P-spliced_seq_B726P).

[0496] SEQ ID NO:464 is the determined cDNA sequence of a second splice form of B726P (referred to as 27490.seq_B726P).

[0497] SEQ ID NO:465 is the determined cDNA sequence of a third splice form of B726P (referred to as 27068.seq_B726P).

[0498] SEQ ID NO:466 is the determined cDNA sequence of a second splice form of B726P (referred to as 23113.seq_B726P).

[0499] SEQ ID NO:467 is the determined cDNA sequence of a second splice form of B726P (referred to as 23103.seq_B726P).

[0500] SEQ ID NO:468 is the determined cDNA sequence of a second splice form of B726P (referred to as 19310.seq_B726P).

[0501] SEQ ID NO:469 is the predicted amino acid sequence encoded by the upstream ORF of SEQ ID NO:463.

[0502] SEQ ID NO:470 is the predicted amino acid sequence encoded by SEQ ID NO:464.

[0503] SEQ ID NO:471 is the predicted amino acid sequence encoded by SEQ ID NO:465.

[0504] SEQ ID NO:472 is the predicted amino acid sequence encoded by SEQ ID NO:466.

[0505] SEQ ID NO:473 is the predicted amino acid sequence encoded by SEQ ID NO:467.

[0506] SEQ ID NO:474 is the determined cDNA sequence for an alternative splice form of B726P.

[0507] SEQ ID NO:475 is the amino acid sequence encoded by SEQ ID NO:474.

[0508] SEQ ID NO:476 is the isolated cDNA sequence of B720P.

[0509] SEQ ID NO:477 is the cDNA sequence of a known keratin gene.

[0510] SEQ ID NO:478 is the amino acid sequence encoded by SEQ ID NO:477.

[0511] SEQ ID NO:479 is the determined cDNA sequence for clone 19465.

[0512] SEQ ID NO:480 and 481 are PCR primers.

[0513] SEQ ID NO:482 is the cDNA sequence for the expressed downstream ORF of B726P.

[0514] SEQ ID NO:483 is the amino acid sequence for the expressed recombinant downstream ORF of B726P.

[0515] SEQ ID NO:484 is the determined full-length cDNA sequence for B720P.

[0516] SEQ ID NO:485 is the amino acid sequence encoded by SEQ ID NO:484.

[0517] SEQ ID NO:486 is the determined cDNA sequence of a truncated form of B720P, referred to as B720P-tr.

[0518] SEQ ID NO:487 is the amino acid sequence of B720P-tr.

[0519] SEQ ID NO:488 is the amino acid sequence of a naturally processed epitope of B726P recognized by B726P-specific CTL.

[0520] SEQ ID NO:489 is a DNA sequence encoding the B726P epitope set forth in SEQ ID NO:488.

[0521] SEQ ID NO:490 is a DNA sequence encoding a fusion protein wherein mammaglobin is fused to the B726P combined upstream and downstream open reading frame (ORF) (the amino acid sequence of the B726P combined ORF is disclosed herein as SEQ ID NO:475 which is encoded by the DNA sequence of SEQ ID NO:474).

[0522] SEQ ID NO:491 is a DNA sequence encoding a fusion protein wherein mammaglobin is fused to the B726P upstream ORF (the amino acid sequence of the B726P upstream ORF is disclosed herein as SEQ ID NO:469 which is encoded by the DNA sequence of SEQ ID NO:463).

[0523] SEQ ID NO:492 is a DNA sequence encoding a fusion protein wherein mammaglobin is fused to the B726P downstream ORF (the amino acid sequence of the B726P downstream ORF is disclosed herein as SEQ ID NO:176 which is encoded by the DNA sequence of SEQ ID NO:175).

[0524] SEQ ID NO:493 is the amino acid sequence encoded by the DNA sequence of SEQ ID NO:490.

[0525] SEQ ID NO:494 is the amino acid sequence encoded by the DNA sequence of SEQ ID NO:491.

[0526] SEQ ID NO:495 is the amino acid sequence encoded by the DNA sequence of SEQ ID NO:492.

[0527] SEQ ID NO:496 is amino acids 59-78 of SEQ ID NO:493.

[0528] SEQ ID NO:497 is amino acids 55-69 of SEQ ID NO:493.

[0529] SEQ ID NO:498 is amino acids 13-33 of SEQ ID NO:493.

[0530] SEQ ID NO:499 is amino acids 41-60 of SEQ ID NO:493.

[0531] SEQ ID NO:500 is amino acids 2-10 of SEQ ID NO:493.

[0532] SEQ ID NO:501 is amino acids 47-59 of SEQ ID NO:493.

[0533] SEQ ID NO:502 is amino acids 62-74 of SEQ ID NO:493.

[0534] SEQ ID NO:503 is amino acids 1-93 of SEQ ID NO:493.

[0535] SEQ ID NO:504 is the full-length cDNA sequence for B718P.

[0536] SEQ ID NO:505 is the cDNA sequence of the open reading frame of B718P including stop codon.

[0537] SEQ ID NO:506 is the cDNA sequence of the open reading frame of B718P without stop codon.

[0538] SEQ ID NO:507 is the full-length amino acid sequence of B718P.

[0539] SEQ ID NO:508 represents amino acids 1-158 of SEQ ID NO:507.

[0540] SEQ ID NO:509 represents amino acids 159-243 of SEQ ID NO:509.

[0541] SEQ ID NO:510 is the entire cDNA sequence of the open reading frame, including stop codon, of a first variant of B723P, referred to as B723P-short.

[0542] SEQ ID NO:511 is the entire cDNA sequence of the open reading frame, without stop codon, of a first variant of B723P, referred to as B723P-short.

[0543] SEQ ID NO:512 is the entire cDNA sequence of the open reading frame, including stop codon, of a second variant of B723P, referred to as B723P-long.

[0544] SEQ ID NO:513 is the entire cDNA sequence of the open reading frame, without stop codon, of a second variant of B723P, referred to as B723P-long.

[0545] SEQ ID NO:514 is the amino acid sequence of B723P-short.

[0546] SEQ ID NO:515 is the amino acid sequence of B723P-long.

[0547] SEQ ID NO:516 is amino acids 1-197 of B723P-short.

[0548] SEQ ID NO:517 is amino acids 1-232 of B723P-long.

[0549] SEQ ID NO:518 is amino acids 198-243 of B723P-short.

[0550] SEQ ID NO:519 is amino acids 218-243 of B723P-short.

[0551] SEQ ID NO:520-533 are the DNA sequences of epitopes of B726P.

[0552] SEQ ID NO:534-547 are the amino acid sequences of epitopes of B726P.

[0553] SEQ ID NO:548 is the cDNA sequence of B726P Combined ORF coding_region for expression in *E. coli*.

[0554] SEQ ID NO:549 is the cDNA sequence of B726P Upstream ORF coding_region for expression in *E. coli*.

[0555] SEQ ID NO:550 is the cDNA sequence of B726P Downstream ORF coding region for expression in *E. coli*.

[0556] SEQ ID NO:551 is the amino acid sequence of B726P Downstream ORF encoded by the cDNA set forth in SEQ ID NO:550.

[0557] SEQ ID NO:552 is the amino acid sequence of B726P Upstream ORF with HIS, encoded by the cDNA set forth in SEQ ID NO:549.

[0558] SEQ ID NO:553 is the amino acid sequence of B726P Combined ORF correct, encoded by the cDNA set forth in SEQ ID NO:548.

[0559] SEQ ID NO:554-563 are PCR primers as described in Example 8.

[0560] SEQ ID NO:564 is the cDNA sequence for NY-BR-1, an extended sequence of B726P.

[0561] SEQ ID NO:565 is the amino acid sequence for NY-BR-1, an extended sequence of B726P, and encoded by the nucleotide sequence set forth in SEQ ID NO:564.

[0562] SEQ ID NO:566 is the cDNA sequence for B726P XC coding region with changes.

[0563] SEQ ID NO:567 is the cDNA sequence for B726P XB clone 83686 with 2 changes from the published NY-BR-1 sequence in SEQ ID NO:564.

[0564] SEQ ID NO:568 is the cDNA sequence for B726P XB clone 84330 with 4 changes from the published NY-BR-1 sequence in SEQ ID NO:564.

[0565] SEQ ID NO:569 is the cDNA sequence for B726P XB clone 84328 with 3 changes from the published NY-BR-1 sequence in SEQ ID NO:564.

[0566] SEQ ID NO:570 is the amino acid sequence for B726P XB clone 84328, encoded by the sequence set forth in SEQ ID NO:569.

[0567] SEQ ID NO:571 is the amino acid sequence for B726P XB clone 84330, encoded by the sequence set forth in SEQ ID NO:568.

[0568] SEQ ID NO:572 is the amino acid sequence for B726P XB clone 83686, encoded by the sequence set forth in SEQ ID NO:567.

[0569] SEQ ID NO:573 is the amino acid sequence for B726P XC, encoded by the sequence set forth in SEQ ID NO:566.

[0570] SEQ ID NO:574-575 are PCR primers as described in Example 12.

[0571] SEQ ID NO:576 is the full-length cDNA sequence for NY-BR-1.1.

[0572] SEQ ID NO:577 is the full-length amino acid sequence for NY-BR-1.1, encoded by the nucleotide sequence set forth in SEQ ID NO:576.

[0573] SEQ ID NO:578 is amino acids 289-308 of the B726P downstream ORF and corresponds to the peptide recognized by the 220A2.1 antibody.

[0574] SEQ ID NO:579 is amino acids 225-244 of the B726P downstream ORF and corresponds to the peptide recognized by the 220A19.1 antibody.

[0575] SEQ ID NO:580 is amino acids 232-252 of the B726P downstream ORF and corresponds to the peptide recognized by the 220A19.1 and the 220A43 antibodies.

[0576] SEQ ID NO:581 is amino acids 73-92 of the B726P downstream ORF and corresponds to the peptide recognized by the 220A94.1 antibody.

[0577] SEQ ID NO:582 is amino acids 145-164 of the B726P downstream ORF and corresponds to the peptide recognized by the 220A151.1 and 220A86 antibodies.

[0578] SEQ ID NO:583 is amino acids 153-172 of the B726P downstream ORF and corresponds to the peptide recognized by the 220A151.1 and 220A86 antibodies.

[0579] SEQ ID NO:584 is amino acids 1-20 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

[0580] SEQ ID NO:585 is amino acids 9-28 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

[0581] SEQ ID NO:586 is amino acids 17-36 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

[0582] SEQ ID NO:587 is amino acids 24-44 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

[0583] SEQ ID NO:588 is amino acids 97-116 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

[0584] SEQ ID NO:589 is amino acids 105-124 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

[0585] SEQ ID NO:590 is amino acids 113-132 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

[0586] SEQ ID NO:591 is amino acids 121-140 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

[0587] SEQ ID NO:592 is amino acids 129-148 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

[0588] SEQ ID NO:593 is amino acids 137-156 of the B726P downstream ORF and corresponds to the peptide recognized by purified B726 polyclonal antibodies.

[0589] SEQ ID NO:594 is the amino acid sequence of peptide #2732 and corresponds to amino acids 1-20 of the B726P downstream ORF.

[0590] SEQ ID NO:595 is the amino acid sequence of peptide #2733 and corresponds to amino acids 11-30 of the B726P downstream ORF.

[0591] SEQ ID NO:596 is the amino acid sequence of peptide #2734 and corresponds to amino acids 21-40 of the B726P downstream ORF.

[0592] SEQ ID NO:597 is the amino acid sequence of peptide #2735 and corresponds to amino acids 31-50 of the B726P downstream ORF.

[0593] SEQ ID NO:598 is the amino acid sequence of peptide #2736 and corresponds to amino acids 41-60 of the B726P downstream ORF.

[0594] SEQ ID NO:599 is the amino acid sequence of peptide #2737 and corresponds to amino acids 51-70 of the B726P downstream ORF.

[0595] SEQ ID NO:600 is the amino acid sequence of peptide #2738 and corresponds to amino acids 61-80 of the B726P downstream ORF.

[0596] SEQ ID NO:601 is the amino acid sequence of peptide #2739 and corresponds to amino acids 71-90 of the B726P downstream ORF.

[0597] SEQ ID NO:602 is the amino acid sequence of peptide #2740 and corresponds to amino acids 81-100 of the B726P downstream ORF.

[0598] SEQ ID NO:603 is the amino acid sequence of peptide #2741 and corresponds to amino acids 91-110 of the B726P downstream ORF.

[0599] SEQ ID NO:604 is the amino acid sequence of peptide #2742 and corresponds to amino acids 101-120 of the B726P downstream ORF.

[0600] SEQ ID NO:605 is the amino acid sequence of peptide #2743 and corresponds to amino acids 111-130 of the B726P downstream ORF.

[0601] SEQ ID NO:606 is the amino acid sequence of peptide #2744 and corresponds to amino acids 121-140 of the B726P downstream ORF.

[0602] SEQ ID NO:607 is the amino acid sequence of peptide #2745 and corresponds to amino acids 130-151 of the B726P downstream ORF.

[0603] SEQ ID NO:608 is the amino acid sequence of peptide #2746 and corresponds to amino acids 141-160 of the B726P downstream ORF.

[0604] SEQ ID NO:609 is the amino acid sequence of peptide #2747 and corresponds to amino acids 151-170 of the B726P downstream ORF.

[0605] SEQ ID NO:610 is the amino acid sequence of peptide #2748 and corresponds to amino acids 161-180 of the B726P downstream ORF.

[0606] SEQ ID NO:611 is the amino acid sequence of peptide #2749 and corresponds to amino acids 170-190 of the B726P downstream ORF.

[0607] SEQ ID NO:612 is the amino acid sequence of peptide #2750 and corresponds to amino acids 181-200 of the B726P downstream ORF.

[0608] SEQ ID NO:613 is the amino acid sequence of peptide #2751 and corresponds to amino acids 191-210 of the B726P downstream ORF.

[0609] SEQ ID NO:614 is the amino acid sequence of peptide #2752 and corresponds to amino acids 201-220 of the B726P downstream ORF.

[0610] SEQ ID NO:615 is the amino acid sequence of peptide #2753 and corresponds to amino acids 211-230 of the B726P downstream ORF.

[0611] SEQ ID NO:616 is the amino acid sequence of peptide #2765 and corresponds to amino acids 221-240 of the B726P downstream ORF.

[0612] SEQ ID NO:617 is the amino acid sequence of peptide #2766 and corresponds to amino acids 231-250 of the B726P downstream ORF.

[0613] SEQ ID NO:618 is the amino acid sequence of peptide #2767 and corresponds to amino acids 240-260 of the B726P downstream ORF.

[0614] SEQ ID NO:619 is the amino acid sequence of peptide #2768 and corresponds to amino acids 251-270 of the B726P downstream ORF.

[0615] SEQ ID NO:620 is the amino acid sequence of peptide #2769 and corresponds to amino acids 261-280 of the B726P downstream ORF.

[0616] SEQ ID NO:621 is the amino acid sequence of peptide #2770 and corresponds to amino acids 271-290 of the B726P downstream ORF.

[0617] SEQ ID NO:622 is the amino acid sequence of peptide #2771 and corresponds to amino acids 281-300 of the B726P downstream ORF.

[0618] SEQ ID NO:623 is the amino acid sequence of peptide #2772 and corresponds to amino acids 291-310 of the B726P downstream ORF.

[0619] SEQ ID NO:624 is the amino acid sequence of peptide #2773 and corresponds to amino acids 298-317 of the B726P downstream ORF.

[0620] SEQ ID NO:625 is the amino acid sequence of peptide #3535 of B726P.

[0621] SEQ ID NO:626 is the amino acid sequence of peptide #3536 of B726P.

[0622] SEQ ID NO:627 is the amino acid sequence of peptide #3534 of B726P.

DETAILED DESCRIPTION OF THE INVENTION

[0623] The present invention is directed generally to compositions and their use in the therapy and diagnosis of cancer, particularly breast cancer. As described further below, illustrative compositions of the present invention include, but are not restricted to, polypeptides, particularly immunogenic polypeptides, polynucleotides encoding such polypeptides, antibodies and other binding agents, antigen presenting cells (APCs) and immune system cells (e.g., T cells).

[0624] The practice of the present invention will employ, unless indicated specifically to the contrary, conventional methods of virology, immunology, microbiology, molecular biology and recombinant DNA techniques within the skill of the art, many of which are described below for the purpose of illustration. Such techniques are explained fully in the literature. See, e.g., Sambrook, et al. *Molecular Cloning: A Laboratory Manual* (2nd Edition, 1989); Maniatis et al. *Molecular Cloning: A Laboratory Manual* (1982); DNA Cloning: A Practical Approach, vol. I & II (D. Glover, ed.); *Oligonucleotide Synthesis* (N. Gait, ed., 1984); *Nucleic Acid Hybridization* (B. Hames & S. Higgins, eds., 1985); *Transcription and Translation* (B. Hames & S. Higgins, eds., 1984); *Animal Cell Culture* (R. Freshney, ed., 1986); Perbal, *A Practical Guide to Molecular Cloning* (1984).

[0625] All publications, patents and patent applications cited herein, whether supra or infra, are hereby incorporated by reference in their entirety.

[0626] As used in this specification and the appended claims, the singular forms "a," "an" and "the" include plural references unless the content clearly dictates otherwise.

Polypeptide Compositions

[0627] As used herein, the term "polypeptide" is used in its conventional meaning, i.e., as a sequence of amino acids. The polypeptides are not limited to a specific length of the product; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide, and such terms may be used interchangeably herein unless specifically indicated otherwise. This term also does not refer to or exclude post-expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like, as well as other modifications known in the art, both naturally occurring and non-naturally occurring. A polypeptide may be an entire protein, or a subsequence thereof. Particular polypeptides of interest in the context of this invention are amino acid subsequences comprising epitopes, i.e., antigenic determinants substantially responsible for the immunogenic properties of a polypeptide and being capable of evoking an immune response.

[0628] Particularly illustrative polypeptides of the present invention comprise those encoded by a polynucleotide sequence set forth in any one of SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576, or a sequence that hybridizes under moderately stringent conditions, or, alternatively, under highly stringent conditions, to a polynucleotide sequence set forth

in any one of SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576. Certain other illustrative polypeptides of the invention comprise amino acid sequences as set forth in any one of SEQ ID NO: 62, 176, 179, 181, 469-473, 475, 478, 483, 485, 487, 488, 493-503, 507-509, 514-519, 534-547, 551-553, 565, 570-573, and 577-627.

[0629] The polypeptides of the present invention are sometimes herein referred to as breast tumor proteins or breast tumor polypeptides, as an indication that their identification has been based at least in part upon their increased levels of expression in breast tumor samples. Thus, a "breast tumor polypeptide" or "breast tumor protein," refers generally to a polypeptide sequence of the present invention, or a polynucleotide sequence encoding such a polypeptide, that is expressed in a substantial proportion of breast tumor samples, for example preferably greater than about 20%, more preferably greater than about 30%, and most preferably greater than about 50% or more of breast tumor samples tested, at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in normal tissues, as determined using a representative assay provided herein. A breast tumor polypeptide sequence of the invention, based upon its increased level of expression in tumor cells, has particular utility both as a diagnostic marker as well as a therapeutic target, as further described below.

[0630] In certain preferred embodiments, the polypeptides of the invention are immunogenic, i.e., they react detectably within an immunoassay (such as an ELISA or T-cell stimulation assay) with antisera and/or T-cells from a patient with breast cancer. Screening for immunogenic activity can be performed using techniques well known to the skilled artisan. For example, such screens can be performed using methods such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one illustrative example, a polypeptide may be immobilized on a solid support 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, ¹²⁵I-labeled Protein A.

[0631] As would be recognized by the skilled artisan, immunogenic portions of the polypeptides disclosed herein are also encompassed by the present invention. An "immunogenic portion," as used herein, is a fragment of an immunogenic polypeptide of the invention that itself is immunologically reactive (i.e., specifically binds) with the B-cells and/or T-cell surface antigen receptors that recognize the polypeptide. Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (i.e., they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well-known techniques.

[0632] In one preferred embodiment, an immunogenic portion of a polypeptide of the present invention is a portion

that reacts with antisera and/or T-cells at a level that is not substantially less than the reactivity of the full-length polypeptide (e.g., in an ELISA and/or T-cell reactivity assay). Preferably, the level of immunogenic activity of the immunogenic portion is at least about 50%, preferably at least about 70% and most preferably greater than about 90% of the immunogenicity for the full-length polypeptide. In some instances, preferred immunogenic portions will be identified that have a level of immunogenic activity greater than that of the corresponding full-length polypeptide, e.g., having greater than about 100% or 150% or more immunogenic activity.

[0633] In certain other embodiments, illustrative immunogenic portions may include peptides in, which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other illustrative immunogenic portions will contain a small N- and/or C-terminal deletion (e.g., 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

[0634] In another embodiment, a polypeptide composition of the invention may also comprise one or more polypeptides that are immunologically reactive with T cells and/or antibodies generated against a polypeptide of the invention, particularly a polypeptide having an amino acid sequence disclosed herein, or to an immunogenic fragment or variant thereof.

[0635] In another embodiment of the invention, polypeptides are provided that comprise one or more polypeptides that are capable of eliciting T cells and/or antibodies that are immunologically reactive with one or more polypeptides described herein, or one or more polypeptides encoded by contiguous nucleic acid sequences contained in the polynucleotide sequences disclosed herein, or immunogenic fragments or variants thereof, or to one or more nucleic acid sequences which hybridize to one or more of these sequences under conditions of moderate to high stringency.

[0636] The present invention, in another aspect, provides polypeptide fragments comprising at least about 5, 10, 15, 20, 25, 50, or 100 contiguous amino acids, or more, including all intermediate lengths, of a polypeptide compositions set forth herein, such as those set forth in SEQ ID NO: 62, 176, 179, 181, 469-473, 475, 478, 483, 485, 487, 488, 493-503, 507-509, 514-519, 534-547, 551-553, 565, 570-573, and 577-627, or those encoded by a polynucleotide sequence set forth in a sequence of SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576.

[0637] In another aspect, the present invention provides variants of the polypeptide compositions described herein. Polypeptide variants generally encompassed by the present invention will typically exhibit at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more identity (determined as described below), along its length, to a polypeptide sequences set forth herein.

[0638] In one preferred embodiment, the polypeptide fragments and variants provide by the present invention are immunologically reactive with an antibody and/or T-cell that reacts with a full-length polypeptide specifically set forth herein.

[0639] In another preferred embodiment, the polypeptide fragments and variants provided by the present invention exhibit a level of immunogenic activity of at least about 50%, preferably at least about 70%, and most preferably at least about 90% or more of that exhibited by a full-length polypeptide sequence specifically set forth herein.

[0640] A polypeptide "variant," as the term is used herein, is a polypeptide that typically differs from a polypeptide specifically disclosed herein in one or more substitutions, deletions, additions and/or insertions. Such variants may be naturally occurring or may be synthetically generated, for example, by modifying one or more of the above polypeptide sequences of the invention and evaluating their immunogenic activity as described herein and/or using any of a number of techniques well known in the art.

[0641] For example, certain illustrative variants of the polypeptides of the invention include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other illustrative variants include variants in which a small portion (e.g., 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

[0642] In many instances, a variant will contain conservative substitutions. 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. As described above, modifications may be made in the structure of the polynucleotides and polypeptides of the present invention and still obtain a functional molecule that encodes a variant or derivative polypeptide with desirable characteristics, e.g., with immunogenic characteristics. When it is desired to alter the amino acid sequence of a polypeptide to create an equivalent, or even an improved, immunogenic variant or portion of a polypeptide of the invention, one skilled in the art will typically change one or more of the codons of the encoding DNA sequence according to Table 1.

[0643] For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated that various changes may be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences which encode said peptides without appreciable loss of their biological utility or activity.

TABLE 1

Amino Acids			Codons		
Alanine	Ala	A	GGA	GGG	GGC
Cysteine	Gys	C	UGC	UGU	

TABLE 1-continued

Amino Acids			Codons		
Aspartic acid	Asp	D	GAC	GAU	
Glutamic acid	Glu	E	GAA	GAG	
Phenylalanine	Phe	F	UUG	UUU	
Glycine	Gly	G	GGA	GGG	GGU
Histidine	His	H	GAG	CAU	
Isoleucine	Ile	I	AUA	AUG	AUU
Lysine	Lys	K	AAA	AAG	
Leucine	Leu	L	UUA	UUG	CUA CUC CUG CUU
Methionine	Met	M	AUG		
Asparagine	Asn	N	AAG	AAU	
Proline	Pro	P	CCA	CCC	CCG CCU
Glutamine	Gln	Q	CAA	CAG	
Arginine	Arg	R	AGA	AGG	CGA CGC CGG CGU
Serine	Ser	S	AGC	AGU	UCA UCC UCG UGU
Threonine	Thr	T	ACA	ACC	ACG ACU
Valine	Val	V	GUA	GUC	GUG GUU
Tryptophan	Trp	W	UGG		
Tyrosine	Tyr	Y	UAC	UAU	

[0644] In making such changes, the hydrophobic index of amino acids may be considered. The importance of the hydrophobic amino acid index in conferring interactive biological function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporated herein by reference). It is accepted that the relative hydrophobic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydrophobic index on the basis of its hydrophobicity and charge characteristics (Kyte and Doolittle, 1982). These values are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (−0.4); threonine (−0.7); serine (−0.8); tryptophan (−0.9); tyrosine (−1.3); proline (−1.6); histidine (−3.2); glutamate (−3.5); glutamine (−3.5); aspartate (−3.5); asparagine (−3.5); lysine (−3.9); and arginine (−4.5).

[0645] It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydrophobic index or score and still result in a protein with similar biological activity, i.e. still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydrophobic indices are within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U.S. Pat. No. 4,554,101 (specifically incorporated herein by

reference in its entirety), states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein.

[0646] As detailed in U.S. Pat. No. 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0±1); glutamate (+3.0±1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5±1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ±2 is preferred, those within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

[0647] As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that take various of the foregoing characteristics into consideration are well known to those of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

[0648] In addition, any polynucleotide may be further modified to increase stability in vivo. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetylmethyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

[0649] Amino acid substitutions may further be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (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. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

[0650] As noted above, polypeptides may comprise 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.

[0651] When comparing polypeptide sequences, two sequences are said to be "identical" if the sequence of amino acids in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

[0652] Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, Wis.), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M. O. (1978) A model of evolutionary change in proteins—Matrices for detecting distant relationships. In Dayhoff, M. O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington D.C. Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, Calif.; Higgins, D. G. and Sharp, P. M. (1989) *CABIOS* 5:151-153; Myers, E. W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E. D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P. H. A. and Sokal, R. R. (1973) *Numerical Taxonomy—the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, Calif.; Wilbur, W. J. and Lipman, D. J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

[0653] Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, Wis.), or by inspection.

[0654] One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. For amino acid sequences, a scoring matrix can be used to calculate the cumulative score. Extension of the word hits in each direc-

tion are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment.

[0655] In one preferred approach, the “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (i.e., the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

[0656] Within other illustrative embodiments, a polypeptide may be a fusion polypeptide that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the polypeptide or to enable the polypeptide to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the polypeptide.

[0657] Fusion polypeptides may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion polypeptide is expressed as a recombinant polypeptide, allowing the production of increased levels, relative to a non-fused polypeptide, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion polypeptide that retains the biological activity of both component polypeptides.

[0658] A peptide linker sequence may be employed to separate the first and second polypeptide components 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 polypeptide 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 confor-

mation; (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. Pat. No. 4,935,233 and U.S. Pat. No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker 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.

[0659] 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 required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

[0660] The fusion polypeptide can comprise a polypeptide as described herein together with an unrelated immunogenic protein, such as an immunogenic protein capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (see, for example, Stoute et al. *New Engl. J. Med.*, 336:86-91, 1997).

[0661] In one preferred embodiment, the immunological fusion partner is derived from a *Mycobacterium* sp., such as a *Mycobacterium tuberculosis*-derived Ra12 fragment. Ra12 compositions and methods for their use in enhancing the expression and/or immunogenicity of heterologous polynucleotide/polypeptide sequences is described in U.S. Patent Application 60/158,585, the disclosure of which is incorporated herein by reference in its entirety. Briefly, Ra12 refers to a polynucleotide region that is a subsequence of a *Mycobacterium tuberculosis* MTB32A nucleic acid. MTB32A is a serine protease of 32 KD molecular weight encoded by a gene in virulent and avirulent strains of *M. tuberculosis*. The nucleotide sequence and amino acid sequence of MTB32A have been described (for example, U.S. Patent Application 60/158,585; see also, Skeiky et al., *Infection and Immun.* (1999) 67:3998-4007, incorporated herein by reference). C-terminal fragments of the MTB32A coding sequence express at high levels and remain as a soluble polypeptides throughout the purification process. Moreover, Ra12 may enhance the immunogenicity of heterologous immunogenic polypeptides with which it is fused. One preferred Ra12 fusion polypeptide comprises a 14 KD C-terminal fragment corresponding to amino acid residues 192 to 323 of MTB32A. Other preferred Ra12 polynucleotides generally comprise at least about 15 consecutive nucleotides, at least about 30 nucleotides, at least about 60 nucleotides, at least about 100 nucleotides, at least about 200 nucleotides, or at least about 300 nucleotides that encode a portion of a Ra12 polypeptide. Ra12 polynucleotides may comprise a native sequence (i.e., an endogenous sequence that encodes a Ra12 polypeptide or a portion thereof) or may comprise a variant of such a sequence. Ra12 polynucleotide variants may contain one or more substitutions, additions,

deletions and/or insertions such that the biological activity of the encoded fusion polypeptide is not substantially diminished, relative to a fusion polypeptide comprising a native Ra12 polypeptide. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native Ra12 polypeptide or a portion thereof.

[0662] Within other preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza* B (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (e.g., the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenza virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

[0663] In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *Lyta* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (see *Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion polypeptide. A repeat portion is found in the C-terminal, region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

[0664] Yet another illustrative embodiment involves fusion polypeptides, and the polynucleotides encoding them, wherein the fusion partner comprises a targeting signal capable of directing a polypeptide to the endosomal/lysosomal compartment, as described in U.S. Pat. No. 5,633,234. An immunogenic polypeptide of the invention, when fused with this targeting signal, will associate more efficiently with MHC class II molecules and thereby provide enhanced in vivo stimulation of CD4⁺ T-cells specific for the polypeptide.

[0665] Polypeptides of the invention are prepared using any of a variety of well known synthetic and/or recombinant techniques, the latter of which are further described below. Polypeptides, portions and other variants generally less than about 150 amino acids can be generated by synthetic means, using techniques well known to those of ordinary skill in the art. In one illustrative example, such polypeptides are 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 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, Calif.), and may be operated according to the manufacturer's instructions.

[0666] In general, polypeptide compositions (including fusion polypeptides) of the invention are isolated. An "isolated" polypeptide is one that is removed from its original environment. For example, a naturally-occurring protein or polypeptide is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are also purified, e.g., are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure.

Polynucleotide Compositions

[0667] The present invention, in other aspects, provides polynucleotide compositions. The terms "DNA" and "polynucleotide" are used essentially interchangeably herein to refer to a DNA molecule that has been isolated free of total genomic DNA of a particular species. "Isolated," as used herein, means that a polynucleotide is substantially away from other coding sequences, and that the DNA molecule does not contain large portions of unrelated coding DNA, such as large chromosomal fragments or other functional genes or polypeptide coding regions. Of course, this refers to the DNA molecule as originally isolated, and does not exclude genes or coding regions later added to the segment by the hand of man.

[0668] As will be understood by those skilled in the art, the polynucleotide compositions of this invention can include genomic sequences, extra-genomic and plasmid-encoded sequences and smaller engineered gene segments that express, or may be adapted to express, proteins, polypeptides, peptides and the like. Such segments may be naturally isolated, or modified synthetically by the hand of man.

[0669] As will be also recognized by the skilled artisan, polynucleotides of the invention may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules may include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

[0670] Polynucleotides may comprise a native sequence (i.e., an endogenous sequence that encodes a polypeptide/protein of the invention or a portion thereof) or may comprise a sequence that encodes a variant or derivative, preferably and immunogenic variant or derivative, of such a sequence.

[0671] Therefore, according to another aspect of the present invention, polynucleotide compositions are provided that comprise some or all of a polynucleotide sequence set forth in any one of SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492,

504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576, complements of a polynucleotide sequence set forth in any one of SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576, and degenerate variants of a polynucleotide sequence set forth in any one of SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576. In certain preferred embodiments, the polynucleotide sequences set forth herein encode immunogenic polypeptides, as described above.

[0672] In other related embodiments, the present invention provides polynucleotide variants having substantial identity to the sequences disclosed herein in SEQ ID NO: 1-61, 63-175, 178, 180, 182-468, 474, 476, 477, 479, 482, 484, 486, 489-492, 504-506, 510-513, 520-533, 548-550, 564, 566-569, and 576, for example those comprising at least 70% sequence identity, preferably at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a polynucleotide sequence of this invention using the methods described herein, (e.g., BLAST analysis using standard parameters, as described below). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like.

[0673] Typically, polynucleotide variants will contain one or more substitutions, additions, deletions and/or insertions, preferably such that the immunogenicity of the polypeptide encoded by the variant polynucleotide is not substantially diminished relative to a polypeptide encoded by a polynucleotide sequence specifically set forth herein). The term "variants" should also be understood to encompass homologous genes of xenogenic origin.

[0674] In additional embodiments, the present invention provides polynucleotide fragments comprising various lengths of contiguous stretches of sequence identical to or complementary to one or more of the sequences disclosed herein. For example, polynucleotides are provided by this invention that comprise at least about 10, 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the sequences disclosed herein as well as all intermediate lengths there between. It will be readily understood that "intermediate lengths", in this context, means any length between the quoted values, such as 16, 17, 18, 19, etc.; 21, 22, 23, etc.; 30, 31, 32, etc.; 50, 51, 52, 53, etc.; 100, 101, 102, 103, etc.; 150, 151, 152, 153, etc.; including all integers through 200-500; 500-1,000, and the like.

[0675] In another embodiment of the invention, polynucleotide compositions are provided that are capable of hybridizing under moderate to high stringency conditions to a polynucleotide sequence provided herein, or a fragment thereof, or a complementary sequence thereof. Hybridization techniques are well known in the art of molecular biology. For purposes of illustration, suitable moderately stringent conditions for testing the hybridization of a polynucleotide of this invention with other polynucleotides include prewashing in a solution of 5×SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50° C.-60° C., 5×SSC,

overnight; followed by washing twice at 65° C. for 20 minutes with each of 2×, 0.5× and 0.2×SSC containing 0.1% SDS. One skilled in the art will understand that the stringency of hybridization can be readily manipulated, such as by altering the salt content of the hybridization solution and/or the temperature at which the hybridization is performed. For example, in another embodiment, suitable highly stringent hybridization conditions include those described above, with the exception that the temperature of hybridization is increased, e.g., to 60-65° C. or 65-70° C.

[0676] In certain preferred embodiments, the polynucleotides described above, e.g., polynucleotide variants, fragments and hybridizing sequences, encode polypeptides that are immunologically cross-reactive with a polypeptide sequence specifically set forth herein. In other preferred embodiments, such polynucleotides encode polypeptides that have a level of immunogenic activity of at least about 50%, preferably at least about 70%, and more preferably at least about 90% of that for a polypeptide sequence specifically set forth herein.

[0677] The polynucleotides of the present invention, or fragments thereof, regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol. For example, illustrative polynucleotide segments with total lengths of about 10,000, about 5000, about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated to be useful in many implementations of this invention.

[0678] When comparing polynucleotide sequences, two sequences are said to be "identical" if the sequence of nucleotides in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

[0679] Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, Wis.), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M. O. (1978) A model of evolutionary change in proteins—Matrices for detecting distant relationships. In Dayhoff, M. O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington D.C. Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, Calif.; Higgins, D. G. and Sharp, P. M. (1989) *CABIOS* 5:151-153; Myers, E. W. and

Muller W. (1988) *CABIOS* 4:11-17; Robinson, E. D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P. H. A. and Sokal, R. R. (1973) *Numerical Taxonomy—the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, Calif.; Wilbur, W. J. and Lipman, D. J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

[0680] Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, Wis.), or by inspection.

[0681] One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. In one illustrative example, cumulative scores can be calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=4 and a comparison of both strands.

[0682] Preferably, the “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (i.e., the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

[0683] It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

[0684] Therefore, in another embodiment of the invention, a mutagenesis approach, such as site-specific mutagenesis, is employed for the preparation of immunogenic variants and/or derivatives of the polypeptides described herein. By this approach, specific modifications in a polypeptide sequence can be made through mutagenesis of the underlying polynucleotides that encode them. These techniques provides a straightforward approach to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the polynucleotide.

[0685] Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Mutations may be employed in a selected polynucleotide sequence to improve, alter, decrease, modify, or otherwise change the properties of the polynucleotide itself, and/or alter the properties, activity, composition, stability, or primary sequence of the encoded polypeptide.

[0686] In certain embodiments of the present invention, the inventors contemplate the mutagenesis of the disclosed polynucleotide sequences to alter one or more properties of the encoded polypeptide, such as the immunogenicity of a polypeptide vaccine. The techniques of site-specific mutagenesis are well-known in the art, and are widely used to create variants of both polypeptides and polynucleotides. For example, site-specific mutagenesis is often used to alter a specific portion of a DNA molecule. In such embodiments, a primer comprising typically about 14 to about 25 nucleotides or so in length is employed, with about 5 to about 10 residues on both sides of the junction of the sequence being altered.

[0687] As will be appreciated by those of skill in the art, site-specific mutagenesis techniques have often employed a phage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially-available and their use is generally well-known to those skilled in the art. Double-stranded plasmids are also routinely employed in site directed mutagenesis that eliminates the step of transferring the gene of interest from a plasmid to a phage.

[0688] In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double-stranded vector that includes within its sequence a DNA sequence that encodes the desired peptide. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement.

[0689] The preparation of sequence variants of the selected peptide-encoding DNA segments using site-directed mutagenesis provides a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of peptides and the DNA sequences encoding them may be obtained. For example, recombinant vectors encoding the desired peptide sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants. Specific details regarding these methods and protocols are found in the teachings of Maloy et al., 1994; Segal, 1976; Prokop and Bajpai, 1991; Kuby, 1994; and Maniatis et al., 1982, each incorporated herein by reference, for that purpose.

[0690] As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known rules of complementary base pairing (see, for example, Watson, 1987). Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U.S. Pat. No. 4,237, 224, specifically incorporated herein by reference in its entirety.

[0691] In another approach for the production of polypeptide variants of the present invention, recursive sequence recombination, as described in U.S. Pat. No. 5,837,458, may be employed. In this approach, iterative cycles of recombination and screening or selection are performed to "evolve" individual polynucleotide variants of the invention having, for example, enhanced immunogenic activity.

[0692] In other embodiments of the present invention, the polynucleotide sequences provided herein can be advantageously used as probes or primers for nucleic acid hybridization. As such, it is contemplated that nucleic acid segments that comprise a sequence region of at least about 15

nucleotide long contiguous sequence that has the same sequence as, or is complementary to, a 15 nucleotide long contiguous sequence disclosed herein will find particular utility. Longer contiguous identical or complementary sequences, e.g., those of about 20, 30, 40, 50, 100, 200, 500, 1000 (including all intermediate lengths) and even up to full length sequences will also be of use in certain embodiments.

[0693] The ability of such nucleic acid probes to specifically hybridize to a sequence of interest will enable them to be of use in detecting the presence of complementary sequences in a given sample. However, other uses are also envisioned, such as the use of the sequence information for the preparation of mutant species primers, or primers for use in preparing other genetic constructions.

[0694] Polynucleotide molecules having sequence regions consisting of contiguous nucleotide stretches of 10-14, 15-20, 30, 50, or even of 100-200 nucleotides or so (including intermediate lengths as well), identical or complementary to a polynucleotide sequence disclosed herein, are particularly contemplated as hybridization probes for use in, e.g., Southern and Northern blotting. This would allow a gene product, or fragment thereof, to be analyzed, both in diverse cell types and also in various bacterial cells. The total size of fragment, as well as the size of the complementary stretch(es), will ultimately depend on the intended use or application of the particular nucleic acid segment. Smaller fragments will generally find use in hybridization embodiments, wherein the length of the contiguous complementary region may be varied, such as between about 15 and about 100 nucleotides, but larger contiguous complementary stretches may be used, according to the length complementary sequences one wishes to detect.

[0695] The use of a hybridization probe of about 15-25 nucleotides in length allows the formation of a duplex molecule that is both stable and selective. Molecules having contiguous complementary sequences over stretches greater than 15 bases in length are generally preferred, though, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of specific hybrid molecules obtained. One will generally prefer to design nucleic acid molecules having gene-complementary stretches of 15 to 25 contiguous nucleotides, or even longer where desired.

[0696] Hybridization probes may be selected from any portion of any of the sequences disclosed herein. All that is required is to review the sequences set forth herein, or to any continuous portion of the sequences, from about 15-25 nucleotides in length up to and including the full length sequence, that one wishes to utilize as a probe or primer. The choice of probe and primer sequences may be governed by various factors. For example, one may wish to employ primers from towards the termini of the total sequence.

[0697] Small polynucleotide segments or fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer. Also, fragments may be obtained by application of nucleic acid reproduction technology, such as the PCR™ technology of U.S. Pat. No. 4,683,202 (incorporated herein by reference), by introducing selected sequences into recombinant vectors for recombinant production, and by other recombinant DNA techniques generally known to those of skill in the art of molecular biology.

[0698] The nucleotide sequences of the invention may be used for their ability to selectively form duplex molecules with complementary stretches of the entire gene or gene fragments of interest. Depending on the application envisioned, one will typically desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of probe towards target sequence. For applications requiring high selectivity, one will typically desire to employ relatively stringent conditions to form the hybrids, e.g., one will select relatively low salt and/or high temperature conditions, such as provided by a salt concentration of from about 0.02 M to about 0.15 M salt at temperatures of from about 50° C. to about 70° C. Such selective conditions tolerate little, if any, mismatch between the probe and the template or target strand, and would be particularly suitable for isolating related sequences.

[0699] Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying template, less stringent (reduced stringency) hybridization conditions will typically be needed in order to allow formation of the heteroduplex. In these circumstances, one may desire to employ salt conditions such as those of from about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20° C. to about 55° C. Cross-hybridizing species can thereby be readily identified as positively hybridizing signals with respect to control hybridizations. In any case, it is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide, which serves to destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method of choice depending on the desired results.

[0700] According to another embodiment of the present invention, polynucleotide compositions comprising antisense oligonucleotides are provided. Antisense oligonucleotides have been demonstrated to be effective and targeted inhibitors of protein syntheses, and, consequently, provide a therapeutic approach by which a disease can be treated by inhibiting the synthesis of proteins that contribute to the disease. The efficacy of antisense oligonucleotides for inhibiting protein synthesis is well established. For example, the synthesis of polygalacturonase and the muscarine type 2 acetylcholine receptor are inhibited by antisense oligonucleotides directed to their respective mRNA sequences (U.S. Pat. No. 5,739,119 and U.S. Pat. No. 5,759,829). Further, examples of antisense inhibition have been demonstrated with the nuclear protein cyclin, the multiple drug resistance gene (MDG1), ICAM-1, E-selectin, STK-1, striatal GABA_A receptor and human EGF (Jaskulski et al., *Science*, Jun. 10, 1988;240(4858):1544-6; Vasanthakumar and Ahmed, *Cancer Commun.* 1989; 1(4):225-32; Peris et al., *Brain Res Mol Brain Res.* Jun. 15, 1998;57(2):310-20; U.S. Pat. No. 5,801,154; U.S. Pat. No. 5,789,573; U.S. Pat. No. 5,718,709 and U.S. Pat. No. 5,610,288). Antisense constructs have also been described that inhibit and can be used to treat a variety of abnormal cellular proliferations, e.g. cancer (U.S. Pat. No. 5,747,470; U.S. Pat. No. 5,591,317 and U.S. Pat. No. 5,783,683).

[0701] Therefore, in certain embodiments, the present invention provides oligonucleotide sequences that comprise all, or a portion of, any sequence that is capable of specifically binding to polynucleotide sequence described herein,

or a complement thereof. In one embodiment, the antisense oligonucleotides comprise DNA or derivatives thereof. In another embodiment, the oligonucleotides comprise RNA or derivatives thereof. In a third embodiment, the oligonucleotides are modified DNAs comprising a phosphorothioated modified backbone. In a fourth embodiment, the oligonucleotide sequences comprise peptide nucleic acids or derivatives thereof. In each case, preferred compositions comprise a sequence region that is complementary, and more preferably substantially-complementary, and even more preferably, completely complementary to one or more portions of polynucleotides disclosed herein. Selection of antisense compositions specific for a given gene sequence is based upon analysis of the chosen target sequence and determination of secondary structure, T_m , binding energy, and relative stability. Antisense compositions may be selected based upon their relative inability to form dimers, hairpins, or other secondary structures that would reduce or prohibit specific binding to the target mRNA in a host cell. Highly preferred target regions of the mRNA, are those which are at or near the AUG translation initiation codon, and those sequences which are substantially complementary to 5' regions of the mRNA. These secondary structure analyses and target site selection considerations can be performed, for example, using v.4 of the OLIGO primer analysis software and/or the BLASTN 2.0.5 algorithm software (Altschul et al., *Nucleic Acids Res.* 1997, 25(17):3389-402).

[0702] The use of an antisense delivery method employing a short peptide vector, termed MPG (27 residues), is also contemplated. The MPG peptide contains a hydrophobic domain derived from the fusion sequence of HIV gp41 and a hydrophilic domain from the nuclear localization sequence of SV40 T-antigen (Morris et al., *Nucleic Acids Res.* Jul. 15, 1997;25(14):2730-6). It has been demonstrated that several molecules of the MPG peptide coat the antisense oligonucleotides and can be delivered into cultured mammalian cells in less than 1 hour with relatively high efficiency (90%). Further, the interaction with MPG strongly increases both the stability of the oligonucleotide to nuclease and the ability to cross the plasma membrane.

[0703] According to another embodiment of the invention, the polynucleotide compositions described herein are used in the design and preparation of ribozyme molecules for inhibiting expression of the tumor polypeptides and proteins of the present invention in tumor cells. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cech, *Proc Natl Acad Sci USA.* 1987 December;84(24):8788-92; Forster and Symons, *Cell.* Apr. 24, 1987;49(2):211-20). For example, a large number of ribozymes accelerate phosphoester transfer reactions with a high degree of specificity, often cleaving only one of several phosphoesters in an oligonucleotide substrate (Cech et al., *Cell.* 1981 December;27(3 Pt 2):487-96; Michel and Westhof, *J Mol Biol.* Dec. 5, 1990;216(3):585-610; Reinhold-Hurek and Shub, *Nature.* May 14, 1992;357(6374):173-6). This specificity has been attributed to the requirement that the substrate bind via specific base-pairing interactions to the internal guide sequence ("IGS") of the ribozyme prior to chemical reaction.

[0704] Six basic varieties of naturally-occurring enzymatic RNAs are known presently. Each can catalyze the

hydrolysis of RNA phosphodiester bonds in trans (and thus can cleave other RNA molecules) under physiological conditions. In general, enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

[0705] The enzymatic nature of a ribozyme is advantageous over many technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its translation) since the concentration of ribozyme necessary to affect a therapeutic treatment is lower than that of an antisense oligonucleotide. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme. Similar mismatches in antisense molecules do not prevent their action (Woolf et al., *Proc Natl Acad Sci USA*. Aug. 15, 1992;89(16):7305-9). Thus, the specificity of action of a ribozyme is greater than that of an antisense oligonucleotide binding the same RNA site.

[0706] The enzymatic nucleic acid molecule may be formed in a hammerhead, hairpin, a hepatitis δ virus, group I intron or RNaseP RNA (in association with an RNA guide sequence) or Neurospora VS RNA motif. Examples of hammerhead motifs are described by Rossi et al. *Nucleic Acids Res.* Sep. 11, 1992;20(17):4559-65. Examples of hairpin motifs are described by Hampel et al. (*Eur. Pat. Appl. Publ. No. EP 0360257*), Hampel and Tritz, *Biochemistry Jun.* 13, 1989;28(12):4929-33; Hampel et al., *Nucleic Acids Res.* Jan. 25, 1990;18(2):299-304 and U.S. Pat. No. 5,631,359. An example of the hepatitis δ virus motif is described by Perrotta and Been, *Biochemistry.* Dec. 1, 1992;31(47):11843-52; an example of the RNaseP motif is described by Guerrier-Takada et al., *Cell.* 1983 December;35(3 Pt 2):849-57; Neurospora VS RNA ribozyme motif is described by Collins (Saville and Collins, *Cell.* May 18, 1990;61(4):685-96; Saville and Collins, *Proc Natl Acad Sci USA.* Oct. 1, 1991;88(19):8826-30; Collins and Olive, *Biochemistry.* Mar. 23, 1993;32(11):2795-9); and an example of the Group I intron is described in (U.S. Pat. No. 4,987,071). All that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an RNA cleaving activity to the molecule. Thus the ribozyme constructs need not be limited to specific motifs mentioned herein.

[0707] Ribozymes may be designed as described in Int. Pat. Appl. Publ. No. WO 93/23569 and Int. Pat. Appl. Publ. No. WO 94/02595, each specifically incorporated herein by reference) and synthesized to be tested in vitro and in vivo, as described. Such ribozymes can also be optimized for delivery. While specific examples are provided, those in the art will recognize that equivalent RNA targets in other species can be utilized when necessary.

[0708] Ribozyme activity can be optimized by altering the length of the ribozyme binding arms, or chemically synthesizing ribozymes with modifications that prevent their degradation by serum ribonucleases (see e.g., Int. Pat. Appl. Publ. No. WO 92/07065; Int. Pat. Appl. Publ. No. WO 93/15187; Int. Pat. Appl. Publ. No. WO 91/03162; *Eur. Pat. Appl. Publ. No. 92110298.4*; U.S. Pat. No. 5,334,711; and Int. Pat. Appl. Publ. No. WO 94/13688, which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules), modifications which enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times and reduce chemical requirements.

[0709] Sullivan et al. (Int. Pat. Appl. Publ. No. WO 94/02595) describes the general methods for delivery of enzymatic RNA molecules. Ribozymes may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, ribozymes may be directly delivered ex vivo to cells or tissues with or without the aforementioned vehicles. Alternatively, the RNA/vehicle combination may be locally delivered by direct inhalation, by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of ribozyme delivery and administration are provided in Int. Pat. Appl. Publ. No. WO 94/02595 and Int. Pat. Appl. Publ. No. WO 93/23569, each specifically incorporated herein by reference.

[0710] Another means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters may also be used; providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells. Ribozymes expressed from such promoters have been shown to function in mammalian cells. Such transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated vectors), or viral RNA vectors (such as retroviral, semliki forest virus, sindbis virus vectors).

[0711] In another embodiment of the invention, peptide nucleic acids (PNAs) compositions are provided. PNA is a DNA mimic in which the nucleobases are attached to a pseudopeptide backbone (Good and Nielsen, *Antisense Nucleic Acid Drug Dev.* 1997 7(4) 431-37). PNA is able to be utilized in a number methods that traditionally have used RNA or DNA. Often PNA sequences perform better in techniques than the corresponding RNA or DNA sequences and have utilities that are not inherent to RNA or DNA. A review of PNA including methods of making, characteristics of, and methods of using, is provided by Corey (*Trends Biotechnol* 1997 June;15(6):224-9). As such, in certain embodiments, one may prepare PNA sequences that are complementary to one or more portions of the ACE mRNA sequence, and such PNA compositions may be used to regulate, alter, decrease, or reduce the translation of ACE-specific mRNA, and thereby alter the level of ACE activity in a host cell to which such PNA compositions have been administered.

[0712] PNAs have 2-aminoethyl-glycine linkages replacing the normal phosphodiester backbone of DNA (Nielsen et al., *Science* Dec. 6, 1991;254(5037):1497-500; Hanvey et al., *Science*. Nov. 27, 1992;258(5087):1481-5; Hyrup and Nielsen, *Bioorg Med Chem.* 1996 January;4(1):5-23). This chemistry has three important consequences: firstly, in contrast to DNA or phosphorothioate oligonucleotides, PNAs are neutral molecules; secondly, PNAs are achiral, which avoids the need to develop a stereoselective synthesis; and thirdly, PNA synthesis uses standard Boc or Fmoc protocols for solid-phase peptide synthesis, although other methods, including a modified Merrifield method, have been used.

[0713] PNA monomers or ready-made oligomers are commercially available from PerSeptive Biosystems (Framingham, Mass.). PNA syntheses by either Boc or Fmoc protocols are straightforward using manual or automated protocols (Norton et al., *Bioorg Med Chem.* 1995 April;3(4):437-45). The manual protocol lends itself to the production of chemically modified PNAs or the simultaneous synthesis of families of closely related PNAs.

[0714] As with peptide synthesis, the success of a particular PNA synthesis will depend on the properties of the chosen sequence. For example, while in theory PNAs can incorporate any combination of nucleotide bases, the presence of adjacent purines can lead to deletions of one or more residues in the product. In expectation of this difficulty, it is suggested that, in producing PNAs with adjacent purines, one should repeat the coupling of residues likely to be added inefficiently. This should be followed by the purification of PNAs by reverse-phase high-pressure liquid chromatography, providing yields and purity of product similar to those observed during the synthesis of peptides.

[0715] Modifications of PNAs for a given application may be accomplished by coupling amino acids during solid-phase synthesis or by attaching compounds that contain a carboxylic acid group to the exposed N-terminal amine. Alternatively, PNAs can be modified after synthesis by coupling to an introduced lysine or cysteine. The ease with which PNAs can be modified facilitates optimization for better solubility or for specific functional requirements. Once synthesized, the identity of PNAs and their derivatives can be confirmed by mass spectrometry. Several studies have made and utilized modifications of PNAs (for example,

Norton et al., *Bioorg Med Chem.* 1995 April;3(4):437-45; Petersen et al., *J Pept Sci.* 1995 May-June;1(3):175-83; Orum et al., *Biotechniques.* 1995 September;19(3):472-80; Footer et al., *Biochemistry.* Aug. 20, 1996;35(33):10673-9; Griffith et al., *Nucleic Acids Res.* Aug. 11, 1995;23(15):3003-8; Pardridge et al., *Proc Natl Acad Sci USA.* Jun. 6, 1995;92(12):5592-6; Boffa et al., *Proc Natl Acad Sci USA.* Mar. 14, 1995;92(6):1901-5; Gambacorti-Passerini et al., *Blood.* Aug. 15, 1996;88(4):1411-7; Armitage et al., *Proc Natl Acad Sci USA.* Nov. 11, 1997;94(23):12320-5; Seeger et al., *Biotechniques.* 1997 September;23(3):512-7). U.S. Pat. No. 5,700,922 discusses PNA-DNA-PNA chimeric molecules and their uses in diagnostics, modulating protein in organisms, and treatment of conditions susceptible to therapeutics.

[0716] Methods of characterizing the antisense binding properties of PNAs are discussed in Rose (*Anal Chem.* Dec. 15, 1993;65(24):3545-9) and Jensen et al. (*Biochemistry.* Apr. 22, 1997;36(16):5072-7). Rose uses capillary gel electrophoresis to determine binding of PNAs to their complementary oligonucleotide, measuring the relative binding kinetics and stoichiometry. Similar types of measurements were made by Jensen et al. using BIAcore™ technology.

[0717] Other applications of PNAs that have been described and will be apparent to the skilled artisan include use in DNA strand invasion, antisense inhibition, mutational analysis, enhancers of transcription, nucleic acid purification, isolation of transcriptionally active genes, blocking of transcription factor binding, genome cleavage, biosensors, in situ hybridization, and the like.

Polynucleotide Identification Characterization and Expression

[0718] Polynucleotides compositions of the present invention may be identified, prepared and/or manipulated using any of a variety of well established techniques (see generally, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, N.Y., 1989, and other like references). For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (i.e., expression that is at least two fold greater in a tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed, for example, using the microarray technology of Affymetrix, Inc. (Santa Clara, Calif.) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polynucleotides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as tumor cells.

[0719] Many template dependent processes are available to amplify a target sequences of interest present in a sample. One of the best known amplification methods is the polymerase chain reaction (PCR™) which is described in detail in U.S. Pat. Nos. 4,683,195, 4,683,202 and 4,800,159, each of which is incorporated herein by reference in its entirety. Briefly, in PCR™, two primer sequences are prepared which are complementary to regions on opposite complementary strands of the target sequence. An excess of deoxynucleoside triphosphates is added to a reaction mixture along with a

DNA polymerase (e.g., Taq polymerase). If the target sequence is present in a sample, the primers will bind to the target and the polymerase will cause the primers to be extended along the target sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the target to form reaction products, excess primers will bind to the target and to the reaction product and the process is repeated. Preferably reverse transcription and PCR™ amplification procedure may be performed in order to quantify the amount of mRNA amplified. Polymerase chain reaction methodologies are well known in the art.

[0720] Any of a number of other template dependent processes, many of which are variations of the PCR™ amplification technique, are readily known and available in the art. Illustratively, some such methods include the ligase chain reaction (referred to as LCR), described, for example, in Eur. Pat. Appl. Publ. No. 320,308 and U.S. Pat. No. 4,883,750; Qbeta Replicase, described in PCT Intl. Pat. Appl. Publ. No. PCT/US87/00880; Strand Displacement Amplification (SDA) and Repair Chain Reaction (RCR). Still other amplification methods are described in Great Britain Pat. Appl. No. 2 202 328, and in PCT Intl. Pat. Appl. Publ. No. PCT/US89/01025. Other nucleic acid amplification procedures include transcription-based amplification systems (TAS) (PCT Intl. Pat. Appl. Publ. No. WO 88/10315), including nucleic acid sequence based amplification (NASBA) and 3SR. Eur. Pat. Appl. Publ. No. 329,822 describes a nucleic acid amplification process involving cyclically synthesizing single-stranded RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA). PCT Intl. Pat. Appl. Publ. No. WO 89/06700 describes a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. Other amplification methods such as "RACE" (Frohman, 1990), and "one-sided PCR" (Ohara, 1989) are also well-known to those of skill in the art.

[0721] An amplified portion of a polynucleotide of the present invention may be used to isolate a full length gene from a suitable library (e.g., a tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

[0722] For hybridization techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with ³²P) using well known techniques. A bacterial or bacteriophage library is then generally screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, N.Y., 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to

identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences can then be assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

[0723] Alternatively, amplification techniques, such as those described above, can be useful for obtaining a full length coding sequence from a partial cDNA sequence. One such amplification technique is inverse PCR (see Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

[0724] In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (e.g., NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

[0725] In other embodiments of the invention, polynucleotide sequences or fragments thereof which encode polypeptides of the invention, or fusion proteins or functional equivalents thereof, may be used in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences that encode substantially the same or a functionally equivalent amino acid sequence may be produced and these sequences may be used to clone and express a given polypeptide.

[0726] As will be understood by those of skill in the art, it may be advantageous in some instances to produce polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

[0727] Moreover, the polynucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter polypeptide encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. For example, DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. In addition, site-directed mutagenesis may be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

[0728] In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of polypeptide activity, it may be useful to encode a chimeric protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the polypeptide-encoding sequence and the heterologous protein sequence, so that the polypeptide may be cleaved and purified away from the heterologous moiety.

[0729] Sequences encoding a desired polypeptide may be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers, M. H. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 215-223; Horn, T. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 225-232). Alternatively, the protein itself may be produced using chemical methods to synthesize the amino acid sequence of a polypeptide, or a portion thereof. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J. Y. et al. (1995) *Science* 269:202-204) and automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer, Palo Alto, Calif.).

[0730] A newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (e.g., Creighton, T. (1983) *Proteins, Structures and Molecular Principles*, WH Freeman and Co., New York, N.Y.) or other comparable techniques available in the art. The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure). Additionally, the amino acid sequence of a polypeptide, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

[0731] In order to express a desired polypeptide, the nucleotide sequences encoding the polypeptide, or functional equivalents, may be inserted into appropriate expression vector, i.e., a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding a polypeptide of interest and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. Such techniques are described, for example, in Sambrook, J. et al. (1989) *Molecular Cloning*, A Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. et al. (1989) *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, N.Y.

[0732] A variety of expression vector/host systems may be utilized to contain and express polynucleotide sequences. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (e.g., baculovirus); plant cell systems transformed with virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems.

[0733] The "control elements" or "regulatory sequences" present in an expression vector are those non-translated regions of the vector—enhancers, promoters, 5' and 3' untranslated regions—which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the PBLUE-SCRIPT phagemid (Stratagene, La Jolla, Calif.) or PSORT1 plasmid (Gibco BRL, Gaithersburg, Md.) and the like may be used. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are generally preferred. If it is necessary to generate a cell line that contains multiple copies of the sequence encoding a polypeptide, vectors based on SV40 or EBV may be advantageously used with an appropriate selectable marker.

[0734] In bacterial systems, any of a number of expression vectors may be selected depending upon the use intended for the expressed polypeptide. For example, when large quantities are needed, for example for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence encoding the polypeptide of interest may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of beta.-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S. M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509); and the like. pGEX Vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

[0735] In the yeast, *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel et al. (supra) and Grant et al. (1987) *Methods Enzymol.* 153:516-544.

[0736] In cases where plant expression vectors are used, the expression of sequences encoding polypeptides may be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV may

be used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311. Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; and Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (see, for example, Hobbs, S. or Murry, L. E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, N.Y.; pp. 191-196).

[0737] An insect system may also be used to express a polypeptide of interest. For example, in one such system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia larvae*. The sequences encoding the polypeptide may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of the polypeptide-encoding sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, *S. frugiperda* cells or *Trichoplusia larvae* in which the polypeptide of interest may be expressed (Engelhard, E. K. et al. (1994) *Proc. Natl. Acad. Sci.* 91 :3224-3227).

[0738] In mammalian host cells, a number of viral-based expression systems are generally available. For example, in cases where an adenovirus is used as an expression vector, sequences encoding a polypeptide of interest may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is capable of expressing the polypeptide in infected host cells (Logan, J. and Shenk, T. (1984) *Proc. Natl. Acad. Sci.* 81:3655-3659). In addition, transcription enhancers, such as the *Rous sarcoma virus* (RSV) enhancer, may be used to increase expression in mammalian host cells.

[0739] Specific initiation signals may also be used to achieve more efficient translation of sequences encoding a polypeptide of interest. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding the polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162).

[0740] In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences

or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as CHO, COS, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

[0741] For long-term, high-yield production of recombinant proteins, stable expression is generally preferred. For example, cell lines which stably express a polynucleotide of interest may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

[0742] Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler, M. et al. (1977) *Cell* 11:223-32) and adenine phosphoribosyltransferase (Lowy, I. et al. (1990) *Cell* 22:817-23) genes which can be employed in tk.sup.- or apt.sup.-cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M. et al. (1980) *Proc. Natl. Acad. Sci.* 77:3567-70); npt, which confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin, F. et al (1981) *J. Mol. Biol.* 150:1-14); and als or pat, which confer resistance to chloresulfuron and phosphinotricin acetyltransferase, respectively (Murry, supra). Additional selectable genes have been described, for example, trpB, Which allows cells to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in place of histidine (Hartman, S. C. and R. C. Mulligan (1988) *Proc. Natl. Acad. Sci.* 85:8047-51). The use of visible markers has gained popularity with such markers as anthocyanins, beta-glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C. A. et al. (1995) *Methods Mol. Biol.* 55:121-131).

[0743] Although the presence/absence of marker gene expression suggests that the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding a polypeptide is inserted within a marker gene sequence, recombinant cells containing sequences can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a polypeptide-encoding sequence under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

[0744] Alternatively, host cells that contain and express a desired polynucleotide sequence may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques which include, for example, membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

[0745] A variety of protocols for detecting and measuring the expression of polynucleotide-encoded products, using either polyclonal or monoclonal antibodies specific for the product are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on a given polypeptide may be preferred for some applications, but a competitive binding assay may also be employed. These and other assays are described, among other places, in Hampton, R. et al. (1990; *Serological Methods*, a Laboratory Manual, APS Press, St Paul, Minn.) and Maddox, D. E. et al. (1983; *J. Exp. Med.* 158:1211-1216).

[0746] A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences, or any portions thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits. Suitable reporter molecules or labels, which may be used include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

[0747] Host cells transformed with a polynucleotide sequence of interest may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a recombinant cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides of the invention may be designed to contain signal sequences which direct secretion of the encoded polypeptide through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences encoding a polypeptide of interest to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAG extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego, Calif.) between the purification domain and the encoded polypeptide may be

used to facilitate purification. One such expression vector provides for expression of a fusion protein containing a polypeptide of interest and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography) as described in Porath, J. et al. (1992, *Prot. Exp. Purif.* 3:263-281) while the enterokinase cleavage site provides a means for purifying the desired polypeptide from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J. et al. (1993; *DNA Cell Biol.* 12:441-453).

[0748] In addition to recombinant production methods, polypeptides of the invention, and fragments thereof, may be produced by direct peptide synthesis using solid-phase techniques (Merrifield J. (1963) *J. Am. Chem. Soc.* 85:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Alternatively, various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

Antibody Compositions Fragments Thereof and Other Binding Agents

[0749] According to another aspect, the present invention further provides binding agents, such as antibodies and antigen-binding fragments thereof, that exhibit immunological binding to a tumor polypeptide disclosed herein, or to a portion, variant or derivative thereof. An antibody, or antigen-binding fragment thereof, is said to "specifically bind," "immunologically bind," and/or is "immunologically reactive" to a polypeptide of the invention if it reacts at a detectable level (within, for example, an ELISA assay) with the polypeptide, and does not react detectably with unrelated polypeptides under similar conditions.

[0750] Immunological binding, as used in this context, generally refers to the non-covalent interactions of the type which occur between an immunoglobulin molecule and an antigen for which the immunoglobulin is specific. The strength, or affinity of immunological binding interactions can be expressed in terms of the dissociation constant (K_d) of the interaction, wherein a smaller K_d represents a greater affinity. Immunological binding properties of selected polypeptides can be quantified using methods well known in the art. One such method entails measuring the rates of antigen-binding site/antigen complex formation and dissociation, wherein those rates depend on the concentrations of the complex partners, the affinity of the interaction, and on geometric parameters that equally influence the rate in both directions. Thus, both the "on rate constant" (K_{on}) and the "off rate constant" (K_{off}) can be determined by calculation of the concentrations and the actual rates of association and dissociation. The ratio of K_{off}/K_{on} enables cancellation of all parameters not related to affinity, and is thus equal to the dissociation constant K_d . See, generally, Davies et al. (1990) *Annual Rev. Biochem.* 59:439-473.

[0751] An "antigen-binding site," or "binding portion" of an antibody refers to the part of the immunoglobulin molecule that participates in antigen binding. The antigen binding site is formed by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L")

chains. Three highly divergent stretches within the V regions of the heavy and light chains are referred to as "hypervariable regions" which are interposed between more conserved flanking stretches known as "framework regions," or "FRs". Thus the term "FR" refers to amino acid sequences which are naturally found between and adjacent to hypervariable regions in immunoglobulins. In an antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each other in three dimensional space to form an antigen-binding surface. The antigen-binding surface is complementary to the three-dimensional surface of a bound antigen, and the three hypervariable regions of each of the heavy and light chains are referred to as "complementarity-determining regions," or "CDRs."

[0752] Binding agents may be further capable of differentiating between patients with and without a cancer, such as breast cancer, using the representative assays provided herein. For example, antibodies or other binding agents that bind to a tumor protein will preferably generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, more preferably at least about 30% of patients. Alternatively, or in addition, the antibody will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (e.g., blood, sera, sputum, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. Preferably, a statistically significant number of samples with and without the disease will be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

[0753] 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 polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies 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 general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or 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.

[0754] Monoclonal antibodies specific for an 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 their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

[0755] 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.

[0756] A number of therapeutically useful molecules are known in the art which comprise antigen-binding sites that are capable of exhibiting immunological binding properties of an antibody molecule. The proteolytic enzyme papain preferentially cleaves IgG molecules to yield several fragments, two of which (the "F(ab)" fragments) each comprise a covalent heterodimer that includes an intact antigen-binding site. The enzyme pepsin is able to cleave IgG molecules to provide several fragments, including the "F(ab')₂" fragment which comprises both antigen-binding sites. An "Fv" fragment can be produced by preferential proteolytic cleavage of an IgM, and on rare occasions IgG or IgA immunoglobulin molecule. Fv fragments are, however, more commonly derived using recombinant techniques known in the art. The Fv fragment includes a non-covalent V_H::V_L heterodimer including an antigen-binding site which retains much of the antigen recognition and binding capabilities of the native antibody molecule. Inbar et al. (1972) *Proc. Nat. Acad. Sci. USA* 69:2659-2662; Hochman et al. (1976) *Biochem* 15:2706-2710; and Ehrlich et al. (1980) *Biochem* 19:4091-4096.

[0757] A single chain Fv ("sFv") polypeptide is a covalently linked V_H::V_L heterodimer which is expressed from a gene fusion including V_H- and V_L-encoding genes

linked by a peptide-encoding linker. Huston et al. (1988) *Proc. Nat. Acad. Sci. USA* 85(16):5879-5883. A number of methods have been described to discern chemical structures for converting the naturally aggregated—but chemically separated—light and heavy polypeptide chains from an antibody V region into an sFv molecule which will fold into a three dimensional structure substantially similar to the structure of an antigen-binding site. See, e.g., U.S. Pat. Nos. 5,091,513 and 5,132,405, to Huston et al.; and U.S. Pat. No. 4,946,778, to Ladner et al.

[0758] Each of the above-described molecules includes a heavy chain and a light chain CDR set, respectively interposed between a heavy chain and a light chain FR set which provide support to the CDRs and define the spatial relationship of the CDRs relative to each other. As used herein, the term “CDR set” refers to the three hypervariable regions of a heavy or light chain V region. Proceeding from the N-terminus of a heavy or light chain, these regions are denoted as “CDR1,” “CDR2,” and “CDR3” respectively. An antigen-binding site, therefore, includes six CDRs, comprising the CDR set from each of a heavy and a light chain V region. A polypeptide comprising a single CDR, (e.g., a CDR1, CDR2 or CDR3) is referred to herein as a “molecular recognition unit.” Crystallographic analysis of a number of antigen-antibody complexes has demonstrated that the amino acid residues of CDRs form extensive contact with bound antigen, wherein the most extensive antigen contact is with the heavy chain CDR3. Thus, the molecular recognition units are primarily responsible for the specificity of an antigen-binding site.

[0759] As used herein, the term “FR set” refers to the four flanking amino acid sequences which frame the CDRs of a CDR set of a heavy or light chain V region. Some FR residues may contact bound antigen; however, FRs are primarily responsible for folding the V region into the antigen-binding site, particularly the FR residues directly adjacent to the CDRs. Within FRs, certain amino residues and certain structural features are very highly conserved. In this regard, all V region sequences contain an internal disulfide loop of around 90 amino acid residues. When the V regions fold into a binding-site, the CDRs are displayed as projecting loop motifs which form an antigen-binding surface. It is generally recognized that there are conserved structural regions of FRs which influence the folded shape of the CDR loops into certain “canonical” structures—regardless of the precise CDR amino acid sequence. Further, certain FR residues are known to participate in non-covalent interdomain contacts which stabilize the interaction of the antibody heavy and light chains.

[0760] A number of “humanized” antibody molecules comprising an antigen-binding site derived from a non-human immunoglobulin have been described, including chimeric antibodies having rodent V regions and their associated CDRs fused to human constant domains (Winter et al. (1991) *Nature* 349:293-299; Lobuglio et al. (1989) *Proc. Nat. Acad. Sci. USA* 86:4220-4224; Shaw et al. (1987) *J Immunol.* 138:4534-4538; and Brown et al. (1987) *Cancer Res.* 47:3577-3583), rodent CDRs grafted into a human supporting FR prior to fusion with an appropriate human antibody constant domain (Riechmann et al. (1988) *Nature* 332:323-327; Verhoeyen et al. (1988) *Science* 239:1534-1536; and Jones et al. (1986) *Nature* 321:522-525), and rodent CDRs supported by recombinantly veneered rodent

FRs (European Patent Publication No. 519,596, published Dec. 23, 1992). These “humanized” molecules are designed to minimize unwanted immunological response toward rodent antihuman antibody molecules which limits the duration and effectiveness of therapeutic applications of those moieties in human recipients.

[0761] As used herein, the terms “veneered FRs” and “recombinantly veneered FRs” refer to the selective replacement of FR residues from, e.g., a rodent heavy or light chain V region, with human FR residues in order to provide a xenogeneic molecule comprising an antigen-binding site which retains substantially all of the native FR polypeptide folding structure. Veneering techniques are based on the understanding that the ligand binding characteristics of an antigen-binding site are determined primarily by the structure and relative disposition of the heavy and light chain CDR sets within the antigen-binding surface. Davies et al. (1990) *Ann. Rev. Biochem.* 59:439-473. Thus, antigen binding specificity can be preserved in a humanized antibody only wherein the CDR structures, their interaction with each other, and their interaction with the rest of the V region domains are carefully maintained. By using veneering techniques, exterior (e.g., solvent-accessible) FR residues which are readily encountered by the immune system are selectively replaced with human residues to provide a hybrid molecule that comprises either a weakly immunogenic, or substantially non-immunogenic veneered surface.

[0762] The process of veneering makes use of the available sequence data for human antibody variable domains compiled by Kabat et al., in *Sequences of Proteins of Immunological Interest*, 4th ed., (U.S. Dept. of Health and Human Services, U.S. Government Printing Office, 1987), updates to the Kabat database, and other accessible U.S. and foreign databases (both nucleic acid and protein). Solvent accessibilities of V region amino acids can be deduced from the known three-dimensional structure for human and murine antibody fragments. There are two general steps in veneering a murine antigen-binding site. Initially, the FRs of the variable domains of an antibody molecule of interest are compared with corresponding FR sequences of human variable domains obtained from the above-identified sources. The most homologous human V regions are then compared residue by residue to corresponding murine amino acids. The residues in the murine FR which differ from the human counterpart are replaced by the residues present in the human moiety using recombinant techniques well known in the art. Residue switching is only carried out with moieties which are at least partially exposed (solvent accessible), and care is exercised in the replacement of amino acid residues which may have a significant effect on the tertiary structure of V region domains, such as proline, glycine and charged amino acids.

[0763] In this manner, the resultant “veneered” murine antigen-binding sites are thus designed to retain the murine CDR residues, the residues substantially adjacent to the CDRs, the residues identified as buried or mostly buried (solvent inaccessible), the residues believed to participate in non-covalent (e.g., electrostatic and hydrophobic) contacts between heavy and light chain domains, and the residues from conserved structural regions of the FRs which are believed to influence the “canonical” tertiary structures of the CDR loops. These design criteria are then used to prepare recombinant nucleotide sequences which combine

the CDRs of both the heavy and light chain of a murine antigen-binding site into human-appearing FRs that can be used to transfect mammalian cells for the expression of recombinant human antibodies which exhibit the antigen specificity of the murine antibody molecule.

[0764] In another embodiment of the invention, monoclonal antibodies of the present invention may be 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, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

[0765] 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.

[0766] 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.

[0767] 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, Ill.), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, e.g., U.S. Pat. No. 4,671,958, to Rodwell et al.

[0768] 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. Pat. No. 4,489,710, to Spitler), by irradiation of a photolabile bond (e.g., U.S. Pat. No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (e.g., U.S. Pat. No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (e.g., U.S. Pat. No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (e.g., U.S. Pat. No. 4,569,789, to Blattler et al.).

[0769] 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 that provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

[0770] 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. Pat. No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (e.g., U.S. Pat. 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. Pat. Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Pat. 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. Pat. No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

T Cell Compositions

[0771] The present invention, in another aspect, provides T cells specific for a tumor polypeptide disclosed herein, or for a variant or derivative thereof. Such cells may generally be prepared in vitro or ex vivo, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the Isoplex™ System, available from Nexell Therapeutics, Inc. (Irvine, Calif.; see also U.S. Pat. No. 5,240,856; U.S. Pat. No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

[0772] T cells may be stimulated with a polypeptide, polynucleotide encoding a polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide of interest. Preferably, a tumor polypeptide or polynucleotide of the invention is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

[0773] T cells are considered to be specific for a polypeptide of the present invention if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For

example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a tumor polypeptide (100 ng/ml–100 µg/ml, preferably 200 ng/ml–25 µg/ml) for 3–7 days will typically result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2–3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-γ) is indicative of T cell activation (see Coligan et al., *Current Protocols in Immunology*, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Tumor polypeptide-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from a patient, a related donor or an unrelated donor, and are administered to the patient following stimulation and expansion.

[0774] For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to a tumor polypeptide, polynucleotide or APC can be expanded in number either in vitro or in vivo. Proliferation of such T cells in vitro may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of the tumor polypeptide can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

Pharmaceutical Compositions

[0775] In additional embodiments, the present invention concerns formulation of one or more of the polynucleotide, polypeptide, T-cell and/or antibody compositions disclosed herein in pharmaceutically-acceptable carriers for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy.

[0776] It will be understood that, if desired, a composition as disclosed herein may be administered in combination with other agents as well, such as, e.g., other proteins or polypeptides or various pharmaceutically-active agents. In fact there is virtually no limit to other components that may also be included, given that the additional agents do not cause a significant adverse effect upon contact with the target cells or host tissues. The compositions may thus be delivered along with various other agents as required in the particular instance. Such compositions may be purified from host cells or other biological sources, or alternatively may be chemically synthesized as described herein. Likewise, such compositions may further comprise substituted or derivatized RNA or DNA compositions.

[0777] Therefore, in another aspect of the present invention, pharmaceutical compositions are provided comprising one or more of the polynucleotide, polypeptide, antibody, and/or T-cell compositions described herein in combination with a physiologically acceptable carrier. In certain preferred embodiments, the pharmaceutical compositions of the invention comprise immunogenic polynucleotide and/or

polypeptide compositions of the invention for use in prophylactic and therapeutic vaccine applications. Vaccine preparation is generally described in, for example, M. F. Powell and M. J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Generally, such compositions will comprise one or more polynucleotide and/or polypeptide compositions of the present invention in combination with one or more immunostimulants.

[0778] It will be apparent that any of the pharmaceutical compositions described herein can contain pharmaceutically acceptable salts of the polynucleotides and polypeptides of the invention. Such salts can be prepared, for example, from pharmaceutically acceptable non-toxic bases, including organic bases (e.g., salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (e.g., sodium, potassium, lithium, ammonium, calcium and magnesium salts).

[0779] In another embodiment, illustrative immunogenic compositions, e.g., vaccine compositions, of the present invention comprise DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated in situ. As noted above, the polynucleotide may be administered within any of a variety of delivery systems known to those of ordinary skill in the art. Indeed, numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143–198, 1998, and references cited therein. Appropriate polynucleotide expression systems will, of course, contain the necessary regulatory DNA regulatory sequences for expression in a patient (such as a suitable promoter and terminating signal). Alternatively, bacterial delivery systems may involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope.

[0780] Therefore, in certain embodiments, polynucleotides encoding immunogenic polypeptides described herein are introduced into suitable mammalian host cells for expression using any of a number of known viral-based systems. In one illustrative embodiment, retroviruses provide a convenient and effective platform for gene delivery systems. A selected nucleotide sequence encoding a polypeptide of the present invention can be inserted into a vector and packaged in retroviral particles using techniques known in the art. The recombinant virus can then be isolated and delivered to a subject. A number of illustrative retroviral systems have been described (e.g., U.S. Pat. No. 5,219,740; Miller and Rosman (1989) *BioTechniques* 7:980–990; Miller, A. D. (1990) *Human Gene Therapy* 1:5–14; Scarpa et al. (1991) *Virology* 180:849–852; Burns et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:8033–8037; and Boris-Lawrie and Temin (1993) *Cur. Opin. Genet. Develop.* 3:102–109.

[0781] In addition, a number of illustrative adenovirus-based systems have also been described. Unlike retroviruses which integrate into the host genome, adenoviruses persist extrachromosomally thus minimizing the risks associated with insertional mutagenesis (Haj-Ahmad and Graham (1986) *J. Virol.* 57:267–274; Bett et al. (1993) *J. Virol.* 67:5911–5921; Mittereder et al. (1994) *Human Gene Therapy* 5:717–729; Seth et al. (1994) *J. Virol.* 68:933–940; Barr et al. (1994) *Gene Therapy* 1:51–58; Berkner, K. L.

(1988) *BioTechniques* 6:616-629; and Rich et al. (1993) *Human Gene Therapy* 4:461-476).

[0782] Various adeno-associated virus (AAV) vector systems have also been developed for polynucleotide delivery. AAV vectors can be readily constructed using techniques well known in the art. See, e.g., U.S. Pat. Nos. 5,173,414 and 5,139,941; International Publication Nos. WO 92/01070 and WO 93/03769; Lebkowski et al. (1988) *Molec. Cell. Biol.* 8:3988-3996; Vincent et al. (1990) *Vaccines 90* (Cold Spring Harbor Laboratory Press); Carter, B. J. (1992) *Current Opinion in Biotechnology* 3:533-539; Muzyczka, N. (1992) *Current Topics in Microbiol. and Immunol.* 158:97-129; Kotin, R. M. (1994) *Human Gene Therapy* 5:793-801; Shelling and Smith (1994) *Gene Therapy* 1:165-169; and Zhou et al. (1994) *J. Exp. Med.* 179:1867-1875.

[0783] Additional viral vectors useful for delivering the polynucleotides encoding polypeptides of the present invention by gene transfer include those derived from the pox family of viruses, such as vaccinia virus and avian poxvirus. By way of example, vaccinia virus recombinants expressing the novel molecules can be constructed as follows. The DNA encoding a polypeptide is first inserted into an appropriate vector so that it is adjacent to a vaccinia promoter and flanking vaccinia DNA sequences, such as the sequence encoding thymidine kinase (TK). This vector is then used to transfect cells which are simultaneously infected with vaccinia. Homologous recombination serves to insert the vaccinia promoter plus the gene encoding the polypeptide of interest into the viral genome. The resulting TK^{sup}(-) recombinant can be selected by culturing the cells in the presence of 5-bromodeoxyuridine and picking viral plaques resistant thereto.

[0784] A vaccinia-based infection/transfection system can be conveniently used to provide for inducible, transient expression or coexpression of one or more polypeptides described herein in host cells of an organism. In this particular system, cells are first infected in vitro with a vaccinia virus recombinant that encodes the bacteriophage T7 RNA polymerase. This polymerase displays exquisite specificity in that it only transcribes templates bearing T7 promoters. Following infection, cells are transfected with the polynucleotide or polynucleotides of interest, driven by a T7 promoter. The polymerase expressed in the cytoplasm from the vaccinia virus recombinant transcribes the transfected DNA into RNA which is then translated into polypeptide by the host translational machinery. The method provides for high level, transient, cytoplasmic production of large quantities of RNA and its translation products. See, e.g., Elroy-Stein and Moss, *Proc. Natl. Acad. Sci. USA* (1990) 87:6743-6747; Fuerst et al. *Proc. Natl. Acad. Sci. USA* (1986) 83:8122-8126.

[0785] Alternatively, avipoxviruses, such as the fowlpox and canarypox viruses, can also be used to deliver the coding sequences of interest. Recombinant avipox viruses, expressing immunogens from mammalian pathogens, are known to confer protective immunity when administered to non-avian species. The use of an Avipox vector is particularly desirable in human and other mammalian species since members of the Avipox genus can only productively replicate in susceptible avian species and therefore are not infective in mammalian cells. Methods for producing recombinant Avipox-viruses are known in the art and employ genetic

recombination, as described above with respect to the production of vaccinia viruses. See, e.g., WO 91/12882; WO 89/03429; and WO 92/03545.

[0786] Any of a number of alphavirus vectors can also be used for delivery of polynucleotide compositions of the present invention, such as those vectors described in U.S. Pat. Nos. 5,843,723; 6,015,686; 6,008,035 and 6,015,694. Certain vectors based on Venezuelan Equine Encephalitis (VEE) can also be used, illustrative examples of which can be found in U.S. Pat. Nos. 5,505,947 and 5,643,576.

[0787] Moreover, molecular conjugate vectors, such as the adenovirus chimeric vectors described in Michael et al. *J. Biol. Chem.* (1993) 268:6866-6869 and Wagner et al. *Proc. Natl. Acad. Sci. USA* (1992) 89:6099-6103, can also be used for gene delivery under the invention.

[0788] Additional illustrative information on these and other known viral-based delivery systems can be found, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 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. Pat. Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Pat. 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., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993.

[0789] In certain embodiments, a polynucleotide may be integrated into the genome of a target cell. This integration may be in the specific location and orientation via homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the polynucleotide may be stably maintained in the cell as a separate, episomal segment of DNA. Such polynucleotide segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle. The manner in which the expression construct is delivered to a cell and where in the cell the polynucleotide remains is dependent on the type of expression construct employed.

[0790] In another embodiment of the invention, a polynucleotide is administered/delivered as "naked" DNA, for example as described in Ulmer et al., *Science* 259:1745-1749, 1993 and 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.

[0791] In still another embodiment, a composition of the present invention can be delivered via a particle bombardment approach, many of which have been described. In one illustrative example, gas-driven particle acceleration can be achieved with devices such as those manufactured by Powderject Pharmaceuticals PLC (Oxford, UK) and Powderject Vaccines Inc. (Madison, Wis.), some examples of which are described in U.S. Pat. Nos. 5,846,796; 6,010,478; 5,865,196; 5,584,807; and EP Patent No. 0500 799. This approach offers a needle-free delivery approach wherein a dry powder formulation of microscopic particles, such as polynucleotide or polypeptide particles, are accelerated to

high speed within a helium gas jet generated by a hand held device, propelling the particles into a target tissue of interest.

[0792] In a related embodiment, other devices and methods that may be useful for gas-driven needle-less injection of compositions of the present invention include those provided by Bioject, Inc. (Portland, Oreg.), some examples of which are described in U.S. Pat. Nos. 4,790,824; 5,064,413; 5,312,335; 5,383,851; 5,399,163; 5,520,639 and 5,993,412.

[0793] According to another embodiment, the pharmaceutical compositions described herein will comprise one or more immunostimulants in addition to the immunogenic polynucleotide, polypeptide, antibody, T-cell and/or APC compositions of this invention. An immunostimulant refers to essentially any substance that enhances or potentiates an immune response (antibody and/or cell-mediated) to an exogenous antigen. One preferred type of immunostimulant comprises an adjuvant. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, Mich.); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, N.J.); AS-2 (SmithKline Beecham, Philadelphia, Pa.); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

[0794] Within certain embodiments of the invention, the adjuvant composition is preferably one that induces an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

[0795] Certain preferred adjuvants for eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A, together with an aluminum salt. MPL $\text{\textcircled{R}}$ adjuvants are available from Corixa Corporation (Seattle, Wash.; see, for example, U.S. Pat. Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555, WO 99/33488 and U.S. Pat. Nos. 6,008,200 and 5,856,462. Immunostimulatory DNA

sequences are also described, for example, by Sato et al., *Science* 273:352, 1996. Another preferred adjuvant comprises a saponin, such as Quil A, or derivatives thereof, including QS21 and QS7 (Aquila Biopharmaceuticals Inc., Framingham, Mass.); Escin; Digitonin; or *Gypsophila* or *Chenopodium quinoa* saponins. Other preferred formulations include more than one saponin in the adjuvant combinations of the present invention, for example combinations of at least two of the following group comprising QS21, QS7, Quil A, β -escin, or digitonin.

[0796] Alternatively the saponin formulations may be combined with vaccine vehicles composed of chitosan or other polycationic polymers, polylactide and poly(lactide-co-glycolide) particles, poly-N-acetyl glucosamine-based polymer matrix, particles composed of polysaccharides or chemically modified polysaccharides, liposomes and lipid-based particles, particles composed of glycerol monoesters, etc. The saponins may also be formulated in the presence of cholesterol to form particulate structures such as liposomes or ISCOMs. Furthermore, the saponins may be formulated together with a polyoxyethylene ether or ester, in either a non-particulate solution or suspension, or in a particulate structure such as a paucilamellar liposome or ISCOM. The saponins may also be formulated with excipients such as Carbowax $\text{\textcircled{R}}$ to increase viscosity, or may be formulated in a dry powder form with a powder excipient such as lactose.

[0797] In one preferred embodiment, the adjuvant system includes the combination of a monophosphoryl lipid A and a saponin derivative, such as the combination of QS21 and 3D-MPL $\text{\textcircled{R}}$ adjuvant, as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. Another particularly preferred adjuvant formulation employing QS21, 3D-MPL $\text{\textcircled{R}}$ adjuvant and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

[0798] Another enhanced adjuvant system involves the combination of a CpG-containing oligonucleotide and a saponin derivative particularly the combination of CpG and QS21 is disclosed in WO 00/09159. Preferably the formulation additionally comprises an oil in water emulsion and tocopherol.

[0799] Additional illustrative adjuvants for use in the pharmaceutical compositions of the invention include Montanide ISA 720 (Seppic, France), SAF (Chiron, Calif., United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (e.g., SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Enhancyn $\text{\textcircled{R}}$) (Corixa, Hamilton, Mont.), RC-529 (Corixa, Hamilton, Mont.) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in pending U.S. patent application Ser. Nos. 08/853,826 and 09/074,720, the disclosures of which are incorporated herein by reference in their entireties, and polyoxyethylene ether adjuvants such as those described in WO 99/52549A1.

[0800] Other preferred adjuvants include adjuvant molecules of the general formula



wherein, n is 1-50, A is a bond or —C(O)—, R is C₁₋₅₀ alkyl or Phenyl C₁₋₅₀ alkyl.

[0801] One embodiment of the present invention consists of a vaccine formulation comprising a polyoxyethylene ether of general formula (I), wherein n is between 1 and 50, preferably 4-24, most preferably 9; the R component is C₁₋₅₀, preferably C₄₋₂₀ alkyl and most preferably C₁₂ alkyl, and A is a bond. The concentration of the polyoxyethylene ethers should be in the range 0.1-20%, preferably from 0.1-10%, and most preferably in the range 0.1-1%. Preferred polyoxyethylene ethers are selected from the following group: polyoxyethylene-9-lauryl ether, polyoxyethylene-9-stearyl ether, polyoxyethylene-8-stearyl ether, polyoxyethylene-4-lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether. Polyoxyethylene ethers such as polyoxyethylene lauryl ether are described in the Merck index (12th edition: entry 7717). These adjuvant molecules are described in WO 99/52549.

[0802] The polyoxyethylene ether according to the general formula (I) above may, if desired, be combined with another adjuvant. For example, a preferred adjuvant combination is preferably with CpG as described in the pending UK patent application GB 9820956.2.

[0803] According to another embodiment of this invention, an immunogenic composition described herein is delivered to a host via antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects per se and/or to be immunologically compatible with the receiver (i.e., matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

[0804] Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (see Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate in situ, with marked cytoplasmic processes (dendrites) visible in vitro), their ability to take up, process and present antigens with high efficiency and their ability to activate naive T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells in vivo or ex vivo, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel et al., *Nature Med.* 4:594-600, 1998).

[0805] Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated ex vivo by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells

harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

[0806] Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (e.g., CD54 and CD11) and costimulatory molecules (e.g., CD40, CD80, CD86 and 4-1BB).

[0807] APCs may generally be transfected with a polynucleotide of the invention (or portion or other variant thereof) such that the encoded polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place ex vivo, and a pharmaceutical composition comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs in vivo. In vivo and ex vivo transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (e.g., vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

[0808] 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 typically vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, mucosal, intravenous, intracranial, intraperitoneal, subcutaneous and intramuscular administration.

[0809] Carriers for use within such pharmaceutical compositions are biocompatible, and may also be biodegradable. In certain embodiments, the formulation preferably provides a relatively constant level of active component release. In other embodiments, however, a more rapid rate of release immediately upon administration may be desired. The formulation of such compositions is well within the level of ordinary skill in the art using known techniques. Illustrative

carriers useful in this regard include microparticles of poly-(lactide-co-glycolide), polyacrylate, latex, starch, cellulose, dextran and the like. Other illustrative delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (e.g., a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (see e.g., U.S. Pat. No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

[0810] In another illustrative embodiment, biodegradable microspheres (e.g., polylactate polyglycolate) are employed as carriers for the compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Pat. Nos. 4,897,268; 5,075,109; 5,928,647; 5,811,128; 5,820,883; 5,853,763; 5,814,344, 5,407,609 and 5,942,252. Modified hepatitis B core protein carrier systems, such as described in WO/99 40934, and references cited therein, will also be useful for many applications. Another illustrative carrier/delivery system employs a carrier comprising particulate-protein complexes, such as those described in U.S. Pat. No. 5,928,647, which are capable of inducing a class I-restricted cytotoxic T lymphocyte responses in a host.

[0811] The pharmaceutical compositions of the invention will often further comprise one or more buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide), solutes that render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate.

[0812] The pharmaceutical compositions described herein may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are typically sealed in such a way to preserve the sterility and stability of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

[0813] The development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including e.g., oral, parenteral, intravenous, intranasal, and intramuscular administration and formulation, is well known in the art, some of which are briefly discussed below for general purposes of illustration.

[0814] In certain applications, the pharmaceutical compositions disclosed herein may be delivered via oral administration to an animal. As such, these compositions may be formulated with an inert diluent or with an assimilable edible carrier, or they may be enclosed in hard- or soft-shell gelatin capsule, or they may be compressed into tablets, or they may be incorporated directly with the food of the diet.

[0815] The active compounds may even be incorporated with excipients and used in the form of ingestible tablets, buccal tables, troches, capsules, elixirs, suspensions, syrups, wafers, and the like (see, for example, Mathiowitz et al., *Nature* Mar. 27, 1997;386(6623):410-4; Hwang et al., *Crit Rev Ther Drug Carrier Syst* 1998;15(3):243-84; U.S. Pat. No. 5,641,515; U.S. Pat. No. 5,580,579 and U.S. Pat. No. 5,792,451). Tablets, troches, pills, capsules and the like may also contain any of a variety of additional components, for example, a binder, such as gum tragacanth, acacia, corn-starch, or gelatin; excipients, such as dicalcium phosphate; a disintegrating agent, such as corn starch, potato starch, alginic acid and the like; a lubricant, such as magnesium stearate; and a sweetening agent, such as sucrose, lactose or saccharin may be added or a flavoring agent, such as peppermint, oil of wintergreen, or cherry flavoring. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar, or both. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compounds may be incorporated into sustained-release preparation and formulations.

[0816] Typically, these formulations will contain at least about 0.1% of the active compound or more, although the percentage of the active ingredient(s) may, of course, be varied and may conveniently be between about 1 or 2% and about 60% or 70% or more of the weight or volume of the total formulation. Naturally, the amount of active compound(s) in each therapeutically useful composition may be prepared in such a way that a suitable dosage will be obtained in any given unit dose of the compound. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as such, a variety of dosages and treatment regimens may be desirable.

[0817] For oral administration the compositions of the present invention may alternatively be incorporated with one or more excipients in the form of a mouthwash, dentifrice, buccal tablet, oral spray, or sublingual orally-administered formulation. Alternatively, the active ingredient may be incorporated into an oral solution such as one containing sodium borate, glycerin and potassium bicarbonate, or dispersed in a dentifrice, or added in a therapeutically-effective amount to a composition that may include water, binders, abrasives, flavoring agents, foaming agents, and humectants. Alternatively the compositions may be fashioned into a tablet or solution form that may be placed under the tongue or otherwise dissolved in the mouth.

[0818] In certain circumstances it will be desirable to deliver the pharmaceutical compositions disclosed herein parenterally, intravenously, intramuscularly, or even intraperitoneally. Such approaches are well known to the skilled artisan, some of which are further described, for example, in U.S. Pat. No. 5,543,158; U.S. Pat. No. 5,641,515 and U.S. Pat. No. 5,399,363. In certain embodiments, solutions of the active compounds as free base or pharmacologically acceptable salts may be prepared in water suitably mixed with a

surfactant, such as hydroxypropylcellulose. Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations generally will contain a preservative to prevent the growth of microorganisms.

[0819] Illustrative pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (for example, see U.S. Pat. No. 5,466,468). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (e.g., glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and/or by the use of surfactants. The prevention of the action of microorganisms can be facilitated by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

[0820] In one embodiment, for parenteral administration in an aqueous solution, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, a sterile aqueous medium that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. Moreover, for human administration, preparations will of course preferably meet sterility, pyrogenicity, and the general safety and purity standards as required by FDA Office of Biologics standards.

[0821] In another embodiment of the invention, the compositions disclosed herein may be formulated in a neutral or salt form. Illustrative pharmaceutically-acceptable salts include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon for-

mulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective.

[0822] The carriers can further comprise any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions. The phrase "pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human.

[0823] In certain embodiments, the pharmaceutical compositions may be delivered by intranasal sprays, inhalation, and/or other aerosol delivery vehicles. Methods for delivering genes, nucleic acids, and peptide compositions directly to the lungs via nasal aerosol sprays has been described, e.g., in U.S. Pat. No. 5,756,353 and U.S. Pat. No. 5,804,212. Likewise, the delivery of drugs using intranasal microparticle resins (Takenaga et al., J Controlled Release Mar. 2, 1998;52(1-2):81-7) and lysophosphatidyl-glycerol compounds (U.S. Pat. No. 5,725,871) are also well-known in the pharmaceutical arts. Likewise, illustrative transmucosal drug delivery in the form of a polytetrafluoroethylene support-matrix is described in U.S. Pat. No. 5,780,045.

[0824] In certain embodiments, liposomes, nanocapsules, microparticles, lipid particles, vesicles, and the like, are used for the introduction of the compositions of the present invention into suitable host cells/organisms. In particular, the compositions of the present invention may be formulated for delivery either encapsulated in a lipid particle, a liposome, a vesicle, a nanosphere, or a nanoparticle or the like. Alternatively, compositions of the present invention can be bound, either covalently or non-covalently, to the surface of such carrier vehicles.

[0825] The formation and use of liposome and liposome-like preparations as potential drug carriers is generally known to those of skill in the art (see for example, Lasic, Trends Biotechnol 1998 July;16(7):307-21; Takakura, Nippon Rinsho 1998 March;56(3):691-5; Chandran et al., Indian J Exp Biol. 1997 August;35(8):801-9; Margalit, Crit Rev Ther Drug Carrier Syst. 1995;12(2-3):233-61; U.S. Pat. No. 5,567,434; U.S. Pat. No. 5,552,157; U.S. Pat. No. 5,565,213; U.S. Pat. No. 5,738,868 and U.S. Pat. No. 5,795,587, each specifically incorporated herein by reference in its entirety).

[0826] Liposomes have been used successfully with a number of cell types that are normally difficult to transfect by other procedures, including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Renneisen et al., J Biol Chem. Sep. 25, 1990;265(27):16337-42; Muller et al., DNA Cell Biol. 1990 April;9(3):221-9). In addition, liposomes are free of the DNA length constraints that are typical of viral-based delivery systems. Liposomes have been used effectively to introduce genes, various drugs, radiotherapeutic agents, enzymes, viruses, transcription factors, allosteric effectors and the like, into a variety of cultured cell lines and animals. Furthermore, the use of liposomes does not appear

to be associated with autoimmune responses or unacceptable toxicity after systemic delivery.

[0827] In certain embodiments, liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs)).

[0828] Alternatively, in other embodiments, the invention provides for pharmaceutically-acceptable nanocapsule formulations of the compositions of the present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (see, for example, Quintanar-Guerrero et al., *Drug Dev Ind Pharm.* 1998 December;24(12):1113-28). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 μm) may be designed using polymers able to be degraded in vivo. Such particles can be made as described, for example, by Couvreur et al., *Crit Rev Ther Drug Carrier Syst.* 1988;5(1):1-20; zur Muhlen et al., *Eur J Pharm Biopharm.* 1998 March;45(2):149-55; Zambaux et al. *J Controlled Release.* Jan. 2, 1998;50(1-3):31-40; and U.S. Pat. No. 5,145,684.

Cancer Therapeutic Methods

[0829] In further aspects of the present invention, the pharmaceutical compositions described herein may be used for the treatment of cancer, particularly for the immunotherapy of breast cancer. Within such methods, the pharmaceutical compositions described herein are administered to a patient, typically a warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs. As discussed above, administration of the pharmaceutical compositions may be by any suitable method, including administration by intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intradermal, anal, vaginal, topical and oral routes.

[0830] Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the in vivo stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides as provided herein).

[0831] Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adop-

tive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Pat. No. 4,918,164) for passive immunotherapy.

[0832] Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth in vitro, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition in vivo are well known in the art. Such in vitro culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast and/or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term in vivo. Studies have shown that cultured effector cells can be induced to grow in vivo and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (see, for example, Cheever et al., *Immunological Reviews* 157:177, 1997).

[0833] Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated ex vivo for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

[0834] Routes and frequency of administration of the therapeutic compositions described herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. 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. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (i.e., untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells in vitro. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (e.g., more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patient as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose

ranges from about 25 μg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

[0835] In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (e.g., more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

Cancer Detection and Diagnostic Compositions, Methods and Kits

[0836] In general, a cancer may be detected in a patient based on the presence of one or more breast tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, sputum urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as breast cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a breast tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

[0837] There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

[0838] In a preferred embodiment, the assay involves the use of binding agent 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 detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. 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 agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full

length breast tumor proteins and polypeptide portions thereof to which the binding agent binds, as described above.

[0839] The solid support may be any material known to those of ordinary skill in the art to which the tumor protein 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. Pat. 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 agent 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.

[0840] 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).

[0841] 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 detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

[0842] 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 20TM (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 a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with breast 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.

[0843] 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 those groups recited above.

[0844] The detection reagent 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 detection reagent is then removed and bound detection reagent 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.

[0845] To determine the presence or absence of a cancer, such as breast 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 for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the 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 a cancer.

[0846] In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent 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 binding agent 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. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. 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.

[0847] Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such tumor protein specific antibodies may correlate with the presence of a cancer.

[0848] A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated in vitro for 2-9 days (typically 4 days) at 37° C. with polypeptide (e.g., 5-25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of tumor polypeptide to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating

proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

[0849] As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (i.e., hybridizes to) a polynucleotide encoding the tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

[0850] To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a tumor protein of the invention that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence as disclosed herein. Techniques for both PCR based assays and hybridization assays are 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).

[0851] One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

[0852] In another embodiment, the compositions described herein may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or poly-

nucleotide(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, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

[0853] Certain in vivo diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

[0854] As noted above, to improve sensitivity, multiple tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

[0855] The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

[0856] Alternatively, a kit may be designed to detect the level of mRNA encoding a tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a tumor protein.

[0857] The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Isolation and Characterization of breast Tumor Polypeptides

[0858] This Example describes the isolation of breast tumor polypeptides from a breast tumor cDNA library.

[0859] A cDNA subtraction library containing cDNA from breast tumor subtracted with normal breast cDNA was constructed as follows. Total RNA was extracted from

primary tissues using Trizol reagent (Gibco BRL Life Technologies, Gaithersburg, Md.) as described by the manufacturer. The polyA+RNA was purified using an oligo(dT) cellulose column according to standard protocols. First strand cDNA was synthesized using the primer supplied in a Clontech PCR-Select cDNA Subtraction Kit (Clontech, Palo Alto, Calif.). The driver DNA consisted of cDNAs from two normal breast tissues with the tester cDNA being from three primary breast tumors. Double-stranded cDNA was synthesized for both tester and driver, and digested with a combination of endonucleases (MluI, MscI, PvuII, SalI and StuI) which recognize six base pairs DNA. This modification increased the average cDNA size dramatically compared with cDNAs generated according to the protocol of Clontech (Palo Alto, Calif.). The digested tester cDNAs were ligated to two different adaptors and the subtraction was performed according to Clontech's protocol. The subtracted cDNAs were subjected to two rounds of PCR amplification, following the manufacturer's protocol. The resulting PCR products were subcloned into the TA cloning vector, pCRII (Invitrogen, San Diego, Calif.) and transformed into ElectroMax *E. coli* DH10B cells (Gibco BRL Life, Technologies) by electroporation. DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division (Foster City, Calif.) Automated Sequencer Model 373A.

[0860] Sixty-three distinct cDNA clones were found in the subtracted breast tumor-specific cDNA library. The determined one strand (5' or 3') cDNA sequences for the clones are provided in SEQ ID NO:1-61, 72 and 73, respectively. Comparison of these cDNA sequences with known sequences in the gene bank using the EMBL and GenBank databases (Release 97) revealed no significant homologies to the sequences provided in SEQ ID NO:14, 21, 22, 27, 29, 30, 32, 38, 44, 45, 53, 57, 72 and 73. The sequences of SEQ ID NO: 1, 3, 16, 17, 34, 48, 60 and 61 were found to represent known human genes. The sequences of SEQ ID NO:2, 4, 23, 39 and 50 were found to show some similarity to previously identified non-human genes. The remaining clones (SEQ ID NO:5-13, 15, 18-20, 24-26, 28, 31, 33, 35-37, 40-43, 46, 47, 49, 51, 52, 54-56, 58 and 59) were found to show at least some degree of homology to previously identified expressed sequence tags (ESTs).

[0861] Further studies resulted in the isolation of the full-length cDNA sequence for the clone of SEQ ID NO:57 (referred to as B718P). By computer analysis, the full-length sequence was found to contain a putative transmembrane domain at amino acids 137-158. The full-length cDNA sequence of B718P is provided in SEQ ID NO:504, with the cDNA sequence of the open reading frame including stop codon being provided in SEQ ID NO:505 and the cDNA sequence of the open reading frame without stop codon being provided in SEQ ID NO:506. The full-length amino acid sequence of B718P is provided in SEQ ID NO:507. SEQ ID NO:508 represents amino acids 1-158 of B718P, and SEQ ID NO:509 represents amino acids 159-243 of B718P.

[0862] To determine mRNA expression levels of the isolated cDNA clones, cDNA clones from the breast subtraction described above were randomly picked and colony PCR amplified. Their mRNA expression levels in breast tumor, normal breast and various other normal tissues were determined using microarray technology (Synteni, Palo Alto,

Calif.). Briefly, the PCR amplification products were arrayed 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. Data was analyzed using Synteni provided GEMTOOLS Software. Of the seventeen cDNA clones examined, those of SEQ ID NO:40, 46, 59 and 73 were found to be over-expressed in breast tumor and expressed at low levels in all normal tissues tested (breast, PBMC, colon, fetal tissue, salivary gland, bone marrow, lung, pancreas, large intestine, spinal cord, adrenal gland, kidney, pancreas, liver, stomach, skeletal muscle, heart, small intestine, skin, brain and human mammary epithelial cells). The clones of SEQ ID NO:41 and 48 were found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested, with the exception of bone marrow. The clone of SEQ ID NO:42 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested except bone marrow and spinal cord. The clone of SEQ ID NO:43 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of spinal cord, heart and small intestine. The clone of SEQ ID NO:51 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of large intestine. The clone of SEQ ID NO:54 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of PBMC, stomach and small intestine. The clone of SEQ ID NO:56 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of large and small intestine, human mammary epithelia cells and SCID mouse-passaged breast tumor. The clone of SEQ ID NO:60 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of spinal cord and heart. The clone of SEQ ID NO:61 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of small intestine. The clone of SEQ ID NO:72 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of colon and salivary gland.

[0863] The results of a Northern blot analysis of the clone SYN18C6 (SEQ ID NO:40) are shown in **FIG. 1**. A predicted protein sequence encoded by SYN18C6 is provided in SEQ ID NO:62.

[0864] Additional cDNA clones that are over-expressed in breast tumor tissue were isolated from breast cDNA subtraction libraries as follows. Breast subtraction libraries were prepared, as described above, by PCR-based subtraction employing pools of breast tumor cDNA as the tester and pools of either normal breast cDNA or cDNA from other normal tissues as the driver. cDNA clones from breast subtraction were randomly picked and colony PCR amplified and their mRNA expression levels in breast tumor, normal breast and various other normal tissues were determined using the microarray technology described above. Twenty-four distinct cDNA clones were found to be over-expressed in breast tumor and expressed at low levels in all normal tissues tested (breast, brain, liver, pancreas, lung, salivary gland, stomach, colon, kidney, bone marrow, skeletal muscle, PBMC, heart, small intestine, adrenal gland,

spinal cord, large intestine and skin). The determined cDNA sequences for these clones are provided in SEQ ID NO:63-87. Comparison of the sequences of SEQ ID NO:74-87 with those in the gene bank as described above, revealed homology to previously identified human genes. No significant homologies were found to the sequences of SEQ ID NO:63-73.

[0865] Three DNA isoforms for the clone B726P (partial sequence provided in SEQ ID NO:71) were isolated as follows. A radioactive probe was synthesized from B726P by excising B726P DNA from a pT7Blue vector (Novagen) by a BamHI/XbaI restriction digest and using the resulting DNA as the template in a single-stranded PCR in the presence of [α -³²P]dCTP. The sequence of the primer employed for this PCR is provided in SEQ ID NO:177. The resulting radioactive probe was used to probe a directional cDNA library and a random-primed cDNA library made using RNA isolated from breast tumors. Eighty-five clones were identified, excised, purified and sequenced. Of these 85 clones, three were found to each contain a significant open reading frame. The determined cDNA sequence of the isoform B726P-20 is provided in SEQ ID NO:175, with the corresponding predicted amino acid sequence being provided in SEQ ID NO:176. The determined cDNA sequence of the isoform B726P-74 is provided in SEQ ID NO:178, with the corresponding predicted amino acid sequence being provided in SEQ ID NO:179. The determined cDNA sequence of the isoform B726P-79 is provided in SEQ ID NO:180, with the corresponding predicted amino acid sequence being provided in SEQ ID NO:181.

[0866] Efforts to obtain a full-length clone of B726P using standard techniques led to the isolation of five additional clones that represent additional 5' sequence of B726P. These clones appear to be alternative splice forms of the same gene. The determined cDNA sequences of these clones are provided in SEQ ID NO:464-468, with the predicted amino acid sequences encoded by SEQ ID NO: 464-467 being provided in SEQ ID NO:470-473, respectively. Using standard computer techniques, a 3,681 bp consensus DNA sequence (SEQ ID NO:463) was created that contains two large open reading frames. The downstream ORF encodes the amino acid sequence of SEQ ID NO:176. The predicted amino acid sequence encoded by the upstream ORF is provided in SEQ ID NO:469. Subsequent studies led to the isolation of an additional splice form of B726P that has 184 bp insert relative to the other forms. This 184 bp insert causes a frameshift that brings the down stream and upstream ORFs together into a single ORF that is 1002 aa in length. The determined cDNA sequence of this alternative splice form is disclosed in SEQ ID NO:474, with the corresponding amino acid sequence being provided in SEQ ID NO:475.

[0867] Comparison of the cDNA sequence of SEQ ID NO:63 (referred to as B723P) with the sequences in the GeneSeq™ DNA database showed matches to 5 DNA sequences (Accession nos. A26456, A37144, A26424, V84525 and T22133), 4 of which appear to represent the full-length sequence of the gene. Three of these sequences encode a 243 amino acid open reading frame (ORF), while one of the DNA sequences (Accession no. A37144) contains an extra C at position 35, resulting in a 278 amino acid ORF. The open reading frame, including stop codon, of the first variant of B723P (referred to as B723P-short) is provided in

SEQ ID NO:510, with the open reading frame without stop codon being provided in SEQ ID NO:511. The open reading frame, including stop codon, of the second variant of B723P (referred to as B723P-long) is provided in SEQ ID NO:512, with the open reading frame without stop codon being provided in SEQ ID NO:513. The amino acid sequences of B723P-short and B723P-long are provided in SEQ ID NO:514 and 515, respectively. Computer analysis of these sequences demonstrated the presence of putative transmembrane domains at amino acids 233-252 of the B723P-long ORF and amino acids 198-217 of the B723P-short ORF. SEQ ID NO:516, 518 and 519 represent amino acids 1-197, 198-243 and 218-243, respectively of B723P-short. SEQ ID NO:517 represents amino acids 1-232 of B723P-long.

[0868] Further isolation of individual clones that are over-expressed in breast tumor tissue was conducted using cDNA subtraction library techniques described above. In particular, a cDNA subtraction library containing cDNA from breast tumors subtracted with five other normal human tissue cDNAs (brain, liver, PBMC, pancreas and normal breast) was utilized in this screening. From the original subtraction, one hundred seventy seven clones were selected to be further characterized by DNA sequencing and microarray analysis. Microarray analysis demonstrated that the sequences in SEQ ID NO:182-251 and 479 were 2 or more fold over-expressed in human breast tumor tissues over normal human tissues. No significant homologies were found for nineteen of these clones, including, SEQ ID NO:185, 186, 194, 199, 205, 208, 211, 214-216, 219, 222, 226, 232, 236, 240, 241, 245, 246 and 479, with the exception of some previously identified expressed sequence tags (ESTs). The remaining clones share some homology to previously identified genes, specifically SEQ ID NO:181-184, 187-193, 195-198, 200-204, 206, 207, 209, 210, 212, 213, 217, 218, 220, 221, 223-225, 227-231, 233-235, 237-239, 242-244 and 247-251.

[0869] One of the cDNA clones isolated by PCR subtraction as described above (SEQ ID NO:476; referred to as B720P) which was shown by microarray to be over-expressed in breast tumor tissues, was found to be identical to a known keratin gene. The full-length cDNA sequence of the known keratin gene is provided in SEQ ID NO:477, with the corresponding amino acid sequence being provided in SEQ ID NO:478. Primers were generated based on the sequence of SEQ ID NO:477 and used to clone full-length cDNA from mRNA which was obtained from total RNA showing high expression of B720P in real-time PCR analysis. Products were then cloned and sequenced. The determined full-length cDNA sequence for B720P is provided in SEQ ID NO:484, with the corresponding amino acid sequence being provided in SEQ ID NO:485.

[0870] In further studies, a-truncated form of B720P (referred to as B720P-tr) was identified in breast carcinomas. This antigen was cloned from mRNA derived from total breast tumor RNA that showed high expression of B720P-tr in real-time PCR analysis. mRNA was used to generate a pool of cDNA which was then used as a template to amplify the cDNA corresponding to B720P-tr by PCR. The determined cDNA sequence for B720P-tr is provided in SEQ ID NO:486. B720P-tr has an ORF of 708 base pairs which encodes a 236 amino acid protein (SEQ ID NO:487). The size of the transcript was confirmed by northern analysis.

[0871] Of the seventy clones showing over-expression in breast tumor tissues, fifteen demonstrated particularly good expression levels in breast tumor over normal human tissues. The following eleven clones did not show any significant homology to any known genes. Clone 19463.1 (SEQ ID NO:185) was over-expressed in the majority of breast tumors and also in the SCID breast tumors tested (refer to Example 2); additionally, over-expression was found in a majority of normal breast tissues. Clone 19483.1 (SEQ ID NO:216) was over-expressed in a few breast tumors, with no over-expression in any normal tissues tested. Clone 19470.1 (SEQ ID NO:219) was found to be slightly over-expressed in some breast tumors. Clone 19468.1 (SEQ ID NO:222) was found to be slightly over-expressed in the majority of breast tumors tested. Clone 19505.1 (SEQ ID NO:226) was found to be slightly over-expressed in 50% of breast tumors, as well as in SCID tumor tissues, with some degree of over-expression in found in normal breast. Clone 1509.1 (SEQ ID NO:232) was found to be over-expressed in very few breast tumors, but with a certain degree of over-expression in metastatic breast tumor tissues, as well as no significant over-expression found in normal tissues. Clone 19513.1 (SEQ ID NO:236) was shown to be slightly over-expressed in few breast tumors, with no significant over-expression levels found in normal tissues. Clone 19575.1 (SEQ ID NO:240) showed low level over-expression in some breast tumors and also in normal breast. Clone 19560.1 (SEQ ID NO:241) was over-expressed in 50% of breast tumors tested, as well as in some normal breast tissues. Clone 19583.1 (SEQ ID NO:245) was slightly over-expressed in some breast tumors, with very low levels of over-expression found in normal tissues. Clone 19587.1 (SEQ ID NO:246) showed low level over-expression in some breast tumors and no significant over-expression in normal tissues.

[0872] Clone 19520.1 (SEQ ID NO:233), showing homology to clone 102D24 on chromosome 11q13.31, was found to be over-expressed in breast tumors and in SCID tumors. Clone 19517.1 (SEQ ID NO:237), showing homology to human PAC 128M19 clone, was found to be slightly over-expressed in the majority of breast tumors tested. Clone 19392.2 (SEQ ID NO:247), showing homology to human chromosome 17, was shown to be over-expressed in 50% of breast tumors tested. Clone 19399.2 (SEQ ID NO:250), showing homology to human Xp22 BAC GSHB-184P14, was shown to be slightly over-expressed in a limited number of breast tumors tested.

[0873] In subsequent studies, 64 individual clones were isolated from a subtracted cDNA library containing cDNA from a pool of breast tumors subtracted with cDNA from five normal tissues (brain, liver, PBMC, pancreas and normal breast). The subtracted cDNA library was prepared as described above with the following modification. A combination of five six-base cutters (MluI, MscI, PvuII, Sall and StuI) was used to digest the cDNA instead of RsaI. This resulted in an increase in the average insert size from 300 bp to 600 bp. The 64 isolated clones were colony PCR amplified and their mRNA expression levels in breast tumor tissue, normal breast and various other normal tissues were examined by microarray technology as described above. The determined cDNA sequences of 11 clones which were found to be over-expressed in breast tumor tissue are provided in SEQ ID NO:405-415. Comparison of these sequences to those in the public database, as outlined above, revealed

homologies between the sequences of SEQ ID NO:408, 411, 413 and 414 and previously isolated ESTs. The sequences of SEQ ID NO:405-407, 409, 410, 412 and 415 were found to show some homology to previously identified sequences.

[0874] In further studies, a subtracted cDNA library was prepared from cDNA from metastatic breast tumors subtracted with a pool of cDNA from five normal tissues (breast, brain, lung, pancreas and PBMC) using the PCR-subtraction protocol of Clontech, described above. The determined cDNA sequences of 90 clones isolated from this library are provided in SEQ ID NO:316-404. Comparison of these sequences with those in the public database, as described above, revealed no significant homologies to the sequence of SEQ ID NO:366. The sequences of SEQ ID NO:321-325, 343, 354, 368, 369, 377, 382, 385, 389, 395, 397 and 400 were found to show some homology to previously isolated ESTs. The remaining sequences were found to show homology to previously identified gene sequences.

[0875] In yet further studies, a subtracted cDNA library (referred to as 2BT) was prepared from cDNA from breast tumors subtracted with a pool of cDNA from six normal tissues (liver, brain, stomach, small intestine, kidney and heart) using the PCR-subtraction protocol of Clontech, described above. cDNA clones isolated from this subtraction were subjected to DNA microarray analysis as described above and the resulting data subjected to four modified Gemtools analyses. The first analysis compared 28 breast tumors with 28 non-breast normal tissues. A mean over-expression of at least 2.1 fold was used as a selection cut-off. The second analysis compared 6 metastatic breast tumors with 29 non-breast normal tissues. A mean over-expression of at least 2.5 fold was used as a cut-off. The third and fourth analyses compared 2 early SCID mouse-passaged with 2 late SCID mouse-passaged tumors. A mean over-expression in the early or late passaged tumors of 2.0-fold or greater was used as a cut-off. In addition, a visual analysis was performed on the microarray data for the 2BT clones. The determined cDNA sequences of 13 clones identified in the visual analysis are provided in SEQ ID NO:427-439. The determined cDNA sequences of 22 clones identified using the modified Gemtools analysis are provided in SEQ ID NO:440-462, wherein SEQ ID NO:453 and 454 represent two partial, non-overlapping, sequences of the same clone.

[0876] Comparison of the clone sequences of SEQ ID NO:436 and 437 (referred to as 263G6 and 262B2) with those in the public databases, as described above, revealed no significant homologies to previously identified sequences. The sequences of SEQ ID NO:427, 429, 431, 435, 438, 441, 443, 444, 445, 446, 450, 453 and 454 (referred to as 266B4, 266G3, 264B4, 263G1, 262B6, 2BT2-34, 2BT1-77, 2BT1-62, 2BT1-60, 61, 2BT1-59, 2BT1-52 and 2BT1-40, respectively) showed some homology to previously isolated expressed sequences tags (ESTs). The sequences of SEQ ID NO:428, 430, 432, 433, 434, 439, 440, 442, 447, 448, 449, 451, 452 and 455-462 (referred to as clones 22892, 22890, 22883, 22882, 22880, 22869, 21374, 21349, 21093, 21091, 21089, 21085, 21084, 21063, 21062, 21060, 21053, 21050, 21036, 21037 and 21048, respectively), showed some homology to gene sequences previously identified in humans.

EXAMPLE 2

Isolation and Characterization of Breast Tumor Polypeptides Obtained by PCR-Based Subtraction Using SCID-Passaged Tumor RNA

[0877] Human breast tumor antigens were obtained by PCR-based subtraction using SCID mouse passaged breast tumor RNA as follows. Human breast tumor was implanted in SCID mice and harvested on the first or sixth serial passage, as described in patent application Ser. No. 08/556,659 filed Nov. 13, 1995, U.S. Pat. No. 5,986,170. Genes found to be differentially expressed between early and late passage SCID tumor may be stage specific and therefore useful in therapeutic and diagnostic applications. Total RNA was prepared from snap frozen SCID passaged human breast tumor from both the first and sixth passage.

[0878] PCR-based subtraction was performed essentially as described above. In the first subtraction (referred to as T9), RNA from first passage tumor was subtracted from sixth passage tumor RNA to identify more aggressive, later passage-specific antigens. Of the 64 clones isolated and sequenced from this subtraction, no significant homologies were found to 30 of these clones, hereinafter referred to as: 13053, 13057, 13059, 13065, 13067, 13068, 13071-13073, 13075, 13078, 13079, 13081, 13082, 13092, 13097, 13101, 13102, 13131, 13133, 13119, 13135, 13139, 13140, 13146-13149, and 13151, with the exception of some previously identified expressed sequence tags (ESTs). The determined cDNA sequences for these clones are provided in SEQ ID NO:88-116, respectively. The isolated cDNA sequences of SEQ ID NO:117-140 showed homology to known genes.

[0879] In a second PCR-based subtraction, RNA from sixth passage tumor was subtracted from first passage tumor RNA to identify antigens down-regulated over multiple passages. Of the 36 clones isolated and sequenced, no significant homologies were found to nineteen of these clones, hereinafter referred to as: 14376, 14377, 14383, 14384, 14387, 14392, 14394, 14398, 14401, 14402, 14405, 14409, 14412, 14414-14416, 14419, 14426, and 14427, with the exception of some previously identified expressed sequence tags (ESTs). The determined cDNA sequences for these clones are provided in SEQ ID NO:141-159, respectively. The isolated cDNA sequences of SEQ ID NO:160-174 were found to show homology to previously known genes.

[0880] Further analysis of human breast tumor antigens through PCR-based subtraction using first and sixth passage SCID tumor RNA was performed. Sixty three clones were found to be differentially expressed by a two or more fold margin, as determined by microarray analysis, i.e., higher expression in early passage tumor over late passage tumor, or vice versa. Seventeen of these clones showed no significant homology to any known genes, although some degree of homology with previously identified expressed sequence tags (ESTs) was found, hereinafter referred to as 20266, 20270, 20274, 20276, 20277, 20280, 20281, 20294, 20303, 20310, 20336, 20341, 20941, 20954, 20961, 20965 and 20975 (SEQ ID NO:252-268, respectively). The remaining clones were found to share some degree of homology to known genes, which are identified in the Brief Description of the Drawings and Sequence Identifiers section above, hereinafter referred to as 20261, 20262, 20265, 20267,

20268, 20271, 20272, 20273, 20278, 20279, 20293, 20300, 20305, 20306, 20307, 20313, 20317, 20318, 20320, 20321, 20322, 20326, 20333, 20335, 20337, 20338, 20340, 20938, 20939, 20940, 20942, 20943, 20944, 20946, 20947, 20948, 20949, 20950, 20951, 20952, 20957, 20959, 20966, 20976, 20977 and 20978. The determined cDNA sequences for these clones are provided in SEQ ID NO:269-314, respectively.

[0881] The clones 20310, 20281, 20262, 20280, 20303, 20336, 20270, 20341, 20326 and 20977 (also referred to as B820P, B821P, B822P, B823P, B824P, B825P, B826P, B827P, B828P and B829P, respectively) were selected for further analysis based on the results obtained with microarray analysis. Specifically, microarray data analysis indicated at least two- to three-fold overexpression of these clones in breast tumor RNA compared to normal tissues tested. Subsequent studies led to the determination of the complete insert sequence for the clones B820P, B821P, B822P, B823P, B824P, B825P, B826P, B827P, B828P and B829P. These extended cDNA sequences are provided in SEQ ID NO:416-426, respectively.

EXAMPLE 3

Synthesis of Polypeptides

[0882] Polypeptides may be synthesized on an Perkin Elmer/Applied Biosystems Division 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

EXAMPLE 4

elicitation of Breast Antigen-Specific CTL Responses in Human Blood

[0883] This Example illustrates the ability of the breast-specific antigen B726P to elicit a cytotoxic T lymphocyte (CTL) response in peripheral blood lymphocytes from normal humans.

[0884] Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of a normal donor by growth for five days in RPMI medium containing 10% human serum, 30 ng/ml GM-CSF and 30 ng/ml IL-4. Following five days of culture, DC were infected overnight with adenovirus expressing recombinant B726P (downstream ORF; SEQ ID NO:176) at an M.O.I. of 2.5 and matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. CD8 positive cells were enriched for by the

depletion of CD4 and CD14-positive cells. Priming cultures were initiated in individual wells of several 96-well plates with the cytokines IL-6 and IL-12. These cultures were restimulated in the presence of IL-2 using autologous fibroblasts treated with IFN-gamma and transduced with B726P and CD80. Following three stimulation cycles, the presence of B726P-specific CTL activity was assessed in IFN-gamma Elispot assays (Lavani et al., *J. Exp. Med.* 186:859-865, 1997) using IFN-gamma treated autologous fibroblasts transduced to express either B726P or an irrelevant, control, antigen as antigen presenting cells (APC). Of approximately 96 lines, one line (referred to as 6-2B) was identified that appeared to specifically recognize B726P-transduced APC but not control antigen-transduced APC. This microculture was cloned using standard protocols. B726P-specific CTL were identified by Elispot analysis and expanded for further analysis. These CTL clones were demonstrated to recognize B726P-expressing fibroblasts, but not the control antigen MART-1, using chromium-51 release assays. Furthermore, using a panel of allogeneic fibroblasts transduced with B726P in antibody blocking assays, the HLA restriction element for these B726P-specific CTL was identified as HLA-B*1501.

[0885] In order to define more accurately the location of the epitope recognized by the B726P-specific CTL clones, a deletion construct comprising only the N-terminal half (a.a. 1-129) of B726P (referred to as B726Pdelta3') was constructed in the pBIB retroviral expression plasmid. This plasmid, as well as other plasmids containing B726P, were transfected into COS-7 cells either alone or in combination with a plasmid expressing HLA-B*1501. Approximately 48 hours after transfection, a B726P-specific CTL clone (1-9B) was added at approximately 10^4 cells per well. The cells were harvested the next day and the amount of IFN-gamma released was measured by ELISA. The CTL responded above background (EGFP) to COS-7 cells that had been transfected with both B726P and HLA-B*1501. There was no response above background to COS-7 cells that had been transfected with either B726P or HLA-B*1501 alone. Importantly, a higher response was seen with COS-7 cells that had been transfected with both HLA-B*1501 and B726Pdelta3'. This result indicated that the epitope was likely to be located in the N-terminal region (a.a. 1-129) of B726P. This region was examined and amino acid sequences that corresponded to the HLA-B*1501 peptide binding motif (*J. Immunol.* 1999, 162:7277-84) were identified and synthesized. These peptides were pulsed at 10 ug/ml onto autologous B-LCL overnight. The next day, the cells were washed and the ability of the cells to stimulate the B726P-specific CTL clone 1-9B was assayed in a IFN-gamma ELISPOT assay. Of the eleven peptides tested, only one peptide, having the amino acid sequence SLTKRASQY (a.a. 76-84 of B726P; SEQ ID NO: 488) was recognized by the CTL clone. This result identifies this peptide as being a naturally-processed epitope recognized by this B726P-specific CTL clone.

[0886] In further studies, a panel of breast tumor cell lines obtained from the American Type Culture Collection (Manassas, Va.), was analyzed using real time PCR to determine their B726P message level. The cell line that expressed the highest level of B726P (referred to as HTB21) and a line that expressed no B726P (referred to as HTB132) were transduced with HLA-B*1501. These cell lines were grown up and analyzed using FACS to determine their

B1501 expression. The line HTB 21 was found to endogenously express B1501. To determine if clone 1-9A would recognize the tumor cell line HTB2 1, an IFN-gamma ELISPOT assay was performed using 20,000 T cells, low dose IL-2 (5 ug/ml), and 20,000 of the following targets: autologous B726P or Mart-1 fibroblasts, untransduced or B1501-transduced HTB21; or untransduced or B1501-transduced HTB132. These were incubated overnight and the assay was developed the next day. The results of this assay are shown in **FIG. 2**. These studies demonstrate that B726P-specific CTL can recognize and lyse breast tumor cells expressing B726P.

EXAMPLE 5

Identification of Immunogenic CD4 T Cell Epitopes in Breast Antigens

[0887] Immunogenic CD4 T cell epitopes derived from the breast antigen B726P were identified as follows.

[0888] A total of thirty-five 20-mer peptides overlapping by 12 amino acids and derived from the downstream ORF of B726P (corresponding to amino acids 1-317 of SEQ ID NO:176) were generated by standard procedure. Dendritic cells (DC) were derived from PBMC of a normal male donor using GM-CSF and IL-4 by standard protocol. Purified CD4 T cells were generated from the same donor as the DC using MACS beads and negative selection of PBMCs. DC were pulsed overnight with pools of the 20-mer peptides, with each peptide at an individual concentration of 0.5 micrograms/mL. Pulsed DC were washed and plated at 10,000 cells/well of 96-well U bottom plates, and purified CD4 T cells were added at 100,000 cells/well. Cultures were supplemented with 10 ng/mL IL-6 and 5 ng/mL IL-12 and incubated at 37° C. Cultures were restimulated as above on a weekly basis using DC made and pulsed as above as the antigen presenting cell, supplemented with 10 u/mL IL-2 and 5 ng/mL IL-7. Following three in vitro stimulation cycles (the initial priming+two restimulations), cell lines (each corresponding to one well) were tested for specific proliferation and cytokine production in response to the stimulating pool versus an irrelevant pool of peptides derived from unrelated antigens. A number of individual CD4 T cell lines (36/672 by IFN-gamma and 64/672 by proliferation) demonstrated significant cytokine release (IFN-gamma) and proliferation in response to the B726P peptide pools but not to the control peptide pool. Twenty-five of these T cell lines were restimulated on the appropriate pool of B726P peptides and reassayed on autologous DC pulsed with either the individual peptides or recombinant B726P protein made in *E. coli*. Approximately 14 immunogenic peptides were recognized by the T cells from the entire set of peptide antigens tested. The amino acid sequences of these 14 peptides are provided in SEQ ID NO:534-547, with the corresponding DNA sequences being provided in SEQ ID NO:520-533, respectively. In some cases the peptide reactivity of the T cell line could be mapped to a single peptide but some could be mapped to more than one peptide in each pool. Thirteen of the fifteen T cell lines recognized the recombinant B726P protein. These results demonstrate that 13 of the 14 peptide sequences (SEQ ID NO:534-542 and 544-547) may be naturally processed CD4 epitopes of the B726P protein.

EXAMPLE 6

Preparation and Characterization of Antibodies
Against Breast Tumor Antigen B726P

[0889] Polyclonal antibodies against both the downstream (SEQ ID NO:176) and upstream (SEQ ID NO:469) ORF of the breast tumor antigen B726P were prepared as follows.

[0890] The downstream or upstream ORF of B726P expressed in an *E. coli* recombinant expression system was grown overnight in LB broth with the appropriate antibiotics at 37° C. in a shaking incubator. The next morning, 10 ml of the overnight culture was added to 500 ml to 2× YT plus appropriate antibiotics in a 2L-baffled Erlenmeyer flask. When the Optical Density (at 560 nm) of the culture reached 0.4-0.6, the cells were induced with IPTG (1 mM). Four hours after induction with IPTG, the cells were harvested by centrifugation. The cells were then washed with phosphate buffered saline and centrifuged again. The supernatant was discarded and the cells were either frozen for future use or immediately processed. Twenty ml of lysis buffer was added to the cell pellets and vortexed. To break open the *E. coli* cells, this mixture was then run through the French Press at a pressure of 16,000 psi. The cells were then centrifuged again and the supernatant and pellet were checked by SDS-PAGE for the partitioning of the recombinant protein. For proteins that localized to the cell pellet, the pellet was resuspended in 10 mM Tris pH 8.0, 1% CHAPS and the inclusion body pellet was washed and centrifuged again. This procedure was repeated twice more. The washed inclusion body pellet was solubilized with either 8 M urea or 6 M guanidine HCl containing 10 mM Tris pH 8.0 plus 10 mM imidazole. The solubilized protein was added to 5 ml of nickel-chelate resin (Qiagen) and incubated for 45 min to 1 hour at room temperature with continuous agitation. After incubation, the resin and protein mixture were poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer. The antigen was then eluted from the column using 8M urea, 10 mM Tris pH 8.0 and 300 mM imidazole and collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification.

[0891] As a final purification step, a strong anion exchange resin, such as HiPrepQ (Biorad), was equilibrated with the appropriate buffer and the pooled fractions from above were loaded onto the column. Antigen was eluted off the column with a increasing salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool. The pooled fractions were dialyzed against 10 mM Tris pH 8.0. The protein was then vialled after filtration through a 0.22 micron filter and the antigens were frozen until needed for immunization.

[0892] Four hundred micrograms of the B726P antigen was combined with 100 micrograms of muramyl dipeptide (MDP). Every four weeks rabbits were boosted with 100 micrograms mixed with an equal volume of Incomplete Freund's Adjuvant (IFA). Seven days following each boost, the animal was bled. Sera was generated by incubating the blood at 4° C. for 12-24 hours followed by centrifugation.

[0893] Ninety-six well plates were coated with B726P antigen by incubating with 50 microliters (typically 1 micro-

gram) of recombinant protein at 4° C. for 20 hours. 250 Microliters of BSA blocking buffer was added to the wells and incubated at room temperature for 2 hours. Plates were washed 6 times with PBS/0.01% Tween. Rabbit sera was diluted in PBS. Fifty microliters of diluted sera was added to each well and incubated at room temperature for 30 min. Plates were washed as described above before 50 microliters of goat anti-rabbit horse radish peroxidase (HRP) at a 1:10000 dilution was added and incubated at room temperature for 30 min. Plates were again washed as described above and 100 microliters of TMB microwell peroxidase substrate was added to each well. Following a 15 min incubation in the dark at room temperature, the colorimetric reaction was stopped with 100 microliters of 1N H₂SO₄ and read immediately at 450 nm. All the polyclonal antibodies showed immunoreactivity to the appropriate B726P antigen.

B) Preparation of Polyclonal Antibodies Against B709P and B720P

[0894] The breast antigens B709P (SEQ ID NO: 62) and B720P (SEQ ID NO: 485) expressed in an *E. coli* recombinant expression system were grown overnight in LB Broth with the appropriate antibiotics at 37° C. in a shaking incubator. Ten ml of the overnight culture was added to 500 ml of 2×YT plus appropriate antibiotics in a 2L-baffled Erlenmeyer flask. When the optical density (at 560 nanometers) of the culture reached 0.4-0.6, the cells were induced with IPTG (1 mM). Four hours after induction with IPTG, the cells were harvested by centrifugation. The cells were washed with phosphate buffered saline and centrifuged again. The supernatant was discarded and the cells were either frozen for future use or immediately processed. Twenty milliliters of lysis buffer was added to the cell pellets and vortexed. To break open the *E. coli* cells, the mixture was run through a French Press at a pressure of 16,000 psi. The cells were centrifuged again and the supernatant and pellet were checked by SDS-PAGE for the partitioning of the recombinant protein. For proteins that localized to the cell pellet, the pellet was resuspended in 10 mM Tris pH 8.0, 1% CHAPS and the inclusion body pellet was washed and centrifuged again. This procedure was repeated twice more. The washed inclusion body pellet was solubilized with either 8 M urea or 6 M guanidine HCl containing 10 mM Tris pH 8.0 plus 10 mM imidazole. The solubilized protein was added to 5 ml of nickel-chelate resin (Qiagen) and incubated for 45 min to 1 hour at room temperature (RT) with continuous agitation. After incubation, the resin and protein mixture were poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer. The antigen was then eluted from the column using 8M urea, 10 mM Tris pH 8.0 and 300 mM imidazole and collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification. As a final purification step, a strong anion exchange resin such as Hi-Prep Q (Biorad) was equilibrated with the appropriate buffer and the pooled fractions from above were loaded onto the column. Each antigen was eluted off of the column with an increasing salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool. The pooled fractions were dialyzed against 10 mM Tris pH 8.0. The proteins were then vialled after filtration through a 0.22-micron filter and frozen until needed for immunization.

[0895] Four hundred micrograms of antigen was combined with 100 micrograms of muramyl dipeptide (MDP). An equal volume of Incomplete Freund's Adjuvant (IFA) was added and mixed, and the mixture was injected into a rabbit. The rabbit was boosted with 100 micrograms of antigen mixed with an equal volume of IFA every four weeks. The animal was bled seven days following each boost. Sera was generated by incubating the blood at 4° C. for 12-24 hours followed by centrifugation.

[0896] The reactivity of the polyclonal antibodies to recombinant antigen (B709P or B720P) was determined by ELISA as follows. Ninety-six well plates were coated with antigen by incubating with 50 microliters (typically 1 microgram) at 4° C. for 20 hrs. 250 microliters of BSA blocking buffer was added to the wells and incubated at RT for 2 hrs. Plates were washed 6 times with PBS/0.01% Tween. Rabbit sera were diluted in PBS. Fifty microliters of diluted sera was added to each well and incubated at RT for 30 min. Plates were washed as described above before 50 microliters of goat anti-rabbit horse radish peroxidase (HRP) at a 1:10000 dilution was added and incubated at RT for 30 min. Plates were washed as described above and 100 microliters of TMB Microwell Peroxidase Substrate was added to each well. Following a 15-minute incubation in the dark at RT, the colorimetric reaction was stopped with 100 microliters of 1N H₂SO₄ and read immediately at 450 nm. The polyclonal antibodies showed immunoreactivity to the appropriate antigen.

EXAMPLE 7

Protein Expression of Breast Tumor Antigens

[0897] The downstream ORF of B726P (SEQ ID NO:176), together with a C-terminal 6×His Tag, was expressed in insect cells using the baculovirus expression system as follows.

[0898] The cDNA for the full-length downstream ORF of B726P was PCR amplified using the primers of SEQ ID NO:480 and 481. The PCR product with the expected size was recovered from agarose gel, restriction digested with EcoRI and Hind II, and ligated into the transfer plasmid pFastBac1, which was digested with the same restriction enzymes. The sequence of the insert was confirmed by DNA sequencing. The recombinant transfer plasmid pFBB726P was used to make recombinant bacmid DNA and virus using the Bac-To-Bac Baculovirus expression system (BRL Life Technologies, Gaithersburg, Md.). High Five cells were infected with the recombinant virus BVB726P to produce protein. The cDNA and amino acid sequences of the expressed B726P recombinant protein are provided in SEQ ID NO:482 and 483, respectively.

EXAMPLE 8

Generation of Constructs for Protein Expression of B726P in *E. Coli*

[0899] Three different open reading frames (ORFs) of B726P were subcloned into pPDM, a modified pET28 vector for expression in *E. coli*.

[0900] Construct for the expression of B726P Upstream ORF in *E. coli* (cDNA: SEQ ID NO:549; amino acid: SEQ ID NO:552):

[0901] The partial B726P upstream ORF (A) from clone 23113 was PCR amplified with the following primers:

PDM-416 (SEQ ID NO:554)
5' gtcggctccatgagtcgccgcaaaag 3' Tm 63° C.

PDM-431 (SEQ ID NO:555)
5' cgagaattcaataacttaagaagaccatctttaccag 3'
Tm 61° C.

[0902] The amplification conditions were as follows 10 µl 10×Pfu buffer, 1 µl 10 µM dNTPs, 2 µl 10 µM each oligo, 83 µl sterile water, 1.5 µl Pfu DNA polymerase (Stratagene, La Jolla, Calif.), 1 µl PCR 23113. The reaction was first denatured for 2 minutes at 96° C., followed by 40 cycles of 96° C for 20 seconds, 62° C. for 15 seconds, and extension at 72° C. for 2 minutes. This was followed by a final extension of 72° C. for 4 minutes.

[0903] The second partial B726P upstream ORF (B) from clone 19310 was PCR amplified with the following primers:

PDM-432 (SEQ ID NO:556)
5' cataagcttaaggctaactgcggaatgaaag 3' Tm 63° C.

PDM-427 (SEQ ID NO:557)
5' cccgcagaattcaacatgcaattttcatgtaagag 3'
Tm 62° C.

[0904] The amplification and cycling conditions were as described above. The first PCR product was digested with EcoRI and cloned into pPDM His (a modified pET28 vector) that had been digested with EcoRI and Eco721. The second PCR product was digested with BfrI and EcoRI and cloned into the resulting construct: pPDM B726P UP-A-5 at the EcoRI and BfrI sites. The construct (pPDM B726P Up-4) was confirmed to be correct through sequence analysis and transformed into BL21 (DE3) pLys S and BL21 CodonPlus RIL (DE3) cells. Protein expression was confirmed by Coomassie stained SDS-PAGE and N-terminal protein sequence analysis.

[0905] Construct for B726P D-ORF expression in *E. coli* (cDNA: SEQ ID NO:550; amino acid: SEQ ID NO:551):

[0906] The B726P D-ORF was PCR amplified with the following primers:

PDM-290 (SEQ ID NO:558)
5' ctaaatgccggcacaagagctctgc 3' Tm 61° C.

PDM-291 (SEQ ID NO:559)
5' cgccgcagaattctattatataacttctgtttctgc 3'
Tm 61° C.

[0907] The reaction conditions were as described. The cycling conditions were altered slightly in that the annealing temperature was lowered to 61° C. from 62° C. and was held for 15 seconds. The extension time was also increased to 2 minutes and 15 seconds. The PCR product was digested with NaeI and EcoRI and cloned into pPDM His which has been

digested with Eco72I and EcoRI. Construct was confirmed by sequencing and then transformed into BL21 (DE3) pLys S cells (Novagen, Madison, Wis.). Protein expression was confirmed by Coomassie stained SDS-PAGE and N-terminal protein sequence analysis.

[0908] Construct for B726P Combined ORF expression in *E. coli* (cDNA: SEQ ID NO:548; amino acid: SEQ ID NO:553);

[0909] The B726P C-1 coding region was PCR amplified including the 183 bp insert, with the following primers:

PDM-750
(SEQ ID NO:560)
5' ggggaattgtgagcggataacaattc 3' Tm 58° C.

PDM-752
(SEQ ID NO:561)
5' cgtagaattcaacctgatttaataattactttctacac 3'
Tm 59° C.

[0910] The B726P Downstream ORF was PCR amplified with the following primers:

PDM-753
(SEQ ID NO:562)
5' gaaagtaatttaaatcaggtttctcacactc 3' Tm 59° C.

PDM-751
(SEQ ID NO:563)
5' gagggcccaagggttatgctag 3' Tm 61° C.

[0911] The reaction conditions for these PCR reactions were the same as described above. The cycling conditions were as follows: 1st PCR: The reaction was first denatured for 2 minutes at 96° C., followed by 40 cycles of 96° C. for 20 seconds, 58° C. for 15 seconds, and extension at 72° C. for 4 minutes. This was followed by a final extension of 72° C. for 4 minutes; 2nd PCR: The reaction was first denatured for 2 minutes at 96° C., followed by 40 cycles of 96° C. for 20 seconds, 59° C. for 15 seconds, and extension at 72° C. for 2 minutes. This was followed by a final extension of 72° C. for 4 minutes. The first PCR product was digested with EcoRI and cloned into pPDM His (a modified pET28 vector) at the Eco 72I and EcoRI sites. The construct was confirmed to be correct through sequence analysis. The second PCR product was digested with EcoRI and cloned into pPDM His at the same sites. The resulting constructs pPDM B726P UA-8 and pPDM B726P DA-7 respectively were digested with SwaI and EcoRI. The pPDM B726P UA-8 construct was used as vector and the insert from the pPDM B726P DA-7 was cloned into this construct successfully. The construct was confirmed to be correct through sequence analysis and then transformed into BLR (DE3) pLys S and HMS 174 (DE3) pLys S cells (Novagen, Madison, Wis.). Protein expression was confirmed by Coomassie stained SDS-PAGE and N-terminal protein sequence analysis.

EXAMPLE 9

Additional Sequence Identified for Breast Tumor
Antigen B726P by Bioinformatic Analysis

[0912] The combined ORF of the breast tumor antigen, B726P (amino acid sequence set forth in SEQ ID NO:475), was used to search public databases. A sequence essentially

identical to the combined ORF with additional N-terminal sequence was identified in the GenBank nonredundant protein database and the cDNA and predicted amino acid sequences are set forth in SEQ ID NO:564 and 565, respectively. The gene is also referred to as NY-BR-1 and was described in Cancer Research 61(5):2055-2061, Mar. 1, 2001.

EXAMPLE 10

Analysis of B726P Expression Using
Immunohistochemistry

[0913] Affinity purified polyclonal antibodies anti-B726Pup (generated against the B726P upstream ORF protein) and anti-B726Pdown (generated against the B726P downstream ORF) were used to assess B726P protein expression in breast cancer and in a variety of normal tissue sections.

[0914] In order to determine which tissues express the breast cancer antigen protein B726P immunohistochemistry (IHC) analysis was performed on a diverse range of tissue sections. Tissue samples were fixed in formalin solution for 12-24 hrs and embedded in paraffin before being sliced into 8 micron sections. Steam heat induced epitope retrieval (SHIER) in 0.1 M sodium citrate buffer (pH 6.0) was used for optimal staining conditions. Sections were incubated with 10% serum/PBS for 5 minutes. Primary antibody (either rabbit affinity purified anti-B726Pdown or anti-B726Pup) was added to each section for 25 minutes followed by 25 minute incubation with anti-rabbit biotinylated antibody. Endogenous peroxidase activity was blocked by three 1.5 minute incubations with hydrogen peroxidase. The avidin biotin complex/horse radish peroxidase (ABC/HRP) system was used along with DAB chromogen to visualize antigen expression. Slides were counterstained with hematoxylin to visualize cell nuclei. Anti-B726Pup and anti-B726Pdown immunoreactivity was observed in about 30-40% of breast cancer samples analyzed but not observed in a majority of various normal tissues. Anti-B726Pdown and anti-b726Pup also stained roughly the same breast cancer samples. Thus, these data confirm earlier microarray analysis (see Example 1) showing that B726P is overexpressed in breast tumor tissue as compared to normal tissue. Therefore, this antigen may be used in diagnostic and immunotherapeutic applications for breast cancer.

EXAMPLE 11

Generation of Monoclonal Antibodies to B726P
Downstream and Upstream ORFs

[0915] Production and purification of protein used for antibody generation. B726 upstream ORF and B726 downstream ORF proteins were expressed in an *E. coli* recombinant expression system (see Example 8). Cells were grown overnight in LB Broth with the appropriate antibiotics at 37° C. in a shaking incubator. The next morning, 10 ml of the overnight culture was added to 500 ml of 2xYT plus appropriate antibiotics in a 2L-baffled Erlenmeyer flask. When the optical density (at 560 nanometers) of the culture reached 0.4-0.6 the cells were induced with IPTG (1 mM). Four hours after induction with IPTG the cells were harvested by centrifugation. The cells were then washed with phosphate buffered saline and centrifuged again. The super-

natant was discarded and the cells were either frozen for future use or immediately processed. Twenty milliliters of lysis buffer was added to the cell pellets and vortexed. To break open the *E. coli* cells, this mixture was then run through the French Press at a pressure of 16,000 psi. The cells were then centrifuged again and the supernatant and pellet were checked by SDS-PAGE for the partitioning of the recombinant protein. For proteins that localized to the cell pellet, the pellet was resuspended in 10 mM Tris pH 8.0, 1% CHAPS and the inclusion body pellet was washed and centrifuged again. This procedure was repeated twice more. The washed inclusion body pellet was solubilized with either 8 M urea or 6 M guanidine HCl containing 10 mM Tris pH 8.0 plus 10 mM imidazole.

[0916] The solubilized protein was added to 5 ml of nickel-chelate resin (Qiagen, Valencia, Calif.) and incubated for 45 min to 1 hour at room temperature with continuous agitation. After incubation, the resin and protein mixture were poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer. The antigen was then eluted from the column using 8M urea, 10 mM Tris pH 8.0 and 300 mM imidazole and collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification. As a final purification step, a strong anion exchange resin such as Hi-Prep Q (Biorad) was equilibrated with the appropriate buffer and the pooled fractions from above were loaded onto the column. Each antigen was eluted off of the column with an increasing salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool. The pooled fractions were dialyzed against 10 mM Tris pH 8.0. This material was then submitted to Quality Control for final release. The release criteria were purity as determined by SDS-PAGE or HPLC, concentration as determined by Lowry assay or Amino Acid Analysis, identity as determined by amino terminal protein sequence, and endotoxin level as determined by the Limulus (LAL) assay. The proteins were then vialled after filtration through a 0.22-micron filter and the antigens were frozen until needed for immunization.

[0917] To generate anti-B726P mouse monoclonal antibodies, mice were immunized IP with 50 micrograms of recombinant B726P upstream ORF and B726P downstream ORF proteins that had been mixed to form an emulsion with an equal volume of Complete Freund's Adjuvant (CFA). Every three weeks animals were injected IP with 50 micrograms of recombinant B726P upstream ORF and B726P downstream ORF that had been mixed with an equal volume of IFA to form an emulsion. After the fourth injection, spleens were isolated and standard hybridoma fusion procedures were used to generate anti-B726P mouse monoclonal antibody hybridomas. Anti-B726P monoclonal antibodies were screened using the ELISA analysis using the bacterially expressed recombinant B726P upstream ORF and B726P downstream ORF proteins.

[0918] A list of the mouse anti-B726P monoclonal antibodies that were generated, as well as their anti-B726P reactivity in an ELISA assay and Western blot are shown in Table 2. The hybridomas were then subcloned and the subclones further tested for reactivity with B726P upstream ORF and B726P downstream ORF proteins. Several mono-

clonal antibodies showed particularly favorable reactivity: 220A2-21, 220A19-25, 220A94-29, 220A151-33.

[0919] For Western blot analysis, recombinant B726P upstream ORF and B726P downstream ORF protein was diluted with SDS-PAGE loading buffer containing beta-mercaptoethanol, then boiled for 10 minutes prior to loading the SDS-PAGE gel. Protein was transferred to nitrocellulose and probed with each of the anti-B726P hybridoma supernatants. Protein A-HRP was used to visualize the anti-B726P reactive bands by incubation in ECL substrate.

TABLE 2

Anti-B726P	B726PUP AND B726PDOWN MONOCLONAL ANTIBODY REACTIVITY				
	ELISA			Western Blots	
	mAbs	B726PDown	B726PUp	L523S	B726Pdown B726Pup
220A2	+++	+	-	+++	++
220A10	-	-	-	N/A	N/A
220A14	+++	+++	+++	+++	++
220A19	++	-	-	++	+
220A43	+++	+	-	+++	++
220A86	+++	+	-	+++	++
220A94	+++	-	-	++	+/-
220A123	++	-	-	+	-
220A139	+/-	-	-	+	-
220A140	-	-	-	N/A	N/A
220A141	-	-	-	N/A	N/A
220A143	-	-	-	N/A	N/A
220A151	++	-	-	++	-
220A176	+/-	-	-	+	-

EXAMPLE 12

Identification of Additional Sequences for B726P

[0920] Additional 5' sequence was obtained for B726P—this sequence was obtained by PCR from 1st strand cDNA prepared from three separate mRNA sources (metastatic breast tumor, breast tumor, normal testis). Disclosed herein are clones that were isolated, each with differences from the expected published sequence of NY-BR-1.

[0921] A 1300 bp fragment of B726P otherwise known as NY-BR-1 was PCR amplified from 1st strand cDNA and cloned into pPDM, a modified pET28 vector as follows:

[0922] The B726P XB coding region (NY-BR-1) was PCR amplified with the following primers

PDM-784 5' cacacaaagaggaagaagaccatc 3' Tm 56° C.

PDM-814 5' gattctttttaggacatgcaatcatc 3' Tm 55° C.

[0923] The following PCR conditions were used: 10 µl 10×Herculase buffer, 1 µl 10 mM dNTPs, 2 µl 10 µM each oligo, 83 µl sterile water, 1.5 µl Herculase DNA polymerase (Stratagene, La Jolla, Calif.), 50 ng DNA. The thermal-cycling conditions were as follows:

98° C. 3 minutes
 98° C. 40 seconds, 51° C. 15 seconds, 72° C. 4 minutes, ×10 cycles
 98° C. 40 seconds, 51° C. 15 seconds, 72° C. 5 minutes, ×10 cycles
 98° C. 40 seconds, 51° C. 15 seconds, 72° C. 6 minutes, ×10 cycles
 98° C. 40 seconds, 51° C. 15 seconds, 72° C. 7 minutes, ×10 cycles
 72° C. 10 minutes

[0924] The PCR product was ligated into the pPDM vector (a modified pET28) that had been digested with Eco72I and de-phosphorylated. PCR amplification of this gene proved very difficult and required the use of a polymerase lacking proofreading capabilities. However, use of such an enzyme, in this case, Herculase from Stratagene (La Jolla, Calif.), led to what is likely PCR errors in the resulting clones. The cDNA sequence of three of the isolated clones containing mutations are disclosed in SEQ ID NO:567-569 with the corresponding amino acid sequences disclosed in SEQ ID NO:572, 571, and 570, respectively.

[0925] The resulting construct, pPDM B726P XB (clone 83686), was then digested with BglII and the insert which dropped out from the 5' vector BglII site and the internal BglII site at amino acids 390-391 was cloned into the pPDM B726P C-ORF (SEQ ID NO:548) that had been digested with BglII and was de-phosphorylated. This construct, pPDM B726P XC, was then DNA sequenced and showed two nucleotide changes, which result in two amino acid changes. The cDNA of the full-length clone containing these 2 mutations is disclosed in SEQ ID NO:566 with the corresponding amino acid sequence in SEQ ID NO:573. The full-length expected, published NY-BR-1 is disclosed in SEQ ID NO:564 (cDNA); amino acid SEQ ID NO:565.

EXAMPLE 13

Isolation of Additional 3' Sequence and Real-Time PCR Analysis of B726P Homolog NY-BR1.1

[0926] A sequence homolog to the breast candidate B726P, called NY-BR-1.1, was identified and published in Cancer Research 61(5):2055-2061; Mar. 1, 2001. The NY-BR-1.1 gene, thought to be located on chromosome 9 based on 100% sequence identity to genomic sequence from chromosome 9, was shown to be expressed as mRNA in breast tumors as well as in normal brain. However, the published sequence was lacking 3' sequence. Published incomplete sequence for NY-BR-1.1 is represented by GenBank accession number AF269088. A recent BlastN search of the GenBank High Throughput Genomic Sequence database using Ny-Br-1.1 as a query sequence showed a 100% match to the working draft sequence of chromosome 9 (GenBank accession number AL359312), yielding further 3' DNA sequence for Ny-Br-1.1. The compilation of the Ny-Br-1.1 sequence with the additional 3' sequence from chromosome 9 yielded a 3720 bp ORF sequence (SEQ ID NO:576) which encodes a 1240 amino acid protein sequence (SEQ ID NO:577).

[0927] Real time PCR primers were designed to a unique region of NY-BR-1.1 to distinguish its mRNA expression profile from B726P. This experiment represents relative values, as it was done without template. The first-strand cDNA used in the quantitative real-time PCR was synthe-

sized from 20 µg of total RNA that was treated with DNase I (Amplification Grade, Gibco BRL Life Technology, Gaithersburg, Md.), using Superscript Reverse Transcriptase (RT) (Gibco BRL Life Technology, Gaithersburg, Md.). Real-time PCR was performed with a GeneAmp™ 5700 sequence detection system (PE Biosystems, Foster City, Calif.). The 5700 system uses SYBR™ green, a fluorescent dye that only intercalates into double stranded DNA, and a set of gene-specific forward and reverse primers. The increase in fluorescence was monitored during the whole amplification process. The optimal concentration of primers was determined using a checkerboard approach and a pool of cDNAs from tumors was used in this process. The PCR reaction was performed in 25 µl volumes that included 2.5 µl of SYBR green buffer, 2 µl of cDNA template and 2.5 µl each of the forward and reverse primers for the gene of interest. The cDNAs used for quantitative real time PCR reactions were diluted 1:10 for each gene of interest and 1:100 for the β-actin control. Levels of mRNA were expressed relative to ureter where NY-BR-1.1 expression was not observed when compared to the β-actin control.

[0928] The real time PCR results show that mRNA expression for NY-BR-1.1 is present in breast tumors as well as in normal adrenal gland, brain, retina and testis.

EXAMPLE 14

Characterization of B726P Monoclonal and Purified Polyclonal Antibody Epitopes

[0929] Mouse monoclonal antibodies and rabbit polyclonal sera were raised against *E. coli* derived B726P recombinant protein and tested by ELISA as described in further detail below, for antibody epitope recognition against overlapping 20 mer peptides that correspond to the amino acid sequence of the downstream ORF of B726P (B726P dORF, set forth in SEQ ID NO:176, encoded by SEQ ID NO:175). Numerous peptides were recognized by the monoclonal and polyclonal antibodies. The corresponding amino acid sequences of these peptide antibody epitopes are summarized in Table 3 and are set forth in SEQ ID NO:578-593.

[0930] ELISA ANALYSIS: B726P recombinant protein and peptides were coated onto 96 well ELISA plate: 50 ul/well at 2 ug/ml for 20 hrs at 4 C. Plates were then washed 5 times with PBS+0.1% Tween 20 and blocked with PBS+1% BSA for 2 hr. Affinity purified B726P polyclonal antibodies were then added to the wells at 1 ug/ml and B726P monoclonal supernatants were added neat (220A43 and 220A86 were diluted 1/60 and 1/20 respectively). Plates were incubated at room temperature for 30 minutes and then washed again as above, followed by the addition of 50 ul/well donkey anti-mouse-Ig-HRP antibody for 30 minutes at room temperature. Plates were washed, then developed by the addition of 100 ul/well of TMB substrate. The reaction was incubated 15 minutes in the dark at room temperature and then stopped by the addition of 100 ul/well of 1N H2SO4. Plates were read at OD450 in an automated plate reader. Peptides with OD450 readings three times background or above were considered to be positively recognized by the corresponding antibody.

TABLE 3

	Peptides recognized by B726P Antibodies					
	B726P Monoclonal Supernatant					B726P Purified Polyclonal
	220A2.1	220A19.1	220A94.1	220A151.1	220A43	220A86 (1 ug/ml)
B726P peptides (amino acids)	289-308	225-244, 232-252	73-252	145-164, 153-172	232-252	145-164, 153-172, 1-20, 9-28, 17-36, 24-44, 97-116, 105-124, 113-132, 121-140, 129-148, 137-156

EXAMPLE 15

Analysis of Autoantibodies to B726P In Breast Cancer Sera and Epitope Mapping of the Antigenic Sites

[0931] Specific B726P peptide epitopes were identified that react with autoantibodies in the serum of breast cancer patients. Thirty-three overlapping peptides were synthesized spanning the entire B726P protein. These 33 peptides were tested in ELISAs to evaluate which epitopes reacted with breast cancer sera. Reactive epitopes were identified throughout the molecule and a total of 16/74 sera samples from breast cancer patients had reactivity with one or more peptides.

[0932] Thirty-one overlapping synthetic peptides spanning the entire B726P downstream ORF sequence (amino acid sequence set forth in SEQ ID NO:176) were synthesized and 30 of these were tested in ELISA with sera from breast cancer patients as well as control sera. The amino acid sequences of the 31 overlapping peptides of the B726P downstream ORF are set forth in SEQ ID NO:594-624. Three additional peptides of B726P, set forth in SEQ ID NO:625-627 were also tested. Several peptides throughout the molecule showed reactivity, in particular peptide #2735 (amino acids 31-50; SEQ ID NO:597), peptide #2747 (amino acids 151-170; SEQ ID NO:609), peptide #2750 (amino acids 181-200; SEQ ID NO:612), peptide #2753 (amino acids 211-230; SEQ ID NO:615), and peptide #2766 (amino acids 231-250; SEQ ID NO:617). A total of 16/74 breast cancer sera were reactive with at least one peptide.

[0933] B726P antibody epitopes were also mapped using rabbit antisera generated against the B726P downstream ORF (SEQ ID NO:176). The epitopes identified using the rabbit antisera were as follows: peptide #2732 (amino acids 1-20; SEQ ID NO:594), peptide #2733 (amino acids 11-30; SEQ ID NO:595), peptide #2742 (amino acids 101-120; SEQ ID NO:604), peptide #2743 (amino acids 111-130; SEQ ID NO:605), peptide #2744 (amino acids 121-140; SEQ ID NO:606), peptide #2745 (amino acids 130-151; SEQ ID NO:607), peptide #2751 (amino acids 191-210; SEQ ID NO:613), and peptide #2753 (amino acid 211-230; SEQ ID NO:615). Some low level reactivity was observed for peptide #2772 (amino acids 291-310; SEQ ID NO:623) and peptide #2773 (amino acids 298-317; SEQ ID NO:624).

[0934] The above results confirm that B726P can be used alone or in combination with other breast tumor antigens as a vaccine target. Additionally, these results show that detection of antibodies to B726P can be used as a diagnostic indicator of breast cancer either alone or in combination

with detection of antibodies to other antigens (e.g. Her-2/Neu or other antigens known to be expressed in breast cancer tissue).

EXAMPLE 16

Immunohistochemical Analysis of B726P Expression In Metastatic Breast Cancer

[0935] Affinity purified polyclonal antibodies anti-B726Pdown (generated against the B726P downstream ORF) were used to assess B726P protein expression in metastatic breast cancer samples.

[0936] In order to determine which tissues express the breast cancer antigen protein B726P immunohistochemistry (IHC) analysis was performed on a diverse range of tissue sections. Tissue samples were fixed in formalin solution for 12-24 hrs and embedded in paraffin before being sliced into 8 micron sections. Steam heat induced epitope retrieval (SHIER) in 0.1 M sodium citrate buffer (pH 6.0) was used for optimal staining conditions. Sections were incubated with 10% serum/PBS for 5 minutes. Primary antibody (rabbit affinity purified anti-B726Pdown) was added to each section for 25 minutes followed by 25 minute incubation with anti-rabbit biotinylated antibody. Endogenous peroxidase activity was blocked by three 1.5 minute incubations with hydrogen peroxidase. The avidin biotin complex/horse radish peroxidase (ABC/HRP) system was used along with DAB chromogen to visualize antigen expression. Slides were counterstained with hematoxylin to visualize cell nuclei.

[0937] Anti-B726Pdown immunoreactivity was observed in 7 of 10 metastatic breast cancer samples analyzed but not observed in various normal tissues including normal breast. Thus, these data confirm earlier microarray analysis (see Example 1) showing that B726P is overexpressed in breast tumor tissue as compared to normal tissue. Therefore, this antigen may be used in diagnostic and immunotherapeutic applications for breast cancer.

EXAMPLE 17

Analysis of B726P Expression Using Immunoprecipitation and Western Blot Analysis

[0938] Affinity purified polyclonal antibodies generated against the B726P downstream ORF protein set forth in SEQ ID NO:176 (anti-B726Pdown) were used to assess the protein expression of the combined ORF of B726P in breast cancer cell lines as compared to normal cells as described below. Since the combined ORF includes both the upstream and downstream ORFs, the antibodies generated against the

downstream ORF crossreact with the combined ORF polypeptide as set forth in SEQ ID NO:475.

[0939] Cells were lysed in 1% Triton lysis buffer on ice for 10 minutes. Lysates were centrifuge at 15000 rpm and supernatant was saved for immunoprecipitation (IP)/Western analysis. 2 µg of anti-B726down polyclonal antibody was added to the supernatant and rocked overnight at 4° C. 20 µl of protein G bead slurry was added and incubated for 1 hour. Beads were then washed 3 times with 1 ml of lysis buffer. LDS sample buffer and β-mercaptoethanol were added and the samples were heated for 5 min at 95° C. Samples were size fractionated by gel electrophoresis, transferred to nitrocellulose and Western blotted with the mouse anti-B726down monoclonal antibody A2.1.

[0940] ³⁵S methionine labeling/IP analysis was carried out as follows: Cells were grown in 10% Fetal Bovine Serum (FBS) media to desired density. Cells were then starved with DMEM lacking methionine containing 0.1% FBS media for 10-15 minutes. FBS was added to a final concentration of 10% along with ³⁵S-Methionine trislabel (300 µCi -1 mCi). After incubating for 3-4 hours the cells were harvested, washed, and lysed. B726P was immunoprecipitated

as described above and samples were size fractionated by gel electrophoresis before being exposed to autoradiography film.

[0941] The results from the above described experiments showed that the full length 148 kDa form (also called NYBR1), the 110 kDa combined ORF form, and the 35 kDa downstream ORF form are all expressed in breast tumor cell lines HTB21 and BT474 but not in the SKBR3 normal breast cell line. Therefore, these results confirm that these forms of the B726P protein are expressed in breast tumor cell lines and not in normal cells.

[0942] U.S. patents, U.S. patent application publications, U.S. patent applications, foreign patents, foreign patent applications and non-patent publications referred to in this specification and/or listed in the Application Data Sheet, are incorporated herein by reference in their entirety.

[0943] From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

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gccaggatct gggcctgttt cttcccttct gccacattga tggccgactc tcgggtcccc 240
tcagactcta gaactgtggc ccgtttccgc cgctctgcct ccacctgcat ctgcatagac 300
t 301
```

```
<210> SEQ ID NO 27
<211> LENGTH: 301
<212> TYPE: DNA
<213> ORGANISM: Homo sapien
```

```
<400> SEQUENCE: 27
```

```
aaatcagtca tcacatctgt gaaaagagtg ctagtataa caaatgagat cacaaatttg 60
accattttat tagacaccct ctattagtgt taacagacaa agatgaaggt taagttgaaa 120
tcaaattgaa atcatcttcc ctctgtacag attgcaatat ctgataatac cctcaacttt 180
cttggtgcaa attaattgcc tgggtactcac agtccagtgt taacaggcaa taatggtgtg 240
attccagagg agaggactag gtggcaggaa aataaatgag attagcagta tttgacttgg 300
a 301
```

```
<210> SEQ ID NO 28
<211> LENGTH: 286
<212> TYPE: DNA
<213> ORGANISM: Homo sapien
```

```
<400> SEQUENCE: 28
```

```
tttttttttg cacaggatgc acttattcta ttcattctcc cccacccttc ccatatttac 60
atccttagag gaagagaggg gtaagggtgat aaagtaactg aaggaccgca agacgggtat 120
gtcccttggt caccaaatgg tcaaagggtc aaagatcgga ggaggtcagg gggtaacgca 180
ggaacagggt agggcggttc gccctctctc cctctccct tttcaacctc ttaatcactg 240
gctaactcgc gacctcatgg gttaattcgt aagcttacac gcgttg 286
```

```
<210> SEQ ID NO 29
<211> LENGTH: 301
<212> TYPE: DNA
<213> ORGANISM: Homo sapien
```

```
<400> SEQUENCE: 29
```

```
gtcatgttct tgctcttctt tctttacaca tttgagttgt gccttctggt cttaaagaga 60
ttttcctttg ttcaaaggat ttattcctac catttcacaa atccgaaaat aattgaggaa 120
acagggttaca tcattccaat tttgccttgg gtttgaagag tctctcatgg tggcacagtc 180
ctccagggta gctatgttgt tgggtctccc tacatcccag aagctcagag actttgtcaa 240
agggtgtgccg tccacccatt gccactgacc ctcgacaacc tggcttgaca gtccaataaa 300
a 301
```

```
<210> SEQ ID NO 30
<211> LENGTH: 332
<212> TYPE: DNA
<213> ORGANISM: Homo sapien
```

```
<400> SEQUENCE: 30
```

```
gagcagaatt gatgcctatg gctccaagtc aaatactgct aatctcattt attttcctgc 60
cacctagtcc tctcctctgg aatcacacca ttattgcctg ttaacactgg actgtgagta 120
```

-continued

ccaggcaatt aatttgcacc aagaaagttg aggggtattat cagatattgc aatctgtaca	180
gaggggaagat gattttcaatt tgatttcaac ttaaccttca tctttgtctg ttaacactaa	240
tagaggggtgt ctaataaaat ggtcaaatgt gtgatctcat ttgttataac tagcactcct	300
ttcacagatg tgatgactga ttccagcag ac	332

<210> SEQ ID NO 31
 <211> LENGTH: 141
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 31

aaaggctatc aagtactttg aaggacagga aggaatgaac acaccaggt ggacgttttg	60
tttcatttgc aggggttcag ggaggggttc aggggttcag ggagggctct tgtccacaa	120
ccgggggaag ggagaggga c	141

<210> SEQ ID NO 32
 <211> LENGTH: 201
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 32

gagctgatct cacagcacat acagaatgat gctactatgt agaccctcac tcccttgga	60
aatctgtcat ctaccttaaa gagagaaaaa agatggaaca taggccacc tagtttcac	120
catccaccta cataaccaac atagatgtga ggtccactgc actgatagcc agactgcctg	180
gggtaaacct ttccaggag g	201

<210> SEQ ID NO 33
 <211> LENGTH: 181
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 33

tttcaaaaca ctcatatgtt gcaaaaaa catagaaaaa taaagtttg tgggggtgct	60
gactaaactt caagtcacag acttttatgt gacagattgg agcagggttt gttatgcatg	120
tagagaaccc aaactaatgt attaaacagg atagaaacag gctgtctggg tgaaatggtt	180
c	181

<210> SEQ ID NO 34
 <211> LENGTH: 151
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 34

atgtcctgca cagtatagct tggacctctg ggctgaacc agggtagca tcaaggcccc	60
cattttcct caccacggg tcgcttgca gctccaagaa ccagtctggc cccactgaga	120
acttttcagt cgaggcctg atgaatcttg g	151

<210> SEQ ID NO 35
 <211> LENGTH: 291
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 35

-continued

tcttttagggc aaaatcatgt ttctgtgtac ctagcaatgt gttcccatTT tattaagaaa	60
agctttaaca cgtgtaatct gcagtcctta acagtggcgt aattgtacgt acctgttgtg	120
tttcagtttg tttttcacct ataatgaatt gtaaaaacaa acatacttgt ggggtctgat	180
agcaaacata gaaatgatgt atattgtttt ttgttatcta tttatTTtca tcaatacagt	240
atTTtgatgt attgcaaaaa tagataataa tttatataac aggttttctg t	291

<210> SEQ ID NO 36
 <211> LENGTH: 201
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 36

ctgatacaat tataataacg gttccctgaa ctttttagag tgcaattaag acaaaaaact	60
aaatTTtggt tacatgaata tggaataaat acaataatca aaatatgact ctccctaaaa	120
gtgaaacaca caagccaatc cggaactgct gtgcgaaaga taaaatcgag aaaggcaagg	180
tttcggtagg aggacgcgat g	201

<210> SEQ ID NO 37
 <211> LENGTH: 121
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 37

catcacactg gcggccgctc gagcatgcat ctagagggcc caattcgccc tataatgagt	60
cgtattacaa ttcaactggcc gtcgttttac aacgtcgtga ctgggaaaac cctggcggtta	120
c	121

<210> SEQ ID NO 38
 <211> LENGTH: 200
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 38

aaacatgtat tactctatat ccccaagtcc tagagcatga cctgcatggt ggagatgttg	60
tacagcaatg tttttatcca gacatacata tatgatattt agagacacag tgattctttt	120
gataacacca cacatagaac attataatta cacacaaatt tatggtaaaa gaattaatat	180
gctgtctggt gctgctgtta	200

<210> SEQ ID NO 39
 <211> LENGTH: 760
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 39

gcgtggtcgt cggccgaggt cctgggctag acctaatggt ttattattgg tggagagaaa	60
gatctggaaa tacttgaggt tattacatac tagattagct tctaattgtga accatttttc	120
ttttaacagt gatcaaatTA ttatttcgaa gttaatcgtt cccttggtgg ctgcatacac	180
atcgcattaa caaacatact gttgtatttt ttcccagttt tgtttggcta tgccaccaca	240
gtcatcccca gggctctatac atactatggt tcaactgtat tatttgccat ttttggcatt	300
agaatgcttc gggaaggcct aaagatgagc cctgatgagg gtcaagagga actggaagaa	360

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```

gttcaagctg aattaaagaa gaaagatgaa gaagtaagcc atggcactgt tgatctggac 420
caaaaaggca ctcaactagg aataaacact ctacagaggt ttctcagtg ccccatctgt 480
gtgatatgcg gggctacaca aaaatagctt cttttgcttt gttctgttct tatacctgtc 540
tgtgatctga cttggggttg gtgtgaatgt agtagagaaa ggaagctgac agatgaatac 600
tgaacacagg taatcagttt ccttaattag gttgattata agctcctgaa aagcaggaac 660
tgtattttat aattttacct gtttctccc tggtgtctag gatagtaagt ggcagagca 720
gtaaatactg tttggtttgt tcagacctgc ccgggcggcc 760

```

```

<210> SEQ ID NO 40
<211> LENGTH: 452
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

```

```

<400> SEQUENCE: 40

```

```

aatcactaaa gatattgact agagaatgct gtgtgctatt tcaattacat ttgtttttct 60
tttattaaca ggaattttga ttcttcaagg aagtggctca atttcaattt caggtgacca 120
ggtttatcgt gacttttctt tcttgtttac ttttcgctag gaaggggagt tgtaggggca 180
gattcaggta ttggaatagg aaaattacgt ctaaacctg gaaatcttgg aaatggaatt 240
ggtggaagtg ggcgaatagg atatgggtaa gggaacacaa aaaaccctga agctaattca 300
tcgctgtcac tgatacttct tttttctcgt tcctgggtctt gagagactgg gaaaccaaca 360
gccactgcca agatggctgt gatcaggagg agaactttct tcatctcaaa cgtttcagtc 420
agttctttct ctcacctcgg ccgcgaccac gc 452

```

```

<210> SEQ ID NO 41
<211> LENGTH: 676
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

```

```

<400> SEQUENCE: 41

```

```

aatctttgaa tgccaagtct cttctgtact ttcttttatt aacatcatag tctttgcatc 60
aagatacata gcaatgatag caggttttct tttaaagctt agtattaata ttaaattatt 120
ttccccattt aaattttaca ttacttgcca agaaaaaaaa aaaattaaaa ctcaagttac 180
ttgaagcctg gacacacttc catgattagc cgggctaggt aaaagttggt ggctttattc 240
ttctgtctct ataagcagat ccaggcccta gaaagatggg accaggggat ataattgttt 300
ttgaaaagtg tgctacaaaa atggatggcc tgttataagc caggatacaa agttaaggat 360
gggggtaagg gagggacatt ttcttcaga agaaaagaca gaatttctga agagtcccag 420
tcataaattt tcccaaatg gttggaggag agggtaaaat ctcaacatga gtttcaaagt 480
actgtctctg tgaggggccc gtagatgcct tgctgaggag ggatggctaa tttggaccat 540
gccccatccc cagctaggag aatggaaatg gaaactttaa ttgccagtg ggtgtgaaag 600
tgggctgaag cttggttggt actgaattct ctaagaggtt tcttctagaa acagacaact 660
cagacctgcc cgggcg 676

```

```

<210> SEQ ID NO 42
<211> LENGTH: 468
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

```

-continued

<400> SEQUENCE: 42

```
agcgtgggtcg cggccgaggt ttggccggga gectgatcac ctgccctgct gagtcccagg    60
ctgagcctca gtctccctcc ctggggcct atgcagaggt ccacaacaca cagatttgag    120
ctcagccctg gtgggcagag aggtagggat ggggctgtgg gtagatgag gcatcgcaat    180
gtaagactcg ggattagtac acacttggtg attaatggaa atgtttacag atccccaagc    240
ctggcaaggg aattttctca actccctgcc cccagccct cttatcaaa ggacaccatt    300
ttggcaagct ctatgaccaa ggagccaaac atcctacaag acacagtac cataactaatt    360
aaaaacccct gcaaagccca gcttgaaacc ttacttagg aacgtaatcg tgtcccctat    420
cctacttccc cttcctaatt ccacagacct gcccgggcgg ccgctcga                468
```

<210> SEQ ID NO 43

<211> LENGTH: 408

<212> TYPE: DNA

<213> ORGANISM: Homo sapien

<400> SEQUENCE: 43

```
atcatatcaa aacactatct tcccactgtg ttctcaatgc ctgctacttc ttgtagatat    60
ttcatttcag gagagcagca gttaaacccg tggattttgt agttaggaac ctgggttcaa    120
acctctttcc actaattggc tatgtctctg gacagttttt tttttttttt ttttttttaa    180
accctttctg aactttcact ttctatggct acctcaaaga attgttgtga ggcttgagat    240
aatgcatttg taaagggctc gccagatagg aagatgctag ttatggattt acaaggttgt    300
taaggctgta agagtctaaa acctacagtg aatcacaatg catttaccct cactgacttg    360
gacataagtg aaaactagcc cgaagtctct ttttcaaatt acttacag                408
```

<210> SEQ ID NO 44

<211> LENGTH: 160

<212> TYPE: DNA

<213> ORGANISM: Homo sapien

<400> SEQUENCE: 44

```
tggtcgcggc cgaggctctg tgtgcctgt ggtccagggg accaagaaca acaagatcca    60
ctctctgtgc tacaatgatt gcaccttctc acgcaacact ccaaccagga ctttcaacta    120
caacttctcc gctttggcaa acaccgtcac tcttgctgga                160
```

<210> SEQ ID NO 45

<211> LENGTH: 231

<212> TYPE: DNA

<213> ORGANISM: Homo sapien

<400> SEQUENCE: 45

```
cgagcggccg cccgggcagg tctggggagg tgattccatc cagagtcata tctgttgtca    60
ccccataag tcgatcagca aggctgacag gctgtgagga aaccccggcc ttgtagcctg    120
tcacctctgg ggggatgatg actgcctggc agacgtaggc tgtgatagat ttgggagaaa    180
acctgactca ccctcaggaa tccggaggtc ggtgacattg tcggtgcaca c                231
```

<210> SEQ ID NO 46

<211> LENGTH: 371

<212> TYPE: DNA

<213> ORGANISM: Homo sapien

-continued

<400> SEQUENCE: 46

```
ccccggcagg tctgtgtaac atgccaaggc ttgcaacttt ctgcagagca gttttttatt    60
ttccttatca ggtacagggt ttggtttttc ttgactatct ctgatgaatt tttcatgagt    120
ctgtatatgc agaatctttt ccctaataac tgcttcgtcc catgtctgaa ggcgtaaaat    180
aaagtcattc atcatttttt ctttgtacat gtttatttgt tctttttcaa ttacaccaag    240
cattactagt cagaaggaag cacttgctac ctcttgctct tcctctgcct ctggtttgga    300
tcattttgat gacattgccc acattactca tgaaggatga caagattgca ctgtgcaatg    360
tcaattgcct t                                     371
```

<210> SEQ ID NO 47

<211> LENGTH: 261

<212> TYPE: DNA

<213> ORGANISM: Homo sapien

<400> SEQUENCE: 47

```
gccctgtttt tatacacttc acatttgcaag aaatataatg atgccctcat tatcagtgaag    60
catgcacgaa tgaaagatgc tctggattac ttgaaagact tcttcagcaa tgtccgagca    120
gcaggattcg atgagattga gcaagatctt actcagagat ttgaagaaa gctgcaggaa    180
ctagaaaagt tttccaggga tcccagcaat gagaatccta aacttgaaga cctctgcttc    240
atcttacaag aagagtacca c                                     261
```

<210> SEQ ID NO 48

<211> LENGTH: 701

<212> TYPE: DNA

<213> ORGANISM: Homo sapien

<400> SEQUENCE: 48

```
cgagcgcccc ccgggcagggt ccaattagta caagtctcat gatataatca ctgcctgcat    60
acatatgcac agatccagtt agtgagtttg tcaagcttaa tctaattggt taagtctcaa    120
agagattatt attcttgatg ttgtctttgt attggctaac aaatgtgcag aggtaatata    180
tatgtgatgt ccgatgtctc tgtctttttt ttgtcttta aaaaataatt ggcagcaact    240
gtatttgaat aaaatgatgt cttagtatga ttgtaccgta atgaatgaaa gtggaacatg    300
tttctttttg aaaggagag aattgacat ttattattgt gatgtttaag ttataactta    360
ttgagcactt ttagtagtga taactgtttt taaacttgcc taataccttt cttgggtatt    420
gtttgtaatg tgacttattt aaccoccttt ttgtttgtt taagttgctg ctttaggtta    480
acagcgtggt ttagaagatt taaatttttt tcctgtctgc acaattagtt attcagagca    540
agagggcctg attttataga agccccttga aaagaggctc agatgagagc agagatacag    600
tgagaaatta tgtgatctgt gtgtgtggg aagagaattt tcaatatgta actacggagc    660
tgtagtgcca ttagaaactg tgaatttcca aataaatttg a                                     701
```

<210> SEQ ID NO 49

<211> LENGTH: 270

<212> TYPE: DNA

<213> ORGANISM: Homo sapien

<400> SEQUENCE: 49

```
agcggccgcc cgggcaggtc tgatattagt agctttgcaa ccctgataga gtaaataaat    60
```

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```

tttatgggcg ggtgccaaat actgctgtga atctatttgt atagtatcca tgaatgaatt 120
tatggaaata gatatttgtg cagctcaatt tatgcagaga ttaaatgaca tcataatact 180
ggatgaaaac ttgcatagaa ttctgattaa atagtgggtc tgtttcacat gtgcagtttg 240
aagtatttaa attaaccact cctttcacag 270

```

```

<210> SEQ ID NO 50
<211> LENGTH: 271
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

```

```

<400> SEQUENCE: 50

```

```

atgcatttat ccatatgaac ttgattattc tgaattactg actataaaaa ggctattgtg 60
aaagatatca cactttgaaa cagcaaatga attttcaatt ttacatttaa ttataagacc 120
acaataaaaa gttgaacatg cgcataatcta tgcatttcac agaagattag taaaactgat 180
ggcaacttca gaattatttc atgaagggtg caaacagtct ttaccacaat ttcccatgg 240
tcttatcctt caaaataaaa ttccacacac t 271

```

```

<210> SEQ ID NO 51
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

```

```

<400> SEQUENCE: 51

```

```

tggtcgcggc cgagggtgtga ggagatgaac tttgtgttaa tggggggcac tttaaactga 60
aatggcttat ccccaccgcc atgtaagtta ccatgcctgt ctctccctc ctacacattt 120
ccagctcctg ctgcagttat tcctacagaa gctgccattt accagccctc tgtgattttg 180
aatccacgag cactgcaggc cctccacagc gttactaccc agcaggcact cagctcttca 240
t 241

```

```

<210> SEQ ID NO 52
<211> LENGTH: 271
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

```

```

<400> SEQUENCE: 52

```

```

tccaagactt aaaacttagg aaacacctat gatgccactt taactggaag taatggagac 60
atctgattcc aaattcacat tttaaagtc tatttgcaat cagcaaagag ccaggatatgc 120
tgcatgctgc ttgctgtaag ttacgatttg gottcactag ctcaaatttt ttcactccac 180
caaaagataa ggcacaggcc cgtttgtcca atcaagtttg ctgaaaatac tgcagcctga 240
gtgtagacaa acttcccctg aatttgctag a 271

```

```

<210> SEQ ID NO 53
<211> LENGTH: 493
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

```

```

<400> SEQUENCE: 53

```

```

ttagcgtggt cgcgggccga ggtctggcct gactagctca ctctgaagag tgtctttcac 60
atggattaac caaaaaatgc attactgcct ttggcacact gtcttgaata ttctttctga 120
caatgagaaa atatgattta atggagtcgt tcaataacct cacaatctcg ctgttccgag 180

```

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cagatagttt tcgtgccaac aggaactggc acatctagca gggtcacggc atgacctttt	240
tgtggactgg ctggcataat tggaatgggt ttgatTTTT cttctgctaa taactcttca	300
agcttttgaa gttttcaagc attcctctcc agttgcctgt ggttggttct tgaacaccat	360
ctccaacccc accacctcca gatgcaacct tgtctcgtga tacagacctg cccgggctggc	420
cctcaagggc gaattctgca gatatccatc aactggcgg ccgctcgagc atgcatctag	480
agggcccaat tcg	493

<210> SEQ ID NO 54
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 54

cggtgtcgcg gccgaggtct gtttgcctgt tgggtgaggt tttcttctg gagactttgt	60
actgaatgtc aataaactct gtgattttgt taggaagtaa aactgggatc tatttagcca	120
ctggtaagct tctgaggtga aggattcagg gacatctcgt ggaacaaaca ctccccactg	180
gactttctct ctggagatac ccttttgaat atacaatggc cttggctcac taggtttaaa	240
tacaaacaag tctgaaaccc actgaagact gagagattgc agcaatattc tctgaattag	300
gatcgggttc cataactcta a	321

<210> SEQ ID NO 55
<211> LENGTH: 281
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 55

ttgcaaatga aactgtggat gtataataag aaaacacaag ggtttattct taacactaaa	60
attaacatgc cacacgaaga ctgcattaca gctctctgtt tctgtaatgc agaaaaatct	120
gaacagccca ccttggttac agctagcaaa gatggttact tcaaagtatg gatattaaca	180
gatgactctg acatatacaa aaaagctgtt ggctggacct gtgactttgt tggtagttat	240
cacaagtatc aagcaactaa ctgttggttc tccgaagatg g	281

<210> SEQ ID NO 56
<211> LENGTH: 612
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 56

gcgtggtcgc ggccgaggtc ctgtccgggg gcactgagaa ctccctctgg aattcttggg	60
gggtgttggg gagagactgt gggcctggag ataaaacttg tctcctctac caccacctg	120
taccctagcc tgcacctgtc ctcatctctg caaagttcag cttccttccc caggtctctg	180
tgccactctg tcttggtatg tctggggagc tcatgggtgg aggagtctcc accagaggga	240
ggctcagggg actggttggg ccagggatga atatttgagg gataaaaatt gtgtaagagc	300
caaagaattg gtagtagggg gagaacagag aggagctggg ctatgggaaa tgatttgaat	360
aatggagctg ggaatatggc tggatatctg gtactaaaaa aggttcttta agaacctact	420
tcctaattct tccccaatc caaacatag ctgtctgtcc agtgctctct tctgcctcc	480
agctctgccc caggctcctc ctgactctg tccctgggct agggcagggg aggagggaga	540

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gcagggttg gggagaggct gaggagagtg tgacatgtgg ggagaggacc agacctgccc 600
gggcggccgt cg 612

<210> SEQ ID NO 57
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 57

gtcgcggccg aggtcctgag cgtcacccta gttctgcccc tttttagctg tgtagacttg 60
gacaagacat ttgacttccc tttctccttg tctataaaat gtggacagtg gacgtctgtc 120
acccaagaga gttgtgggag acaagatcac agctatgagc acctcgcacg gtgtccagga 180
tgcacagcac aatccatgat gcgttttctc cccttacgca ctttgaaacc catgctagaa 240
aagtgaatac atctgactgt gctccactcc aacctccagc gtggatgtcc ctgtctgggc 300
cctttttctg ttttttattc tatgttcagc accactggca ccaaatacat tttaattcac 360
cga 363

<210> SEQ ID NO 58
<211> LENGTH: 750
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 58

cgtaggtcgcg gccgaggtct aattccacct gactggcaga acctgcgccc ctgcctaacc 60
ctgcgccctt ctcccaactc gcgtgcctca cagaaccagc gtgctgcaca gcccagagat 120
gtggcccttc ttcaggaaag agcaaataag ttggtccaag tacttgatgc ttaaggaata 180
cacaagggtg cccatcaagc gctcagaaat gctgagagat atcatccgtg aatacactga 240
tgtttatcca gaaatcattg aacgtgcatg ctttgtccta gagaagaaat ttgggattca 300
actgaaagaa attgacaagc aagaacacct gtatattctc atcagtaccc ccgagtcctt 360
ggctggcata ctgggaacga ccaaagacac acccaagctc ggtctcttct tggtgattct 420
gggtgtcatc ttcattgaatg gcaaccgtgc cagtgaggct gtcttttggg aggcactacg 480
caagatggga ctgcgtcctg gggtagagaca tcccctccct tggagatcta aggaaacttc 540
tcacctatga gtttgtaaag cagaaatacc tggactacag acgagtgcc ccaacagcaacc 600
ccccggagta tgagttcctc tggggcctcc gtccctacca tgagactagc aagatgaaaa 660
tgctgagatt cattgcagag gttcagaaaa gagaccctcg tgactggact gcacagttca 720
tggaggctgc agatgaggac ctgcccgggc 750

<210> SEQ ID NO 59
<211> LENGTH: 505
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 59

tggccgcccc gccaggtcca gtctacaagc agagcactct catggggagc accagatgag 60
ttccagccgc agttctttta taagctttta gtgcctcatg aagacgcgag gatctcttcc 120
aagtgaacc tggtcacatc agggcacatt cagcagcaga agtctgtttc cagtatagtc 180
cttggtatgg ctaaattcca ctgtcccttt ctcagcagtc aataatccat gataaattct 240

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gtacaacact gtagtcaata acagcagcac cagacagcat attaattctt ttaccataaa 300
tttgtgtgta attataatgt tctatgtgtg gtgttatcaa aagaatcact gtgtctctaa 360
atatcatata tgtatgtctg gataaataca ttgctgtaca acatctccaa catgcaggtc 420
atgctctaag acttggggat atagagtaat acatgtttcg tggacctcgg ccgcgaccac 480
gctaaggggc aattctgcag atatc 505

```

```

<210> SEQ ID NO 60
<211> LENGTH: 520
<212> TYPE: DNA
<213> ORGANISM: Homo sapien
<400> SEQUENCE: 60

```

```

cgtggtcgcg gccgaggtcc tcaggacaag gaaacaggta tcagcatgat ggtagcagaa 60
accttatcac caaggtgcag gagctgactt cttccaaaga gttgtggttc cgggcagcgg 120
tcattgcctg cccttgctgg agggctgatt ttagtggtgc ttattatggt gccctgagg 180
atgcttcgaa gtgaaaaata gaggtgcag gatcagcggc aacagatgct ctcccgtttg 240
cactacagct ttcacggaca ccattccaaa aaggggcagg ttgcaaagtt agacttgga 300
tgcatgggtc cggtcagtgg gcacgagaac tgctgtctga cctgtgataa aatgagacaa 360
gcagacctca gcaacgataa gatcctctcg cttgttcact ggggcagtga cagtgggcac 420
gggaagctgg aattcgtatg acggagtctt atctgaacta cacttactga acagcttgaa 480
ggacctgccc gggcgccgcg tcgaaagggg cgaattctgc 520

```

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<210> SEQ ID NO 61
<211> LENGTH: 447
<212> TYPE: DNA
<213> ORGANISM: Homo sapien
<400> SEQUENCE: 61

```

```

agagaggtgt ttttattctt tggggacaaa gccgggttct gtgggtgtag gattctccag 60
gttctccagg ctgtagggcc cagaggctta atcagaatth tcagacaaaa ctggaacctt 120
tcttttttcc cgttggttta ttgtagtcc ttgggcaaac caatgtcttt gttcgaaaga 180
gggaaaaata tccaaacgtt tttcttttaa cttttttttt aggttcaggg gcacatgtgt 240
aggcttgcta tataggtaaa ttgcatgtca ccagggtttg ttgtacagat tatttcatca 300
tccagataaa aagcatagta ccagataggt agttttttga tcctcacctt ctttccatgc 360
tccgacctca ggtaggcccc agtgtctgac ctgcccggcg gcccgctcga aagggccaat 420
tctgcagata tccatcacac tggccgg 447

```

```

<210> SEQ ID NO 62
<211> LENGTH: 83
<212> TYPE: PRT
<213> ORGANISM: Homo sapien
<400> SEQUENCE: 62

```

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Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val Gly
 1             5             10             15
Phe Pro Val Ser Gln Asp Gln Glu Arg Glu Lys Arg Ser Ile Ser Asp
 20             25             30
Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr Pro

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35	40	45	
Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg		Phe Pro Trp Phe Arg	
50	55	60	
Arg Asn Phe Pro Ile Pro Ile Pro Ser Ala Pro		Thr Thr Pro Leu Pro	
65	70	75	80
Ser Glu Lys			
<210> SEQ ID NO 63			
<211> LENGTH: 683			
<212> TYPE: DNA			
<213> ORGANISM: Homo sapien			
<400> SEQUENCE: 63			
acaagattg gtagctttta tttttttta aaaatgctat actaagagaa aaaacaaaag		60	
accacaacaa tattccaaat tataggttga gagaatgtga ctatgaagaa agtattctaa		120	
ccaactaaaa aaaatattga aaccactttt gattgaagca aaatgaataa tgctagattt		180	
aaaaacagtg tgaaatcaca ctttggctctg taaacatatt tagctttgct tttcattcag		240	
atgtatacat aaactttattt aaaatgtcat ttaagtgaac cattccaagg cataataaaa		300	
aaagwggtag caaatgaaaa ttaaagcatt ttttttggtta gttcttcaat aatgatrcga		360	
gaaactgaat tccatccagt agaagcatct ctttttggtt aatctgaaca agtrccaacc		420	
cagatagcaa catccactaa tccagcacca attccttcac aaagtccttc cacagaagaa		480	
gtgcgatgaa tattaattgt tgaattcatt tcagggttc cttggtccaa ataaattata		540	
gcttcaatgg gaagagggtcc tgaacattca gctccattga atgtgaaata ccaacgctga		600	
cagcatgcat ttctgcattt tagccgaagt gagccactga acaaaactct tagagcacta		660	
tttgaacgca tctttgtaaa tgt		683	
<210> SEQ ID NO 64			
<211> LENGTH: 749			
<212> TYPE: DNA			
<213> ORGANISM: Homo sapiens			
<220> FEATURE:			
<221> NAME/KEY: misc_feature			
<222> LOCATION: 534			
<223> OTHER INFORMATION: n = A,T,C or G			
<400> SEQUENCE: 64			
ctgttcattt gtccgccagc tcctggactg gatgtgtgaa aggcatacaca ttccattttt		60	
cctccgtgta aatgtttttat gtgttcgcct actgatccca ttcgttgctt ctattgtaaa		120	
tatttgtcat ttgtatttat tatctctgtg ttttcccctt aaggcataaa atggtttact		180	
gtgttcattt gaaccttatt actgatctct gttgtatatt tttcatgcca ctgctttgtt		240	
ttctcctcag aagtcgggta gatagcattt ctatcccatc cctcacgtta ttggaagcat		300	
gcaacagtat ttattgctca gggctctctg cttaaaactg aggaaggtcc acattcctgc		360	
aagcattgat tgagacattt gcacaatcta aaatgtaagc aaagtaagtc attaaaaata		420	
caccctctac ttgggcttta tactgcatac aaatttactc atgagccttc ctttgaggaa		480	
ggatgtggat ctccaaaata agatttagtg tttattttga gctctgcac ttancaagat		540	
gatctgaaca cctctccttt gtatcaataa atagccctgt tattctgaag tgagaggacc		600	
aagtatagta aaatgctgac atctaaaact aaataaatag aaaacaccag gccagaacta		660	

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tagtcatact cacacaaagg gagaaattta aactcgaacc aagcaaaagg cttcacggaa 720

atagcatgga aaaacaatgc ttccagtgg 749

<210> SEQ ID NO 65

<211> LENGTH: 612

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 65

acagcagcag tagatggctg caacaacctt cctcctaccc cagcccagaa aatatttctg 60

ccccacccca ggatccggga ccaaaataaa gagcaagcag gcccccttca ctgagggtgct 120

gggtagggct cagtgcacac ttactgtgct ttgagaaaga ggaaggggat ttgtttggca 180

ctttaaaaat agaggagtaa gcaggactgg agaggccaga gaagatacca aaattggcag 240

ggagagacca tttggcgcca gtcccttagg agatgggagg agggagatag gtatgagggt 300

aggcgctaag aagagttaga ggggtccact ccaagtggca ggggtctgaa atgggctagg 360

accaacagga cactgactct aggtttatga cctgtccata ccggttcac agcagctggg 420

tgggagaaat caccattttg tgacttctaa taaaataatg ggtctaggca acagttttca 480

atggatgcta aaacgattag gtgaaaagtt gatggagaat ttttaattcag gggaattagg 540

ctgataccat ctgaaacat ttggcatcat taaaaatgtg acaacctggt ggctgccagg 600

gaggaagggg ag 612

<210> SEQ ID NO 66

<211> LENGTH: 703

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 66

tagcgtggtc gcggccgagg tacattgatg ggctggagag cagggttggc agcctgttct 60

gcacagaacc aagaattaca gaaaaaagtc caggagctgg agaggcacia catctccttg 120

gtagctcagc tccgccagct gcagacgcta attgctcaa cttccaacia agctgcccag 180

accagcactt gtgttttgat tcttcttttt tccctggctc tcatcatcct gccagcttc 240

agtccattcc agagtcgacc agaagctggg totgaggatt accagcctca cggagtgact 300

tccagaaata tcctgaccca caaggacgta acagaaaatc tggagaccca agtggttagag 360

tccagactga gggagccacc tggagccaag gatgcaaatg gctcaacaag gacactgctt 420

gagaagatgg gagggaagcc aagaccagtc gggcgcatcc ggtccgtgct gcatgcagat 480

gagatgtgag ctggaacaga ccttcctggc ccacttcttg atcacaagga atcctgggct 540

tccttatggc tttgcttccc actgggattc ctacttaggt gtctgccctc aggggtccaa 600

atcacttcag gacaccccaa gagatgtcct ttagtctctg cctgaggcct agtctgcatt 660

tgtttgcata tatgagaggg tacctgcccg ggcggccgct cga 703

<210> SEQ ID NO 67

<211> LENGTH: 1022

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 67

cttgagaaag caggattggt ttaagttcca agatttaaca aacttactgt tcagcatcat 60

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attcaagcct aaaaggaaga taggattttc aagatatatt tccaacttct ttaacatggc 120
accatggatg aactgtttct cagcactgtg ctgcttcact tggaattaag gatgaattgg 180
gaggagacag tatgacatag gtgggtaggt tgggtggtga ggggaaccag ttctaatagt 240
cctcaactcc actccagctg ttcctgttcc acacggtcca ctgagctggc ccagtccctt 300
tcactcagtg tgtcaccaaa ggcagettca aggetcaatg gcaagagacc acctataacc 360
tcttcacctt ctgctgcctc tttctgctgc cactgactgc catggccatc tgcataagcc 420
gcattgtcct cagtgtgtcc agggcccaga caaggaaggg gagccatggt gagactccaa 480
ttcccaggcc ttaatcctta accctagacc tgttgccctc agcatcattt atttatctac 540
ctacctaata gctatctacc agtcattaaa ccatgggtgag attctaacca tgtctagcac 600
ctgatgctag agataatttt gttgaatccc ttcaattata aacagctgag ttagctggac 660
aaggactagg gaggcaatca gtattattta ttcttgaaca ccatcaagtc tagacttggc 720
ggcttcatat ttctatcata atcccgggg gtaagaaatc atatagcccc aggttgggaa 780
ggggaaaacg gtttgcaaca ttctcctcct tgtaggaggc gagctctgtc tcactagcta 840
tgcccctcca tcaattcacc ctatactcag atcagaagct gagtgtctga attacagtat 900
attttctaaa ttcctagccc ctgctggtga atttgccctc ccccgctcct ttgacaattg 960
tccccgtggt cgtctccggg ccctgagact ggccctgctt atcttctga ccttcacct 1020
ct 1022

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<210> SEQ ID NO 68
<211> LENGTH: 449
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 68

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```

ccagatccat tttagtggt ctggatttct ttttattttc ttttcaactt gaaagaaact 60
ggacattagg ccactatgtg ttgttactgc cactagtgtt caagtgcctc ttgttttccc 120
agagatttcc tgggtctgcc agaggcccag acaggctcac tcaagctctt taactgaaaa 180
gcaacaagcc actccaggac aaggttcaaa atggttataa cagcctctac ctgtcgcccc 240
agggagaaa gggtagtgat acaagtctca tagccagaga tggttttcca ctctctctag 300
atattcccaa aaagaggctg agacaggagg ttattttcaa ttttattttg gaattaaata 360
cttttttccc ttattactg ttgtagtccc tcacttggt atacctctgt tttcacgata 420
gaaataaggg aggtctagag cttctattc 449

```

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<210> SEQ ID NO 69
<211> LENGTH: 387
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 22, 26, 36, 45, 54, 56, 62, 63, 73, 92, 98, 105, 155,
174, 194, 302, 312, 358, 375, 378, 381
<223> OTHER INFORMATION: n = A,T,C or G

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<400> SEQUENCE: 69

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gcccttagcg tgggtcgcg cncgangtct ggagcntatg tgatncctat ggtncncagg 60
cnnatactgc tantctcatt tattctctcg cnacctantc ctctnctctg gaatcacacc 120
attattgcct gttaacactg gactgtgagt accangcaat taatttgcac caanaaagtt 180

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gaggggtatta tcanatattg caatctgtac agaggggaaga tgattttcaat ttgatttcaa	240
cttaaccttc atctttgtct gttaacacta atagaggggtg tctaataaaa tggcaaat	300
gngatctcat tnggtataac tacactcttt ttcacagatg tgatgactga atttccanca	360
acctgcccgg gcggncgntc naagggc	387

<210> SEQ ID NO 70

<211> LENGTH: 836

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 70

tattccattt aaaaaataaa ttcagccctg cactttcttt agatgccttg atttccagaa	60
tggagcttag tgctactgaa taccctggcc acagagccac ctcaggatat tcttttctcc	120
accttagttt atttatttat agatatctgt ttacaaagtc tgtagtaaat cctgatgctg	180
accatctgaa atgtactttt tttctgaatg ctgtttcaat ctaaaatagc agcttttgag	240
aaaaaatga tgtaattcc ttatgataaa aggatgattc tatatatctt ttaatgat	300
taaatatgcc gaagccaagc acacagtctt tctaaagtgt gtgtatgttt gtgtgaatgt	360
gaatgatact gatcttata tctgttaaaag ttgttttaaa aagctgtggc atccattgt	420
tcataattgc caagtcttct gtaaagatgt ctaggacgaa atattttatg tgctaattgca	480
tgtatttgta aaccagattt gtttaccact caaaattaac ttgttttctt catccaaaaa	540
agtttatttc ttccacgtac ttaaatttct tgtgtgggta taatatagct ttctaatttt	600
tttctttcac aaaggcaggt tcaaaattct gttgaaagaa aaatgctttc tgaaactgag	660
gtataacacc agagcttgct gtttaaggga ttatatgatg tacatcagtt ctataaatgt	720
gctcagcagt ttaacatgtg aatcctgttt taaagtgtc agatttcaac tgtgtaagcc	780
attgatataa cgctgtaatt aaaaatgttt atatgaaaaa aaaaaaaaaa aaaaaa	836

<210> SEQ ID NO 71

<211> LENGTH: 618

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 71

gttgacgtga gctcaagtgt tgggtgtatc agtcaaaac accatgtgat gccaatcatc	60
tccacaggag caatttgttt accttttttt tctgatgctt tactaacttc atcttttaga	120
tttaaatcat tagtagatcc tagaggagcc agtttcagaa aatatagatt ctagttcagc	180
accaccgta gttgtgcatt gaaataatta tcattatgat tatgtatcag agcttctggt	240
tttctcattc ttatttcatt tattcaacaa ccacgtgaca aacactggaa ttacaggatg	300
aaatgagat aatccgctcc ttggcagtggt tatactatta tataacctga aaaaacaaac	360
aggtaatttt cacacaaagt aatagatata atgacacatt taaaataggg cactactgga	420
acacacagat aggacatcca ggttttgggt caatattgta gacttttttg tgatgagat	480
atgcagggtg atrccagaag gacaacaaaa acatatgtca gatagaaggg aggagcaa	540
gccaaagact ggagctgagg aagatcactg tgaaattcta tgtagtctag ttggctggat	600
gctagagcaa agaggtgg	618

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<210> SEQ ID NO 72
<211> LENGTH: 806
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 72

```
tctacgatgg ccatttgctc attgtcttcc ctctgtgtgt agtgagtgac cctggcagtg      60
tttgctgctc cagagtggcc cctcagaaca acagggtctg ccttgaaaaa accccaaaac    120
aggactgtgg tgacaactct ggtcagggtg gatttgacat gagggccgga ggcgggttgct    180
gacggcagga ctggagaggc tgcgtgcccg gcaactggcag cgaggctcgt gtgtcccca      240
ggcagatctg ggcactttcc caaccagggt ttatgccgtc tccaggaag cctcggtgcc      300
agagtgggtg gcagatctga ccatcccccac agaccagaaa caaggaattt ctgggattac    360
ccagtccccc ttcaaccagc ttgatgtaac cacctcattt tttacaaata cagaatctat    420
tctactcagg ctatgggctc cgtcctcact cagttattgc gagtgttgct gtccgcatgc    480
tccgggcccc acgtggctcc tgtgctctag atcatggtga ccccccgcc ctgtggttg      540
aatcgatgcc acggattgca ggccaaattt cagatcgtgt ttccaaacac ccttgctgtg      600
ccctttaatg ggattgaaag cacttttacc acatggagaa atatattttt aatttgtgat    660
gcttttctac aaggctcact atttctgagt ttaatgtggt tccaacactt aaggagactc    720
taatgaaagc tgatgaattt tcttttctgt ccaacaaggt aaaataaaaa taaaagtcta    780
tttagatggt gaaaaaaaaa aaaaaa      806
```

<210> SEQ ID NO 73
<211> LENGTH: 301
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 59
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 73

```
actctggtaa gcttggtggt gtccaagtga agtccctca gatgaggcgt gttggccana      60
gagccattgt caacagcaga gatgctgttg aaactcaatc ccaacttagc caaattattc    120
agtcctttca ggctagctgc atcaactctg ctgattttgt tgccatcaag atgtaattcc    180
gtaagggaag gaggaagacc ttgaggaatg ctggygatat tggyatcagc aatgcggatg    240
tasgaagagc ttcttcmctc cctggaaagc cccattttca atyccttgag ctcttcakcg    300
g                                          301
```

<210> SEQ ID NO 74
<211> LENGTH: 401
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 74

```
agtttacatg atccctgtaa cagccatggt ctcaaactca gatgcttcc ccatctgcca      60
agtgtgttct ggatacagag cacatcgtgg cttctggggg cactcagc ttaggctgtg    120
ggccacaga gcaactcatc ggctgggcta tgggtgggtg ggctctactc aagaagcaaa    180
gcagttacca gcacattcaa acagtgtatt gaacatcttt taaatatcaa agtgagaaac    240
aagaaggcaa cataataatg ttatcagaaa gatgttagga agtaaggaca gctgtgtaaa    300
```

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gcttgaggct gaaaagtagc ttgccagctt catttctttg gtttcttggg tagtgggccg 360
ccggaacagc aagatgtgag gttctggttc atggatcata t 401

```

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<210> SEQ ID NO 75
<211> LENGTH: 612
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 75
ttatattttca atttttattt tggttttctt acaaagggtg acattttcca taacagggtg 60
aagagtgttg aaaaaaaaaa tcaaattttt ggggagcgag ggaaggagtt aatgaaactg 120
tattgcacaa tgctctgac aatccttctt tttctctttt gccacaatt taagcaagta 180
gatgtgcaga agaaatggaa ggattcagct ttcagttaaa aaagaagaag aagaaatggc 240
aaagagaaa gtttttcaaa tttctttctt ttttaattta gattgagttc atttatttga 300
aacagactgg gccaatgtcc acaaagaatt cctggtcagc accaccgatg tccaaagggtg 360
caatatcaag gaaggcgag cgtgatggct tatttgtttt gtattcaatg attgtctttc 420
cccattcatt tgtcttttta gagcagccat ctacaagaac agtgaagtg aacctgctgt 480
tgccctcagc aacaagttca acatcattag agccctgtag aatgacagcc tttttcaggt 540
tgccagtctc ctcatccatg tatgcaatgc tgttcttgca gtggtagggtg atgttctgag 600
aggcatagtt gg 612

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<210> SEQ ID NO 76
<211> LENGTH: 844
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 76
ggcttttcgag cggccgcccg ggcaggctcg atggttctcg taaaaacccc gctagaaact 60
gcagagacct gaaattctgc catcctgaac tcaagagtgg agaatactgg gttgacccta 120
accaaggatg caaattggat gctatcaagg tattctgtaa tatggaaact ggggaaacat 180
gcataagtgc caatcctttg aatgttccac ggaacactg gtggacagat tctagtgtctg 240
agaagaaaca cgtttggttt ggagagtcca tggatggtgg ttttcagttt agctacggca 300
atcctgaact tcctgaagat gtccttgatg tgcagcykgc attccttcga cttctctcca 360
gccgagcttc ccagaacatc acatatcact gcaaaaatag cattgcatac atggatcagg 420
ccagtggaaa tgtaaaaga gcccctgaagc tgatggggtc aatgaagggt gaattcaagg 480
ctgaaggaaa tagcaaatcc acctacacag ttctggagga tggttgcacg aaacacactg 540
gggaatggag caaaacagtc tttgaatata gaacacgcaa tgctgttctt tgacattgca 600
ccaccaatgt ccagagggtc aatgtcaagg aacggcaggc gagatggctt atttgttttg 660
tattcaatga ttgtcttgcc ccattcattt gtcttttttg agcagccatc gactaggaca 720
gagtaggtga acctgctgtt gccctcagca acaagttcca catcggttga accctgcaga 780
agcacagcct tgttcaarct gcccgtctcc tcattccagat acctcggccg cgaccacgct 840
aatc 844

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<210> SEQ ID NO 77
<211> LENGTH: 314

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<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 77

```

ccagtcctcc acttgccctg atgagagtgg ggagtggcaa gggacgtttc tcctgcaata    60
gacacttaga tttctctctt gtgggaagaa accacctgtc catccactga ctcttctaca    120
ttgatgtgga aattgctgct gctaccacca cctcctgaag aggcttcctt gatgccaatg    180
ccagccatcc tggcatcctg gccctcgagc aggctgcggt aagtagcgat ctctgtctcc    240
agcgtgtctt ttatgtcaag cagcatcttg tactcctggt tctgagcctc catctcgcat    300
cggagctcac tcag                                     314

```

<210> SEQ ID NO 78

<211> LENGTH: 548

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 78

```

accaagagcc aagtgttaca caggatattt taaaaataaa atgttttttg aatcctcacc    60
tcccatgcta tcttctaaga taactacaaa tattcttcaa agatttaact gagtcttgcc    120
aaggacctcc caggactcta tccagaatga ttattgtaaa gctttacaaa tcccaccttg    180
gccctagcga taattaggaa atcacaggca aacctcctct ctccgagacc aatgaccagg    240
ccaatcagtc tgcacattgg ttttgtaga tactttgttg agaaaaacaa aggcctcgtga    300
tagtgcagct ctgtgcctac agagagcctc ccttttggtt ctgaaattgc tgatgtgaca    360
gagacaaaag tgctatgggt ctaaaacctt caataaagta actaatgaca ctcaagggtc    420
tgggactctg agacagacgg tggtaaaacc cacagctgcg attcacattt ccaatttatt    480
ttgagctctt tctgaagctg ttgcttccta cctgagaatt cccatttaga gagctgcaca    540
gcacagtc                                     548

```

<210> SEQ ID NO 79

<211> LENGTH: 646

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 79

```

accccgctac tatgtgaata aaggcagcta gaaaatggac tcaattctgc aagccttcat    60
ggcaacagcc catattaaga cttctagaac aagttaaaaa aaatcttcca ttccatcca    120
tgcatgggaa aagggcttta gtatagttta ggatggatgt gtgtataata ataaaatgat    180
aagatatgca tagtggggga ataaagcctc agagtccttc cagtatgggg aatccattgt    240
atcttagaac cgagggattt gtttagattg ttgatctact aatttttttc ttcacttata    300
tttgaatttt caatgatagg acttattgga aattggggat aattctgttg tggattataa    360
taatatcat tttttaaaaa ctcatcttgg tattgagtta gtgcattgac ttccaatgaa    420
ttgacataag cccatatttc attttaacca gaaacaaaaa ctgaaaaatg ttactcccta    480
aataggcaac aatgtatttt ataagcactg cagagattta gtaaaaaaca tgtatagtta    540
ctttagaaac aacttctgac acttgagggt tacccaatgg tctccttccc attctttata    600
tgaggtaaat gcaaaccagg gagccaccga ataaacagcc ctgagt                                     646

```

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<210> SEQ ID NO 80
<211> LENGTH: 276
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 16, 29, 32, 45, 53, 55, 58, 59, 65, 66, 75, 77, 85, 90, 97, 109, 112, 163, 170
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 80

gtctgaatga gcttcnctgc gagatgganc ancataaccc agaantccaa aancntanng 60
aacgnnaaaa cccgntngaa caagnaaacn gcaactnacg gccgcctgnt gnagggcgag 120
gagcccccacc tctcctcctc ccagttctcc tctggatcgc agncatccan agatgtgacc 180
tcttccagcc gccaaatccg caccaaggtc atggatgtgc acgatggcaa ggtgggtgtc 240
caccacgaa caggtccttc gcaccaagaa ctgagg 276

<210> SEQ ID NO 81
<211> LENGTH: 647
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 81

gtcctgcctt tcatcttttc tttaaaaaaa ataaatgttt aaaaaacatt tccctcagat 60
tttaaaattc atggaagtaa taaacagtaa taaaatatgg atactatgaa aactgacaca 120
cagaaaaaca taaccataaa atattgttcc aggatacaga tattaattaa gagtgacttc 180
gttagcaaca cgtagacatt catacatatc cggtggaaga ctggtttctg agatgcgatt 240
gccatccaaa cgcaaatgct tgatcttgga gtaggrtaat ggccccagga tcttcagaa 300
gctctttatg tcaaacttct caagttgatt gacctccagg taatagtttt caaggttttc 360
attgacagtt ggtatgtttt taagcttggt ataggacaga tccagctcaa ccagggatga 420
cacattgaaa gaatttcag gtattccact atcagccagt tcgttgtgag ataaacgcag 480
atactgcaat gcattaaaac gcttgaaata ctcatcaggg atgttgctga tcttattgtt 540
gtctaagtag agagttagaa gagagacagg gagaccagaa ggcagtctgg ctatctgatt 600
gaagctcaag tcaaggtatt cgagtgtttt aagaccttta aaagcag 647

<210> SEQ ID NO 82
<211> LENGTH: 878
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 82

ccttctttcc cactcaatt cttcctgccc tgttattaat taagatatct tcagcttgta 60
gtcagacaca atcagaatya cagaaaaatc ctgcctaagg caaagaaata taagacaaga 120
ctatgatatc aatgaatgtg ggtaagtaa tagatttcca gctaaattgg tctaaaaaag 180
aatattaagt gtggacagac ctatttcaaa ggagcttaat tgatctcact tgttttagtt 240
ctgatccagg gagatcacc cttctaattat ttctgaactt ggtaataaa agttttataag 300
atttttatga agcagccact gtatgatatt ttaagcaaat atgtttattha aaatattgat 360
ccttcccttg gaccaccttc atgttagttg ggtattataa ataagagata caacctgaa 420
tatattatgt ttatacaaaa tcaatctgaa cacaattcat aaagatttct cttttatacc 480

-continued

ttcctcactg gccccctcca cctgcccata gtcaccaa	540
aat tctgttttaa atcaatgacc	
taagatcaac aatgaagtat ttataaatg tatttatgct	600
gctagactgt gggtaaatg	
ttccatttt caaattattt agaattctta tgagttaaa	660
atttgtaaat ttctaaatcc	
aatcatgtaa aatgaaactg ttgctccatt ggagtagtct	720
cccacctaaa tatcaaatg	
gctatatgct aaaaagagaa aatatggta agtctaaa	780
ggctaattgt cctatgatgc	
tattatcata gactaatgac atttatcttc aaaacaccaa	840
attgtcttta gaaaaattaa	
tgtgattaca ggtagagaac ctgggccgcg accacgct	878

<210> SEQ ID NO 83
 <211> LENGTH: 645
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 83

acaaacattt tacaaaaag aacattacca atatcagtgg	60
cagtaagggc aagctgaaga	
ataaatagac tgagtttccg ggcaatgtct gtcctcaa	120
acatccaaac tgcgttcagg	
cagctgaaac aggcctcttt ccagtgaca agcatatgtg	180
gtcagtaata caaacgatgg	
taaatgaggc tactacatag gccaggttaa caaactctc	240
ttctcctcgg gtaggccatg	
atacaagtgg aactcatcaa ataatttaa ccaaggcga	300
taacaacgct atttcccatc	
taaaactcatt taagccttca caatgtcgca atggattcag	360
ttacttgcaa acgatcccgg	
gttgtcatac agatacttgt ttttacacat aacgctgtgc	420
catcccttcc ttactgccc	
cagtcagggtt tcctgttgtt ggaccgaaag gggatacatt	480
ttagaaatgc ttccctcaag	
acagaagtga gaaagaaagg agaccctgag gccaggatct	540
attaaacctg gtgtgtgctgc	
aaaaggagg gggaaggcag gaatttgaaa ggataaacgt	600
ctcctttgcg ccgaggaatc	
aggaagcgtg actcacttgg gtctgggacg ataccgaaat	645
ccggt	

<210> SEQ ID NO 84
 <211> LENGTH: 301
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 270, 284
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 84

tctgatgtca atcacaactt gaaggatgcc aatgatgtac	60
caatccaatg tgaatctct	
cctcttatct cctatgctgg agaaggatta gaaggttatg	120
tggcagataa agaattccat	
gcacctctaa tcatcgatga gaatggagtt catgggctgg	180
tgaaaatgg tatttgaacc	
agataccaag ttttgtttgc cacgatagga atagctttta	240
tttttgatag accaactgtg	
aacctacaag acgtcttgga caactgaagn ttaaatatcc	300
acanggggtt attttgcttg	
g	301

<210> SEQ ID NO 85
 <211> LENGTH: 296
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 16, 20, 240

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<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 85

```
agcgtgggtc gcggcncgan gtagagaacc gactgaaacg tttgagatga agaaagtctt 60
cctcctgata acagccatct tggcagtggc tgttggtttc ccagtctctc aagaccagga 120
acgagaaaaa agaagtatca gtgacagcga tgaattagct tcagggtttt ttgtgttccc 180
ttacccatat ccatttcgcc cacttcacac aattccattt ccaagatttc catggtttan 240
acgtaatttt cctattccaa tacctgaatc tgcccctaca actccccttc cttagcg 296
```

<210> SEQ ID NO 86

<211> LENGTH: 806

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 86

```
tctacgatgg ccatttgctc attgtctttc ctctgtgtgt agtgagtgc cctggcagtg 60
tttgctgct cagagtggcc cctcagaaca acagggtctg ccttggaata accccaaaac 120
aggactgtgg tgacaactct ggtcagggtg gatttgacat gagggccgga ggcggttgct 180
gacggcagga ctggagaggg tgcgtgcccg gactggcag cgaggctcgt gtgtcccca 240
ggcagatctg ggcactttcc caaccagggt ttatgccgtc tccaggaag cctcggtgcc 300
agagtgggtg gcagatctga ccatccccc acaccagaaa caaggaattt ctgggattac 360
ccagtcccc ttcaaccag ttgatgtaac cacctcattt ttacaaata cagaatctat 420
tctactcagg ctatgggctc cgtcctcact cagtattgc gagtgttgc gtccgcatgc 480
tccgggcccc acgtggctcc tgtgctctag atcatggtga cccccgcc ctgtggttg 540
aatcgatgcc acggattgca ggccaaattt cagatcgtgt ttccaaacac ccttgctgtg 600
ccctttaatg ggattgaaag cacttttacc acatggagaa atatattttt aatttgtgat 660
gcttttctac aaggctcact atttctgagt ttaatgtgtt tccaacactt aaggagactc 720
taatgaaagc tgatgaattt tcttttctgt ccaacaagt aaaataaaaa taaaagtcta 780
tttagatggtt gaaaaaaaa aaaaaa 806
```

<210> SEQ ID NO 87

<211> LENGTH: 620

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 87

```
tttttgcatc agatctgaaa tgtctgagag taatagtctt tgttgaaatt tttttgttc 60
atttttctgc acagtccatt ctgtttttat tactatctag gcttgaaata tatagtgtga 120
aattatgaca tccttcctct ttgttatttt cctcatgatt gctttggcta ttcaaagt 180
attttagttt catgtaaatt tttgaattgt attttccatt attgtgaaaa tagtaccact 240
gcaattttta taggaagttt attgaatcta tagattactt tggataatat ggcacttcaa 300
taatatcat gttttcaatt catagacaaa atatttttaa atttattgt atcttttcta 360
atttttcctt tttttattgt aaagatttac ctcccttggt aatattttcc tcagaaattt 420
atttttaag gtatagtcaa taaaattttc ttcctctatt ttgtcagata gtttaagtgt 480
atgaaaccat agatatactt gtatgttaat tttatatttt gctaatttac tgagtgtatt 540
```

-continued

tattagtitta gagaggtttt aatgtactgt ttatggtttt ttaaatataa gattacttat	600
tttttaaaaa aaaaaaaaaa	620

<210> SEQ ID NO 88
 <211> LENGTH: 308
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 9, 189, 194, 206, 238, 296
 <223> OTHER INFORMATION: n = A,T,C or G
 <400> SEQUENCE: 88

tagctgtgnt cagcaggccg aggttttttt tttttttgag atggagtctc gccctgtcac	60
ccaggctgga gtgcagtggc ctgatctcag ctcaactgcaa gctccacctc ctggattcac	120
gctattctcc tgcctcagcc tcccaagtag ctgggactac aggcgcccgc caccacgccc	180
agctaattnt ttgnattttt agtacnagat gcggtttcat cgtgttagcc agcatggnet	240
cgatctcctg acctcgtgaa ctgccgcct cgccctccca aagacctgcc cgggcnggcc	300
gctcgaaa	308

<210> SEQ ID NO 89
 <211> LENGTH: 492
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 448
 <223> OTHER INFORMATION: n = A,T,C or G
 <400> SEQUENCE: 89

agcggccgcc cgggcaggtc tgtaagtaa catacatatc accttaataa aaatcaagat	60
gaaatgtttt agaaactatt ttatcaaaaag tggctctgat acaaagactt gtacatgatt	120
gttcacagca gcactattaa tgccaaaaag tagacaaaac ctaaatgtcc attaactgat	180
aagcaaaatg tggatatatcc atacaatgga atattatgta gcccaaca tggcatggag	240
tactacaaca tggatgagcc tcaaaaacgt tatgctaaat gaaaaaagtc agatatagga	300
aaccacatgt catatgatcc catttatatg aaatagccag aaaaggcaag tcatagaaac	360
aagatagatc ggaaaatggg ttggaggact acaaatggca ccagggatct ttgaagtga	420
tggaatggt ctaaaatcag actgtggnntg tggttgaaca agtctgtaaa ttaccaaaa	480
tcggttaata ca	492

<210> SEQ ID NO 90
 <211> LENGTH: 390
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 106, 184, 206, 209, 234, 314
 <223> OTHER INFORMATION: n = A,T,C or G
 <400> SEQUENCE: 90

tcgagcggcc gcccgggcag gtacaagctt tttttttttt tttttttttt ttttctaaca	60
gttctctgtt ttattgcaat acagcaaagt ctggttaata ttaagngata tcaacataaa	120
gtattggtga ggagtctttt gtgacatttt ttaccatccc accttaataa tttctgtgca	180

-continued

```

aaanaaatcca catcattgtt tgggtancana ggatctctta aaaagttccc taanacactg 240
agggcataaa accaaacaaa ataaaataag gagtgatagg ctaaagcagt atcttcccct 300
ccatccacat ttgncaagca ttatatctta accaaaaaat gatcacacca ggccatgcaa 360
aactgtccaa tattaccgag aaaaaaccct 390

```

```

<210> SEQ ID NO 91
<211> LENGTH: 192
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 91

```

```

agcgtggtcg cggccgaggt ctgtcaatta atgctagtcc tcaggattta aaaaataatc 60
ttaactcaaa gtccaatgca aaaacattaa gttggtaatt actcttgatc ttgaattact 120
tccgttacga aagtccttca cttttttcaa actaagctac tatatttaag gcctgcccgg 180
gcggccgctc ga 192

```

```

<210> SEQ ID NO 92
<211> LENGTH: 570
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 519, 559
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 92

```

```

agcgtggtcg cggccgaggt ctgacaacta acaaagaagc aaaaactggc atcttggaca 60
tcctagtatt acacttgcaa gcaattagaa cacaaggagg gccaaggaaa aagtttagct 120
ttgaatcact tccaaatcta ctgattttga ggttccgcag tagttctaac aaaacttttc 180
agacaatggt aactttcgat taagaaagaa aaaaacccca aacatcttca ggaattccat 240
gccaggttca gtctcttcca gtgagcccg cttgctaaaag tccacgtgca ccattaatta 300
gtgtgggtcg cagcaccatg taaaaagaag cctattcacc accaaccaca cagactagac 360
atgtaaaagta ggatcaagta atggatgaca accatggtcg tggaatatgg tcaatgagag 420
tcagaaaagt acaggcacca gtacaagcag cagataacag aattgacggg ccaaaggata 480
aaaataggct tatttaataa ggatgctaca gaacacatnc acttctaatt ggaagctgct 540
ttacactggg tggcattgna ccatatgcat 570

```

```

<210> SEQ ID NO 93
<211> LENGTH: 446
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 328, 389
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 93

```

```

tcgagcggcc gcccgggcag gtccaggttt ttatttagtt gtgtaatctt ggacaagtta 60
cctaactttt ttgagtctga atatatttaa tctgcaaaat gagaatcatg ataatacgtc 120
ataggcttaa ttaggaggat taaatgaaat aatttatagg tggtgccatg gttacatata 180
agtattagta gttaattctt ttcctttgtt tacttttata gtatagggtg gatgaagggt 240

```

-continued

```

ccagtatagg caaaaataact acttgggggt aaagtagagt gtgatacttt atttgaatg    300
ttccctgaat ctgatcttta ctttttgnta ctgctgcact acccaaatcc aaattttcat    360
cccaacattc ttggatttgt gggacagcng tagcagcttt tccaatataa tctatactac    420
atcttttctt actttggtgc tttttg                                         446

```

```

<210> SEQ ID NO 94
<211> LENGTH: 409
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 94

```

```

cgagcgcccg cccgggcagg tccatcagct cttctgctta gaatacgagg cagacagtgg    60
agaggtcaca tcagtattcg tctatcaggg tgatgaccca agaaaggtga gtgagaaggt    120
gtcggcacac acgcctcttg atccacccat gcgagaagcc ctcaagttgc gtatccagga    180
ggagattgca aagcgccaga gccaacactg accatgttga aggcgttctc tccaggctgg    240
attcactgca ctcggaagaa ttctgccag ggaatttagt gtgggggtac caggaccagt    300
ttgtcttgat cttgagaccc ccagagctgc tgcattccata ggggtgttga ggactacacc    360
tggcctgcct tgcagtcatt ctttcttata tgttgaccca tttgcccac                    409

```

```

<210> SEQ ID NO 95
<211> LENGTH: 490
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 486
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 95

```

```

tcgagcgccc gccggggcag gtccacttgg tttgcagctt ccacacactg cacctaccta    60
ctacctctct tccatgctta actgggttta gaaaggtgag ctatgcgtag aagaactact    120
tgggatattc aagtgtgtga ttgaacgat aagcctatag ataacagtct gaagctgcaa    180
gggagacttt gttagtagac tactataaac aggtaaacta cctgtttgta cttgatatag    240
tgcatatgaa atgactgatt taatacaaaa ctacagaaca tgcaaaatth tttctgagat    300
gttaagtatt acttcagtgg agaacaaaac ttacttaacc tttcgctaata gcatgtagta    360
ccagaaaagca aacatggttt tagcttcctt tactcaaaat atgaacatta agtggttgtg    420
aattttgtct gccaaagtgtg tcagaaaata cattataaat aacctaagtt aaaaaaaga    480
aactgngaac                                         490

```

```

<210> SEQ ID NO 96
<211> LENGTH: 223
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 96

```

```

agcgtggtcg cggccgaggt ctggaagccc accctaggac ttgaatggca ccttgtcctt    60
tctctgccag taatgcaatc caacacaata tgctacaggg aaaacagaat ttccacggtg    120
ccgcctctgt gtacaaggga aacagcacgc aaagcaaaag gccacagagg gctccctgag    180
aatccagtac aactaagcga ggacctgccc gggcgggcgc tcg                                         223

```

-continued

<210> SEQ ID NO 97
<211> LENGTH: 527
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 404, 436, 451, 476
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 97

tcgagcggcc gcccgggcag gtctgtgcag gagacactga agtgggtagt gtccataatc 60
tttttagcct gttgctgaaa ttccagttgt actccttcaa accaaaatgc ttacaggatc 120
atgggaaagc ctcggttgca gaaatcaaga caggcaagtg ggaagataac tcggctttga 180
ggttaaacag atctgggttc aaagcatagt ttactctct gtctgtgaa gtgtcctggg 240
tgaagtcatt tcctctcttg aatttcagag aggatgaaaa tataaaaagt ataataacta 300
tcttcataat cttgtgaggg attaaagaag acgaagtgtg tgaaaagcta agcacagagc 360
aggcattcta caataagtag ttattatttt tggaaccatc ccgncctag cccagccca 420
attaccttct cttagnctct tcatatcgaa ngccgtaatc ttgaccttct cttgcnactg 480
gattggtgct ggttgatgcc caaacttccc gagatgctgt ctgggaa 527

<210> SEQ ID NO 98
<211> LENGTH: 514
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 455
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 98

tcgagcggcc gcccgggcag gtctgggtcc catggccctt ggggtggcct gactctgtca 60
ctattcctaa aaccttctag gacatctgct ccaggaagaa ctttcaacac caaaattcat 120
ctcaatttta cagatgggaa aagtgttct gagaccgac cagggtcagg ccaaggatcat 180
ccagcatcag tggtgggct gagactgggc ccagggaacc ctgtctgtc ctctttttcc 240
cagagctgtg agttctctag ccaaggctgc actcttgagg gagagccagg aagcatagct 300
gaggccatga caacctcact cttcacctga aaatttaacc cgtggcagag gatccaggca 360
catataggct tcggagccaa acaggacctc ggccgcgacc acgctaagcc gaattccagc 420
acactggcgg ccgttactag tggatcccg gcttnggtac caagcttggc gtaatcatgg 480
gcatagctgg ttctgggggt gaaaatggta tccg 514

<210> SEQ ID NO 99
<211> LENGTH: 530
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 430, 522
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 99

tcgagcggcc gcccgggcag gtctgaagaa acaggataaa atttggcagc cagtaatttt 60
gacaggaag ttacagcttg catgacttta aatatgtaaa tttgaaaata ctgaatttcg 120

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agtaatcatt gtgctttgtg ttgatctgaa aaatataaca ctggctgtcg aagaagcatg 180
ttcaaaaata tttaattcac ttcaaaatgt catacaaatt atggtgggtt ctatgcaccc 240
ctaaagcttc aagtcattta gctcaggtag atactaaagt aatatattaa ttcttccagt 300
acagtgggtg ttcataccat tgacatttgc ataccctaga ataatttaag aaagacatgt 360
gtaatatcca caatgttcag aaaagcaagc aaaagggtcaa ggaacctgct ttggttcttc 420
tggagatggn ctcatatcag cttcataaac attcattcta caaaatagta agctaaccat 480
ttgaacccca atttccagat taagcatatt ttctcataaa tnatgaagcc 530

```

```

<210> SEQ ID NO 100
<211> LENGTH: 529
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 100

```

```

agcgtggtcg cggccgaggt ccaggcacgg tggcttatgt gtgtaatccc agcacttggg 60
gaggctgagg gaggtggatc acttgagtcc aggagtttga gaccagtctg ggcaacatgg 120
cgaaacttca tcaactacca agaagaaaa aattagccag gtgtgggtgt gtatgcctgt 180
agtcccagat actctggtgg ctgaggtgag aggatagctt gagcccagga aattgaggct 240
gcagtgaact atgattgcac tactgtgtct cagcttgggc aacagagtga gatcttgtct 300
ccaaaagtcc ttgaaggatt ttaggaagtt gttaaaagtc ttgaaacgat gtttgggggc 360
atgttagggt tcttgaatgt ttaattcctc taataactgc ttattcaaga gaagcatttc 420
tgactgggtg cggggcagtg gcttcatgcc ccataatccc agtactttgg gaggtgaag 480
caggaacatt gcttgagccc aggacttcaa gaacagcctg ggtaacata 529

```

```

<210> SEQ ID NO 101
<211> LENGTH: 277
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 101

```

```

tcgagcggcc gcccgggcag gtcgcaggaa gaggatggaa actgaggagt ccaggaagaa 60
gagggaacga gatcttgagc tggaaatggg agatgattat attttggatc ttcagaagta 120
ctgggattta atgaatttgt ctgaaaaaca tgataagata ccagaaatct gggaaggcca 180
taatatagct gatttatattg atccagccat catgaagaaa ttggaagaat tagaaaaaga 240
agaagagctg agaacagacc tcggccgcga ccacgct 277

```

```

<210> SEQ ID NO 102
<211> LENGTH: 490
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 102

```

```

gcgtggtcgc ggccgaggtc tgacggcttt gctgtcccag agccgcctaa acgcaagaaa 60
agtcgatggg acagtttagg gggatgtgct aaagcgtgaa atcagttgtc cttaattttt 120
agaaagatth ttgtaactag gtgtctcagg gctgggttgg ggtccaaagt gtaaggaccc 180
cctgccctta gtggagagct ggagcttggg gacattaccc cttcatcaga aggaattttc 240
ggatgttttc ttgggaagct gttttggtcc ttggaagcag tgagagctgg gaagcttctt 300

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ttggctctag gtgagttgtc atgtgggtaa gttgaggta tcttgggata aagggctctc	360
tagggcacaa aactcactct aggtttatat tgtatgtagc ttatatTTTT tactaaggtg	420
tcacctata agcatctata aattgacttc ttttcttag ttgtatgacc tgccccgggc	480
ggccgctcga	490

<210> SEQ ID NO 103
 <211> LENGTH: 490
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 103

gagcggccgc ccgggcaggt ccaaaccagc ttgctcataa gtcattaacc aaatccatta	60
taggtaattt gttcagttca atgtttacaa ttcttatgga aaaaattagc aacacacaca	120
tttaaacgt gtgcatttac ctttgcgtga gtgcttaaaa tacatatctt tatttcaaga	180
tgacatttaa aaattattct aatatatcag cagcaaaaat ataatttgca attacaaaaa	240
actaaactag aatccttaag ttattctcat gtttacagtt gtgattcttt aataaatact	300
attatgcagc tctattgttt aagctttctg gatttggttt aaacacatgc atatatattg	360
tcaattgtgg gaagctttac aagttatatt ccatgcactt tttggacaga gttctaacag	420
agccagccag tccacaaaac aggaagaca aaagtgaat taactggggc aaaataggac	480
tcttatgcaa	490

<210> SEQ ID NO 104
 <211> LENGTH: 489
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 104

cgtggtcgcg gccgaggtcc aggcgtgtct cgaactcctg accttgatgat ctgccgcct	60
cggcctccca aagtgttggg attacaggca tgagccactg cgcccgaccg agttgaacat	120
ttaatgtcag actagccag agtttctcaa tctttttatt ctacttccc aaaggagccg	180
ttggagattt tcccctcaat ctctctcctt catgaaattt cataccacaa atatagtatg	240
ttttatttat gtactgtgac cctttgaagg atcacaaacc aatataatag tttttctttt	300
taaccctgca aggaccaagt ttttcccct gttggaaatg cataaactgg actgatgaat	360
tggtatagat ggcttttata atgaggatca gaaaaacttg aaattccttg gctacgacac	420
tccatattta tcaccgtata gggaggacct tggatatggg aagtagaac acttctacac	480
tttacagca	489

<210> SEQ ID NO 105
 <211> LENGTH: 479
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 142, 453
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 105

gcgtggtcgc gccgaggtc tgactggctt cagccccaga agttgagctg gcctttagac	60
aaaataattg cacctccctc tgctgcttat tcccttccgt ttttcatttg agtgtgaaca	120

-continued

gttagataaa atctgtggct gnetcttcca ccttgctcta gtttccattg ctgtgagcag	180
gccctcctat gcccgcatt tagctacaat gctgtggact cacttgattc tttttctccg	240
agctttgtct agaaatatgt gaaggtagg ttaagtgctt ctctgtgtag atccacttag	300
ccctgtctgc tgtctcgtg ggcgttgctt cgtctctcct ctcttccatc ctttccattt	360
gcttctcacc accctctggc ttcttttctt aatgcaataa aggcagtctt taacaaagaa	420
agaatgtggg ctttgagatt agacagacct ggnnttaaat tctgcttctg gctctccaa	479

<210> SEQ ID NO 106
 <211> LENGTH: 511
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 106

tcgcgccga ggtccaaac gtggattcca atgacctgcc ttgagccgc ggttgccagg	60
agttggacct gcagtagtat gggaagtca cggcctaaat accgactgcc ctctgacccc	120
accgtccagc gattctagaa catttctagt aggaagaca tagcaaggga ttttcatgat	180
tgggaaatac tgggagacaa gctgaagatt tgttaagggc tatgcttctg tcatctttta	240
ggtatttaag gctactcctt tagctagcta ctttgagctg tttaaagtga ctatctccct	300
acacagagtt acacaatgag catctctgaa agagaatatt accctggatt tccaaagatg	360
tactctaaca ggatgaccag gcaaagggtg acccggggga ggagtctgtt ataacactcg	420
gaccacatg ttctcaaggc acttcagaac tttgggaaat cattttgtac cggatcctca	480
gaaagcattt atggaaatac acatccttta g	511

<210> SEQ ID NO 107
 <211> LENGTH: 451
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 107

ggcgcgccg gcaggtccag aatatcaaat caaaaggta caaatgttca ctctctctc	60
cacctctta catattggat cttcaattgc aatagggagt gtaagatggg catttttagag	120
acgtagttgc atcagcagaa gcaaaccat cttatacaa tgggttttgg gtagagaaa	180
aggctgctaa aaattcacia gtcaccattc ccagaagca atgaatagcc gtagaagacc	240
aaggaagatc aacaagtctt caaagtgcta aagccagaga tttggccctt ccaaaatacc	300
accaggacgc ctggacccgt gggctctccg catgtcacca ctgactgcca ggatgctgct	360
gcacctccct tccttgagac acaacagaga gacagtgaag tcaccaaga ctgggatcat	420
cagaggctcc tcatgcttgc tacagagaag c	451

<210> SEQ ID NO 108
 <211> LENGTH: 461
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 108

ccgccccggc aggtcctgaa aacattcaga ctaatcaaaa tgggtactact gtaacttctt	60
ataatacata atataaaagt ttttgaaaga tatagacaca attaaccctt aaacaacaca	120
ctatctgatt ctcaaaagca atggctatctt aacaagatgt aaaaggacaa taacatatca	180

-continued

```

aagaactttc acacacctaa agatagcatt tagcagcaag ttagtcagac aaaacaaaca    240
caaatatfff cacatttcct atgtttgttt ttaactttac ttcataaagc cactgataat    300
tgaggtttct ttcaagtata agattttctaa aattaaaaac tgtttttgac atatfttttat    360
aaagaaataa aaagcaaaac gcaatccaac tatttatatg agtccctctt ctccaacagc    420
tttagatggt tttctgagta ctttttttaca cagaatatftt t                      461

```

```

<210> SEQ ID NO 109
<211> LENGTH: 441
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 109

```

```

ggccgcccgg gcaggctctga ttataagaga aagaaatcca gtgacacgag ggcaggcagg    60
ccccgctctg ctctgactga gaaaagcttc ctgatgtcag ggagatggaa ctgccaccat    120
cagaaccatg gcactttggg tgaagggtgtg tcagcgacca agggggcagg aaatgggcag    180
tgactaaggg ggcaggaaac aggcaggcac atggcaagggt tctcccagcc catcagccca    240
gtgatggcct cgattttgaa gctgcactac tgtctgaaaa gcacaattac tggtgactct    300
taacaaactt cagcatactg gggaaggaga ctgtcaagta actgaattgg aaagatgaaa    360
aagaaccatc tctaaaagtt gatgcttgtc agaagaataa cctcctttgt gcaagtcttg    420
caacatcttc attcaaccac a                      441

```

```

<210> SEQ ID NO 110
<211> LENGTH: 451
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 260, 361
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 110

```

```

ggtcgcggcc gaggtctggg gaaggggtga gaatccctgg gccttgccca gtcctgagct    60
ctgggtgtct gcagggaagc acagtgggtga gttagtgtta aagaaagcat ccagagaggt    120
aagaggggct tgggtagcac cctttgcctc tgtcacttcc gcaaaaactt cttgttgagg    180
aggaagatga gaaggttgac attgactttg gccttggtga agagtttcat gacagccaca    240
ccctcatact ggagctgcan gagatcctga tagtgaagct tgaaatcgct ccatgtccac    300
accaggaac ttggcattta cttcaaaactt tctgcctca tctccggcg tgatgtcaaa    360
natgacgttt cttgaagtga gaggcgggaa agatcttcaa tttccaccaa agacaccctt    420
tttccaggaa gcttgagcaa caagtgaat g                      451

```

```

<210> SEQ ID NO 111
<211> LENGTH: 407
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 26, 33, 36, 79, 105, 111, 133, 149, 186, 206, 220, 239,
245, 259, 336, 375, 383, 393
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 111

```

```

ggccgacgtt cgacctgact tcttngagc agntgncact acccgctctg aggaatgccg    60

```

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```

actgcagaca gtggcccang gcaaagagtg tgcgtcatcg atganattgg naagatggag 120
ctcttcagtc agnttttcat tcaagctgnt cgtcagacgc tgtctacccc agggactata 180
atcctnngca caatcccagt tcctanagga aagccactgn ctcttgtaga agaaatcana 240
cacanaaagg atgtgaacng tgtttaatgt caccaaggga aaacatgaaa ccaccttctg 300
ccagatatcg ggacgttgcg tgcagatcaa gcacgnaagt gaagacgcgt gcattccttg 360
ccttccgtga acgantgccc agntcaagaa gancctgatg gaaccct 407

```

```

<210> SEQ ID NO 112
<211> LENGTH: 401
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 363
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 112
tcgcggccga ggtcggccga ggtctgacat ctgttgctcg tgataaccac ttctgtattg 60
cgtcttaacc acttctgtat tgtgtggttt taactgccta aggcggcaat gggcagtggg 120
cccccttccc ttaggatggg tatcaattca acaatattta taaggcattt actgtgtgct 180
aagcatttgg aagaccacag ctacaaaata agacatagtt cctgccctcc aggccagcag 240
agggaggcac aaataccacg gaatctctga tgggtgtgaa gtgcggctcg gggccacaga 300
aaatgaccgt catggagacc ctgctaaagg tcggaccctg agcccaaagg ggtattcaga 360
agnggagatg attttggccc cactcataga tgggtggcaa a 401

```

```

<210> SEQ ID NO 113
<211> LENGTH: 451
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 113
gtcgcggccg aggtccatat taaaaagtcc atcataaaca aagactcctc ctcatggtat 60
gaatatgctc catatgccca taatggtgca taacggactt agaaattcca atgagtctta 120
gggttgaaat ttccaatgac ctgagcaagg cagctcccta tagcttcttg ataacatttt 180
acaccagag ttcaggctta aacagaccta tcaacacaat tattttcgga ttgtctgtct 240
agaaaacggc aatgctcaaa ggaatataaa taagggtggg gggacatatg cttccagcct 300
ggcctttctc catgtggtaa aaaacaatgg aatggctgtg ttaatttttt tttaatcttt 360
tctgaccttt actatgtttg gtaatggaaa taagtcaggg aaaacaaaat gaacaggtct 420
catcacttaa ttaatactgg gttttcttct t 451

```

```

<210> SEQ ID NO 114
<211> LENGTH: 441
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 114
ggccgcccgg gcaggcccat cctgtcagag atgggagaag tcacagacgg aatgatggat 60
acaaagatgg ttcactttct tacacactat gctgacaaga ttgaatctgt tcatttttca 120
gaccagttct ctggtccaaa aattatgcaa gaggaaggtc agcctttaaa gctacctgac 180

```

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```

actaagagga cactgttggt tacatttaaat gtgcctggct caggtaacac ttacccaaag 240
gatatggagg cactgctacc cctgatgaac atgggtgattt attctattga taaagccaaa 300
aagttccgac tcaacagaga aggcaaacaa aaagcagata agaaccgtgc ccgagtagaa 360
gagaacttct tgaaacttga cacatgtgca aagacaggaa gcagcacagt ctggcgggga 420
ggaagaaaaa aagaacagag a 441

```

```

<210> SEQ ID NO 115
<211> LENGTH: 431
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 317
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 115

```

```

gccgcccggg cagggtccatt ggcggtgaca aaaggaaaag aagcaaagag actcagtcca 60
taatgctgat tagttagaag aaagggctag gattgagaaa gtaccaggaa cttttaatta 120
tttaaaagag aatgctgact gttaatgttt taaatcttac tgttcaaatg tactaatatg 180
aatTTTTacc ctttgtgcat gaatattcta aacaactaga agacctccac aatttagcag 240
ttatgaaagt taaacttttt attataaaaa ttctaaacct tactgctcct ttaccaggaa 300
catgacacac tatttancat cagttgcata cctcgccaat agtataattc aactgtcttg 360
cccgaacaat catctccatc tggaagacgt aagcctttag aaacacattt ttctattaat 420
ttctctagaa c 431

```

```

<210> SEQ ID NO 116
<211> LENGTH: 421
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 116

```

```

gtcgcggccg aggtccagaa atgaagaaga agtttgaga tgtatttgca aagaagacga 60
aggcagagtg gtgtcaaatc ttgacggca cagatgcctg tgtgactccg gttctgactt 120
ttgaggaggt tgttcatcat gatcacaaca aggaaccggg gtcggtttat caccagttag 180
gagcaggacg tgagcccccg ccctgcacct ctgctgttaa acacccagc catcccttct 240
ttcaaaaggg atccttttcat aggagaacac actgaggaga tacttgaaga atttgattc 300
agcccgcgaa gagatttatc aagcttaact cagataaaat cattgaaagt aataaggtaa 360
aagctaagtc tctaacttcc aggccacggt ctcaagttaa tttcgaatac tgcatttaca 420
g 421

```

```

<210> SEQ ID NO 117
<211> LENGTH: 489
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 117

```

```

agcgtggtcg cggccgaggt aaggctgcga ggttggtgtg tctgggaaac tccgaggaca 60
gagggctaaa tccatgaagt ttgtggatgg cctgatgatc cacagcggag accctgttaa 120
ctactacgtt gacactgctg tgcgccacgt gttgctcaga cagggtgtgc tgggcatcaa 180

```

-continued

```

ggggaagatc atgctgccct gggacccaac tggtaagatt ggcctaaga agcccctgcc 240
tgaccacgtg agcattgttg aacccaaaga tgagatactg cccaccaccc ccatctcaga 300
acagaagggt gggaagccag agccgcctgc catgccccag ccagtcccca cagcataaca 360
gggtctcctt ggcagacctg cccgggcggc cgctcgaaag cccgaattcc agcacactgg 420
cgcccgttac tagtggatcc cagctcggtt ccaagcttgg cgtaatcatg gtcatactg 480
gtttcctgt 489

```

```

<210> SEQ ID NO 118
<211> LENGTH: 489
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 118
tcgagcgccc gcccgggcag gtattgaata cagcaaaatt ctatatacaa agtgacctgg 60
acctgtgct tcaaacatg atcctttctt actaatatct tgatagtcgg tccatagagc 120
attagaaagc aattgactct taaataaaca gaaaagtgcc taatgcacat taaatgaatg 180
gcctaactac tggaaactta gtatttctat aagggtgatta acataggtag gatccagttc 240
ctatgacagg ctgctgaaga acagatatga gcatacaagag gccattttgt gcaactgccac 300
cgtgatgcc tctgttttct ggatcataat gttccatta tctgattcta gacacaccac 360
aggaatatca gtggggtcag aggttagctt agctgcttgc tgggctagaa cagatatcac 420
tccagcatgc tcatctgaca ggggtccgcg gcaaccaga ttaagtcctt gtgaatctgt 480
gcacaggga 489

```

```

<210> SEQ ID NO 119
<211> LENGTH: 181
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 119
taggttccag agacttttgg cccaggagga atatttactt ttagctctgg acatcattac 60
aaaaaggaat atttccaaa cctcttcaga ccgagaatac atgggtaaaa ttattaaata 120
gttgataat aaaaataatt ttttccttaa aaaaaaaaaa aacctcgcc gcgaccacgc 180
t 181

```

```

<210> SEQ ID NO 120
<211> LENGTH: 489
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 422, 487
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 120
gcgtggtcgc ggccgaggtc catttaaac aaagaaaaat actaaagcca ctagtaaaca 60
tctgatgtgc aaaatacaac atcctctagt tggctttatg ccattattac ataagctcca 120
aatagctcat cttaaatata aaagaaaaag tggctgtccc atctctgctg cataaatcag 180
atTTTTTTTT aaaggtttag agtactttta ggaagggaag ttcaaaactg ccagtgaat 240
tcacagagaa tacaaattta gcaatttaat ttcccaaagc tctttgaaga agcaagagag 300

```

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```

tctctcttct taatgcagtg ttctcccaag aggaactgta attttgcttg gtacttatgc 360
tgaggagatat gcaaaatgtg tttttcaatg tttgctagaa tataatgggt cctcttcagt 420
gnctggttca tcctggaact catgggttaa gaaggacttc ttggagccga actgcccggt 480
cgggccttt 489

```

```

<210> SEQ ID NO 121
<211> LENGTH: 531
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 121

```

```

cgagcggcgc cccgggcagg tggccagcgc tggccccga gacgccgaga tggaggaaat 60
at ttgatgat gcgtcacctg gaaagcaaaa ggaaatccaa gaaccagatc ctacctatga 120
agaaaaaatg caaactgacc gggcaaatag attcgagtat ttattaaagc agacagaact 180
ttttgcacat ttcatccaac ctgctgctca gaagactcca acttcacctt tgaagatgaa 240
accagggcgc ccacgaataa aaaaagatga gaagcagaac ttactatccg ttggcgatta 300
ccgacaccgt agaacagagc aagaggagga tgaagagcta ttaacagaaa gctccaaagc 360
aaccaatggt tgcaactcgt ttgaagactc tccatcgtat gtaaaatggg gtaaaactgag 420
agattatcag gtcccagga ttaaactggc tcatttcttt gtatgagaat ggcacatcatg 480
gtatccttgc agatgaaatg ggccataggaa agactcttca acaatttctc t 531

```

```

<210> SEQ ID NO 122
<211> LENGTH: 174
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 122

```

```

tcgagcggcc gcccgggcag gtctgccaac agcagaggcg gggcctccgg catcttcaaa 60
gcacctctga gcaggctcca gccctctggc tgccggagggt gtctggggtc tcctctgagc 120
tcggcagcaa agcagatggt atttctctcc cgcgacctcg gccgcgacca cgct 174

```

```

<210> SEQ ID NO 123
<211> LENGTH: 531
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 152, 373, 482, 494, 496, 502
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 123

```

```

agcgtggtcg cggccaggt cctcaaccaa gagggttgat ggcctccagt caagaaactg 60
tggctcatgc cagcagagct ctctcctcgt ccagcaggcg ccatgcaagg gcaggctaaa 120
agacctccag tgcacaaaca tccatctagc anagagaaaa ggggcactga agcagctatg 180
tgtgccaggg gctaggggct cccttgcaaga cagcaatgct acaataaagg acacagaaat 240
gggggagggt ggggaagccc tttttttata acaaagtcaa acagatctgt gccgttcatt 300
ccccagaca cacaagtaga aaaaaaccaa tgcttggtgt ttctgccaag atggaatatt 360
ctccttctct aanttcaca catggccgtt tgcaatgctc gacagcattg cactgggctg 420
cttgtctctg tggctctggc accagtagct tgggccccat atacacttct cagttccac 480

```

-continued

anggccttatg gccnangggc angctccaat tttcaagcac cacgaaggaa g 531

<210> SEQ ID NO 124

<211> LENGTH: 416

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 124

tcgagcggcc gcccgggcag gtccatctat actttctaga gcagtaaatc tcataaattc 60
acttaccaag ccaggaata atgactttta aagccttgaa tatcaactaa gacaaattat 120
gccaaattctg attttctaca tatacttaga ttacacaaag ataaagcttt agatgtgatc 180
attgtttaat gtagacttat ctttaaagtt ttttaattaaa aactacagaa gggagtaaac 240
agcaagccaa atgatttaac caaatgattt aagagtaaaa ctactcaga aagcattata 300
cgtaactaaa tatacatgag catgattata tacatacatg aaactgcaat tttatggcat 360
tctaagtaac tcatttaagt acatttttgg catttaaaca aagatcaaata caagct 416

<210> SEQ ID NO 125

<211> LENGTH: 199

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 112, 160, 195

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 125

agcgtggtcg cggccgaggt gctttttttt tttttttttt tttttttttt gctattctaa 60
aggggaaggc ccctttttat taaacttgta cattttactt tccttctttc anaatgctaa 120
taaaaaactt ttgtttatag ttaaaaaaac cataaatcan acaaacaaaa gaaacgattc 180
caacatcact tctgngatg 199

<210> SEQ ID NO 126

<211> LENGTH: 490

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 126

cgtaggtcgc gccgaggtcc agttgctcta agtggattgg atatggttgg agtggcacag 60
actggatctg ggaaaacatt gtcttatttg cttcctgcc a ttgtccacat caatcatcag 120
ccattcctag agagaggcga tgggcctatt tgtttggtgc tggcaccaac tcgggaactg 180
gccaacagg tgcagcaagt agctgctgaa tattgtagag catgtcgctt gaagtctact 240
tgtatctacg gtggtgctcc taagggaacca caaatacgtg atttgagag aggtgtggaa 300
atctgtattg caacacctgg aagactgatt gacttttttag agtgtggaaa aaccaatctg 360
agaagaacaa cctaccttgt ccttgatgaa gcagatagaa tgcttgatat gggctttgaa 420
cccaaaataa ggaagattgt ggatcaaata agacotgata ggcaaactct aatgtggagt 480
gcgacttggc 490

<210> SEQ ID NO 127

<211> LENGTH: 490

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

-continued

<400> SEQUENCE: 127

```

cgtggtcgcg gccgaggtcg gccgaggtct ggagatctga gaacgggcag actgcctcct    60
caagtgggtc cctgaccctt gacccccgag cagcctaact gggaggcacc cccagcagg    120
ggcacactga cacctcacac gccaggggtat tccaacagac ctgaagctga gggctcctgtc    180
tgttagaagg aaaactaaca agcagaaaagg acagccacat caaaaaccca tctgtacatc    240
accatcatca aagaccaaaa gtataataaa ccacaaagat gggaaaaaaa cagaacagaa    300
aaactggaaa ctctaaaaag cagagcacct ctctctctcc aaaggaacgc agttcctcac    360
cagcaatgga acaaagctgg atggagaatg actttgacga gctgagaaaa gaacgcttca    420
gacgatcaaa ttactctgag ctacgggagg acattcaaac caaaggcaaa gaagttgaaa    480
actttgaaaa                                490

```

<210> SEQ ID NO 128

<211> LENGTH: 469

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 69, 106, 140, 152, 165, 196, 224, 233, 241, 258, 260, 267, 291, 347, 395

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 128

```

cgtggtcgcg gccgaggtgc tttttttttt tttttttttt tttttttttt tgctgattta    60
ttttttctnt ttattgttac atacaatgta taaacacata aaacanaaaa cagtagggat    120
cctctaggat ctctagggan acagtaaagt anaaagaggt ctcanaaaca ttttttttaa    180
gtacaagaca ttcagngctc ggcccaaagg cgtaaaaggt ttanagccag canatagctg    240
nactaaaggc tccgtctntn tccccanagc caggacaacc ccagggagct ntccattagc    300
agccagtcca cgcaggcagg atgctgcgga aaaagctcta tgctganaac attccccttg    360
atggaaagaa gggcaacaca aaaggggtaa ctaanagctc cttcctctcg tgagggcgac    420
aactgaggaa cagaaaagga gtgtcccatg tcacttttga cccctctccc    469

```

<210> SEQ ID NO 129

<211> LENGTH: 419

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 129

```

gcgtggtcgc gccgaggtgc tgattttcat ttaaatattt cagagctata gcatttgcct    60
ccatgctcaa atccacacca ttggggctta agccgctcat gccaacatta gcaaatgaca    120
tgcagtttaa tccagagatc actgcttctg ggctgatgca tgccaacaca ctggcgtgat    180
ccacgttatg tgcatttttc ttcaactttg tgggagaatc aatttttact ccaaggcttc    240
ttagttgctt aagagttgca ttaaggacac aatctttgtc caccagtctt gaatgatgtg    300
tttttttctt tgtatggtaa acgttttggg ttctgggtgca ttcatgactg ataattactg    360
ctttggtaga cggctgctca agtttctctg gaggaactat ttaataggtg ggttacttg    419

```

<210> SEQ ID NO 130

<211> LENGTH: 354

<212> TYPE: DNA

-continued

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 130

```
agcgtgggtcg cggccgaggt ccatctgagg agataaccac atcactaaca aagtgggagt    60
gaccccgagc agcacgctgt ggaattccat agttggtctc atccctggtc agtttccaca    120
tgatgatggt cttatctcga gaggcggaga ggatcatgtc cgggaactgc ggggtagtag    180
cgatctgggt taccagccg ttgtggccct tgagggtgcc acgaagggtc atctgctcag    240
tcatggcggc ggcgagagcg tgtgtcgctg cagcgacgag gatggcactg gatggcttag    300
agaaactagc accacaacct ctctgcccgc acctgcccgg gcggcccgtc cgaa        354
```

<210> SEQ ID NO 131

<211> LENGTH: 474

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 421

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 131

```
cgagcggccg cccgggcagg tctggcagca gcttcctctg gaataattga cagctttgtg    60
ctgcctgact aaaatttgaa atgacaaccg ctgaatgtaa aatgatgtac ctacaatgag    120
agagatttag gaatactatc tgtcaatcca tagatgtaga aacaaaacaa actacagaat    180
gaaaacaaac ttatttttaa ccaaagaaac aaatgtatcc aaaatatagt ccatgatata    240
tttgattact agtataacca cagttgaaaa cttaaaaaaa aaaattgaca ttttttgtaa    300
tggttactaa tggatttata aaaggtttct gtttccaaag atgttattgg ggtccacata    360
ttccttgaag acttcagcat ccaaagccc gacatcagag atactttcct ttagccattg    420
nttcccgtaa cttgcccact ccatggtgat gtgacaggct tcccttcatt agca        474
```

<210> SEQ ID NO 132

<211> LENGTH: 474

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 403

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 132

```
ggccgagggt gggaattcat gtggagggtc gagtggaagc aggtgtgaga ggggccagca    60
gaaggaaaca tggtgcca agtgtttgag tccattggca agtttggcct ggccttagct    120
gttgaggag gcgtgggtgaa ctctgcctta tataatgtgg atgctgggca cagagctgtc    180
atctttgacc gattccgtgg agtgcaggac attgtggtag ggaagggtc tcattttctc    240
atcccggtgg tacagaaacc aattatcttt gactgccgtt ctgcaccacg taatgtgcca    300
gtcatcactg gtagcaaaga ttacagaat gtcaacatca cactgcgcat cctctccggg    360
cctgtcgcca gccagcttcc tcgcatcttc accagcatcg ganaggacta tgatgaaccg    420
tgtgtgcggt tccatcaca ctgagatcct caagtcagtg gtggctcgct ttga        474
```

<210> SEQ ID NO 133

<211> LENGTH: 387

<212> TYPE: DNA

-continued

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 133

```

tgctcgagcg gccgccatg tgatggatat ctgcagaatt cggcttagcg tggtcgcggc    60
cgaggtctgc gggccctta gcctgccctg cttccaagcg acggccatcc cagtagggga    120
ctttccaca ctgtgccttt acgatcagcg tgacagagta gaagctggag tgcctcacca    180
cacggcccg aaacagcggg aagtaactgg aaagagcttt aggacagctt agatgccgag    240
tggggcaatg ccagaccaat gatacccaga gctacctgcc gccaaactgt tgagatgtgt    300
gtttgactgt gagagagtgt gtgtttgtgt gtgtgttttg ccatgaaactg tggccccagt    360
gtatagtgtt tcagtggggg agaactg                                     387

```

<210> SEQ ID NO 134

<211> LENGTH: 401

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 134

```

ggccgcccgg gcaggtctga tgaagaacac ggggtgtgac cttgccaatg acgccaatgc    60
tgagcggctc aagagtgttg tgggcaactt gcacggctg ggagtcacca acaccattat    120
cagccactat gatggggccc agttcccaa ggtggtgggg ggctttgacc gactactgct    180
ggatgctccc tgcagtggca ctggggtcat ctccaaggat ccagccgtga agactaacia    240
ggatgagaag gacatcctgc gcttgctgc acctccagaa ggaagttgct cctgagtgtc    300
attgactctt gtcaatgcga ccttcaagac aggaggctac ctggtttact gcacctgttc    360
tatcacagtg agacctctgc catggcagaa caggggaagc t                                     401

```

<210> SEQ ID NO 135

<211> LENGTH: 451

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 135

```

ggtcgcgccc gaggtctgtt cctgagaaca gcctgcattg gaatctacag agaggacaac    60
taatgtgagt gaggaagtga ctgtatgttg actgtggaga aagtaagtca cgtgggccct    120
tgaggacctg gactgggtta ggaacagttg tactttcaga ggtgaggtgt cgagaaggga    180
aagtgaatgt ggtctggagt gtgtccttgg ccttggctcc acagggtgtg ctttcctctg    240
gggcccgtcag ggagctcatc ccttggttgc tgccagggtg gggtaaccgg gtttgacact    300
gaggagggtg acctgctggc tggagcggca gaacagtggc cttgatttgt cttttggaag    360
attttaaaaa ccaaaaagca taaacattct ggtccttcac aatgctttct ctgaagaaat    420
acttaacgga aggacttctc cattcaccat t                                     451

```

<210> SEQ ID NO 136

<211> LENGTH: 411

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 136

```

ggccgcccgg gcaggtctga atcacgtaga atttgaagat caagatgatg aagccagagt    60
tcagtatgag ggttttcgac ctgggatgta tgtccgcgtt gagattgaaa atgttcctctg    120

```

-continued

tgaatttggtg cagaactttg acccccttta cccattatc ctgggtggct tgggcaacag	180
tgagggaaat gttggacatg tgcaggtggg tccctttgct gcgtatttg tgcctgaggc	240
tctgtggatt tccccccat caatcatctt accctctcat cccctcaga tgcgtctgaa	300
gaaacatctc tggataaga aaatcctcaa gtcccaagat ccaatcatat tttctgtagg	360
gtggagggaag tttcagacca tcctgctcta ttatatccga agaccacaat g	411

<210> SEQ ID NO 137
 <211> LENGTH: 211
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 186
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 137

cggccgcccc ggacagtcgg ttggtgcggc ctccattgtt cgtgttttaa ggcgccatga	60
ggggtgacag aggcctgtgt cgtgtggggc gctttggttc cagaggaggc ccaggaggag	120
ggttcaggcc ctttgaccca catatcccat ttgacttcta tttgtgtgaa atggcctttc	180
cccggntcaa gccagcacct cgatgaaact t	211

<210> SEQ ID NO 138
 <211> LENGTH: 471
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 138

gccgccccgg caggtctggg ctggcgactg gcattccaggc cgtaactgca aatctatgct	60
aggcggggtc tcccttctgt gtgttcaagt gttctcgact tggattctta actattttta	120
aaaaatgact gagtttgggt taaaaaccaa ccacaaaat ggatttcaac acagctctaa	180
agccaagggc gtggccggct ctccaacac agcgactcct ggaggccagg tgcccatggg	240
cctacatccc ctctcagcac tgaacagtga gttgattttt ctttttaca taaaaaagc	300
tgagtaatat tgcattggag taccaagaaa ctgcctcatt ggaacaaaa actatttaca	360
ttaataaaaa agcctggccg caggctgcgt ctgccacatt tacagcacgg tgcgatgcac	420
acggtgacca aaccacggag gcaagcttct ggcactcaca ccacgaccgc c	471

<210> SEQ ID NO 139
 <211> LENGTH: 481
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 384
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 139

gtcgcggccg aggtctgttc tttagctcag atttaaacct gctgtctctt ctttatttgc	60
agaatgaatt ccagttcct gagcagttca agaccctatg gaacgggcag aagttggtca	120
ccacagtgc agaaattgct ggataagcga agtgccactg ggttctttgc cctcccttca	180
caccatggga taaatctgta tcaagacggt tcttttctag atttcctcta cttttttgct	240
cttaaaactg cttctctgct ctgagaagca cagctacctg ctttactga aatatacctc	300

-continued

```

aggctgaaat ttgggggtggg atagcaggtc agttgatctt ctgcaggaag gtgcagcttt 360
tccatatcag ctcaaccacg ccgncagtc attcttaagg aactgccgac taggactgat 420
gatgcatttt agcttttgag cttttggggg gtattctacc aaccaacagt ccatttgaa 480
a 481

```

```

<210> SEQ ID NO 140
<211> LENGTH: 421
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 372
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 140

gtcgcggcgg aggtttccca tttaagaaaa atagatcttg agattctgat tcttttccaa 60
acagtccctt gctttcatgt acagcttttt ctttacctta cccaaaattc tggccttgaa 120
gcagttttcc tctatggcct tgccctttctg atttctctcag aggcctcgagt ctttaatata 180
accccaaatg aaagaaccaa ggggaggggt gggatggcac tttttttgt tggctctgtt 240
ttgttttgtt tttgtgttg ttgggttcgg ttatttttta agattagcca ttctctgctg 300
ctatttccct acataatgtc aatttttaac cataattttg acatgattga gatgtacttg 360
aggctttttt gntttaattg agaaaagact ttgcaatttt ttttttagga tgagcctctc 420
c 421

```

```

<210> SEQ ID NO 141
<211> LENGTH: 242
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 4, 6, 20, 31, 35, 39, 72, 94, 141, 142, 211, 222
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 141

cgantngccc gcccgggcan gtctgtctaa nttntcang gaccacgaac agaaactcgt 60
gcttcaccga anaacaatat cttaaacatc gaanaattta aatattatga aaaaaaacat 120
tgcaaaatat aaaataaata nnaaaaggaa aggaaacttt gaaccttatg taccgagcaa 180
atccaggtct agcaaacagt gctagtccta nattacttga tntacaacaa cacatgaata 240
ca 242

```

```

<210> SEQ ID NO 142
<211> LENGTH: 551
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 15, 19, 32, 73, 110, 278, 405, 436, 473, 510
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 142

agcgtggtcg cggcncgang tccacagggc anatattctt ttagtgtctg gaattaaaat 60
gtttgaggtt tangtttgcc attgtctttc caaaaggcca aataattcan atgtaaccac 120
accaagtgca aacctgtgct ttctatttca cgtactgttg tccatacagt tctaaatata 180

```

-continued

tgtgcagggg attgtagcta atgcattaca cagtcgttca gtcttctctg cagacacact	240
aagtgatcat accaacgtgt tatacactca actagaanat aataagcttt aatctgaggg	300
caagtacagt cctgacaaaa gggcaagttt gcataataga tcttcgatca attctctctc	360
caagggggccc gcaactaggc tattattcat aaaacacaac tgaanagggg attggtttta	420
ctggtaaadc atgtgntgct aaatcatttt ctgaacagtg gggctctaat cantcattga	480
tttagtggca gccacctgcc cggcgccgcn tcgaagccca attctgcaga tatccatcac	540
actggcgccc g	551

<210> SEQ ID NO 143
 <211> LENGTH: 515
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 5, 286, 498
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 143

cgagngggccc gcccgggcag gtatcttcac aaactcaaca aaggcactac atgagacttc	60
acattcccct agtccaatag ctgacaaatt tttgcaacgt tctgcaatgc gaattaactc	120
ttcatcaagt gggcgtaate catttgcaca cactactagt tcaaccagtc tagggcatgt	180
cattcccaca cggccaagca catctttgct tactgatctc ccaaagtaca gatgggtggc	240
aggtatttca tagcgaaaga aggggtcaaa ttcttcttca tataanaaaa aatacatcac	300
taagttcact ttgggtgaat gtctgatgaa agcatcccag ctactcttct gaatagtatg	360
gaagtgtgtc tgtccaggat tctcactgac tacatcaatg cgcaaagtgt ctaatcgaac	420
atgtttttca gaagacaatg caagtaacaa ctcactctc aataagtggt aagttcaggg	480
ctagttctct taagccngca cactgatcag cacac	515

<210> SEQ ID NO 144
 <211> LENGTH: 247
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 11, 20, 42, 115, 152, 165, 181, 195, 208, 221
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 144

tgcattctct ntggatgcan acctgcccgt tggtagggac tntgctcaca cggaacatgg	60
acggttacac ctgtgccgtg ggtgacgtcc accagcttct ggatcatctc ggcnggggtg	120
ttgtggaagg gcagactatc cacctccatg cncacgatgc ccganacgcc actccggact	180
ntgtgctgca ccaanatgcc cagcatntta tcttcaagca nagcacttat cagggtcctt	240
ggcacac	247

<210> SEQ ID NO 145
 <211> LENGTH: 309
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 18, 155, 247
 <223> OTHER INFORMATION: n = A,T,C or G

-continued

<400> SEQUENCE: 145

```

cgtgggtcgc ggccccgagt ctgctgtaac aaaacacccat agtctgggca gtcctagac      60
aatggaattt tttttctcac gcttttgag gctggattcc aagatcaagg ttccaggaga      120
ctcagtgtct ggcaaggtct cggtttctgc ctcanagatg gtgccatctg gctgtgtcct      180
cacaagtagg aaggtgcaag aagctcccct caggctctgt ctgtaagaca ctgatcccat      240
tcatganggg gaaacgtaat gacctaatca gccccagag accccacttc taacaccatc      300
accttgggg                                     309

```

<210> SEQ ID NO 146

<211> LENGTH: 486

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 16, 97, 154, 244, 275, 322, 347, 349, 352, 357, 449, 460, 472

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 146

```

agcgtgggtc gcggcncgac gtccgtgcc ttttcacag cccgagaact aatacaagat      60
gctgacatca tttttgtcc ctacaactat cttctanatg cacaataag ggaaagtatg      120
gatttaaatc tgaaagaaca gttgtcatt ttanatgaag ctcataacat cgaggactgt      180
gctcgggaat cagcaagtta cagtgtaca gaagttcagc ttcggtttgc tcgggatgaa      240
ctanatagta tggtaacaa taatataagg aaganagatc atgaaccctc acgagctgtg      300
tgctgtagcc tcattaattg gntagaagca aacgctgaat atcttgnana angagantat      360
gaatcagctt gtaaaatatg gagtggaaat gaaatgctct taactttaca caaaatgggt      420
atcaccactg ctacttttcc cttttgcng gtaagatatn tttctacct gngaaacgta      480
tttaag                                     486

```

<210> SEQ ID NO 147

<211> LENGTH: 430

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 13, 26, 28, 289, 299, 352, 390, 399

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 147

```

gccgccccgg cangttcgac attacntnga gttccatgat gtacaattct ttcacgaaaa      60
acaatgaatg caagaatttg aggatctcct tactcctccc ttttacagat ggtctctcaa      120
tcccttcttc ttctctttca tttcatctt cttctgaacg cgctgccggg taccacggct      180
ttctttgtct ttatcgtgag atgaagtgta tgcttctgtt tctctacca taactgaaga      240
aatttcgctg caagtctctt gactggctgt ttctccgact tcgccttnt gtcaaacng      300
agtcttttta cctcatgccc ctcagcttca cagcatcttc atctggatgt tnattttctca      360
aagggtcac tgaggaaact tctgattcan atgtcgaana gcaactgtgaa gttttctctt      420
cattttgctg                                     430

```

<210> SEQ ID NO 148

<211> LENGTH: 483

-continued

<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 20, 24, 53, 55, 374, 381, 423, 431, 459
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 148

ccccggcagg tctgtgttgn ttttcaaccg gtgtcctccc cagcgtccag aananggaaa	60
tgtggagcgg gtgatgatga cccctcgtg tcctgtcacc tcctgcacag ctctgtatgt	120
gggtctggtc tgggaccacc cgtacagggt gtgcacgttg tagtgctcca cgggggagct	180
gtccggcagg atctgtgtgac tctccatgca cagagtcttg ctgctcaggc ccttgtccct	240
agattccaaa tatggcatat aggggtgggt tatttagcat ttcattgtg cagcccctga	300
cagatccatc cacaaaaatt gatggctcat tcatatcaat ccacaatcca tcaaaactca	360
agctcttctc tggntctcga nggtttgcat agaactcttc tatctctttc ttccaccacg	420
canacctcgg ncgcgaccac gctaagccga attctgcana tatccatcac actggcggcc	480
gct	483

<210> SEQ ID NO 149
<211> LENGTH: 439
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 11, 359, 384, 402
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 149

ctttcacgaa nacaatgaat gcaagaattt gaggatctcc ttactcctcc cttttacaga	60
tgggtctctca atcccttctt cttcctcttc atcttcatct tcttctgaac gcgctgccg	120
gtaccacggc tttctttgtc tttatcgtga gatgaagggt atgcttctgt tttttctacc	180
ataactgaag aaatttcgct gcaagtctct tgactggctg tttctccgac ttgcctttt	240
tgcaaacgtg agtcttttta cctcatgccc ctacgcttcc acagcatctt catctggatg	300
ttcatttctc aaagggtcta ctgaggaaac ttctgactca catgtcgaag aagcactgng	360
agtttctctt catttctgtc aaanttgctc tttgctggct gngctctcag accaccatt	420
tggctgcatg ggggctgac	439

<210> SEQ ID NO 150
<211> LENGTH: 578
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 4, 15, 260, 336, 371, 430, 461, 535, 572
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 150

ggcncgccc ggcangtcca ctccactttt gagctctgag ggaatacctt caggaggag	60
agggtcagg agtcctggca gctccgcagc agagattcac attcattcag agacttggtg	120
tccagtgcga tgccattgat cgcaacgata ctgtctccca cagcaaggga cccttcttta	180
gcggcagggc ttccaggcag cacagcggca gcatacactc cattctccag actgatgcca	240
ctgtctttct gtccactgan gttgatgtgc agcggcgtga ccaccttccc acccaggag	300

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```

ttcctccgcc gcacgacccat gttgatgggc cccctnccca ttgaggagcg ccttgatggc 360
ctgcttcttg nccttggtga tgaagtccac atcggtgatt ctacacagcca gtcattgacc 420
cttaagcggg catcagcaat gcttcctttg gccactttag ngacaaatat gccacagtcc 480
ccgggaaaca aggggtcattc acaccttctg gcatatcaaa cacctcggcc gggancacta 540
agccgaattc tgcagatatt catcacactg gngggccg 578

```

```

<210> SEQ ID NO 151
<211> LENGTH: 503
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 392, 464
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 151

```

```

cgagcggccc gcccgggcag gtctgggaga tcagcgactg ctgccacgtg cccagaaatg 60
gctcgtcctt tcactacagc ggaatgcaat gaggtggtt gagaagatga tgggtcgggt 120
atttcattcc ttttcttttt acaacttcac tttcagagac ttcagcgttc catgtctgct 180
gtgctgtgga acccagagtg ctcttgccctg gatggctgag aatcccttgg accctggaag 240
cacctactcc atgatggccc ggtatagtgc aggtcaata taatcttccc ggtatcttga 300
gttgataact cgttgccgtt tcttttcttg cttaacctct ttctctgtga aaatctcatt 360
gaagcgcatt tctgaagcta ctgacagtct anatttgact ctcttgga gctcttcatt 420
cagtgtgtat acatcatctc tcttaaccac aagttggagc catncttaaa cttcacctgg 480
tacatttgga tagggtggga ggc 503

```

```

<210> SEQ ID NO 152
<211> LENGTH: 553
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 293, 432, 459, 481, 536
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 152

```

```

agcgtggtcg cggcccagag tccactgagc tccgccttcc ccgggctccc tgaggaagca 60
gagtcctgac ttccaggaag gacaggacac agaggcaaga actcagcctg tgaggctctg 120
ggtggctcct gagggcagag gacgccttcc gogatccatg gtcagcattc gtccttcttg 180
cttcccagcc ccggggccga cgttcgggtt aataagcaga gcagttattc ggctcctggc 240
aggagctccc ccgttagttt ccacgttggt agcacattca tacttaagac tgnntctctt 300
tgtgttttaa gcgtctgtct ctgtagtaaa ctgaaatgtt aacagaaatg cagacctgcc 360
cgggcggccg ctcgaaagcc gaattctgca gatatccatc aactggcg cgctcgagc 420
atgcatttag anggcccaat tcgccctata gtgagtcgna ttacaattca ctgggcgcgc 480
ntttacaacg tcgtgactgg gaaaaccctg cggtaaccac ttaatcgct tgcagnacat 540
ccccctttcg cca 553

```

```

<210> SEQ ID NO 153
<211> LENGTH: 454

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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 198, 307, 325, 347, 386, 389, 392, 415, 425
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 153

tcgagcggct cgcccgggca ggtccaccta gcatggctcc tctaaacacg caactcagcg 60
aggggacccc cttcacctct ggcaagagag ctgggtagat cagaaacttg gtgacacctg 120
gctagcacag agcaggtctca cttgtcttgg tcccactacc cagattcctg cagacattgc 180
aaaccaaagt aaggttgntg aatgaccctt gtccccagcc acttgttttg gtatcatctg 240
ctctgcagtg gaatgcctgt gtgtttgagt tcaactctgca tctgtatatt tgagtataga 300
aaccgantca agtgcctgt gcatncagac aactggggc acctgancac agaacaatc 360
accttaacga tctggaatga aactgnganc antgcccgcc tgggtgggtc tgganaaaact 420
gccgncttct tgttggaact tggccgcacc acct 454

<210> SEQ ID NO 154
<211> LENGTH: 596
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 19, 33, 37, 131, 377, 425, 439, 505
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 154

agcgtggtcg cggcccgang gcggcctcct gantganggg aaggacgtg ggggcggcca 60
cggcaggatt aacctccatt tcagctaatt atgggagaga ttaaagtctc tcctgattat 120
aactggttta naggtacagt tccccttaaa aagattattg tggatgatga tgacagtaag 180
atatggtcgc tctatgacgc gggccccga agtatcaggt gtcctctcat attcctgccc 240
cctgtcagtg gaactgcaga tgtctttttc cggcagattt tggctctgac tggatggggt 300
taccgggtta tcgcttttga gtatccagtt tattgggacc atctcgagtt cttgtgatgg 360
attcacaaaa cttttanacc atttacaatt ggataaagtt catctttttg gcgcttcttt 420
gggagctttt ttggccana aatttgctga atacactcac aaatctccta gaagccattc 480
cctaactctc tgcaattcct tcagngacac ctctatcttc aaccaacttg gactggaaac 540
agctttggct gatgcctgca tttatgtcga aaaaatagtt cttggaaatt ttcac 596

<210> SEQ ID NO 155
<211> LENGTH: 343
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 6, 12, 23, 44, 58, 86, 99, 279, 310, 319
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 155

ctcganttgg cncgcccggg cangtctgcc tggtttttga ccngcgcagc tatttagnct 60
ctggctctgt ttccggagct caaggnaaaa atcttgaana actcgagcag cttctgtgga 120
tagccttggg tacacatact gccgagcata gccaatgtac tttctcaata gctgggtggg 180
aatgggatct attgtttctc caggaaccac ctttagtctt tctgataatg gcttctcaga 240

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```
aactacttca agtacggaag tatttgaatc ttgactatnc atacgagcta ctgtggcact 300
gctaattgggn tctctgctnt ccagctctta ttgcaatcac atg 343
```

```
<210> SEQ ID NO 156
<211> LENGTH: 556
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 34, 375, 530
<223> OTHER INFORMATION: n = A,T,C or G
```

```
<400> SEQUENCE: 156
```

```
tcgagcggcc cgcccgggca ggtctggcac cacncagatc gattaactgg ctcatctgat 60
ctcgtggccc ccaccttga actgacttag cacaaaagga cacctcaatt ccttatgatt 120
tcatctccga cccaaccaat caacaccctt gactcactgg ccttccccct cccaccaa 180
tattcctaaa aactctgac cccgaatgct caggagatc gatttgagta ctaataagac 240
tccagtctcc tgcacaagca gctctgtgta ctcttcctct attgcaattc ctgtcttgat 300
aaatcggtct tgtgtaggcg gcggaagaag tgaacctgtt gggcggttac cacctctgtc 360
gtgtgtgaca gttgntttga atctctaatt gctcagtaca gatccacatg cagggttaagt 420
aagaagcttt tgaagaaaat ggaaagtctt aagtgatggc ttccaagaaa tcaaacctac 480
attaattagg gaacaacgga ctttactgat cacaatgaa gagactgacn aagtaaatca 540
acttggcctt ttctta 556
```

```
<210> SEQ ID NO 157
<211> LENGTH: 333
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 18, 40, 55, 57, 60, 91, 97, 103, 110, 161, 173, 193,
195, 196, 214, 231, 233, 238, 263, 264, 266, 283, 284, 287, 297,
298, 323, 331
<223> OTHER INFORMATION: n = A,T,C or G
```

```
<400> SEQUENCE: 157
```

```
ggtccacaaa aatatatnaa ataagctgga tatataaaan caaacactta acatngncan 60
cattccttca gttattcaaa ctactgata nctaacnggg agnagttggn attctggaag 120
acttcctaag ctaaaagtat atttcatat ttacaacaca ngtaaatata acngaagaac 180
tacttcaaat aangnnagaa ttccagaatt ctanagattt atagctatag ntnacaanta 240
tcaccaattg gtttgcaatc aanngnccag cactacttat gannaangtt taactannaa 300
acccaaaagg gagaaaacct ggnagggaaa nat 333
```

```
<210> SEQ ID NO 158
<211> LENGTH: 629
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 345, 565
<223> OTHER INFORMATION: n = A,T,C or G
```

```
<400> SEQUENCE: 158
```

```
tcgagcggcc gcccgggcag gtctggtaca tttgtgcgag gtccggcact ctgttctcat 60
```

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ccagtaagtg gtcgagccct ttctgcagaa ttgctgttaa atgttctcct aatagctgtt 120
tctccacaca agcaatcagt ggtttctgtg tgctgtggtc caagtaagtg attactctgt 180
ctccctcttc ttctaagcgt ttacttacat ggtaagata ttctggaacc tctctttcct 240
gcattaacct ttggccttcg gcagcatata agcaattagt ctcttccaaa aatttcagtt 300
caaatgaatc ttataacacc tgcaggtcag acagcatgcc caggaggct ccgcaacagg 360
ctccggtcca cggcctcgcc gctcctctcg cgctcgatca gcagtaggat tccatcaatg 420
gttttactct gaaccatttt atcactaata atatgggttc taaacagttc taatcccata 480
tcccagatgg agggcagcgt ggagttctgc agcacatagg tgcggtccaa gaacaggaag 540
atgcttctga tcatgaatca ttgnctggc aatggtcctg ccagcacgtg gtaatctttc 600
ttttaaaaat aaacccttat ctaaaagtc 629

<210> SEQ ID NO 159
<211> LENGTH: 629
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 33, 546, 576
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 159

tcgagcggcc gcccgggcag gttctagagg ganaatctgg ctgatttggg aataaaatat 60
aatcgaatat tcaacacccat gaagataaat cttattttgg aaatctactg accttaatac 120
cccaagcttg ccctgaatac ttgattgga attggaatat atcaaaaaag gtagtagttt 180
ttgtgtagt taggatacta aaaggatatt agttacccaa gagatccaat ttgtttttct 240
gatgaatagt gttcagtaaa atgaagcagt cttgaagtg actaataatt tcaaagtgat 300
ttttcgtcta ttcttaatat tttttaatta tttattttta agagttttat accttgagca 360
gatacaatga tccgctttag tgagaggaca atttctgatt gattgttttc tcttcaggcc 420
atctcacctc ttcattctct tgttacattt gaagcagttg atataatggg tttatacttt 480
aaaagataga catggtgcc tgaagtttg ggaagttggg tgaattatcc cattctagtt 540
acagangagc tttccttaaa tgccctttac ttctangttt ggtcaagaag tcattttctg 600
agtaaaagtt attttcatat atgttggg 629

<210> SEQ ID NO 160
<211> LENGTH: 519
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 46, 309, 397, 430, 434, 471, 497
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 160

tcgagcggcg cgccgggga ggtctgctgg gattaatgcc aagtntttca gccataaggt 60
agcgaatct agcagaatcc agattacatc cacttccaat cacgcggtgt ttgggtaatc 120
cacttagttt ccagataaca tacgtaagaa tgtccactgg gttggaaacc acaattatga 180
tgcaatcagg actgtacttg acgatctgag gaataatgaa tttgaagaca ttaacatttc 240
tctgcaccag attgagccga ctctcccctt cttgctgacg gactcctgca gttaccacta 300

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```

caatcttana attgggcggg tcacagaata atctttatct gccacaattt taggtgctga    360
agaaataaagc tcccatgctg cagatccatc atttctnctt taagcttata ttccaaaaca    420
tccacaagan caangttcat cagccagaga ctttccaga atgctgatag nacacgccat    480
accaacttgt ccaacancca ctacagcgat cttattggt                            519

```

```

<210> SEQ ID NO 161
<211> LENGTH: 446
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 5, 32, 36, 269, 354, 381
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 161
cgagngggccc gcccgggcag gtccagtaag cnttnnacga tgatgggaaa ggttatgcaa    60
ggccccagcg gtacaacgag ctgtttctac atcatttgta ttctgcatgg tacgtacaat    120
agcagacacc atctgaggag aacgcatgat agcgtgtctg gaagcttcct ttttagaaag    180
ctgatggacc ataactgcag ccttattaac caccacctgg tcctcgatcat ttagcagttt    240
tgtcagttca gggattgcac gtgtggcang ttctgcatca tcttgatagt taatcaagtt    300
tacaactggc atgtttcagc atctgcgatg ggctcagcaa acgctggaca ttantgggat    360
gagcagcatc aaactgtgta natgggatct gcatgccctc atctaattgc tcagggaaca    420
tagcagctcg taccctctga gctcga                            446

```

```

<210> SEQ ID NO 162
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 6, 19, 36, 116, 152, 174, 186, 196, 223, 249
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 162
agcgtngtcg cggcccgang tcctgggaag ccttntttgc tgagcctcac agcctctgtc    60
aggcggctgc ggatccagcg gtccaccagg ctctcatggc ctccgggctg ggaggnggg    120
gagggcacaa aacccttccc aaggccacga anggcaaact tggtggcatt ccanagcttg    180
ttgcanaagt ggcggnaacc cagtatccgg ttcacatcca ggntgatgtc acgaccttg    240
gacatgtang cacataatcc aaaccggaga gcacgggtgc cacattcacg aatccccgct    300
gggaagtcat ctttctgccc ttctttggcc ttctccacct cgctgggatc cagg        354

```

```

<210> SEQ ID NO 163
<211> LENGTH: 258
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 7, 24, 32, 153, 198, 205
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 163
tttttcncca agtcctcttg ccgngggatc tngactgcaa ttttaagacac ttctaattag    60
ttataccag gccttgcaaa attgctgggt ttatataata tattcttgct gcacgaagat    120

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ttattattct gttgcatgat tctattttta ttntatttat tctggccaaa aaagaacctt 180
ctccgctcgt caagagangc caatntgtct tgaaggacaa gagaaagatg ctaacacaca 240
ctttcttctt cttgagga 258

<210> SEQ ID NO 164
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 97, 130, 163, 178, 203, 204
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 164

ggaacatatt acttttaaat tacttgggtc aatgaaacat ttaataaaaa catttgcttc 60
tctatataat acgtatgtat aaaataagcc ttttcanaaa ctctggttct cataatcctc 120
tataaatcan atgatctgac ttctaagagg aacaaattac agnaaggggt atacattnat 180
gaatactggt agtactagag ganngacgct aaaccactct actaccactt gcggaactct 240
cacagggtaa atgacaaaagc caatgactga ctctaaaaac aa 282

<210> SEQ ID NO 165
<211> LENGTH: 462
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 10, 33, 36, 49, 198, 222, 243, 278, 357, 385, 399, 405,
437
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 165

gccccggcan gtcctgtaat cccagctact cangangctg agtcatgana atcgcctgaa 60
tccgggaggt agaggccgca gcgagcaaag attaagccac tgcactccag tctgggtgac 120
agagtgagaa tctgtctgtt gtcctctctg cattggtctg aaatgggttt gtagaacatg 180
ccacagaagg accagcanca gcaacaaatg gatttgtgga angcgtagct ccaaatggag 240
cangcacact tgatgaagca cgctgtgtct gtgcagangc aaccactggc actgttccaa 300
aaacattgct gctagcatta cttgtggaag tatacgcatc actggagggt gctgcanaac 360
tgaaaacgct gtctagtctt gccanagctg catacttgnc tgaanatgca cttgactgac 420
tggggaactga accacanaac caacaggacc tttacctgtg ga 462

<210> SEQ ID NO 166
<211> LENGTH: 365
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 14, 18
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 166

cgtaggtcgc ggcncgngt ctgaaaccaa tccagaacta aacatcagca cacaaaaaat 60
accaggatag atggaatcaa aagactctga agccaaaagg aggctaggga gagcaactga 120
acttagcaag ctgaggactt cagtgtccat catccgatcc tgccctgtaa caacagggtc 180

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```

atatgataga gatattccat ctgagctgga ggccattatc cttagcaaac taacacagaa    240
cagaaaacca aatacatggt ctcatttaga agtaggagct aaatgatgag aactcaagga    300
cacaaagaaa ggaacaacag acactggggc ctacttgagg gtggaggggtg ggaggaggga    360
gaaga                                              365

```

```

<210> SEQ ID NO 167
<211> LENGTH: 364
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 19, 342, 361
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 167

```

```

agcgtgggtcg cggcgcgang tccagcccta gcttgccctgt gactccgcct tcaactgggtg    60
ctctctctaa aagttgtctga ctctttactg tatctcccaa ttcccactcc attggttcca    120
taaggggagg ggtgtctcac tcaacatggt gttcctggta ccaagaactg gctgacgaag    180
ctgggtgccg tggctcatgc ctgtaatccc agcacttttg ggaggccaag aagggcggat    240
cacctgaggt ctggagtcca agatcagcct gaccaacatg atgaaaccaa gtctccacta    300
aaaatataaa acaattagcc aggcattggt gtgggtgcct gnaatcccag ctactgggga    360
ngct                                              364

```

```

<210> SEQ ID NO 168
<211> LENGTH: 447
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 407, 414, 437
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 168

```

```

cccgggcagg tcaaaaccca aaacctttca ttttagccca aaccagctca tgattaggta    60
tacaaggata acagaaccag ttgtcaggac gagcatttga caagtaaaag caattcttgc    120
aaagctgcag ttcattccagc tcatggcatg tgtctttata tagcatcctc gcaatgtcag    180
cttgctcact gtctgtctca tagaaaatca cggtattgtg gagaagcaat tgggcatcag    240
ctttgaactc ttcataaact cggtatttcc cttcattcac tttctcttga atggtgggaa    300
cgtccacaga cctcggccgc gaccacgcta agcccgaatt ctgcagatat ccatcacact    360
ggcggccggt cgagcatggc atctagaagg cccaattcgc ctatagngag tcgnattacc    420
aattcactgg ccgtcgnntt acaacgc                                              447

```

```

<210> SEQ ID NO 169
<211> LENGTH: 524
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 4, 6, 39, 40, 235, 248, 313, 340, 359, 382, 389, 420,
434, 442, 453, 496
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 169

```

```

cgantngcgc gcccgggcag gtctgagcag ctttctggnn tgctggacta ttgggattgg    60

```

-continued

```

gttcacccaa cagagactgt atggatgta gaatggaaga cacatcatag gttggactcc 120
aacggttctg aagtatgtcc agacatatac taccatctgc atagactaag aacaaagaag 180
taggtacatt aaacgtaaca agaccactaa ggttttaaca ttatagacaa aacanaaata 240
gtcaaganta ctttgctttt gaagtttaaa gattcctatg ttgcttccca gttaactgcc 300
taaaaagata agncataacc accactagtg aaataatcan gatgatcaga gaatgtcana 360
tgtgatcagt ataaaactgg angatattna gtgtcatcct ttggaaaagg ctgccctatn 420
atccaggaaa tcanaaacat tnttgaacag ggnccctagc tatccacaga catgtgggaa 480
attcattccc caaatngtag gctggatccc ctatctgaaa taac 524

```

```

<210> SEQ ID NO 170
<211> LENGTH: 332
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 5, 10, 63, 66, 90, 93, 96, 186, 207, 261, 290, 324, 326
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 170

```

```

tcgancggcn cgcccgggca ggtgacaaac ctgttattga agatgttggt tctgatgagg 60
aanaanatca gaaggatggt tgacaagaan aanaanaaga agattaagga aaagtacatc 120
gatcaagaag agctcaacaa aacaaagccc atctggacca gaaatcccga cgatattact 180
aatgangagt acggagaatt ctataanagc ttgaccaatg actgggaaga tcacttggca 240
gtgaagcatt tttcagttga nggacagttg gaattcagag cccttctatn tgtccacga 300
cgtgctcctt ttgatctggt tganancaga aa 332

```

```

<210> SEQ ID NO 171
<211> LENGTH: 334
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 5, 9, 200, 228, 232
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 171

```

```

cgagnggcnc gcccgggcag gtctgttgat agcgacttaa cagaaaagtc tagacaaaca 60
taagcataaa aaattacagt ctttctaccc ttgggaatgg ggagaaaaag gaatctctac 120
cccaagacca gaaataataa gtcctgtttc tggctctgaa catccagaat tatggaggct 180
ttggcctgac accacattan aatttggctt ggaaatcaaa ctttaganac angagatcgt 240
aagccathtt atactatcga cctaaattcc agtctaacgg ttcctttaca aagttgcgga 300
aagccctctt atatgctagc tgtaggaaat atag 334

```

```

<210> SEQ ID NO 172
<211> LENGTH: 439
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 19, 375, 388, 390, 395, 409, 426, 434
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 172

```

-continued

```

agcgtggctcg cggcccgang tctgcctata aaactagact tctgacgctg ggctccagct    60
tcattctcac aggtcatcat cctcatccgg gagagcagtt gtctgagcaa cctctaagtc    120
gtgctcatac tgtgtcgcca aagctgggtc catgacaact tctggtgggg cgagagcagg    180
catggcaaca aattccaagt tagggctctcc aatgagcttc ctgcaagcc agaggaaggg    240
cttttcaaag ttgtagttac ttttggcaga aatgtcgtag tactgaagat tcttctttcg    300
gtggaagaca atggatttcg ccttcacttt ctgccttaat atccactttg gtgccacaca    360
acacaatggg gatgntttca cacacttngn accanatctc tatgccagnt aggccatttt    420
ggaagnactt cganggtac                                     439

```

```

<210> SEQ ID NO 173
<211> LENGTH: 599
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 5, 31
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 173

```

```

cgatnggccg cccgggcagg tcctgtaaaa naggaaattc agacatcgta cgactcgtaa    60
ttgaatgtgg agctgactgc aatattttgt caaagcacca gaatagtgcc ctgcactttg    120
cgaagcagtc taacaatgtg cttgtgtacg acttgtctgaa gaaccattta gagacacttt    180
caagagtagc agaagagaca ataaaggatt actttgaagc tcgccttgct ctgctagaac    240
cagtttttcc aatcgcatgt catcgactct gtgaggggtc agatttttca acagatttca    300
attaccaacc cccacagaac ataccagaag gctctggcat cctgctgttt atcttccatg    360
caaaactttt gggtaaagaa gttattgtct ggctctgtgg accgtgtagt gtacaagctg    420
tagttctgaa tgataaatth cagcttctct ttttctctgg tctcgctctg ttgtccaggc    480
tggagtgcag tggcgcggat tacagctcac tggagtcttg acttcccagg cacaagcaat    540
cctcccacct cagcctccta actacctggg actaaaaatg caccgccacc acattccgg    599

```

```

<210> SEQ ID NO 174
<211> LENGTH: 458
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 30, 32, 35, 51, 61, 213, 261, 327, 347, 359, 377, 418
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 174

```

```

tcgatttggc cggccgggca ggtccatgcn gnttntgccc attcccatgg ngcccacaaa    60
ncccccccc gagggcgaca tccccatgtt catgttcatg cccaccatgc cctggctcat    120
ccctgcgctg tccccagag gggccattcc catggtgccc gtcattacac cgggcatgtt    180
cataggcatg ggtcccccca ggagagggtt agnttgaggc cggacaggaa gcatgtttga    240
tggagaactg aggttcacag nctccaaaac tttgagtcac cacattcata ggctgctgca    300
tattctgtct gctgaatcca ttgtatncag tgatggcctg ctggggnttt ggaaggctng    360
cataccagggt agtaagntcg tctaggctga tgtttacacc tggggtcaga ccaagtanga    420
gggcaagggt ttgctgactg attttctgga cccatatac                                     458

```

-continued

<210> SEQ ID NO 175

<211> LENGTH: 1206

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 175

```

ggcacgagga agttttgtgt actgaaaaag aaactgtcag aagcaaaaga aataaaatca    60
cagttagaga accaaaaagt taaatgggaa caagagctct gcagtgtgag gtttctcaca    120
ctcatgaaaa tgaaaattat ctcttacatg aaaattgcat gttgaaaaag gaaattgccca    180
tgctaaaact ggaaatagcc acactgaaac accaatacca ggaaaaggaa aataaatact    240
ttgaggacat taagatttta aaagaaaaga atgctgaact tcagatgacc ctaaaactga    300
aagaggaatc attaactaaa agggcatctc aatatagtgg gcagcttaaa gttctgatag    360
ctgagaacac aatgctcact tctaaattga aggaaaaaca agacaaagaa atactagagg    420
cagaaattga atcacaccat cctagactgg cttctgtgtg acaagaccat gatcaaattg    480
tgacatcaag aaaaagtcaa gaacctgctt tccacattgc aggagatgct tgtttgcaaa    540
gaaaaatgaa tgttgatgtg agtagtacga tatataacaa tgagggtgctc catcaaccac    600
tttctgaagc tcaaaggaaa tccaaaagcc taaaaattaa tctcaattat gccggagatg    660
ctctaagaga aaatacatgt gtttcagaac atgcacaaag agaccaacgt gaaacacagt    720
gtcaaatgaa ggaagctgaa cacatgtatc aaaacgaaca agataatgtg aacaaacaca    780
ctgaacagca ggagtctcta gatcagaaat tatttcaact acaaagcaaa aatatgtggc    840
ttcaacagca attagttcat gcacataaga aagctgacaa caaagcaag ataacaattg    900
atattcattt tcttgagagg aaaatgcaac atcatctcct aaaagagaaa aatgaggaga    960
tatttaatta caataacat ttaaaaaacc gtatatatca atatgaaaaa gagaaagcag   1020
aaacagaagt tatataatag tataacactg ccaaggagcg gattatctca tcttcacct   1080
gtaattccag tgtttgtcac gtggtgttg aataaatgaa taaagaatga gaaaaccaga   1140
agctctgata cataatcata atgataatta tttcaatgca caactacggg tgggtgctgct   1200
cgtgcc                                           1206

```

<210> SEQ ID NO 176

<211> LENGTH: 317

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 176

```

Met Gly Thr Arg Ala Leu Gln Cys Glu Val Ser His Thr His Glu Asn
  1             5             10             15
Glu Asn Tyr Leu Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala
  20             25             30
Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys
  35             40             45
Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala
  50             55             60
Glu Leu Gln Met Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg
  65             70             75             80
Ala Ser Gln Tyr Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr
  85             90             95

```

-continued

Met Leu Thr Ser Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu
100 105 110

Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp
115 120 125

His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His
130 135 140

Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser
145 150 155 160

Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Ser Glu Ala
165 170 175

Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp
180 185 190

Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg Asp Gln
195 200 205

Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr Gln Asn
210 215 220

Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu Ser Leu Asp
225 230 235 240

Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln Gln
245 250 255

Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser Lys Ile Thr Ile
260 265 270

Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu Leu Lys Glu
275 280 285

Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile
290 295 300

Tyr Gln Tyr Glu Lys Glu Lys Ala Glu Thr Glu Val Ile
305 310 315

<210> SEQ ID NO 177
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Made in the lab

<400> SEQUENCE: 177

ccaatcatct ccacaggagc

20

<210> SEQ ID NO 178
<211> LENGTH: 1665
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 178

gcaaactttc aagcagagcc tcccagagaag ccattctgcct tcgagcctgc cattgaaatg 60
caaaagtctg ttccaaataa agccttgga ttgaagaatg aacaaacatt gagagcagat 120
cagatgttcc cttcagaatc aaaacaaaag aaggttgaag aaaattcttg ggattctgag 180
agtctccgtg agactgtttc acagaaggat gtgtgtgtac ccaaggctac acatcaaaaa 240
gaaatggata aaataagtgg aaaattagaa gattcaacta gcctatcaaa aatcttgat 300
acagttcatt cttgtgaaag agcaaggga cttcaaaaag atcactgtga acaacgtaca 360
ggaaaaatgg aacaaatgaa aaagaagttt tgtgtactga aaaagaaact gtcagaagca 420

-continued

```

aaagaaataa aatcacagtt agagaaccaa aaagttaaat gggaacaaga gctctgcagt 480
gtgagggttc tcacactcat gaaaatgaaa attatctctt acatgaaaat tgcatgttga 540
aaaaggaaat tgccatgcta aaactggaaa tagccacact gaaacaccaa taccaggaaa 600
aggaaaataa atactttgag gacattaaga ttttaaaaga aaagaatgct gaacttcaga 660
tgaccctaaa actgaaagag gaatcattaa ctaaaagggc atctcaatat agtgggcagc 720
ttaaagttct gatagctgag aacacaatgc tcaacttctaa attgaaggaa aaacaagaca 780
aagaaatact agaggcagaa attgaatcac accatcctag actggcttct gctgtacaag 840
accatgatca aattgtgaca tcaagaaaaa gtcaagaacc tgctttccac attgcaggag 900
atgcttgttt gcaaagaaaa atgaatgttg atgtgagtag tacgatatat aacaatgagg 960
tgctccatca accactttct gaagctcaaa ggaaatccaa aagcctaaaa attaatctca 1020
attatgccgg agatgctcta agagaaaata cattgggttc agaacatgca caaagagacc 1080
aacgtgaaac acagtgtcaa atgaaggaa ctgaacacat gtatcaaac gaacaagata 1140
atgtgaacaa acacactgaa cagcaggagt ctctagatca gaaattatct caactacaaa 1200
gcaaaaaatat gtggcttcaa cagcaattag ttcatgcaca taagaaagct gacaacaaaa 1260
gcaagataac aattgatatt ctttttcttg agaggaaaat gcaacatcat ctctaaaaag 1320
agaaaaatga ggagatattt aattacaata accattttaa aaaccgtata tatcaatatg 1380
aaaaagagaa agcagaaaca gaaaactcat gagagacaag cagtaagaaa cttcttttgg 1440
agaaacaaca gaccagatct ttactcaaa ctcatgctag gaggccagtc ctgacattac 1500
cttatgttga aaatcttacc aatagtctgt gtcaacagaa tacttatctt agaagaaaaa 1560
ttcatgattt cttctgaag cctggggcag agagcgagac tctgtctcaa aaaaaaaaaa 1620
aaaaaaaaaa agaaagaaat gcctgtgctt acttcgcttc ccagg 1665

```

<210> SEQ ID NO 179

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 179

```

Ala Asn Phe Gln Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro
 1           5           10          15
Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys
          20          25          30
Asn Glu Gln Thr Leu Arg Ala Asp Gln Met Phe Pro Ser Glu Ser Lys
          35          40          45
Gln Lys Lys Val Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu Arg Glu
          50          55          60
Thr Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala Thr His Gln Lys
65          70          75          80
Glu Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser Thr Ser Leu Ser
          85          90          95
Lys Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala Arg Glu Leu Gln
          100         105         110
Lys Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met Lys Lys
          115         120         125
Lys Phe Cys Val Leu Lys Lys Lys Leu Ser Glu Ala Lys Glu Ile Lys

```

-continued

130	135	140	
Ser Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu Cys Ser			
145	150	155	160
Val Arg Phe Leu Thr Leu Met Lys Met Lys Ile Ile Ser Tyr Met Lys			
	165	170	175
Ile Ala Cys			
 <210> SEQ ID NO 180			
<211> LENGTH: 1681			
<212> TYPE: DNA			
<213> ORGANISM: Homo sapiens			
 <400> SEQUENCE: 180			
gatacagtca ttcttgtgaa agagcaaggg aacttcaaaa agatcactgt gaacaacgta			60
caggaaaaat ggaacaaatg aaaaagaagt tttgtgtact gaaaaagaaa ctgtcagaag			120
caaaagaaat aaaatcacag ttagagaacc aaaaagttaa atgggaacaa gagctctgca			180
gtgtgagatt gacttttaac caagaagaag agaagagaag aaatgccgat atattaaatg			240
aaaaaattag ggaagaatta ggaagaatcg aagagcagca taggaaagag ttagaagtga			300
aacaacaact tgaacaggct ctcaagaatac aagatataga attgaagagt gtagaaagta			360
atttgaatca ggtttctcac actcatgaaa atgaaaatta tctcttacct gaaaattgca			420
tgttgaaaaa ggaaattgcc atgctaaaac tggaaatagc cactactgaaa caccaatacc			480
aggaaaagga aaataaatac tttagaggaca ttaagatttt aaaagaaaag aatgctgaac			540
ttcagatgac cctaaaactg aaagaggaaat cattaactaa aagggcatct caatatagtg			600
ggcagcttaa agttctgata gctgagaaca caatgctcac ttctaaattg aaggaaaaac			660
aagacaaaga aatactagag gcagaaattg aatcacacca tcctagactg gcttctgctg			720
tacaagacca tgatcaaatt gtgacatcaa gaaaaagtca agaacctgct ttccacattg			780
caggagatgc ttgtttgcaa agaaaaatga atgttgatgt gagtagtacg atatataaca			840
atgaggtgct ccatcaacca ctttttgaag ctcaaaggaa atccaaaagc ctaaaaatta			900
atctcaatta tgccggagat gctctaagag aaaatacatt ggtttcagaa catgcacaaa			960
gagaccaacg tgaacacag tgtaaatga aggaagctga acacatgtat caaaacgaac			1020
aagataatgt gaacaaacac actgaacagc aggagtctct agatcagaaa ttatttcaac			1080
tacaagcaaa aaatatgtgg cttcaacagc aattagttca tgcacataag aaagctgaca			1140
acaaaagcaa gataacaatt gatattcatt ttcttgagag gaaatgcaa catcatctcc			1200
taaaagagaa aaatgaggag atatttaatt acaataacca tttaaaaaac cgtatatatc			1260
aatatgaaaa agagaaagca gaaacagaaa actcatgaga gacaagcagt aagaaacttc			1320
ttttggagaa acaacagacc agatctttac tcacaactca tgctaggagg ccagtcctag			1380
cattacotta tgttgaaaaa tcttaaccaat agtctgtgtc aacagaatac ttattttaga			1440
agaaaaattc atgattttctt cctgaagcct acagacataa aataacagtg tgaagaatta			1500
cttggtcacg aattgcataa aagctgcccc ggatttccat ctaccctgga tgatgccgga			1560
gacatcattc aatccaacca gaatctcgct ctgtcactca ggctggagtg cagtgggcgc			1620
aatctcggct cactgcaact ctgcctccca gggttcacgcc attctctggc acagcctccc			1680
g			1681

-continued

<210> SEQ ID NO 181

<211> LENGTH: 432

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 181

```

Asp Thr Val His Ser Cys Glu Arg Ala Arg Glu Leu Gln Lys Asp His
 1          5          10          15
Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met Lys Lys Lys Phe Cys
          20          25          30
Val Leu Lys Lys Lys Leu Ser Glu Ala Lys Glu Ile Lys Ser Gln Leu
          35          40          45
Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu Cys Ser Val Arg Leu
          50          55          60
Thr Leu Asn Gln Glu Glu Glu Lys Arg Arg Asn Ala Asp Ile Leu Asn
          65          70          75          80
Glu Lys Ile Arg Glu Glu Leu Gly Arg Ile Glu Glu Gln His Arg Lys
          85          90          95
Glu Leu Glu Val Lys Gln Gln Leu Glu Gln Ala Leu Arg Ile Gln Asp
          100          105          110
Ile Glu Leu Lys Ser Val Glu Ser Asn Leu Asn Gln Val Ser His Thr
          115          120          125
His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn Cys Met Leu Lys Lys
          130          135          140
Glu Ile Ala Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His Gln Tyr
          145          150          155          160
Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys Glu
          165          170          175
Lys Asn Ala Glu Leu Gln Met Thr Leu Lys Leu Lys Glu Glu Ser Leu
          180          185          190
Thr Lys Arg Ala Ser Gln Tyr Ser Gly Gln Leu Lys Val Leu Ile Ala
          195          200          205
Glu Asn Thr Met Leu Thr Ser Lys Leu Lys Glu Lys Gln Asp Lys Glu
          210          215          220
Ile Leu Glu Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser Ala
          225          230          235          240
Val Gln Asp His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu Pro
          245          250          255
Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val
          260          265          270
Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu
          275          280          285
Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr
          290          295          300
Ala Gly Asp Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln
          305          310          315          320
Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His Met
          325          330          335
Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu
          340          345          350
Ser Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu
          355          360          365

```

-continued

Gln Gln Gln Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser Lys
 370 375 380

Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu
 385 390 395 400

Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys
 405 410 415

Asn Arg Ile Tyr Gln Tyr Glu Lys Glu Lys Ala Glu Thr Glu Asn Ser
 420 425 430

<210> SEQ ID NO 182
 <211> LENGTH: 511
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 182

```

gaagtttcat gaggttttagc ttttctgggc tggggagtgg agagaaagaa gttgcagggc    60
ttacaggaaa tcccagagcc tgaggtttcc tcccagattt gagaactcta gattctgcat    120
cattatcttt gagtctatat tctcttgggc tgtaagaaga tgaggaatgt aataggctctg    180
ccccaagcct ttcattgcctt ctgtaccaag cttgtttcct tgtgcatcct tcccaggctc    240
tggtgcccc ttattggaga atgtgatttc caagacaatc aatccacaag tgtctaagac    300
tgaatacaaa gaacttcttc aagagttcat agacgacaat gccactacaa atgccataga    360
tgaattgaag gaatgttttc ttaaccaaac ggatgaaact ctgagcaatg ttgagggtgtt    420
tatgcaatta atatatgaca gcagtctttg tgattttatt taactttctg caagaccttt    480
ggctcacaga actgcagggt atggtgagaa a                               511

```

<210> SEQ ID NO 183
 <211> LENGTH: 260
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 183

```

cacctcgcgg ttcagctcct ctgtcttggt gaagaacccat tcctcggcat ccttgcggtt    60
cttctctgcc atcttctcat actggtcacg catctcgttc agaatgcggc tcagggtccac    120
gccaggtgca gcgtccatct ccacattgac atctccaccc acctggcctc tcagggcatt    180
catctcctcc tcgtgggttct tcttcaggtg ggccagctcc tccttcaggc tctcaatctg    240
catctccagg tcagctctgg                               260

```

<210> SEQ ID NO 184
 <211> LENGTH: 461
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 184

```

gtctgatggg agaccaaaga atttgcaagt ggtgggtttg gtatcactgt aaataaaaag    60
agggcctttt ctagtgtgat gactgttact tgacottctt tgaaaagcat tcccaaaatg    120
ctctatttta gatagattaa cattaaccaa cataattttt tttagatcga gtcagcataa    180
atttctaagt cagcctctag tcgtgggttc tctctttcac ctgcatttta tttggtgttt    240
gtctgaagaa aggaaagagg aaagcaaata cgaattgtac tatttgtacc aaatctttgg    300
gattcattgg caaataatct cagtgtggtg tattattaaa tagaaaaaaa aaattttgtt    360

```

-continued

tcctagggttg aagggtctaata tgataccggtt tgactttatga tgaccatttta tgcactttca 420
aatgaatttg ctttcaaaat aaatgaagag cagacctcgg c 461

<210> SEQ ID NO 185
<211> LENGTH: 531
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 185

tctgattttta tttccttctc aaaaaaagtt atttacagaa ggtatatatc aacaatctga 60
caggcagtga acttgacatg attagctggc atgattttttt cttttttttc ccccaaact 120
tgttttttgtg gccttgaatt ttaagacaaa tattctacac ggcatattgc acaggatgga 180
tggcaaaaaa aagtttataaa acaaaaaccc ttaacggaac tgccttaaaa aggcagacgt 240
cctagtgcct gtcattgttat attaaacata catacacaca atctttttgc ttattataat 300
acagacttaa atgtacaaa atgtttttcca cttttttcaa tttttaaaca caacagctat 360
aaacctgaac acatatgcta tcatcatgcc ataagactaa acaattata ttagcgaca 420
agtagaaagg attaaatagt caaatacaag aatgaaaaac gcagtacata gtgtcgcgaa 480
ctcaaatcgg catttagata gatccagtg tttaaacggc acgtttttgc t 531

<210> SEQ ID NO 186
<211> LENGTH: 441
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 186

cattcctttc ctgcggttg ggtttctctg tgtcagcgag cctcgggtaca ctgatttccg 60
atcaaaagaa tcatcatcct taccttgact tttcaggga ttactgaact ttcttctcag 120
aagatagggc acagccattg ccttggcctc acttgaaggg tctgcatttg ggtcctctg 180
tctcttgcca agtttcccaa ccaactcgag gagaaatata gggagggttg acttctctcg 240
gggctttccc gagggcttca ccgtgagccc tgcggccctc agggctgcaa tcctggattc 300
aatgtctgaa acctcgtct ctgcctgtg gacttctgag gccgtcactg ccaactctgc 360
ctccagctct gacagctcct catctgtggt cctgtgtgac tggacggggg cccaggggtc 420
ctgggggctt ttttctgtc t 441

<210> SEQ ID NO 187
<211> LENGTH: 371
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 187

aaaagtgaat gagtaactat tatattgttg gcaataataa gttgcaaaat catcaggctg 60
caggctgctg atggtgagag tgaactctgt ccagatcca ctgccgtga acctgatgg 120
gacccagat tctaaactag acgccttatg gatcaggagc tttggggctt tccctggttt 180
ctgttgatac caggccaacc aactactaac actctgactg gcccggaag tgatggtgac 240
tctgtctcct acagttgcag acagggtgga aggagactgg gtcactctga tgcacattt 300
ggcacctggg agccagagca gcaggagccc caggagctga gcggggaccc tcatgtccat 360
gctgagtcct g 371

-continued

<210> SEQ ID NO 188
<211> LENGTH: 226
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 188

```
ggtatataaa ttgagatgcc cccccaggcc agcaaatggt cctttttggt caaagtctat    60
ttttattcct tgatattttt cttttttttt tttttgtgga tggggacttg tgaatttttc    120
taaagtgctc atttaacatg ggaggagagc gtgtgcggct ccagcccagc ccgctgctca    180
ctttccaccc tctctccacc tgccctgggc ttctcaggac ctgccc                    226
```

<210> SEQ ID NO 189
<211> LENGTH: 391
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 43, 112, 131, 156, 195, 208, 221, 317, 333, 367
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 189

```
tgggtgaagt ttattctggt ttcacatcta ggttggtggg ganagtgata gacaaagtgc    60
tggattctgg gcatcgctcg cgcctgcttg taatcctact tgggaggttg anacaggaga    120
cctcgccgcg naccacgcta agggcgaatt ctgcanatat ccatcacact ggcggccgct    180
cgagcatgca tctanagggc ccaattcncc ctatagttag ncgtattaca attcactggc    240
cgtcggttta caacgctggt actgggaaaa cctgggcgtt acccaactta atcgccctgc    300
agcacatccc cttttcncca gctggcttaa tancgaagag gcccgaccg atcgcccttc    360
ccaacanttg cgcagcctga atggcgaatg g                                391
```

<210> SEQ ID NO 190
<211> LENGTH: 501
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 190

```
catcttggcc tttttgagct gtttcgctt cttctcatcc cggtcactgt caccctcatt    60
actggaggag ctggcagagg cgttgctgtc aaactcctct gccacatctt cctcctcttc    120
acctgggttg aatgactcat cggtttcttc tcttgagtca tcgctgctgt cattggcatt    180
ctcctcccg atcttgccct cctccttcat cctctccaag taggcatcat gctggtcctc    240
atcagagtca gcatattcat cgtagcttgg gttcatgccc tctttcaatc ctcggttttt    300
gatgttgagc tttttcgctg tgacaaaatc aaacagtttc ccgtactcct cctctcfaat    360
gctgctgaag gtatactgag tgccctgctt ggtctcaatt tcaaagtcaa aggaacgagt    420
agtagtggtg ccacgagcaa agttgacaaa ggagatctca tcgaagcgga tgtgcacagg    480
tggcttgggg acgtagatga a                                501
```

<210> SEQ ID NO 191
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature

```
<210> SEQ ID NO 194
<211> LENGTH: 311
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 194

ctgagacaca gaggcccaat gcgaggggga cagtggcggg gggactgacc tgctgacagt      60
caccctccct ctgctgggat gaggtcagg agccaactaa aacaatggca gaggagacat      120
ctctggtggt cccaccaccc tagatgaaaa tccacagcac agacctctac cgtgtttctc      180
ttccatccct aaaccacttc cttaaaatgt ttggatttgc aaagccaatt tggggcctgt      240
ggagcctggg gttgatagg gccatggctg gtccccccacc atacctcccc tccacatcac      300
tgacacagac c                                     311
```

-continued

<210> SEQ ID NO 195
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 195

```
tgtcagagtg gcactggtag aagttccagg aaccctgaac tgtaaggggt cttcatcagt    60
gccaacagga tgacatgaaa tgatgtactc agaagtgtcc tggaatgggg cccatgagat    120
ggttgtctga gagagagctt cttgtcctgt ctttttcctt ccaatcaggg gctcgctctt    180
ctgattattc ttcagggcaa tgacataaat tgtatattcg gttcccgggt ccaggccagt    240
aatagtagcc tctgtgacac cagggcgggg ccgagggacc acttctctgg gaggagaccc    300
aggcttctca tactttagta ttagccgggt aatcctggca cgtggcggct gccatgatac    360
cagcagggaa ttgggtgtgg t                                     381
```

<210> SEQ ID NO 196
<211> LENGTH: 401
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 196

```
cacaaaacag aggagcacca gacctcctct tggcttcgag atggcttcgc cacaccaaga    60
gccccaaact ggagacctga ttgagatttt ccgccttggc tatgagcact gggccctgta    120
tataggagat ggctacgtga tccatctggc tcctccaagt gagtaccccg gggctggctc    180
ctccagtgtc ttctcagtcc tgagcaacag tgcagagggtg aaacgggagc gcctggaaga    240
tgtgtgtgga ggctgttgtc atcgggtcaa caacagcttg gaccatgagt accaaccacg    300
gcccgtggag gtgatcacca gttctgcgaa ggagatgggt ggtcagaaga tgaagtacag    360
tattgtgagc aggaactgtg agcactttgt caccagacc t                                     401
```

<210> SEQ ID NO 197
<211> LENGTH: 471
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 197

```
ctgtaatgat gtgagcaggg agccttcctc cctggggcac ctgcagagag ctttcccacc    60
aactttgtac cttgattgcc ttacaaagtt atttgtttac aaacagcgac catataaaag    120
cctctgccc caaagcttgt gggcacatgg gcacatacag actcacatac agacacacac    180
atatatgtac agacatgtac tctcacacac acaggcacca gcatacacac gtttttctag    240
gtacagctcc caggaacagc taggtgggaa agtcccatca ctgaggggagc ctaaccatgt    300
ccctgaacaa aaattgggca ctcatctatt cttttctct tgtgtcccta ctattgaaa    360
ccaaactctg gaaaggaccc aatgtaccag tatttatacc tctagtgaag cacagagaga    420
ggaagagagc tgcttaaact cacacaacaa tgaactgcag acacagacct g                                     471
```

<210> SEQ ID NO 198
<211> LENGTH: 201
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 198

-continued

```
ggtcattga ggctctgtcg gccatgccca cagttcgaag ctttgccaac gaggagggcg      60
aagcccagaa gtttagggaa aagctgcaag aaataaagac actcaaccag aaggaggctg      120
tggcctatgc agtcaactcc tggaccacta gtatttcagg tatgctgctg aaagtgggaa      180
tcctctacat tggtagggcag a                                              201
```

```
<210> SEQ ID NO 199
<211> LENGTH: 551
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
```

```
<400> SEQUENCE: 199
```

```
tctggcacag atcttcaccc acacggcggg ccaagtgtctg atcatcttcc gggcttcacc      60
gggcctggaa cacaccatct tccccatgag cccgggtgcc agtctggtga ctcccatctt      120
ggccctgggc cttatgtccc agttatgacc cctgacttca actctggctc ttaccctgta      180
actccagtcc atctctgaca tttttaacac ccggccttgt gaccgtggac atagctcctg      240
acctcgattc ccatcttgag ccagtggtta gtccatgaga tcatgacctg actcctggtc      300
tccaaccttg tgatccta atctgggacct caatcctagc ctctgaactt gggaccctgg      360
agctcctgac cttagtccct accgctaccc ttgattctga cctttgatcc tgtaacttag      420
gggtggcccc tgaccttatt actgtcattt agctccttga ccttgccact tcaatcctgg      480
ctttatgacc tcctactctc aattttaact ttaaccaa atgacaaatt gtgacactaa      540
atgaccacaa t                                              551
```

```
<210> SEQ ID NO 200
<211> LENGTH: 211
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 8, 36, 40, 78, 165, 170, 171, 173, 203, 207, 208
<223> OTHER INFORMATION: n = A,T,C or G
```

```
<400> SEQUENCE: 200
```

```
cagctcancg ggcgacatgc ccctacaagt tggcanaagn ggctgccact gctgggtttg      60
tgtaagagag gctgctgnca ccattacctg cagaaacctt ctcatagggg ctacgatcgg      120
tactgctagg gggcacatag cgcccatggg tgtggtagggt ggggnactcn ntnataggat      180
ggtaggtatc ccgggctgga aanatgnnca g                                              211
```

```
<210> SEQ ID NO 201
<211> LENGTH: 111
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
```

```
<400> SEQUENCE: 201
```

```
ccagtgaag gaaacaaaac tggcagtttg tccatttgaa tatcagacct agtttcttct      60
taatttccac actatttctc ccatattcct taaacttctt ggcattccacc t              111
```

```
<210> SEQ ID NO 202
<211> LENGTH: 331
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
```

```
<400> SEQUENCE: 202
```

-continued

tgaaaataca gaataccagg tgggtcccaa tgtttgaagt tctttgaaca gaaagagaga	60
ggagagagag agagaggaaa attccctaac ccttggttta aagacaatat tcattttattg	120
ctcaaatgat gcttttaagg gaggacagt gaataaaata aacttttttt ttctccctac	180
aatacataga aggggttatca aaccactcaa gtttcaaaat ctttccaggg tccaatatca	240
ctttttttct ttcgggttcaa tgaaaagcta aatgtaataa tactaattat agataaaaatt	300
ttattttact ttttaaaaat ttgtccagac c	331

<210> SEQ ID NO 203
<211> LENGTH: 491
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 203

agtcaccag tctacttagt acctgggtgc tgcctctgac cttttcagct tgataccctg	60
ggcttttagtg taaccaataa atctgtagtg accttacctg tattccctgt gctatcctgt	120
gggaaggtag gaatgggcta agtatgatga atgtataggt tagggatcct ttgggttttaa	180
atcacagaaa acctaattca aactgggtta aaataaaaag gatttattgg ttcagttaac	240
tagaaagtcc ataggtagtg ctggctccag gtgaagactt gaccagtag ttcagtatgt	300
ctctaaatac cggactgact tttttctcac tgttgcatct tctgtaggac catttaagtc	360
tggggcactt aatggctgcc agcattccta agattacact tttccccatt tatgtccaat	420
cagaaaaaga aggcactctt gtaccagaaa tctcagcaa agccctaata ttcacactga	480
ttaggacctg c	491

<210> SEQ ID NO 204
<211> LENGTH: 361
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 204

tcccttcctc ccccatgtga taaatgggtc cagggtgat caaagaactc tgactgcaga	60
actgccgctc tcagtggaca gggcatctgt tatcctgaga cctgtggcag acacgtcttg	120
ttttcatttg atttttgta agagtgcagt attgcagagt ctagaggaat tttgtttcc	180
ttgattaaca tgattttcct ggttggtaca tccagggcat ggcagtggcc tcagccttaa	240
acttttggtc ctactccac cctcagcgaa ctgggcagca cggggagggt ttggctaccc	300
ctgccatcc ctgagccagg taccaccatt gtaaggaaac actttcagaa attcagacct	360
c	361

<210> SEQ ID NO 205
<211> LENGTH: 471
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 2, 3
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 205

cnngtacagt tcttcctgga tggccgacac agatcctggg gaaaggcaat cctggcactg	60
ctctgaaacc agagctcctc ctccctcccc gggcagggtg gagctgagaa gggctgctct	120

-continued

```

agcgttggga ctccacctcc atacacctga tattttgata gggcaggtec ctgctatggg 180
ccactgttct gggcagtata gtatgcttga cagcatcctt ggcattctatc caccagatcc 240
cagagcaccg gctactagct gtgacaacat cctccaaaca ttgcaaaatt tcccctggga 300
ggcaagattg cctcagatgg gagaatcacg ctctagggaa atctgctggg atgagaaccc 360
caactcccca ctccactgag cctccagatg gcgagcaggc tgcagctcca gcacagacac 420
gaagctccct ccagccactg acggtccatg gctgggggta cccaggacct c 471

```

```

<210> SEQ ID NO 206
<211> LENGTH: 261
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```
<400> SEQUENCE: 206
```

```

tagagtattt agagtccatg gataacaagg aatccaggca tccttttagac agtcttctgt 60
tgtcctttct tcccaatcag agatttgtgg atgtgtggaa tgacaccacc accagcaatt 120
gtagccttga tgagagaatc caattcttca tctccacgaa tagcaagttg caagtgcaga 180
ggggtaatac gctttacctt taagtctttt gatgcatttc ctgccagttc aagtacctct 240
gcggtgaggt actccaggat g 261

```

```

<210> SEQ ID NO 207
<211> LENGTH: 361
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```
<400> SEQUENCE: 207
```

```

gctctccggg agcttgaaga agaaactggc tacaaagggg acattgccga atgttctcca 60
gcggtctgta tggacccagg cttgtcaaac tgtactatac acatcgtgac agtcaccatt 120
aacggagatg atgccgaaaa cgcaaggccg aagccaaagc caggggatgg agagtttgtg 180
gaagtcattt ctttacccaa gaatgacctg ctgcagagac ttgatgctct ggtagctgaa 240
gaacatctca cagtggacgc caggggtctat tcctacgctc tagcactgaa acatgcaaatt 300
gcaaagccat ttgaagtgcc cttcttgaaa ttttaagccc aaatatgaca ctggacctgc 360
c 361

```

```

<210> SEQ ID NO 208
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 10, 27, 37, 46, 75, 95, 102, 137, 143, 202, 234, 278,
310, 351
<223> OTHER INFORMATION: n = A,T,C or G

```

```
<400> SEQUENCE: 208
```

```

agaggagatn ttgcccagtc ctgaatnctt tcctatncca ccctancact taacatatta 60
cttagtctgc ttgntaaaa gcaagtatta ccttnaactt gnctcttact ctttgccctt 120
tagctaacta ataaagnttg atntagcatc tattatataa ttctgagtc ttcattggtat 180
ctctcatgtt tgatgtattt tncaactaa gatctatgat agtttttttt ccanagttcc 240
attaatcat ttatttcctt tacttttcca cctctgtnga aacatttaga aactggattt 300

```

-continued

gggaaccan ttttgaaaa ccagattcat agtcatgaaa atggaaactt ncatattctg 360
tttttgaaaa gatgtggacc t 381

<210> SEQ ID NO 209
<211> LENGTH: 231
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 83
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 209

gtggagagca agtgatttat taaagcaaga cgttgaaacc tttacattct gcagtgaaga 60
tcagggtgtc attgaaagac agnggaaacc aggatgaaag tttttacatg tcacacacta 120
catttcttca atattttcac caggacttcc gcaatgaggc ttcgtttctg aagggacatc 180
tgatccgtgc atctcttcac tcctaacttg gctgcaacag cttccacctg c 231

<210> SEQ ID NO 210
<211> LENGTH: 371
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 210

tccatcctgg ttttgcagag atcaggttgt tgacagttcc tggttgaccc acagctaccc 60
atgtcagtta tctccactaa catatccaag aatctttgta ggacaatttc tccacctgca 120
agggttttta ggtagaactc ttcttttaag gcaattagcc cattgccaaa aggttttact 180
gtcttaaagc tgtctttctg agatctaatt ccaaggactt ctccacagct aagtgagatg 240
cctcacacca ttagtgatg ctttggacag aacagagtat tttcatcttg tgtttaaagc 300
aatcctctgg cttcggtctc tcaccacttt ctatgccagt ctcccattta tgtccctagt 360
aatgcctatg c 371

<210> SEQ ID NO 211
<211> LENGTH: 471
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 211

tttattttta aagaaaaaaa ttaaaataga gccaacaaat gcaattaaga aaaaaaaagt 60
attgagacac aaggggacct acatgttctg gtctaagaag catgcaagta ttacaaagca 120
ttccagatac agtatgacag aggaacagtg aacaagcatt ggaacgatgc tctttctttc 180
agaaacggga agtctaacag ttatgttttc acaatggtag tgattaaacc atctttatct 240
ttaaggaatt ttataggaag aattttagca ccatcattaa aggaaaaata ataatacctt 300
tttagccctg cctatctcca gtcttggaat aataacagaa gcatagcacc tttcagtatc 360
taaaatataa acaagaatag taagtccatc ccagcttcta gagatgaggt agtccatgct 420
aagaaatggt gggtcatctt tcctatgaaa gttcaaaggc caaatggtca c 471

<210> SEQ ID NO 212
<211> LENGTH: 401
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

-continued

<400> SEQUENCE: 212

```

tggcctgtct ccttcacata gtccatatca ccacaaatca cacaacaaaa gggagaggat    60
atattttggg ttcaaaaaaa gtaaaaagat aatgtagctg catttctttg gttatttttg    120
gccccaaata tttcctcatc tttttgttgt tgtcatggat ggtggtgaca tggacttggt    180
tatagaggac aggtcagctc tctggctcgg tgatctacat tctgaagttg tctgaaaatg    240
tcttcatgat taaattcagc ctaaacgttt tgccgggaac actgcagaga caatgctgtg    300
agtttccaac ctcagcccat ctgcgggcag agaaggtcta gtttgtccat caccattatg    360
atatcaggac tggttacttg gttaaggagg ggtctacctc g                          401

```

<210> SEQ ID NO 213

<211> LENGTH: 461

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 239, 290, 358, 359, 391, 393

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 213

```

tgtgaagcat acataataaa atgaagtaag ccatactgat ttaatttatt ggatgttatt    60
ttccctaaga cctgaaaatg aacatagtat gctagttatt tttcagtgtt agccttttac    120
tttcctcaca caatttggaa tcatataata taggtacttt gtccctgatt aaataatgtg    180
acggatagaa tgcatacaagt gtttattatg aaaagagtgg aaaagtatat agcttttanc    240
aaaaggtggt tgccattctt aagaaatgag cgaatatata gaaatagtgn gggcatttct    300
tcctgttagg tggagtgtat gtgttgacat ttctcccat ctcttccac tctgtttntt    360
ccccattatt tgaataaagt gactgctgaa nangactttg aatccttata cacttaattt    420
aatgtttaa gaaaaaccta taatggaaag tgagactcct t                          461

```

<210> SEQ ID NO 214

<211> LENGTH: 181

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 214

```

cctgagcttc tactccttcc ccttaagatt cctccaaagc accagctcca taaaatcctt    60
cagctcccca gaccacacc aagaacccca catgttaatt ggatcagcca aatctacaag    120
cagataagtc ctaaggagaa tgccgaagcg tttttcttct tcctcaagcc tagcatgaga    180
c                                              181

```

<210> SEQ ID NO 215

<211> LENGTH: 581

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 215

```

ctgctttaag aatggttttc caccttttcc ccctaattct taccaatcag acacatttta    60
ttattttaat ctgcacctct ctctatttta tttgccaggg gcacgatgtg acatatctgc    120
agtcccagca cagtgggaca aaaagaattt agaccccaaa agtgtcctcg gcatggatct    180
tgaacagaac cagtatctgt catggaactg aacattcatc gatggctctc atgtattcat    240

```

-continued

```

ttattcactt gttcattcaa gtatttattg aatacctgcc tcaagctaga gagaaaagag 300
agtgcgcttt ggaaatttat tccagttttc agcctacagc agattatcag ctcggtgact 360
ttctcttctg ccaccattta ggtgatggtg tttgattcag agatggctga atttctattc 420
ttagcttatt gtgactgttt cagatctagt ttgggaacag attagaggcc attgtcctct 480
gtcctgatca ggtggcctgg ctgtttcttt ggatccctct gtcccagagc caccagaac 540
cctgactctt gagaatcaag aaaacaccca gaaaggacct c 581

```

```

<210> SEQ ID NO 216
<211> LENGTH: 281
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 37, 38, 164, 176, 254
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 216

```

```

ccgatgtcct gcttctgtgg accaggggct cctctgnngg tggcctcaac cacggctgag 60
atccctagaa gtccaggagc tgtggggaag agaagcactt agggccagcc agccgggcac 120
ccccacttgc gccccgacc cgcctcacgc accagacctg ccnnggcggg cgctcnaaag 180
ggcgaattct gcagatatcc atcacactgg cggacgctcg agcatgcac tagagggccc 240
aattcacctt atantgagtc gtattacaat tcaactggccg t 281

```

```

<210> SEQ ID NO 217
<211> LENGTH: 356
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 33, 322
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 217

```

```

atagcaggtt tcaacaattg tcttgtagtt tgnagtaaaa agacataaga aagagaaggt 60
gtggtttgca gcaatccgta gttggtttct caccataccc tgcagttctg tgagccaaag 120
gtcttgcala aagttaaaat aaatcacaaa gactgctgtc atatattaat tgcataaaca 180
cctcaacatt gctcagagtt tcatccgttt ggttaagaaa acattccttc aattcatcta 240
tggcatttgt agtggcattg tcgtctatga actcttgaag aagttctttg tattcagtct 300
tagacacttg tggattgatt gncttggaag tcacattctc caataaggga cctcgg 356

```

```

<210> SEQ ID NO 218
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 218

```

```

ttgtccatcg ggagaaaggt gtttgtcagt tgtttcataa accagattga ggaggacaaa 60
ctgctctgcc aatttctgga tttctttatt ttcagcaaac actttcttta aagcttgact 120
gtgtgggcac tcatccaagt gatgaataat catcaagggt ttgttgcttg tcttgatttt 180
atatagagct tcttcatatg tctgagtcca gatgagttgg tcacccaac ctctggagag 240
ggtctggggc agtttgggtc gagagtcctt tgtgtccttt ttggctccag gtttgactgt 300

```

-continued

ggtatctctg gacctgctg g 321

<210> SEQ ID NO 219
<211> LENGTH: 271
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 41
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 219

ccggttaggt ccacgcgggg gcagtggagg cacaggctca nggtggccgg gctacctggc 60
accctatggc ttacaaagta gagtggccc agtttccttc cacctgaggg gagcactctg 120
actcctaaca gtcttccttg ccctgccatc atctgggggtg gctggctgtc aagaaaggcc 180
gggcatgctt tctaaacaca gccacaggag gctttagagg catcttccag gtggggaaac 240
agtcttagat aagtaagggt acttgtctaa g 271

<210> SEQ ID NO 220
<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 32, 43
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 220

gtctacgac gaggaccagc ttttcttctt cnacttttcc canaacactc gggcgcctcg 60
cctgcccga a tttgctgact gggctcagga acaggagat gctcctgcca ttttatttga 120
caaagagttc tgcgagtga tgatccagca aatagggcc aacttgatg ggaaatccc 180
gggtccaga gggtttctta tcgctgaagt gttcacgtg aagccctgg agtttgcaa 240
gcccaacact ttggtctgtt ttgtcagtaa tctcttcca ccatgctga cagtgaactg 300
gtagcatcat tccgtccctg tggaaggatt tgggcctact tttgtctcag a 351

<210> SEQ ID NO 221
<211> LENGTH: 371
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 221

gtctgcagaa gcgtgtctga ggtgtccggt ggaggtggca gccgagctct gggactaatc 60
accgtgctgg ggacggcacc gcgtcaggat gcaggcagat ccctgcagaa gtgtctaaaa 120
ttcacactcc tcttctggag ggacgtcgat ggtattagga tagaagcacc aggggacccc 180
acgaacgggt tcgtcgaaac agcagccctt atttgacac tgggagggcg tgacaccagg 240
aaaaccacaa ttctgtcttt cacggggggc cactgtacac gtctctgtct gggcctcggc 300
cagggtgccg agggccagca tggacaccag gaccagggcg cagatcacct tgttctccat 360
ggtggacctc g 371

<210> SEQ ID NO 222
<211> LENGTH: 471
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

-continued

<400> SEQUENCE: 222

```
gtccatgttc catcattaat gttccaacat caccaggac acaaagctgc aaaaatgaga    60
agggaataa ggtagagaa aggatccggg caatcttaag gactgaggaa gacatgttcc    120
ccaacccttg aactcacaaa ccctgaagct caaggattgc atccttcctc caaatctcac    180
tcaacataat aagtgcagaa caacatgcc aagcactgta tgaagcacta gggacaaaga    240
caaggtaaaa atccttgtaa ccaaatttaa tgggtattgta atgcagtgtt aacacaggac    300
agtaacagaa caccacaaga ccaaacagaa gagggtaggg ataagcataa atgaagtaac    360
atgaaataaa cttccaaatg gaaaacttgt ccataccccc agggcaagtc aactacagtc    420
tcccaaagga cataaattcc acttagggca cactagacag aaaacaatat t          471
```

<210> SEQ ID NO 223

<211> LENGTH: 411

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 223

```
agttgtctca caatgacaca caaatcccg taaataaatt ataacaagg gtcaattcaa    60
atgtgaagta atgttttagt aaggagagat tagaagacaa caggcatagc aaatgacata    120
agctaccgat taactaatcg gaacatgtaa aacagttaca aaaataaacg aactctcctc    180
ttgtcctaca atgaaagccc tcatgtgcag tagagatgca gtttcatcaa agaacaaaca    240
tccttgcaaa tgggtgtgac gcggttcag atgtggattt ggcaaacct catttaagta    300
aaaggttagc agagcaaagt gcggtgcttt agctgtgct tgtgccgtg tggcgtcggg    360
gaggctcctg cctgagcttc cttccccagc tttgtgcct gagaggaacc a          411
```

<210> SEQ ID NO 224

<211> LENGTH: 321

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 31

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 224

```
ggtctgaagt ttgataacaa agaaatatat ntaagacaaa aatagacaag agttaacaat    60
aaaaacacaa ctatctgttg acataacata tggaaacttt ttgtcagaaa gctacatctt    120
cttaacttga ttgtccaaat cattaataa tggatgattc agtgccattt tgccagaaat    180
tcgtttggct ggatcataga ttaacatttt cgagagcaaa tccaagccat tttcatccaa    240
gtttttgaca tgggatgcta ggcttctcgg tttccatttg ggaaatgtat tcttatagtc    300
ctgtaaagat tccacttctg g          321
```

<210> SEQ ID NO 225

<211> LENGTH: 251

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 34

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 225

-continued

atgtctgggg aaagagttca ttggcaaaa tgtnctccca agaatggttt acaccaagca	60
gagaggacat gtcactgaat ggggaaaggg aacccccgta tccacagtca ctgtaagcat	120
ccagtaggca ggaagatggc ttggggcagt ggctggatga aagcagattt gagataccca	180
gctccggaac gaggtcatct tctacagggt cttccttcac tgagacaatg aattcagggt	240
gatcattctc t	251

<210> SEQ ID NO 226
 <211> LENGTH: 331
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 26, 34, 35, 36, 37, 39
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 226

gttaggtccc agggcccccg ccaagnggtt accnnntna ccactcctga cccaaaaatc	60
aggcatggca ttaaaacgtt gcaaattcct ttactgttat cccccccacc accaggacca	120
tgtaggggtgc agtctttact ccctaaccgg tttcccgaaa aaggtgctac ctcccttcca	180
gacagatgag agagggcagg acttcaggct ggatccacca ctgggctctc cctccccag	240
cctggagcac gggaggggag gtgacggctg gtgactgatg gatgggtagt gggctgagaa	300
gaggggacta ggaagggcta ttccaggctc a	331

<210> SEQ ID NO 227
 <211> LENGTH: 391
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 227

aggtctgccc ttgaagtata ggaaggaatc atagttggag gacttctgca ttatttgttg	60
gctgaagcta gaagtgcaac cccctcctga tttctgcagc aagatgaact gccttatccc	120
cagccccgag gaatgttcat atctgagcaa tcaatgggca ctgtgttcaa ccacgccatt	180
ttcaagattg gctccttaaa ccaccacaa ggcaccagct ctgggagaag ctgcaggag	240
aagagaacaa agccctcgct gtgatcagga tgggtgtctc ataccttttc tctggggta	300
ttccagggtat gagacagagt tgaacctgcg catgagcgtg gaggccgaca tcaacggcct	360
gcgcagggtg ctggatgagc tgacctgga c	391

<210> SEQ ID NO 228
 <211> LENGTH: 391
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 35
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 228

gttgtccata gccacctcct gggatagaag cttntagtt catagttcga ttagtgtgtc	60
cttaggacat aggtccagcc ctacagatta gctgggtgaa gaaggcaagt gtctcgacag	120
ggcttagtct ccaccctcag gcatggaacc attcagggtg aagcctggga tgtgggcaca	180
ggagactcag gctgatataa aaataacaaa atcagtaata aaaaaattat aaaacctgtt	240

-continued

```

gcttgtctga atagatttga gcaacagtct tgcttttgtt aaaatcctgg agccgttaag 300
tcctgaatat tcttctggac atcattgctg gctggagaaa ggagccccag gcccggtctg 360
gctgacatct gtcaggtttg gaagtctcat c 391

```

```

<210> SEQ ID NO 229
<211> LENGTH: 341
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 202
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 229

```

```

gtccatggct tctcaccag acagtcttct tgggcaactt ggggaagccc ctgttctgct 60
caagtctcac cccatggaag aggtggggga agggggcctt ggtttttcag gaagacgggt 120
tggagagcac gagtctactac aaagcagtaa aagtgaatgg tgtctccagg ggtgggtcc 180
agaacaccgc ggagagcccc anccataaag gtgtgttccg cctctggcct gcaggaatct 240
ctttgaatct ctttgattgg tggctccaag agcaatggga agtcaacagc caggaggctg 300
gactgggttc cctgggaccc cgaggccca gaggtctgct g 341

```

```

<210> SEQ ID NO 230
<211> LENGTH: 511
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 230

```

```

gtccaagcca aggaaacat tcccttacag gagacctccc tgtacacaca ggaccgcctg 60
gggctaaagg aaatggacaa tgcaggacag ctagtgttct tggctacaga aggggacctat 120
cttcagttgt ctgaagaatg gttttatgcc cacatcatac cattccttgg atgaaacccg 180
tatagttcac aatagagctc agggagcccc taactcttcc aaaccacatg ggagacagtt 240
tccttcatgc ccaagcctga gctcagatcc agcttgcaac taatccttct atcatctaac 300
atgccctact tggaaagatc taagatctga atcttatcct ttgccatctt ctgttaccat 360
atggtgttga atgcaagttt aattaccatg gagattgttt taaaaacttt tgatgtggtc 420
aagttcagtt ttagaaaagg gagtctgttc cagatcagtg ccagaactgt gcccaggccc 480
aaaggagaca actaactaaa gtagtgaat a 511

```

```

<210> SEQ ID NO 231
<211> LENGTH: 311
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 231

```

```

ggtccaagta agctgtgggc aggcaagccc ttcggtcacc tgttggtac acagaccct 60
ccccctgtgt cagctcaggc agctcgaggc ccccgaccaa cacttcagcagg ggtccctgct 120
agttagcgcc ccaccgccgt ggagttcgta ccgcttcctt agaacttcta cagaagccaa 180
gctccctgga gccctgttgg cagctctagc tttgcagtcg tgtaattggc ccaagtcaat 240
gtttttctcg cctcacttct caccaagtgt ctagagtcac gtgagcctcg tgatcatctc 300
ggggtggacc t 311

```

-continued

<210> SEQ ID NO 232

<211> LENGTH: 351

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 232

```
tcgttttagct aataatccct tccttgatga tacactccaa cttcttgttt ttctttattt    60
ctaaaaagcg gttctgtaac tctcaatcca gagatgttaa aaatgtttct aggcacggta    120
ttagtaaatc aagtaaatat catgtcctct taaaggacaa acttccagag attggaatat    180
aaatttttat atgtgttatt gattgtcgtg taacaaatgg cccccacaaa ttagtagctt    240
aaaaatagcat ttatgatgtc actgttttct ttgccttttc attaatgttc tgtacagacc    300
tatgtaaaca acttttgtat atgcatatag gatagctttt ttgaggggtat a          351
```

<210> SEQ ID NO 233

<211> LENGTH: 511

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 233

```
aggctctggat gtaaggatgg atgctctcta tacatgctgg gttggggatg ctgggactgc    60
acagccacccc ccagtatgcc gctccaggac tctgggacta gggcgccaaa gtgtgcaaat    120
gaaaatacag gataccacag gaactttgaa tttcagattg tgaaaagaaa acaaatcttg    180
agactccaca atcaccaagc taaaggaaaa agtcaagctg ggaactgctt agggcaaagc    240
tgctctccat tctattcaca gtcctccccc tgagggctcac ctgcatagct gattgcttcc    300
tttcccctat cgcttctgta aaaatgcaga ctactgagc cagactaaat tgtgtgttca    360
gtggaaggct gatcaagaac tcaaaagaat gcaacctttt gtctcttata tactacaacc    420
aggaagcccc cacttaaggg ttgtcccacc ttactggact gaaccaaggt acatcttaca    480
cctactgatt gatgtctcat gtcccctaa g          511
```

<210> SEQ ID NO 234

<211> LENGTH: 221

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 234

```
caggctccagc gaaggggctt cataggctac accaagcatg tccacataac cgaggaagct    60
ctctccatca gcatagcctc cgatgacatc ggtgttccac aaaggggtca tcttcgagcg    120
ccggctgtac atggccctgg tcagccatga atgaatagct ctaggactat agctgtgtcc    180
atctcccaga agctcctcat caatcaccat ctggccgaga c          221
```

<210> SEQ ID NO 235

<211> LENGTH: 381

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 33

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 235

```
ggccaagaa agggacatct atgtgaaagt ganactgaga cagtgtgtgt cacaggatcat    60
```

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```

gctgcagaat aatacattcc caggcactgt cacgtggggg acccaagagg ccccaggagt 120
gacctataac ctctccagaa agaccactct gtgtggcatc acagtccaca cagtttaagg 180
aaatatttag acttaacaat cagacaccag ctcttactca cacttacact cacagcccac 240
acacaagtgt gcaaacatac acacacatat atatttcctg atacattcat ggaatatcag 300
agccctgccc tgaagtcgtt agtgtctctg ctccccaac cgctgctccc acattggcta 360
agctccctca agagacctca g 381

```

```

<210> SEQ ID NO 236
<211> LENGTH: 441
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 236
aggtcctgtt gcccctttct ttgcccac ttcgccattt gggaattgga atatttacc 60
aacacctgta ctgcattgaa tattggaagc aaataacttg gctttgatct tataggctca 120
cagatggagg aacgtacctt gaagttcaga tgagatttcg gacttttgag ttgatgctga 180
aacagcttga gatTTTTTggg gactactgag agatgataat tgtattgtgc aatatgagaa 240
ggacatgaga tttggtgggc ataggtgtga aatgacattg tttggatgtg tttaccctcc 300
aaatctcttg ttgaatgtga tcttaaacgt tgggtggtggg cctagtggaa ggtgttgaat 360
catgggggtg gactcttcat aatttgctta gctccatccc cttggtgatg agcaagtcct 420
tgctctgttg tgtcacatga g 441

```

```

<210> SEQ ID NO 237
<211> LENGTH: 281
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 81, 90, 194, 209, 210, 211, 219, 233
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 237
tcctaaaaaa ttagctgacc ttgttaaaaa tgttggcgtg agcagtatat tattacctat 60
ctttttttat tgtgtgtgtg ngtgtgtgtn ttaaactaat tggctgaaat atctgcctgt 120
ttccctcttt acatttttct tgtttcttct cttattttatc tttgtccatc ttgagatcta 180
ctgtaaagtg aatnttttta tgaaaacann nccaagttnt actctcactg ggnttgggac 240
atcagatgta attgagaggc caacaggtaa gtcttcatgt c 281

```

```

<210> SEQ ID NO 238
<211> LENGTH: 141
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 30, 85
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 238
gtctgcctcc tcctactgtt tccctctatn aaaaagcctc cttggcgcag gttccctgag 60
ctgtgggatt ctgcactggt gcttnggatt ccctgatatg ttccttcaaa tccactgaga 120
attaaataaa catcgctaaa g 141

```

-continued

<210> SEQ ID NO 239
<211> LENGTH: 501
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 29, 30, 65, 86, 471, 489
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 239

aacaatctaa acaaatccct cggttctann atacaatgga ttcccatat tggaaggact	60
ctgangcttt attccccac tatgcntatc ttatcatttt attattatac acacatccat	120
cctaaactat actaaagccc ttttcccatg catggatgga aatggaagat ttttttttaa	180
cttggtctag aagtcttaat atgggctgtt gccatgaagg cttgcagaat tgagtccatt	240
ttctagctgc cttattcac atagtgatgg ggtactaaaa gtactgggtt gactcagaga	300
gtcgtgtca ttctgtcatt gctgtactc taacactgag caacactctc ccagtggcag	360
atccctgta tcattccaag aggagcattc atccctttgc tctaatgac aggaatgatg	420
cttattagaa acaaaactgc ttgacccagg aacaagtggc ttagcttaag naaactggc	480
ttgctcana tccctgatcc t	501

<210> SEQ ID NO 240
<211> LENGTH: 451
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 240

tgctctgaaa ggccattact aatagaaaca cagcctttcc aatcctctgg aacatattct	60
gtctgggttt ttaatgtctg tggaaaaaaa ctaacaagt ctctgtctca gttaagagaa	120
atctattggt ctgaagggtt ctgaacctct ttctggttct cagcagaagt aactgaagta	180
gatcaggaag gggctgcctc aggaaaattc ctagatccta ggaattcagt gagaccctgg	240
gaaggaccag catgctaate agtgtcagt aatccacagt ctttacttcc tgcctcataa	300
agggccaggt ctcccagta ccaagtcctt tctcatgaa gttgtgttc ctcaggctgt	360
ttagggacca ttgcctgtct tggtcacatg agtctgtctc cttactttag tccctgggca	420
atccttgctt aatgcttttg ttgactcaac g	451

<210> SEQ ID NO 241
<211> LENGTH: 411
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 62, 82, 364, 370, 385
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 241

aatctccagt gtgatggtat cggggtaga gottcaatct ccagtgtgat ggtactgcag	60
cnagagcttc aatctccagt gngatggtat tagggtaga tcttcaatct ccagtgtgat	120
ggtatcaggg ttagagcttc agcctccagt gtgatggtat cagggttaga gcttcagcct	180
ccagtgtgat ggtatcggg ttagatcttc aatccccagt ggtgggtggt agagcttcaa	240
tctccagtgt gatggtattg gggtagagc ttcaatctcc agtctgatgg tgtttcggga	300

-continued

tggggctttt aagatgtaat tagggtttaa gatcataagg gacctggtct gatggggatt	360
agtncgcttn tatgaagaga cacangaggg cttgctctat ctctgactct c	411

<210> SEQ ID NO 242
 <211> LENGTH: 351
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 242

ttccccttca caacagtaga gacctacaca gtgaactttg gggacttctg agatcagcgt	60
cctaccaaga ccccgagcca actcaagcta cagcagcagc acttcccaag cctgctgacc	120
acagtcacat caccatcag cacatggaag gcccttggtg tggacactga aaggaagggc	180
tggtcctgcc cctttgaggg ggtgcaaaca tgactgggac ctaagagcca gaggctgtgt	240
agaggtcct gctccacctg ccagtctcgt aagaaatggg gttgctgcag tgttgagta	300
ggggcagagg gagggagcca aggtcactcc aataaaacaa gctcatggca c	351

<210> SEQ ID NO 243
 <211> LENGTH: 241
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 243

gtctgtgctt tatcaggaaa agcacaagaa tatgtttttc tacctaaaac cctcttctac	60
tttaaaaatg gtttgctgaa tttttctatg tttttaaaat gtttttatgc ttttttttaa	120
acacgtaaaag gatggaacct aatcctctcc cgagacgcct cctttgtgtt aatgcctatt	180
cttacaacag agaacaagt acattaatat aaaaacgagt tgattattgg ggtataaaat	240
a	241

<210> SEQ ID NO 244
 <211> LENGTH: 301
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 244

ggtccagagc aatagcgtct gtggtgaagc gcctgcactc ctggggagac atgcctggct	60
tatatgctgc atccacataa ccatagataa aggtgctgcc ggagccacca atggcaaaag	120
gctgtcgagt cagcattcct ccaggggttc catatacttg acctccttca cgttggtccc	180
agccagctac catgagatgt gcagacaagt cctctcgata tttatagctg atatttctca	240
ccacatttgc agcagccaaa acaagtggag gttcctccag ttctatccca tggagctcca	300
g	301

<210> SEQ ID NO 245
 <211> LENGTH: 391
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 245

ctgacactgc tgatgtgggc cggggggcgc cgaggcacia ctggtggccg gaccattgag	60
gcacctggag ggtaggcagc ttgtggtgca gacaccacag agagagaaaa gttggatgga	120
gtggtgggaa taatcaggtt ggcacactgt gcctagaagc ttccagggcc accaagagaa	180

-continued

tggaagga aactacaaca ttcacaacag aaataggagt caattcactt agaccagaa	240
ctccagaaag ggggagtgtg ggaatctaca atttcaaagc cagctcgtgt ctacctagag	300
ccccaaactg cataagcacc aggattgtac accttagtcc ctcaagatag tttcaagtga	360
gcgtgcaatt cactcttaca gaggagggcc t	391

<210> SEQ ID NO 246
 <211> LENGTH: 291
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 26, 80, 82, 185, 255, 259
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 246

tcctccacag gggaagcagg aagttngacc agcttcaggc tggaacgtgc ccagggcaca	60
gagctggcaa ggtgcaaagn cntctgcaga atattcacca ggttgacaca gacctccaca	120
ttcagacata ttccaagctt ctgggggtctt cagggcccca gaatttcctg gtcttgggca	180
tggtncacaa gtcatttgtc cttcctcatt ttggaagggt ccatttggac ataaaatgca	240
agcgttctcg tgctncatna taatagggtc cagcctgcac tgacacattt g	291

<210> SEQ ID NO 247
 <211> LENGTH: 471
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 80, 110, 125, 245, 249, 279, 318, 336, 339, 455, 471
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 247

cactgagtga atgagtatat aatttatgaa aacagaaaag tgctttggaa aaaaaaaag	60
acaacaggag tacatacagn gaaccaaaaa gagtgtacca ggaggagcan accctgaaca	120
gttanaacta tggaatcgc tatgctttgt gttgtcacag gagttaaagt aggaataccc	180
tgcatacaat aaatatattat tggataaata actaagcctg ataccctttt caatgcgtta	240
tacanactnt atcatcacac cactaatcta agttctcana agttaaacad tacaagactt	300
cagaacaaca taggcgtntt tggctccatt taacanaana aggaccatag tgatcattta	360
atctctatga gtctgtctta tcttctggaa aaggggccta acaccatttc cttttgcaaa	420
aaggtagctg ccttgcttcc agttctacca tcctntagca acccatcttt n	471

<210> SEQ ID NO 248
 <211> LENGTH: 551
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 248

ccatgggatc aggaatgggg tcaggtcagt tgacctgagc ataccatta aacatgttca	60
aatgtcccca tcccaccac tcacatgaca tggctccga gccctgagat ctgtatccca	120
agaacctcag ttgagaaata tttatggcag cttcactgtt gctcaagagc ctgggtattg	180
tagcagcctg ggggcagggt gtccctaagt ttctccaagt tcttcacatc agccagaatc	240
ccatctatgc ttgtctccag caaatggagg tggccctct gctgacgtgc cctctcttc	300

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```

agctctgaca tcattgggccc cagttggctg ttgatctggg tcttggtcgc ggaaagcttc 360
tgctccagta agaccagccc ctcttcacat aactgagag gctggtccat cagatgcagg 420
aggccgtcta atgtgttgag tgtgtcttgg attgtaaccc cagcgttctt ggcctctggta 480
tcaaccttct gggcttctgt aatcaccatc tgtactgcat ccatattcgt gtcgaactcc 540
agctccttcc t 551

```

```

<210> SEQ ID NO 249
<211> LENGTH: 181
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 3, 96
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 249

```

```

atntccagag ggaccgtaag actggtacaa gtttacacca taagaggcga cgtggtcagc 60
cacaatgtct tcacctccac aggggctcat caggnggtc agggcaaggc cccccagcat 120
cagagctttg ttaggatca tcctcttccc aaggcagcct tagcagttgc tgacctgccc 180
g 181

```

```

<210> SEQ ID NO 250
<211> LENGTH: 551
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 250

```

```

tctgtagcta ggatgagctg gctctcaagc aaaagtttgt cttcctgggt ccatttgttg 60
ttatcacttg ttattgaatg tacatcacia attaaagtct gcattgttgg acgtaagaga 120
atgtgccgac ttgtgtaacc aggagatttc atgttactgg actgcctgta gtcacgtatt 180
tctgctatga cacatccgca atgaaaaata ttaacctgag atttttctag gagatcaacc 240
aaaaataggag gtaattcttc tgcattccaa tattcaagca actctccttc tcatagggc 300
agtcgaatgg tctcggatc tgatccgttt tttcccctga gcacagaga atatccctca 360
ttcctgggt atagattgac cactaaacat gacaaagtct cttgcataac aagcttctct 420
aacaagtcca catctcttct taatttctta acttcaggtt ctttttcaca ttcttcaata 480
tacaagtcac aaagtttttg aaatacagat tttcttccac ttgataggta tttcctttta 540
ggaggtctct g 551

```

```

<210> SEQ ID NO 251
<211> LENGTH: 441
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 251

```

```

tgtctgctct cccatcctgg ttactatgag tcgctcttgg cagaaaggac cacagatgga 60
gagcttggca ctgcgtccaa ctttgccgaa aagaggacaa ccaccaaagt agtaggtaaa 120
aacacaattt tagcagcagt gaaataaaaa gaggaagtga ggatggggcc aggccgcaac 180
tataattaaa ctgtctgttt aggagaagct gaatccagaa gaaacacaag ctgtaaagtg 240
agagaggaca gggagcaggg cctttggaga gcaggagagg acaggctgtc accaagcgtc 300

```

-continued

```

gctcggactc tgccctgaaa gatttgaatt ggacactgtc cagtcacgtg tgtggcaaac   360
cgtactccaa gcacttttct cacggcagag gaaggagctg ccatggctgt acccctgaac   420
gtttgtgggg ccagcgatgt g                                           441

```

```

<210> SEQ ID NO 252
<211> LENGTH: 406
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 252

```

```

tttttttttg aacaagtaaa aatttcttta ttgtctgaca ataagataac ctacagggaa   60
aacctgatga aatctattaa aaagtacta aaactaataa agaatttag gaaggttata   120
gaatgtaaga ccaagacaca aaaatcaatt acatttctat ataatagcaa tgaacagata   180
ctgaaatttt aaaaactaaa tcattttaca aaagtatcac aatatgaaac actccgggat   240
aaattggata aaagatgtgc aagactgtac aaaagctaca aaacatttat gaaggaaatt   300
ggaagataga aacaagatag aaaatgaaaa tattgtcaag agtttcagat agaaaaatgaa   360
aaacaagcta agacaagtat tggagaagta tagaagatag aaaaat                406

```

```

<210> SEQ ID NO 253
<211> LENGTH: 544
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 224
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 253

```

```

gaaggagttc agtagcaaag tcacacctgt ccaattccct gagctttgct cactcagcta   60
atgggatggc aaaggtggtg gtgctttcat cttcaggcag aagcctctgc ccatccccct   120
caagggctgc aggccaggtt ctcatgtctg ccttgggtgg gcatctgtta acagaggaga   180
acgtctgggt ggccggcagca gctttgctct gagtgcctac aaanctaatg cttgggtgcta   240
gaaacatcat cattattaaa cttcagaaaa gcagcagcca tgttcagtca ggctcatgct   300
gcctcactgc ttaagtgcct gcaggagccg cctgccaagc tcccccttct acacctggca   360
cactggggtc tgcacaaggc ttgtcaacc aaagacagct tccccctttt gattgcctgt   420
agactttgga gccaaagaaac actctgtgtg actctacaca cacttcaggt ggtttgtgct   480
tcaaagtcac tgatgcaact tgaaaggaaa cagtttaaat gtggaaatga actaccattt   540
ataa                                           544

```

```

<210> SEQ ID NO 254
<211> LENGTH: 339
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 254

```

```

tggcattcag ggcagtgtct tctgcatctc ctaggaaacct cgggagcggc agtccggcg   60
cctggtagcg agaggcgggt tccggagatc ccggcctcac ttcgtcccac tgtggttagg   120
ggtgagtcct gcaaagtgtta agtgatttgc tcaagggtgcc catttcgcag gaattggagc   180
ccaggccagt tctctgagcc tatcattagg gctaaaggag tgcgtgatca gaatggtgtc   240

```

-continued

tggaagggttc tacttgctct gcttgctgct ggggtccctg ggctctatgt gcatcctctt 300
cactatctac tggatgcagt actggcgtgg tggctttgc 339

<210> SEQ ID NO 255
<211> LENGTH: 405
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 11, 39, 70, 87, 103, 120, 177, 181, 220, 229, 233, 341,
345, 366, 380, 402
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 255

gagggtttttt nttttttttt tttttttttt caattaaana tttgatttat tcaagtatgt 60
gaaaacattn tacaatggaa acttttntta aatgctgcat gtnctgtgct atggaccacn 120
cacatacagc catgctgttt caaaaaactt gaaatgccat tgatagttaa aaaactntac 180
ncccgatgga aaatcgagga aaacaattta atgtttcatn tgaatccana ggngcatcaa 240
attaaatgac agctccactt ggcaataaat agctgttact tgatgggtatc caaaaaaaaa 300
tggttgggga tggataaatt caaaaatgct tccccaaagg nggngggttt ttaaaaagtt 360
tcaggncaca acccttgcan aaaacactga tgcccaacac antga 405

<210> SEQ ID NO 256
<211> LENGTH: 209
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 6
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 256

gggcangtct ggtcctctcc ccacatgtca cactctcttc agcctctccc ccaaccctgc 60
tctccctcct cccctgccct agcccaggga cagagtctag gaggagcctg gggcagagct 120
ggaggcagga agagagcact ggacagacag ctatgggttg gattggggaa gaggttagga 180
agtaggttct taaagaccct tttttagta 209

<210> SEQ ID NO 257
<211> LENGTH: 343
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 306, 311, 343
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 257

tctggacacc ataatccctt ttaagtggct ggatggtcac acctctccca ttgacaagct 60
gggttaagtc aatagggtga ctaggatcaa cacgaccaa atcaataaga tactgcagtc 120
tattgagact caaagctta tactggcgtc tgaaactatg tccttcgtta aaccgtatt 180
ttgggattcg gatgtaaaat ggagtctggc ctccctcaaa gcccaagcgg gcccggttc 240
ctctttgcct ttctccttta tggcctctgc cacatcttct acctcttctc cgacctcttg 300
gtcttntctc nggtttcttg gagccgggat tcggctttaa gtn 343

-continued

<210> SEQ ID NO 258
<211> LENGTH: 519
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 258

```
gcggcttctg acttctagaa gactaaggct ggtctgtggt tgcttggttg cccacctttg    60
gctgataccc agagaacctg ggcacttgct gctgatgcc caccctgcc agtcattcct    120
ccattcaccg agcgggaggt gggatgtgag acagcccaca ttggaaaatc cagaaaaccg    180
ggaacaggga ttgcccctc acaattctac tcccagatc ctctcccctg gacacaggag    240
acccacaggg caggacccta agatctgggg aaaggaggtc ctgagaacct tgaggtagcc    300
ttagatcctt ttctaccac ttctctatgg aggattcaa gtcaccactt ctctaccgg    360
ctctaccag ggtccaggac taaggcggtt tctccatagc ctcaacattt tgggaatctt    420
cccttaatca ccctgtctc tcctgggtgc ctggaagatg gactggcaga gacctctttg    480
ttgcggtttg tgctttgatg ccaggaatgc cgcctagtt    519
```

<210> SEQ ID NO 259
<211> LENGTH: 371
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 259

```
attgtcaact atatacacag tagtgaggaa taaaatgcac aaaaaacaat ggatagaata    60
tgaaaatgtc ttctaaatat gaccagtcta gcatagaacc ttcttctctt ccttctcagg    120
tcttccagct ccatgtcatc taaccactt aacaaacgtg gacgtatcgc ttccaggaggc    180
cgtcttaaca actccatttc caaaagtcac ctccagaaga catgtatttt ctatgatttc    240
ttttaaacia atgagaattt acaagatgtg taactttcta actctatttt atcatacgtc    300
ggcaacctct ttccatctag aagggtctaga tgtgacaaat gttttctatt aaaagggttg    360
ggtggagttg a    371
```

<210> SEQ ID NO 260
<211> LENGTH: 430
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 57, 189, 208, 256, 426
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 260

```
ttggattttt tgacttgcga ttacgtttt tttacttttt ttttttttt ttttganaaa    60
tactatattt attgtcaaag agtggtacat aggtgagtg tcatcttccc tctcatgccg    120
gtatactctg cttcgtgtt tcagtaaaag ttttccgtag ttctgaacgt cccttgacca    180
caccataana caagcgcaag tactcanaa ttgccactgg aaaactggct caactatcat    240
ttgaggaaag actganaaag cctatoccaa agtaatggac atgcaccaac atcgcggtac    300
ctacatgttc ccgtttttct gccaatctac ctgtgtttcc aagataaatt accaccagg    360
gagtcacttc ctgctatgtg aacaaaaacc cggtttcttt ctggagggtgc ttgactactc    420
tctcngagc    430
```

-continued

<210> SEQ ID NO 261
<211> LENGTH: 365
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 178
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 261

tcctgacgat agccatggct gtaccactta actatgattc tattccaact gttcagaatc	60
atatcacaaa atgacttgta cacagtagtt tacaacgact cccaagagag gaaaaaaaaa	120
aaaaaagacg cctcaaaatt cactcaactt ttgagacagc aatggcaata ggcagcanag	180
aagctatgct gcaactgagg gcacatatca ttgaagatgt cacaggagtt taagagacag	240
gctggaaaaa atctcatact aagcaaacag tagtatctca taccaagcaa aaccaagtag	300
tatctgctca gcctgccgct aacagatctc acaatcacca actgtgcttt aggactgtca	360
ccaaa	365

<210> SEQ ID NO 262
<211> LENGTH: 500
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 262

cctagatgtc atttgggacc cttcacacc attttgaagc cctgtttgag tccctgggat	60
atgtgagctg tttctatgca taatggatat tcgggggttaa caacagtccc ctgcttggtc	120
tctattctga atccttttct ttcaccatgg ggtgcctgaa gggtggtgta tgcataatgg	180
acaatggcac ccagtgtaaa gcagctacaa ttaggagtgg atgtgttctg tagcatccta	240
tttaaataag cctattttat cctttggccc gtcaactctg ttatctgctg cttgtactgg	300
tgctgtact tttctgactc tcattgacca tattccacga ccatggttgt catccattac	360
ttgatcctac tttacatgtc tagtctgtgt ggttggtggt gaataggctt ctttttacat	420
ggtgctgcca gcccagctaa ttaatggtgc acgtggactt ttagcaagcg ggctcactgg	480
aagagactga acctggcatg	500

<210> SEQ ID NO 263
<211> LENGTH: 413
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 263

ctcagagagg ttgaaagatt tgcctacgaa agggacagtg atgaagctaa gctctagatc	60
caggatgtct gacttcaaat tgaaactccc aaagtaatga gtttggaagg gtgggggtgtg	120
gcctttccag gatgggggtc ttttctgctc ccagcggata tgaaacccc tgtctgcacc	180
tggttgggcg tgttgcttct ccaaagggtt tttttttagg tccgtcgtcg tcttgggat	240
taggcattat tatctttact ttgtctccaa ataacctgga gaatggagag agtagtgacc	300
agctcagggc cacagtgcga tgaggaccat cttctcacct ctctaaatgc aggaagaaac	360
gcagagtaac gtggaagtgg tccacaccta ccgccagcac attgtgaatg aca	413

<210> SEQ ID NO 264
<211> LENGTH: 524

-continued

<212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 264

```
tccaatgggg ccctgagagc tgtgacagga actcacactc tggcactggc agcaaaacac    60
cattccaccc cactcatcgt ctgtgcacct atgttcaaac tttctccaca gttccccaat    120
gaagaagact catttcataa gtttgtggct cctgaagaag tcctgccatt cacagaaggg    180
gacattctgg agaaggtcag cgtgcattgc cctgtgtttg actacgttcc cccagagctc    240
attaccctct ttatctccaa cattgggtggg aatgcacctt cctacatcta ccgcctgatg    300
agtgaactct accatcctga tgatcatgtt ttatgaccga ccacacgtgt cctaagcaga    360
ttgcttaggc agatacagaa tgaagaggag acttgagtgt tgctgctgaa gcacatcctt    420
gcaatgtggg agtgcacagg agtccaccta aaaaaaaaaa tccttgatac tgttgccctgc    480
cttttttagtc accccgtaac aagggcacac atccaggact gtgt                    524
```

<210> SEQ ID NO 265
 <211> LENGTH: 344
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 265

```
tcctttcttc tacttcagga gatgattcaa agttacttgt ggacatttct ttaagttctg    60
aagacaaatg agacaggatt tggcctgcgg gttcttcaga cttctctacc acctccatta    120
actcttcatc ttggcttgac gtaggcaatg cactattttg ctcttttggt tctggagatg    180
accacgaccc acttctttct cttggcgggg ttctaagtgt gtctttgaat accagtgaag    240
actcaggcct atcctgtact ggaaagggac taaatttgtc tttctgtcta ggaggtgatg    300
cagtagcatc ctctgaggg ggtaaggcca tttctctttt ttga                    344
```

<210> SEQ ID NO 266
 <211> LENGTH: 210
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 78
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 266

```
ccacaatgtc cataacttga gcaggctttg gcattcccacc acccccttca gaccaatata    60
cactatgttg gaggaacnac tttaaatgtt aaaatgagaa atgggcactg aacactccat    120
cctcactccc aacagcccac ccacacacct cttcaactgc tatccaaaca tggaggagct    180
cttgtggaag agaggctcaa caccaaataa                    210
```

<210> SEQ ID NO 267
 <211> LENGTH: 238
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 5, 19, 31
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 267

```
tcggncctcc caccctctna ctgaaattct ntgaaattct cccctttggg atgaggatgg    60
```

-continued

```

caaccccgag catgtaccct cccaacctgg gacccgacct aataccctaa catcctgctg 120
acagtggctg ttctcgctgg gcaggcgctcc caaagcacat cgagccagat tcaggcagag 180
tggaactggc ccctcagcca tcagtggagg tggcctggga ggctctaccc tgaacggg 238

```

```

<210> SEQ ID NO 268
<211> LENGTH: 461
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 459
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 268
tcctcaagga catgcccctt gatagaaact cagttcctgt ctccagttcc ctccctggacc 60
tgatccccc aatgcagggc ctgggactat atccagttcc ttattttcag aggcccatgc 120
acaagatgca cagcaataa gtgctgaata aagaccagc tactgctagc ttaccctgct 180
ccaaacattc accaagtctc cagcaagag ggccatccat tcacctcttc taaaaacaca 240
ctgagctccc cagtctatac cccaagatat gcttggctcc caactatccc tcctctctca 300
tctccaagcc agtttccctt ttctaagtat actgatatta ccaagacac tgacaatctt 360
cttttctac ctctcccccag tgactagggt tgcagcagga gctctataag tcctagtata 420
cagcagaagc tccataaatg tgtgctgacc taacattang c 461

```

```

<210> SEQ ID NO 269
<211> LENGTH: 434
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 269
ctgtgttggt gagcaccgat tcccactcaa tatggcgtgg cttacagtct tcattaggtt 60
cccgtccca accagaatga ggaatgatca cttcatctgt caaggcatgc agtgcattgt 120
ccacaatctc cattttgatt gagtcatggg atgaaagatt ccacagggtt ccggttaataa 180
cttcagtaag gtccatatca cgagccttcc gaagcaatcg cacaagggca ggcacaccat 240
cacagttttt tatggcaatc ttgttatcct ggtcacgtcc aaaagagata ttcttgagag 300
ctccacaggc tccaaggctc acttcctttt tgggatggtc taacaatccc accagtactg 360
ggatgccttt gagcttccgc acgtcagttt tcaccttgct attgcggtag cataagtgtt 420
gcaggtatgc aaga 434

```

```

<210> SEQ ID NO 270
<211> LENGTH: 156
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 270
ctgcaccagc gattaccagt ggcattcaaa tactgtgtga ctaaggattt tgtatgctcc 60
ccagtagaac cagaatcaga caggtatgag ctagtcaaca gcaagtcttt gttggattcg 120
agtaggtctc ggatctgctg aaggtcggag gagtta 156

```

```

<210> SEQ ID NO 271
<211> LENGTH: 533

```

-continued

<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 100, 137, 383, 385, 411
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 271

```
ccactgtcac ggtctgtctg acacttactg ccaaacgcat ggcaaggaaa aactgcttag    60
tgaagaactt agaagctgtg gagaccttgg ggtccacgtn caccatctgc tctgataaaa    120
ctggaactct gactcanaac cggatgacag tggccacat gtggtttgac aatcaaatcc    180
atgaagctga tacgacagag aatcagagtg gtgtctcttt tgacaagact tcagctacct    240
ggcttgctct gtccagaatt gcagggtctt gtaacagggc agtgtttcag gctaaccagg    300
aaaacctacc tattcttaag cgggcagttg caggagatgc ctctgagtca gcaactctta    360
agtgcataga gctgtgctgt ggnntcgtga aggagatgag agaaagatac nccaaaatcg    420
tcgagatacc cttcaactcc accaacaagt accagttgtc tattcataag aacccaaca    480
catcggagcc ccaacacctg ttggtgatga agggcgcccc agaaaggatc cta          533
```

<210> SEQ ID NO 272
<211> LENGTH: 630
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 272

```
tggtattttt ctttttcttt tggatgtttt atactttttt ttcttttttc ttctctattc    60
ttttcttcgc cttcccgta cttctgtctt cagttttcca cttcaactt ctatcttctc    120
caaatgtttt catcctacca ctcccaatta atctttccat ttctgtctgc gtttagtaaa    180
tgcgtaact aggccttaaa tgacgcaatt ctccctgcgt catggatttc aaggtctttt    240
aatcaccttc ggtttaatct ctttttaaaa gatcgcttc aaattatttt aatcacctac    300
aacttttaaa ctaaacttta agctgtttta gtcaccttca ttttaactta aaagcattgc    360
ccttctattg gtattaattc ggggctctgt agtcctttct ctcaattttc ttttaaatat    420
attttttact ccatgaagaa gcttcatctc aacctccgtc atgttttaga aaccttttat    480
cttttcttc ctcatgtac tcttctaagt cttcataatt tctcttaaaa tcttaagcta    540
ttaaaattac gtaaaaaact taacgctaag caatatctta gtaacctatt gactatattt    600
tttaagtagt tgtattaatc tctatctttc          630
```

<210> SEQ ID NO 273
<211> LENGTH: 400
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 273

```
tctggtttgc cctccagttc attctgaatc tagacttgct cagcctaata aagttcctgt    60
acaaccagaa gcgacacagc ttcctttggt atcatccaca agtgaggggt acacagcatc    120
tcaacccttg taccagcctt ctcatgtac agagcaacga ccacagaagg aaccaattga    180
tcagattcag gcaacaatct ctttaaatat agaccagact acagcatcat catcccttcc    240
tgctgcgtct cagcctcaag tatttcaggc tgggacaagc aaacctttac atagcagtg    300
aatcaatgta aatgcagctc cattccaatc catgcaaagc gtgttcaata tgaatgcccc    360
```

-continued

agttcctcct gttaatgaac cagaaacttt aaaacagcaa 400

<210> SEQ ID NO 274
<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 2
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 274

tntgagtatg tcccagagaa ggtgaagaaa gcggaaaaga aattagaaga gaatccatat 60
gaccttgatg ctggagcat tctcattcga gaggcacaga atcaacctat agacaaagca 120
cggaagactt atgaagcct tgttgcccag ttccccagtt ctggcagatt ctggaaactg 180
tacattgaag cagaggttac tattttattt tattttttct tatatcagta ttgcagcatt 240
cactgtagtg atagaaaaca agttaggaac atagccaatt aggacaagga ggatttaaatt 300
gtgtcttacc tttattttgt aaaataggtg taaaggagta attaaatga a 351

<210> SEQ ID NO 275
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 4, 11, 12, 13
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 275

gcgnggtcgc nnncgaggtc tgagaagccc ataccactat ttgttgagaa atgtgtggaa 60
tttattgaag atacagggtt atgtaccgaa ggactctacc gtgtcagcgg gaataaaact 120
gaccaagaca atattcaaaa gcagtttgat caagatcata atatcaatct agtgtcaatg 180
gaagtaacag taaatgctgt agctggagcc cttaaagctt tctttgcaga tctgccagat 240
cctttaattc catattctct tcatccagaa ctattggaag cagcaaaaat cccggataaa 300
acagaacgtc ttcatgcctt gaaagaaatt gttaagaaat ttcacctgt aaactatgat 360
gtattcagat acgtgataac a 381

<210> SEQ ID NO 276
<211> LENGTH: 390
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 5
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 276

gctcngactc cggcgggacc tgctcggagg aatggcgccg ccgggttcaa gcaactgtctt 60
cctgttggcc ctgacaatca tagccagcac ctgggctctg acgcccactc actacctcac 120
caagcatgac gtggagagac taaaagcctc gctggatcgc cctttcacia atttgaatc 180
tgccttctac tccatcgtgg gactcagcag ccttggtgct cagggtgccag atgcaaagaa 240
agcatgtacc tacatcagat ctaaccttga tccagcaat gtggattccc tcttctacgc 300
tgcccaggcc agccaggccc tctcaggatg tgagatctct atttcaaatg agaccaagaa 360

-continued

tctgcttctg gcagacctcg gccgcgacca

390

<210> SEQ ID NO 277

<211> LENGTH: 378

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 277

tgggaaacttc tggggttagga cgttgtctgc tatctccagt tccacagacc caaccagtta 60
cgatggtttt ggaccattta tgccgggatt cgacatcatt ccctataatg atctgcccgc 120
actggagcgt gctcttcagg atccaaatgt ggctgcgttc atggtagaac caattcaggg 180
tgaagcaggc gttgttgttc cggatccagg ttacctaatg ggagtgcgag agctctgcac 240
caggcaccag gttctcttta ttgctgatga aatacagaca ggattggcca gaactggtag 300
atggctggct gttgattatg aaaatgtcag acctgatata gtcctccttg gaaaggccct 360
ttctgggggc ttataccc 378

<210> SEQ ID NO 278

<211> LENGTH: 366

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 278

ggagggcaca ttccttttca cctcagatgc ggtcggggaa ggccaccagc ataagatttg 60
tgaccaaacc agtgatgctg tccttgatgc ccaccttcag caggatcctg atgccaaagt 120
agcttgtaga actgttgcta aaactggaat gatccttctt gctggggaaa ttacatccag 180
agctgctggt gactaccaga aagtgggtcg tgaagctgtt aaacacattg gatatgatga 240
ttcttccaaa ggttttgact acaagacttg taacgtgctg gtagccttgg agcaacagtc 300
accagatatt gctcaagggt ttcatcttga cagaaatgaa gaagacattg gtgctggaga 360
ccaggg 366

<210> SEQ ID NO 279

<211> LENGTH: 435

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 279

cctaagaact gagacttggt acacaaggcc aacgacctaa gattagccca gggttgtagc 60
tggaagacct acaacccaag gatggaaggc cctgttcaca aagcctacct agatggatag 120
aggacccaag cgaaaaagat atctcaagac taacggcccg aatctggagg cccatgaccc 180
agaacccagg aaggatagaa gcttgaagac ctggggaaat cccaagatga gaaccctaaa 240
ccctacctct tttctattgt ttacacttct tactcttaga tatttccagt tctctgttt 300
atctttaagc ctgattcttt tgagatgtac tttttgatgt tgccggttac ctttagattg 360
acaagtatta tgcttgacca gtcttgagcc agctttaaat cacagctttt acctatttgt 420
taggctatag tgttt 435

<210> SEQ ID NO 280

<211> LENGTH: 435

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

-continued

<400> SEQUENCE: 280

```
tctggatgag ctgctaactg agcacaggat gacctgggac ccagcccagc cccccgaga    60
cctgactgag gccttctctg caaagaagga gaaggccaag gggagccctg agagcagctt    120
caatgatgag aacctgcgca tagtggtggg taacctgttc cttgccggga tggtagccac    180
ctcgaccacg ctggcctggg gcctcctgct catgatccta cacctggatg tgcagcgtga    240
gcccagacct gtccgggcgg ccgctcgaaa ttccagcaca ctggcggccg ttactagtgg    300
atccgagctc ggtaccaagc ttggcgtaat catggtcata gctgtttcct gtgtgaaatt    360
gttatccgct cacaattcca cacaacatac gagccggaag cataaagtgt aaagcctggg    420
gtgcctaatag agtga                                                    435
```

<210> SEQ ID NO 281

<211> LENGTH: 440

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 281

```
catctgatct ataaatgcgg tggcatcgac aaaagaacca ttgaaaaatt tgagaaggag    60
gctgctgaga tgggaaaggg ctccttcaag tatgcctggg tcttgataa actgaaagct    120
gagcgtgaac gtggtatcac cattgatac tccttgtgga aatttgagac cagcaagtac    180
tatgtgacta tcattgatgc cccaggacac agagacttta tcaaaaacat gattacaggg    240
acatctcagg ctgactgtgc tgtcctgatt gttgctgctg gtgttggtga atttgaagct    300
ggtatctcca agaatgggca gacccgagag catgcccttc tggcttacac actgggtgtg    360
aaacaactaa ttgtcgtgtg taacaaaatg gattccactg agccccctac agccagaaga    420
gatatgagga aattgttaag                                                    440
```

<210> SEQ ID NO 282

<211> LENGTH: 502

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 282

```
tctgtggcgc aggagccccc tccccgggca gctctgacgt ctccaccgca gggactggtg    60
cttctcggag ctccactcc tcagactccg gtggaagtga cgtggacctg gatccactg    120
atggcaagct cttccccagc gatggttttc gtgactgcaa gaagggggat cccaagcacg    180
ggaagcggaa acgaggccgg ccccgaaagc tgagcaaaga gtactgggac tgtctcgagg    240
gcaagaagag caagcacgcg cccagaggca cccacctgtg ggagttcatc cgggacatcc    300
tcatccaccc ggagctcaac gagggcctca tgaagtggga gaatcggcac gaaggcgtct    360
tcaagttcct gcgtccgag gctgtggccc aactatgggg ccaaaagaaa aagaacagca    420
acatgacctc cgagaagctg agccgggcca tgaggtacta ctacaaacgg gagatcctgg    480
aacgggtgga tggccggcga ct                                                    502
```

<210> SEQ ID NO 283

<211> LENGTH: 433

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

-continued

<222> LOCATION: 130, 147, 221, 225, 242, 246, 261, 279, 292, 294, 298,
314, 323, 332, 339, 342, 343, 350, 351, 356, 361, 362, 368, 372,
375, 379, 380, 382, 387, 390, 392, 394, 401, 404, 406, 409,
413, 423, 431, 433
<223> OTHER INFORMATION: n = A,T,C or G
<400> SEQUENCE: 283

ccatattaga ttactggaac atctaagcat cagtgtgtga ccatgcgaac aaaagacttc 60
ggggagtgtc tattttttaa aaggtttatg tgtgtcgagg cagttgtaaa agatttactg 120
cagaatcaan cccactttta ggcttangac caggttctaa ctatctaaaa atattgactg 180
ataacaaaaa gtgttctaaa tgtggctatt ctgatccata nttgnttttt aaagaaaaaa 240
antgtnata cagaaagagt ntaaaagttc tgtgaattna atgcaaatta gncnccantc 300
ttgacttccc aaanacttga ttnatacctt tnaactcctnt cnnttcctgn ncttcnttaa 360
nntcaatnat tnggnagtnn anggcctcnc gnanaacacc nttncncgnt cncgcgaatc 420
cancgcctt nan 433

<210> SEQ ID NO 284
<211> LENGTH: 479
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 284

tctggaagga tcagggatct gagcaaagcc aagtttactt aagctaagcc acttgttcct 60
gggtcaagca gtttgttttc taataagcat cattcctgat cattagagca aagggatgaa 120
tgctcctctt ggaatgatac aggggatctg ccaactgggag agtggtgtct agtggttagag 180
tagcagcaat gacagaatga cagcgactct ctgagtcaac ccagtacttt tagtaccctg 240
tcactatgtg aataaaggca gctagaaaat ggactcaatt ctgcaagcct tcatggcaac 300
agcccatatt aagacttcta gaacaagtta aaaaaaaatc ttccatttcc atccatgcat 360
gggaaaaggg ctttagtata gtttaggatg gatgtgtgta taataataaa atgataagat 420
atgcatagtg ggggaataaa gcctcagagt ccttcagta tggggaatcc attgtatct 479

<210> SEQ ID NO 285
<211> LENGTH: 435
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 27, 83, 90, 93, 96, 184, 207, 227, 232, 293, 306, 307,
328, 331, 339, 343, 347, 349, 350, 370, 371, 382, 383, 414, 418,
434
<223> OTHER INFORMATION: n = A,T,C or G
<400> SEQUENCE: 285

tttttttttt tttttttttt tcaatanaaa tgccataatt tattccattg tataaaaaag 60
tcacacctat gtaacaaaat gtnttcttan aanaanaaat atattatttc aggtcataaa 120
taatcagcaa acatacaact gttggcaact aaaaaaaaac ccaacactgg tattttccat 180
cagngctgaa aacaaacctg cttaaanata tatttacagg gatagtncag tntcaaaaa 240
caaaaattga ggtatttttg ttcttctagg agtagacaat gacatttttg gangggcaga 300
ccctnnccc aaaaaataaa ataagggnat nttcttcant atngaanann gggggcgccc 360
cggggaaaaa naaaccttgg gnnnggggtt tggcccaagc ccttgaaaaa aaantttntt 420

-continued

tccccaaaaa aacng 435

<210> SEQ ID NO 286
 <211> LENGTH: 301
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 286

```
cctggtttct ggtggcctct atgaatccca tgtagggtgc agaccgtact ccatccctcc 60
ctgtgagcac cacgtcaacg gctcccgccc cccatgcacg ggggagggag atacccccaa 120
gtgtagcaag atctgtgagc ctggctacag cccgacctac aaacaggaca agcactacgg 180
atacaattcc tacagcgtct ccaatagcga gaaggacatc atggccgaga tctacaaaaa 240
cgcccccggt gagggagctt tctctgtgta ttcggacttc ctgctctaca agtcaggagt 300
g 301
```

<210> SEQ ID NO 287
 <211> LENGTH: 432
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 287

```
tccagcttgt tgccagcatg agaaccgccca ttgatgacat tgaacgccgg gactggcagg 60
atgacttcag agttgccagc caagtcacgc atgtggcggg acagggggac ccccttctca 120
acggcaccag ctttgacagc ggcaagggac acccccagaa tggcgttcgc accaaaactta 180
gatttatttt ctgttccatc catctcgatc atcagtttgt caatcttctc ttgttctgtg 240
acgttcagtt tcttgctaac cagggcaggc gcaatagttt tattgatgtg ctcaacagcc 300
tttgagacac ctttccccat atagcgagtc ttatcattgt cccggagctc tagggcctca 360
tagataccag ttgaagcacc actgggcaca gcagctctga agagaccttt tgagggtgaag 420
agatcaacct ca 432
```

<210> SEQ ID NO 288
 <211> LENGTH: 326
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 254
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 288

```
tctggctcaa gtcaaagtcc tggctcctct ctccgcctcc ttcttcatca tagtaataaa 60
cgttgtcccc ggtgtcatcc tctgggggca gtaagggctc tttgaccacc gctctcctcc 120
gaagaaacag caagagcagc agaatcagaa ttagcaaagc aagaattcct ccaagaatcc 180
ccagaatggc aggaatttgc aatcctgctt cgacaggtg tgccttccta cagacgccgg 240
cgcccccttc acantcacac acgctgacct ctaaggtggt cacttggtct ttattctggt 300
tatccatgag cttgagattg attttg 326
```

<210> SEQ ID NO 289
 <211> LENGTH: 451
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

-continued

<400> SEQUENCE: 289

```

gtcccggtgt ggctgtgccg ttggtcctgt gcggtcactt agccaagatg cctgaggaaa    60
cccagaccca agaccaaccg atggaggagg aggaggttga gacgttcgcc ttccaggcag    120
aaattgcccc gttgatgtca ttgatcatca atactttcta ctccaacaaa gagatctttc    180
tgagagagct catttcfaat tcatcagatg cattggacaa aatccggtat gaaagcttga    240
cagatcccgag taaattagac tctgggaaag agctgcatat taaccttata ccgaacaaac    300
aagatcgaac tctcactatt gtggatactg gaattggaat gaccaaggct gacttgatca    360
ataaccttgg tactatcgcc aagtctggga ccaaagcgtt catggaagct ttgcaggctg    420
gtgcagatat ctctatgatt ggacctcggc c                                451

```

<210> SEQ ID NO 290

<211> LENGTH: 494

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 421

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 290

```

tttttttttt tcaaaacagt atattttatt ttacaatagc aaccaactcc ccagtttgtt    60
tcaattgtga catctagatg gcttaagatt actttctggt ggtcacccat gctgaacaat    120
atttttcaat cttccaaaca gaaaagactc aaaagagatt ctgcatttca catcagttca    180
caagttcaag agtcttccat ttatcttagc ttttggaata aattatcttt gaggtagaag    240
gacaatgacg aagccactta attccttggt tctgcataaa agcagattta ttcatcacia    300
cttcatttat gtgaataaag cagatgatga taaaatgttc tcttattctt gtttaatcag    360
tagtggtagt gatgccagaa acttgtaaat gcacttcaaa ccaattgtgg ctcaagtgtg    420
ngtgggtccc caaggctggt accaatgaga ctgggggttg ggaattagtt ggtcatcatc    480
cctcctgctg ccca                                494

```

<210> SEQ ID NO 291

<211> LENGTH: 535

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 291

```

tcgcggtgctt aacatgaaaa caaactttgt gctgtttggt tcattgtatg cattgatgga    60
gtcttgtctc tcatcatggg gtgtctgacc atccaacctg cagtactcat aatttctcca    120
catgcaataa tcttccaaaa tgtccaatac cttgttcatt tgactgaaga ttagtactcg    180
tgaaccttgt tcttttaact tagggagcag cttgtctaaa accaccattt tgccactggt    240
ggttactaga tgcatatctg ttgtataagg tggaccaggt tctgctccat caaagagata    300
tggatgatta caacattttc tcaactgcat taggatgttc aataacctca ttttgtccat    360
cttgctgctg gagttgagta tatctatata cttcattaat atccgagtat accattccct    420
ttgcattttg ctgagggcca catagatttt tacttccttc tttggaggca aactcttttc    480
aacatcagcc ttaattcgac gaaggaggaa tggacgcaaa accatatgaa gcctc        535

```

<210> SEQ ID NO 292

-continued

<211> LENGTH: 376
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 4, 348
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 292

```
tacnagcccc tgctgatcga gatcctgggtg gaggtgatgg atccttcctt cgtgtgcttg      60
aaaaattggag cctgcccctc ggcccataag cccttggttg gaactgagaa gtgtatatgg      120
ggcccaagct actggtgccca gaacacagag acagcagccc agtgcaatgc tgcgagcat      180
tgcaaacgcc atgtgtggaa ctaggaggag gaatattcca tcttggcaga aaccacagca      240
ttgggttttt tctacttgtg tgtctggggg aatgaacgca cagatctgtt tgactttgtt      300
ataaaaatag ggctccccc cctcccccat ttttgtgtcc tttattgnag cattgtgtgc      360
tgcaaggagg ccccta                                     376
```

<210> SEQ ID NO 293
<211> LENGTH: 320
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 293

```
tcggctgctt cctggctctg cggggatggg tttgctttgg aaatcctcta ggaggctcct      60
cctcgcatgg cctgcagtct ggcagcagcc ccgagttgtt tcctcgctga tcgatttctt      120
tcctccaggt agagttttct ttgcttatgt tgaattccat tgcctctttt ctcatcacag      180
aagtgatgtt ggaatcgttt cttttgtttg tctgatttat ggttttttta agtataaaca      240
aaagtttttt attagcattc tgaaagaagg aaagtaaaat gtacaagttt aataaaaagg      300
ggccttcccc tttagaatag                                     320
```

<210> SEQ ID NO 294
<211> LENGTH: 359
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 294

```
ctgtcataaa ctggtctgga gtttctgacg actccttggt caccaaatgc accatttcct      60
gagacttgct ggctctccg ttgagtccac ttggctttct gtcctccaca gtcctattgc      120
cactgttgat cactagcttt ttctctgcc cacaccttot tcgactgttg actgcaatgc      180
aaactgcaag aatcaagcc aaggccaaga gggatgcaa gatgatcagc cattctggaa      240
tttgggtgtg cttatagga ccagaggttg tgtttgctcc accttcttga ctcccatgtg      300
agtgccatc tgattcagat ccatgagtg tatgggaccc ccactgggg tggaatgtg      359
```

<210> SEQ ID NO 295
<211> LENGTH: 584
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 558
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 295

-continued

cctgagttgg gctgactgcc agagacagac cctcttggtg ctcggtgaac cagccaggca	60
tttacctcag tgggtggcac ctggaacctg tccagggccc tcacctgact gaggagccgc	120
cgggcagtga agtaattgtc cagggtctatg ctcttggtgg ggataccata gccatccaag	180
gtattcctca ggttggtgaa ctgggtctga gtataggcag aactgggccc caggatgac	240
tcccggagtg ggggaagctg tgaggtcagg taagtatcca cgtccacccg taccccaatc	300
aaactcagca gaatggtgaa ctggagaagt ccttccgtta agtatttctt cagagaaagc	360
attgctgaag gaccagaatg tttatgcttt ttggttttta aaatcttcca aaagacaaat	420
caaggccact gctctgccgc tccagccagc aggttacctt cctcagtgtc aaaccccgta	480
ccccaccctg gcagaacaca agggatgagc tccctgacgg cccagagga aagcacacc	540
tgtggagcca aggccaanga cacactccag accacattca cttt	584

<210> SEQ ID NO 296
 <211> LENGTH: 287
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 296

ccttatcatt cattcttagc tcttaattgt tcattttgag ctgaaatgct gcattttaat	60
tttaaccaa acatgtctcc tatcctggtt ttgtagcct tcctccacat cttttctaaa	120
caagatttta aagacatgta ggtgtttgtt catctgtaac tctaaaagat cttttttaa	180
ttcagtccta agaaagagga gtgctgtgcc cctaagagtg tttaatggca aggcagccct	240
gtctgaagga cacttcctgc ctaagggaga gtggtatttg cagacta	287

<210> SEQ ID NO 297
 <211> LENGTH: 457
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 297

ccaattgaaa caaacagttc tgagaccgtt cttccaccac tgattaagag tggggtggca	60
ggtattaggg ataatttca tttagccttc tgagctttct gggcagactt ggtgaccttg	120
ccagctccag cagccttctt gtccactgct ttgatgacac ccaccgcaac tgtctgtctc	180
atatcacgaa cagcaaacgc acccaaaggt ggatagcttg agaagctctc aacacacatg	240
ggcttgccag gaaccatata aacaatggca gcataccag acttcaagaa tttagggcca	300
tcttccagct ttttaccaga acggcgatca atcttttctt tcagctcagc aaacttgcat	360
gcaatgtgag ccgtgtggca atccaatata ggggcatagc cggcgcttat ttggcctgga	420
tggttcagga taatcacctg agcagtgaag ccagacc	457

<210> SEQ ID NO 298
 <211> LENGTH: 469
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 298

tctttgactt tccttgctta cctcctctgg agatctcaa ttctccagg tccatgctcc	60
cagagatctc aatgattcct gattctcttc ttccaggagt ctgaatgtct cttggttcac	120
ttccacagac tccagtgggt cttgaatttc cttttctaga ggattcattg cccctgatt	180

-continued

tattttcttct ggagtcacaca gtggtgcttg agtttctgga gatttcagtg tttccagggt	240
ctcttgctccc gcagacttca gtgattctag gatctctgtt tctaaagatt ttactgcctc	300
tatgtctctct tctttgagtg actttaagaa ctcttgattc tcattttcaa gaggtctagc	360
tatctcctgg tcaagagact tcagtggttc tagatccact tttctctggg gtcttaaatgt	420
catctgatcc tgttccccta gagacctccg tcgctgttga gtctctttt	469

<210> SEQ ID NO 299
 <211> LENGTH: 165
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 37, 82, 144
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 299

tctgtggaga ggatgagggt gagggagggt gggatatnctg ctgctctgac cttaggtaga	60
gtcctccaca gaagcatcaa antggactgg cacatatgga ctcccttcac aggccacaat	120
gagtgtgtctc tccttcgggc tggncggta tgcacagttg gggta	165

<210> SEQ ID NO 300
 <211> LENGTH: 506
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 300

tctgaggaaa gtttgggctt attagtattt gctccagcga acctccaagt tttctccatt	60
gcggacaacg taactaccag ctcccttggt cagtgggttcg cctccactca gaagttccca	120
gtaggttctg tcattattgt tggcacatag gccctgaata caggtgatat agggccccc	180
tgagcgctcc tccattgtga aaccaaatat agtatcattc attttctggg ctttctccat	240
cacactgagg aagacagaac catttagcac agtgacattg gtgaaatatg tttcattgat	300
tctcacagag taattgacgg agatatatga ttgtgagtca ggagggtgca cagttatagg	360
ctcatcagcg gagatgttga agttacctga agcagagacg caagaagagt cttgtttaat	420
atccaagaag gtctttccca tcagggcagg taagacctgg gctgcagcgt ttggattgct	480
gaatgctcct tgagaaattt ccgtga	506

<210> SEQ ID NO 301
 <211> LENGTH: 304
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 221, 223, 252, 275, 280
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 301

tcctaaggca gagccccat cacctcaggc ttctcagttc ccttagccgt cttactcaac	60
tgcccccttc ctctccctca gaatttgtgt ttgctgcctc tatcttggtt tttgtttttt	120
cttctggggg gggctctagaa cagtgcctgg cacatagtag gcgctcaata aatacttggt	180
tggtgaatgt ctctctctct tttccactct gggaaaccta ngnttctgcc attctgggtg	240
accctgtatt tntttctggt gccattcca ttgnccagn taatacttcc tcttaaaaat	300

-continued

ctcc 304

<210> SEQ ID NO 302
<211> LENGTH: 492
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 302

ttttcagtaa gcaacttttc catgctctta atgtattcct ttttagtagg aatccggaag 60
tattagattg aatggaaaag cacttgccat ctctgtctag gggtcacaaa ttgaaatggc 120
tcctgtatca catacgaggg tcttgtgtat ctgtggcaac agggagtttc cttattcact 180
ctttatttgc tgctgtttaa gttgccaacc tcccctccca ataaaaattc acttacacct 240
cctgcctttg tagttctgtg attcacttta ctatgtgata gaagtagcat gttgctgcca 300
gaatacaagc attgcttttg gcaaattaaa gtgcatgtca tttcttaata cactagaaag 360
gggaaataaa ttaaagtaca caagtccaag tctaaaactt tagtactttt ccatgcagat 420
ttgtgcacat gtgagagggt gtccagtttg tctagtgtatt gttatttaga gagttggacc 480
actattgtgt gt 492

<210> SEQ ID NO 303
<211> LENGTH: 470
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 303

tctggggcag caggtagctc ctacggcact agtctacagg gggaaggacg ctctgtgtctg 60
gcagcgggtg ctcacatggc ctgtctgcac tgtaaccaca ggctgggatg tagccaggac 120
ttggtctcct tggaagacag gtctgatgtt tggccaatcc agtccttcag accctgcctg 180
aaacttgtat cttacgtgaa cttaaagaat aaaatgcatt tctaccccca tctcgccccc 240
aggactggca cgacaggccc acggcagatt agatcttttc ccagtactga tcggtgcgtg 300
gaattccagc caccacttct gattcgattc cacagtgatc ctgtcctctg agtattttaa 360
agaagccatt gtcaccccag tcagtgttcc aggagttggc aaccagccag tagggtgtgc 420
cattctccac tcccagccc aggatgcgga tggcatggac ctcgccgcg 470

<210> SEQ ID NO 304
<211> LENGTH: 79
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 304

tgtccattg ttaactcagc ctcaaatctc aactgtcagg ccctacaaag aaaatggaga 60
gcctcttctg gtggatgcg 79

<210> SEQ ID NO 305
<211> LENGTH: 476
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 305

tcactgagcc accctacagc cagaagagat atgaggaaat tgtaaggaa gtcagcactt 60
acattaagaa aattggctac aaccccgaca cagtagcatt tgtgccaatt tctggttgga 120

-continued

```

atggtgacaa catgctggag ccaagtgcta acgtaagtgg ctttcaagac cattgttaaa 180
aagctctggg aatggcgatt tcatgcttac acaaattggc atgcttgtgt ttcagatgcc 240
ttggttcaag ggatggaaa gaccccgtaa ggatggcaat gccagtggaa ccacgctgct 300
tgaggctctg gactgcatcc taccaccaac tcgtccaact gacaagccct tgcgcctgcc 360
tctccaggat gtctacaaaa ttggtggtaa gttggctgta aacaaagttg aatttgagtt 420
gatagagtac tgtctgcctt cataggtatt tagtatgctg taaatatatt taggta 476

```

```

<210> SEQ ID NO 306
<211> LENGTH: 404
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 306

```

```

tctgtctcgg agctcagggc gcagccagca cacacaggag cccacaggac agccacgtct 60
tcacagaaac tacagaagtc aggacccagg cgaggacctc aggaacaagt gccccctgca 120
gacagagaga cgcagtgaac acagcttctg aacaactaca taataatgcg gggagaatcc 180
tgaagaccac tgcattccac aagcactgac aaccacttca ggattttatt tcctccactc 240
taacccccag atccatttat gagaagttag tgaggatggc aggggcatgg aggggtgaagg 300
gacagcaagg atggtctgag ggcttgaaa caatagaaaa tcttcgtcct ttagcatatc 360
ctggactaga aaacaagagt tggagaagag gggggttgat acta 404

```

```

<210> SEQ ID NO 307
<211> LENGTH: 260
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 10, 255, 257
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 307

```

```

tctgcctan acatctgtga gggcctcaag ggctgctgcc tcgactttct ccctagctaa 60
gtccaccctg ccaggagcac agccagggca ctgctctgtg ctgacttcca ctgcagccaa 120
gggtcaaaaat gaagcatctg cggaggccag gactccttgg catcgacac agtcagggga 180
aaagccaccc tgactctgca ggacagaggg tctagggtca tttggcagga gaacactggt 240
tgccaagggt aagcnancat 260

```

```

<210> SEQ ID NO 308
<211> LENGTH: 449
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 308

```

```

tctgtgctcc cgactcctcc atctcaggta ccaccgactg cactgggcgg ggcctctggt 60
ggggaaaggc tccacggggc agggatacat ctgagggcca gtcattctct ggaggcagcc 120
caatcaggtc aaagattttg cccaactggt cggcttcaga gttccacag aagagaggct 180
ttcgacgaaa catctctgca aagatacagc caacactcca catgtccaca ggtgttgcat 240
atgtggactg cagaagaact tcgggagctc ggtaccagag tgtaacaacc ttgatcgttt 300
cggctggcaa gcctgggtgg ggtgccttgt ccagatatgt ccttaggtcc tgggtctacat 360

```

-continued

```
gctcaaacac caggggttacc ttgatctccc ggtcagttcg ggatgtggca cagacgtcca 420
tcagccggac aacattggga tgctcaaaa 449
```

```
<210> SEQ ID NO 309
<211> LENGTH: 411
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 384
<223> OTHER INFORMATION: n = A,T,C or G
```

```
<400> SEQUENCE: 309
```

```
ctgtgaaac ctggggtgcc gggtaaatgg agaactccag cttggatttc ttgccataat 60
caactgagag acgttccatg agcagggagg tgaaccaga accagttccc ccaccaaagc 120
tgtggaaaac caagaagccc tgaagaccgg tgcactggtc agccagcttg cgaattcggg 180
ccaacacaag gtcaatgatc tccttgccaa tgggtgtagt ccctcgggca tagttattgg 240
cagcatcttc cttgcctgtg atgagctgct cagggtgga gagctggcgg taggtgccag 300
tgcgaaactc atcaatgact gtgggttcca agtctacaa cacagccgg ggacagtgtc 360
tgccagcgcc cgtctcactt gaanaagggt gtttgaagga agtcatctcc t 411
```

```
<210> SEQ ID NO 310
<211> LENGTH: 320
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 250
<223> OTHER INFORMATION: n = A,T,C or G
```

```
<400> SEQUENCE: 310
```

```
tcctcgtcca gcttgactcg attagtcctc ataaggtaa caaggcagat ggtggctgac 60
cgggaaatgc ctgcctggca gtggacaaac acccttcctc cagcattctt gatggagtct 120
atgaagtcaa tggcctcgtt gaaccaggag ctgatgtctg ccttgtgggt gtcctccaca 180
gggatgctct tgtactggtg gtgacctca aaatgggttg gacaattggc tgagacgttg 240
atcaaggcan ttatgcccaa ggcattccagc atgtccttgc ggaagcgtg atacgcactg 300
cccaggtaca gaaagggcag 320
```

```
<210> SEQ ID NO 311
<211> LENGTH: 539
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
```

```
<400> SEQUENCE: 311
```

```
tctggcccat gaagctgaag ttgggagaga tgatgcttcg cctctgcttc aaaaactcaa 60
aggcctcgtc cagcttgact cgattagtcc tcataaggta agcaaggcag atgggtggctg 120
accgggaaat gcctgcctgg cagtggacaa acacccttcc tccagcattc ttgatggagt 180
ctatgaagtc aatggcctcg ttgaaccagg agctgatgtc tgccttgttg ttgtcctcca 240
cagggatgct cttgtactgg tagtgacct caaatggtt gggacaattg gctgagacgt 300
tgatcaaggc agttatgccc aaggcatcca gcatgtcctt gcgggaagcg tgatacgac 360
tgcccaggta cagaaagggc aggatattcca ccgggccacc ctgaaatcca gaaatatcca 420
```

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acattcatca agcttgctca aagccaaggc cagtgtcccat acccacaaaa actttctgct 480

ggaaaagtca atttcagata ccgagtgaac tcagtctctgt tgctggagga taaataaat 539

<210> SEQ ID NO 312

<211> LENGTH: 475

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 312

tcaaggatct tcctaaagcc accatgtgag aggattcggg cgagagtctg agctgtatgg 60

cagaccatgt cctgctgttc taggggtcatg actgtgtgta ctctaaagt gccactctca 120

cagggtcag tgataccac tgaacctggc aggaacagtc ctgcagccag aatctgcaag 180

cagcgctgt atgcaacgtt tagggccaaa ggctgtctgg tggggttgtt catcacagca 240

taatggccta gtaggtcaag gatccagggt gtgaggggct caaagccagg aaaacgaatc 300

ctcaagtcct tcagtagtct gatgagaact ttaactgtgg actgagaagc attttcctcg 360

aaccagcggg catgtcggat ggctgctaag gcactctgca atactttgat atccaaatgg 420

agttctggat ccagttttcg aagattgggt ggcactgttg taatgagaat cttca 475

<210> SEQ ID NO 313

<211> LENGTH: 456

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 313

tccacttaaa ggggtgcctct gccaaactgg ggaatcatcg ccacttccag caccacgcca 60

agcctaacat cttccacaag gatcccgatg tgaacatgct gcacgtgttt gttctgggcg 120

aatggcagcc catcgagtac ggcaagaaga agctgaaata cctgccctac aatcaccagc 180

acgaatactt cttcctgatt gggccgccgc tgctcatccc catgtatttc cagtaccaga 240

tcacatgac catgatcgtc cataagaact ggggtggacct ggctggggc gtcagctact 300

acatccgggt cttcatcacc tacatccctt tctacggcat cctgggagcc ctccctttcc 360

tcaacttcat caggttcctg gagagccact ggtttgtgtg ggtcacacag atgaatcaca 420

tcgtcatgga gattgaccag gaggacctcg gcccgcc 456

<210> SEQ ID NO 314

<211> LENGTH: 477

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 314

tgctggggct tctggaagcc tggatctgga atcattcacc agattattct ggaaaactat 60

gcgtaccctg gtgttcttct gattggcact gactcccaca cccccaatgg tggcgccctt 120

gggggcatct gcattggagt tgggggtgac gatgctgtgg atgtcatggc tgggatcccc 180

tgggagctga agtgcccaa ggtgattggc gtgaagctga cgggctctct ctccggttg 240

tcctcaccac aagatgtgat cctgaagggt gcaggcatcc tcacggtgaa aggtggcaca 300

ggtgcaatcg tggaatacca cgggcctggt gtagactcca tctcctgcac tggcatggcg 360

acaactctga acatgggtgc agaaattggg gccaccactt ccgtgttccc ttacaaccac 420

aggatgaaga agtatctgag caagaccggc cggaagaca ttgccaatct agctgat 477

-continued

<210> SEQ ID NO 315
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 35
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 315

cagggtactgg atgtcagggtc tgcgaaactt cttanatttt gacctcagtc cataaaccac 60
actatcacct cggccatcat atgtgtctac tgtggggaca actggagtga aaacttcggt 120
tgctgcagggt ccgtgggaaa atcagtgacc agttcatcag attcatcaga atgggtgagac 180
tcacagact ggtgagaatc atcagtgatc tctacatcat cagagtcgtt cgagtcaatg 240
g 241

<210> SEQ ID NO 316
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 1, 4, 32, 39, 68, 77, 82, 94, 166, 172, 195, 196
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 316

ntntgtgat agtgtggttt atggactgag gncaaaatnt aagaagtttc gcagacctga 60
catccaancc tgcccngcgc gncgctcgaa aggnccaatt ctgcagatat ccatcacact 120
ggcgcccgct cgagcatgca tctagagggc ccaattcgcc ctatantgag tnatattaca 180
attcactggc cgtcnnttta caacgtcgtg actgggaaaa ccctggcggtt acccaactta 240
a 241

<210> SEQ ID NO 317
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 15, 25, 135, 154, 193
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 317

agggtaccctg ctcanagcc tggngcctg ggttgtctcc ttgtccatcc actggtccat 60
tctgctctgc atttttttgt tcctcttttg gaggttccac tttgggtttg ggctttgaaa 120
ttatagggct acaantacct cggccgaaac cacnctaagg gcgaattctg cagatatcca 180
tcacactggc ggncgctcga gcatgcatct agagggccca attcgcccta tagtgagtcg 240
t 241

<210> SEQ ID NO 318
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 3, 5, 10, 11, 24, 28, 31, 34, 40, 42, 47, 53, 74, 80,
96, 101, 127, 129, 136, 138, 205, 241
<223> OTHER INFORMATION: n = A,T,C or G

-continued

<400> SEQUENCE: 318

```
cgngnacaan ntacattgat gganggtntg nggntctgan tntttantta cantggagca    60
ttaatatattt cttnaacgtn cctcaccttc ctgaantaaa nactctgggt tgtagcgctc    120
tgtgctnana accacntnaa ctttcatccc ctcttttgga ttaatccact gcgcggccac    180
ctctgccgcg accacgctaa gggcnaattc tgcagatata catcacactg gcggccgctc    240
n                                                                    241
```

<210> SEQ ID NO 319

<211> LENGTH: 241

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 24, 36, 39

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 319

```
cagggtactga tcggtgcgtg gaantccagc caccantntt gattcgattc cacagtgatc    60
ctgtcctctg agtattttta agaagccatt gtcaccccag tcagtgttcc aggagtggc    120
aaccagccag taggggtgtgc cattctccac tccccagccc aggatgcgga tggcatggcc    180
acccatcatc tctccggtga cgtgttggtc cctcgccgcg gaccacgcta agggcgaatt    240
c                                                                    241
```

<210> SEQ ID NO 320

<211> LENGTH: 241

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 27, 215, 216, 217, 220, 222, 235

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 320

```
ggcaggtacc aacagagctt agtaatntct aaaaagaaaa aatgatcttt ttccgacttc    60
taaaacagtg actatactag cataaatcat tctagtaaaa cagctaaggt atagacattc    120
taataatttg ggaaaccta tgattacaag tgaaaactca gaaatgcaa gatgttggtt    180
ttttgtttct cagtctgctt tagcttttaa ctctnnnaan cncatgcaca cttgnaactc    240
t                                                                    241
```

<210> SEQ ID NO 321

<211> LENGTH: 241

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 2, 25, 26, 228

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 321

```
angtaccaac agagcttagt aattnntaaa aagaaaaaat gatctttttc cgacttctaa    60
acaagtgact atactagcat aatcatttct agtaaacag ctaaggtata gacattctaa    120
taatttggga aaacctatga ttacaagtga aaactcagaa atgcaaagat gttggttttt    180
tgtttctcag tctgctttag cttttaactc tggaagcgca tgcacacntg aactctgctc    240
```

-continued

a 241

<210> SEQ ID NO 322
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 322

ggtaccaaca gagcttagta atttctaaaa agaaaaaatg atctttttcc gacttctaaa 60
caagtgacta tactagcata aatcattctt ctagtaaaac agctaaggta tagacattct 120
aataatttgg gaaaacctat gattacaagt aaaaactcag aaatgcaaag atgttggttt 180
tttgtttctc agtctgcttt agcttttaac tctggaagcg catgcacact gaactctgct 240

c 241

<210> SEQ ID NO 323
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 323

cgaggtagtg tcgtatcctc agccttggtc tatttcttta ttttagcttt acagagatta 60
ggtctcaagt tatgagaatc tccatggctt tcaggggcta aacttttctg ccattctttt 120
gctcttaccg ggctcagaag gacatgtcag gtgggatacg tgtttctctt tcagagctga 180
agaaagggtc tgagctgcgg aatcagtaga gaaagccttg gtctcagtga ctccttggtc 240

t 241

<210> SEQ ID NO 324
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 324

aggtagtgtc gtatcctcag ccttggttcta tttctttatt ttagctttac agagattagg 60
tctcaagtta tgagaatctc catggcttct aggggctaaa cttttctgcc attcttttgc 120
tcttaccggg ctcagaagga catgtcaggt gggatactg tttctcttct agagctgaag 180
aaagggctct agctgcggaa tcagtagaga aagccttggt ctcaagtgact ccttggtctt 240

c 241

<210> SEQ ID NO 325
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 325

ggcaggtaca tttgttttgc ccagccatca ctcttttttg tgaggagcct aaatacattc 60
ttcctggggc ccagagtccc cattcaaggc agtcaagtta agacactaac ttggcccttt 120
cctgatggaa atatttcctc catagcagaa gttgtgttct gacaagactg agagagttac 180
atgttgggaa aaaaaagaa gcattaactt agtagaactg aaccaggagc attaatgtct 240

g 241

-continued

<210> SEQ ID NO 326
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 326

```
gcaggtagcat ttgttttgcc cagccatcac tcttttttgt gagagccta aataattct 60
tcctgggggc cagagtcctc attcaaggca gtcaagttaa gacactaact tggccctttc 120
ctgatggaaa tatttcctcc atagcagaag ttgtgttctg acaagactga gagagttaca 180
tgttgggaaa aaaaagaagc attaacttag tagaactgat ccaggagcat taagttctga 240
a 241
```

<210> SEQ ID NO 327
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 327

```
ggtaccagac caagtgaatg cgacagggaa ttatttcctg tgttgataat tcatgaagta 60
gaacagtata atcaaaatca attgtatcat cattagtttt ccaactgcctc acactagtga 120
gctgtgccaa gtagtagtgt gacacctgtg ttgtcatttc ccacatcacg taagagcttc 180
caaggaaagc caaatcccag atgagtctca gagagggatc aatatgtcca tgattatcag 240
g 241
```

<210> SEQ ID NO 328
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 6, 19, 66, 232, 240
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 328

```
ggtacnagac caaatgaang ccacagggaa ttatttcctg tgttgataat tcatgaagta 60
gaacantata atcaaaatca attgtatcat cattagtttt ccaactgcctc acactagtga 120
gctgtgccaa gtagtagtgt gacacctgtg ttgtcatttc ccacatcacg taagagcttc 180
caaggaaagc caaatcccag atgagtctca gagagggatc aatatgtcca tnatcatcan 240
g 241
```

<210> SEQ ID NO 329
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 33, 61, 220, 228, 229, 240, 241
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 329

```
ttcagggtcga gttgggtgca gatttgtggt gonttctgag ccgtctgtcc tgcgccaaaa 60
ngcttcaag tattattaaa aacatatgga tccccatgaa gccctactac accaaagt 120
accaggagat ttgatagga atggggctga tgggcttcat cgtttataaa atccgggctg 180
ctgataagaa gtaaggcttt gaaagcttca ggcctgtctn ctggctcanna ctaaccatan 240
```

-continued

n 241

<210> SEQ ID NO 330
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 330

ttttgtgcag atttgtggtg cgttctgagc cgtctgtcct gcgccaagat gcttcaaagt 60
attattaaaa acatatggat ccccatgaag ccctactaca ccaaagttta ccaggagatt 120
tggataggaa tggggctgat gggcttcacg gtttataaaa tccgggctgc tgataaaaga 180
agtaaggctt tgaaagcttc agcgctgct cctggtcacg actaaccaga tttacttga 240
g 241

<210> SEQ ID NO 331
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 1, 9, 41, 60, 61, 119, 124, 132, 139, 141, 153, 168
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 331

nttttaggna ctttgggctc cagacttcac tggctctagg nattgaaacc atcacctggn 60
ntgcattcct catgactgag gttaacttaa aacaaaaatg gtaggaaagc tttcctatnc 120
ttcnggtaag anacaaatnt nctttaaaaa aangtggaag gcatgacnta cgtgagaact 180
gcacaaactg gccactgaca aaaatgaccc ccatttgtgt gacttcattg agacacatta 240
c 241

<210> SEQ ID NO 332
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 332

tgtgaggaga gggaacatgc tgagaaactg atgaagctgc agaaccaacg aggtggccga 60
atcttccttc aggatatcaa gaaaccagac tgtgatgact gggagagcgg gctgaatgca 120
atggagtgtg cattacattt ggaaaaaat gtgaatcagt cactactgga actgcacaaa 180
ctggccactg acaaaaaatga ccccatttg tgtgacttca ttgagacaca ttacctgaat 240
g 241

<210> SEQ ID NO 333
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 44, 52, 60, 98, 104, 108, 124, 126, 190, 198, 206, 214
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 333

caggtaacag cttttttttt tttttttttt tttttttttt ttgnaaatac tntttattgn 60
aaatattcta tcctaaatcc catatagcca attaatnttt acanaatntt ttgttaattt 120

-continued

ttgngngtat aaatatttaca aaaataaaagg gtatgtttgt tgcacacaac ttacaaataa 180
taataaaactn tttattgnaa atatntttta ttgnaaatat tctttatcct aaattccata 240
t 241

<210> SEQ ID NO 334
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 10, 16, 22, 24, 49, 158, 159, 237
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 334

tacctgctgn aggggntgaa gncntctctg ctgccccagg catctgcanc ccctgctgct 60
ggttctgccc ctgctgcagc agaggagaag aaagatgaga agaaggagga gtctgaagag 120
tcagatgatg acatgggatt tggccttttt gattaaannc ctgctccctt gcaaataaag 180
cctttttaca caaaaaaaaa aaaaaaaaaa aaaaaaaaaa agcttgttac ctgcccnggc 240
g 241

<210> SEQ ID NO 335
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 39
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 335

ctatgtgctg ggatgactat ggagacccaa atgtctcana atgtatgtcc cagaaacctg 60
tggctgcttc aaccattgac agttttgctg ctgctggctt ctgcagacag tcaagctgca 120
gtccccccaa aggctgtgct gaaacttgag cccccgtgga tcaacgtgct ccaggaggac 180
tctgtgactc tgacatgcca gggggctcgc agccctgaga gcgactccat tcagtggttc 240
c 241

<210> SEQ ID NO 336
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 336

taccaaccta tgcagccaag caacctcagc agttcccatc aaggccacct ccaccacaac 60
cgaaagtatc atctcaggga aacttaattc ctgcccgtcc tgctcctgca cctcctttat 120
atagttccct cacttgattt ttttaacctt ctttttgcaa atgtcttcag ggaactgagc 180
taatactttt ttttttcttg atgttttctt gaaaagcctt tctgttgcaa ctatgaatga 240
a 241

<210> SEQ ID NO 337
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature

-continued

<222> LOCATION: 47, 56, 69, 228
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 337

ggtactgtat gtagctgcac tacaacagat tcttaccgtc tccacanagg tcatanattg 60
taaatggtna atactgactt tttttttatt cccttgactc aagacagcta acttcatttt 120
cagaactgtt ttaaaccctt gtgtgctggt ttataaaata atgtgtgtaa tccttggtgc 180
tttcctgata ccagactgtt tcccgtggtt ggtagaata tttttgntt tgatgcttat 240
a 241

<210> SEQ ID NO 338
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 338

aggtacaggt gtgcgctgag ccgagtttac acggaagga taaagcccat ttagtttctt 60
ctcaaatgga gttttccact ttcctttgaa gtagacagca ttcaccagga tcactcctgt 120
atccccatct acagaacctt caggtaacaa gtttgggatt ttgcctttgg tttgagtctt 180
gacccaggaa ttaatctttt ttctagcttc ttctgcacat tctaggaagt ctactgcctg 240
g 241

<210> SEQ ID NO 339
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 339

taccgacggc tcctggaggg agagagtga gggacacggg aagaatcaaa gtcgagcatg 60
aaagtgtctg caactccaaa gatcaaggcc ataaccagg agaccatcaa cggaagatta 120
gttctttgtc aagtgaatga aatccaaaag cagcagcatg accaatgaaa gtttccgcct 180
gttgtaaaat ctattttccc ccaaggaaag tccttgaca gacaccagtg agtgagttct 240
a 241

<210> SEQ ID NO 340
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 340

gtagccctca cacacacatg cccgtaacag gatttatcac aagacacgcc tgcagttaga 60
ccagacacag ggcgtatgga aagcacgtcc tcaagactgt agtattccag atgagctgca 120
gatgcttacc taccacggcc gtctccacca gaaaaccatc gccaaactct gcgacagct 180
tgtgacttac aaaccttggt taaaagctgc ttacatggac ttctgtcctt taaaagcttc 240
c 241

<210> SEQ ID NO 341
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 341

-continued

gtaccgccta ctttcgtctc atgtctccga acttcttgct gatggccgtt ccaacgttgc	60
tgaagctgc agttgccttt tgccctgcgt gactcagggg ttcattgtgt ttcttgtagg	120
cagtggtagt ctgcattgca tgccagcttt tgctgaagtt ctgttttaatt tcattcatca	180
ggttcatgcc gagttttgtt ttatctcaac tagatgcctt tctttcgctg acaaaacttg	240
t	241

<210> SEQ ID NO 342
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 342

gtacattggt gctataaata taaatgtac ttatgaagca tgaaattaag cttctttttt	60
cttcaagttt tttctcttgt cttagcaatct gttaggcttc tgaaccaaga ccaaatgttt	120
acgttcctct gctgcatacc aacgttactc caaacaataa aaatctatca tttctgctct	180
gtgctgagga atggaaaatg aaacccccac cccctgacct ctaggactat acagtggaaa	240
c	241

<210> SEQ ID NO 343
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 343

gtacatgtgg tagcagtaat ttttttgaag caactgcact gacattcatt tgagttttct	60
ctcattatca gattctgttc caaacaagta ttctgtagat ccaaatggat taccagtgtg	120
ctacagactt cttattatag aacagcattc tattctacat caaaaatagt ttgtgtaagt	180
tagttttggt taccatctaa aatattttta aatgttcttt acataaaaat ttatgttgtg	240
t	241

<210> SEQ ID NO 344
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 344

ggtacaaaat tgttgaatt tagctaatag aaaaacatag taaatattha caaaaacgtt	60
gataacatta ctcaagtcac acacatataa caatgtagac aggtcttaac aaagtttaca	120
aattgaaatt atggagattt cccaaaatga atctaatagc tcattgctga gcatggttat	180
caatataaca tttaagatct tggatcaaat gttgtccccc agtcttctgc aatccagtcc	240
t	241

<210> SEQ ID NO 345
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 345

ggtacgaagc tgagcgacgc ggggttgccc cagcgtggag cctggacctc aaacttcacg	60
gaaaatgctc tctctctttg acaggcttcc agctgtctcc taatttcctg gatgaactct	120

-continued

```

ccccggcgat ttaactgac ctgaaaagtg gtgagaggac tgaggaagac aaccaggtca 180
gcgcttagac ggccctctgag ggtggtgccc ttgcctgagg agccaccctt taccaccttg 240
g 241

```

```

<210> SEQ ID NO 346
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 346

```

```

cagggtaccac tgagcctgag atggggatga gggcagagag aggggagccc cctcttccac 60
tcagttgttc ctactcagac tgttgcactc taaacctagg gaggttgaag aatgagaccc 120
ttaggtttta acacgaatcc tgacaccacc atctataggg tcccaacttg gttattgtag 180
gcaaccttcc ctctctcctt ggtgaagaac atcccaagcc agaaagaagt taactacagt 240
g 241

```

```

<210> SEQ ID NO 347
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 347

```

```

aggtacatct aaaggcatga agcactcaat tgggcaatta acattagtgt ttgttctctg 60
atggtatctc tgagaatact ggttgtagga ctggccagta gtgccttcgg gactgggttc 120
acccccaggt ctgcgcagct tgtcacagcg ccagccccgc tggcctcaa agcatgtgca 180
ggagcaaagt gcaccgagat attccttctg ccaactgttct cctacgtggt atgtcttccc 240
a 241

```

```

<210> SEQ ID NO 348
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 2, 18, 29, 35, 56, 57, 64, 76, 77, 85, 102, 103, 104,
189, 232
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 348

```

```

angtacttgg caagattnga tgctcttngn ctcantgaca tcattcataa cttgtnngtg 60
tgancagagg aggagnncat catctgtgcc tcattcgtea gnnncctctc ctctctgaat 120
ctcaacaag ttgataatgg agaaaaattt gaattctcag gattgaggct ggactgggtc 180
cgcctacang catacactag cgtggctaag gccctcttgc accctgcatg anaacctga 240
c 241

```

```

<210> SEQ ID NO 349
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 349

```

```

gcaggtagca ttgtctgac ctctgtaaaa aatgtgatcc tacagaagtg gagctggata 60

```

-continued

```

atcagatagt tactgctacc cagagcaata tctgtgatga agacagtgct acagagacct 120
gctacactta tgacagaaac aagtgtctaca cagctgtggt ccactctgta tatggtggtg 180
agacaaaat ggtggaaca gccttaaccc cagatgcctg ctatcctgac taatttaagt 240
c 241

```

```

<210> SEQ ID NO 350
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 350

```

```

agggtactgtg gatatttaaa atatcacagt aacaagatca tgcttgttcc tacagtattg 60
cgggccagac acttaagtga aagcagaagt gtttgggtga ctttcctact taaaattttg 120
gtcatatcat ttcaaaacat ttgcatcttg gttggctgca tatgctttcc tattgatccc 180
aaaccaaadc ttagaatcac ttcatttaaa atactgagcg gtattgaata cttcgaagca 240
g 241

```

```

<210> SEQ ID NO 351
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 351

```

```

tacagaaatc atttgagacc gttttgagac agaagtagag gctctgtcaa gtcaatactg 60
cattgcagct tgggtccactg aagaagccac gcctgagata caaagatgc actacacttg 120
acccgcttta tgttcgcttc ctctccctt ctctctcatc aactttatta ggttaaaaca 180
ccacatacag gctttctcca aatgactccc tatgtctggg gtttggttag aattttatgc 240
c 241

```

```

<210> SEQ ID NO 352
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 10, 28, 29, 49, 54, 59, 72, 127, 148, 150, 160, 166, 182
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 352

```

```

gtaccctgtn gagctgcacc aagattannt ggggccatca tgactgcanc cacnacgang 60
acgcaggcgt gnagtgcacg gtctgaccgg gaaacccttt cacttctctg ctcccagggt 120
gtcctcnggc tcatatgtgg gaaggcanan gatctctgan gagttnctg gggacaactg 180
ancagcctct ggagaggggc cattaataaa gctcaacatc attggcaaaa aaaaaaaaaa 240
a 241

```

```

<210> SEQ ID NO 353
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 353

```

```

agggtaccagt gcattaattt gggcaaggaa agtgtcataa tttgatactg tatctgtttt 60

```

-continued

```

ccttcaaaagt atagagcttt tggggaagga aagtattgaa ctgggggttg gtctggccta 120
ctgggctgac attaactaca attatgggaa atgcaaaagt tgtttggata tggtagtgtg 180
tgggtctctt ttggaatfff tttcaggtga ttttaataata atttaaaact actataaaaa 240
c 241

```

```

<210> SEQ ID NO 354
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 1
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 354
ngcagggtccg ggcagggtacc aagattcatt ctcacaaaa actagaaaca gaagggcaaa 60
ttccagtttc cttctgggat tgaatacttt caagtaaggt cttcgacaaa caatcagggg 120
gccaatattt cactgtaga ggtcctaac ttgatccaca gttgaataat aagcccatgg 180
aatacaagca gaatcctctg ttccagctcc agatctttct gggattttcc atacgtaagt 240
g 241

```

```

<210> SEQ ID NO 355
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 355
ggtacccacc ctaaatttga actcttatca agaggctgat gaatctgacc atcaaatagg 60
ataggatgga cttttttttg agttcattgt ataaacaaat tttctgattt ggacttaatt 120
cccaaaggat taggtctact cctgctcatt cactctttca aagctctgtc cactctaaat 180
ttctccagt gtcacagata gggaattgct cactgcgtgc ctactctttc ttcacttacc 240
t 241

```

```

<210> SEQ ID NO 356
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 27
<223> OTHER INFORMATION: n = A,T,C or G

```

```

<400> SEQUENCE: 356
aggtagtgta attgagcatc cggaatntgg agaagtaatt tagctacagg gtgaccaacg 60
caagaacata tgccagttcc tcgtagagat tggactggct aaggacgacg agctgaaggt 120
tcattgggtt taagtgtctg tggctcactg aagcttaagt gaggatttcc ttgcaatgag 180
tagaatttcc cttctctccc ttgtcacagg ttttaaaaacc tcacagcttg tataatgtaa 240
c 241

```

```

<210> SEQ ID NO 357
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

-continued

<400> SEQUENCE: 357

ttttgtacca ccgatatgat caaggaaaat tctgcccatt tttatggctg aagttctaaa 60
aacctaattc aaagttcttc catgaccta cactgcctcc aagatgggcc aggctggcat 120
aaggcctgag cggcggtgag atccgcggct gccagcagct tgtcgctctt cagctgggat 180
gaagcccctc ggccaccga gtctccagga cctgcccggg cgccgctcga aagggcgaat 240
t 241

<210> SEQ ID NO 358

<211> LENGTH: 241

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 25, 57

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 358

aggtacgggg agtgggggtg aagcntgttc tctacatagg caacacagcc gcctaantca 60
caaagtcaagt ggtcgccgcg ttcgaccaac atgtgggtgag cattccacgg gcgcatgaag 120
tctgggtgct gtgctcgagt ctctgaatat ttgatagga agcgacaaga aaattcaaac 180
tgctctttgc tgactactgg aaagtgaaa gatgctcaag tttaccattc aaagaaacca 240
t 241

<210> SEQ ID NO 359

<211> LENGTH: 241

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 359

gaggtagaca aaaggaatac cttctgagag ccaggggagtg aggaaagggg aaggagactt 60
gacgtcaagg gtgcttttga ggaacatgac gggccagcca gcctgcccc aactttgaggc 120
cctgtggggc tcttgtagact ataaatatac tgtctatttc taatgcaatc cgtctttcct 180
gaaagatcct gttatctttt actattgaga catgctttca tttttgtggt cctgtttcca 240
a 241

<210> SEQ ID NO 360

<211> LENGTH: 241

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 1

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 360

ngtactctat actaattctg cctttttata cttaattcta aatttctccc ctctaattta 60
caacaaaattt tgtgattttt ataagaatct atgcctcccc aattctcaga ttcttctctt 120
ttctccttta ttcttttgct taaattcagt ataagctttc ttggattttt aggcttcatg 180
cacattotta ttcttaaaaca ccagcagttc ttcagagacc taaaatccag tataggaata 240
a 241

<210> SEQ ID NO 361

-continued

<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 361

```
aggtactctc cgtgccccga cactgaacat tatccagcca gatctgcccc gtgccagctc      60
ccactttgta cttttcttac tatcctgtct agaatcatgt cttatgattt taacagatat      120
agaaccactc ctagaaaatg ttctttcact ttctcgtttc ctttttaatc tatcatcctg      180
actactgaac ttaaaatctt tttcttcctt tttttgtttc tcttttcttt tatectgttc      240
a                                                                                   241
```

<210> SEQ ID NO 362
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 17, 23
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 362

```
aggtactttt atacctngct tangtcagtg acagatttac caatgacaac acaatttttaa      60
aattccaaca catatattac ttgtcctat gaagggcaaa aagtcaatat attttaaatt      120
ttaaaaacag aatggatata atgacctttt tacacatcag tgatatttaa aagacttaaa      180
gagacaatac tatggttgag acactggcct cctattccag ccctaattaa agaaaaata      240
g                                                                                   241
```

<210> SEQ ID NO 363
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 4
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 363

```
ttangtacta aaaacaaaat cctaattctg ttttaaagag ctgggagatg ttaatcatat      60
gtcagttttt tccacgttat aatttcctaa atgcaaactt ttcaatcagg gcagttcaaa      120
ttcattacat cacagttaat aacagtagcc aactttgatt ttatgcttat aggaaaaaaa      180
atcctgtaga tataaaaaca gcaaattttg acaaataaaa ctcaaaccat tcatccctaa      240
a                                                                                   241
```

<210> SEQ ID NO 364
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 364

```
ggtacaagca gttagtcctg aaggcccctg ataagaatgt catcttctcc ccactgagca      60
tctccaccgc ctgtgccttc ctgtctctgg gggcccataa taccaccctg acagagattc      120
tcaaaggcct caagttcaac ctcacggaga cttctgaggc agaaattcac cagagcttcc      180
agcacctcct gcgcaccctc aatcagtcca gcgatgagct gcagctgagt atgggaaatg      240
```

-continued

c 241

<210> SEQ ID NO 365
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 365

cgagggtactg agattacagg catgagccac cagccccggc caaaaacatt taaaaaatga 60
ctgtccctgc tcaaatactg cagtaggaaa tgtaatttga catatatcac ttccagaaaa 120
aaactttaaa tctttctata aaatgaattt gatacatcat cagcatgaag tgaagttaa 180
atctcttaca aagtaaatc aggtatatca acaatgagat ccaaaagtat cggttcaaga 240

t 241

<210> SEQ ID NO 366
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 366

ggcaggtaca catcaaacac ttcattgcct aaatgcaggg acatgcttcc atctgaccac 60
ttgactatcc gagcattgct tcttttaatt tcatttcctt cttcatctcg gcgtatcctc 120
catcttatag tattttctac ctttaatttt aacctggttc taccttcttc atccagcatt 180
tcttcattct caaattcatc ttcataatac tgggctctac acttgagaaa gttgggcagt 240

t 241

<210> SEQ ID NO 367
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 25
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 367

gcagggtacaa ataattcctg ttgtnacatt tagtggacgc gattatctgt atacctcaaa 60
ttttaattta agaaagtatc acttaaagag catctcattt tctatagatt gaggcttaat 120
tactgaaaag tgactcaacc aaaaagcaca taacctttta aaggagctac acctaccgca 180
gaaagtcaga tgccctgtaa ataactttgg tctttcaaaa tagtggcaat gcttaagata 240

c 241

<210> SEQ ID NO 368
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 368

tttgtacatt gttaatagtg accctcggag gaaatggatt tctcttctat taaaaactct 60
atggtatata agcattacat aataatgcta cttaaccacc ttttgtctca agaattatca 120
ccaaagtttt ctggaaataa gtccacataa gaattaaata ttttaaaggt gaaatgttcc 180
ttattttaac ttttagcaaga tcttttcttt ttcattaaga aacactttaa taattttaaa 240

-continued

g 241

<210> SEQ ID NO 369
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 369

gcagggtactt tattcttatt tcttatccta tattctgtgt tacagaaaa ctactaccat 60
aaacaaaaca ccaaccagcc acagcagttg tgtcaagcat gacaattggc tagtcttca 120
cattttatta gtaagtctat caagtaagag atgaagggtc tagaaaacta gacacaaagc 180
aaccagggtc caaatcacca aggtagatct gtgcttagct aaagggaac acccgaagat 240

t 241

<210> SEQ ID NO 370
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 1
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 370

ngttcacagt gcccctccgg cctcgccatg aggtctcttc tgtcgctccc ggtcctggtg 60
gtggttctgt cgatcgctctt ggaaggccca gcccagccc aggggacccc agacgtctcc 120
agtgccttgg ataagctgaa ggagtttgga aacacactgg aggacaaggc tcgggaactc 180
atcagccgca tcaaacagag tgaactttct gccaatgac gggagtgggt ttcagaagac 240

a 241

<210> SEQ ID NO 371
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 227
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 371

ggcaggtcat cttgagcctt gcacatgata ctcagattcc tcacccttgc ttaggagtaa 60
aacaatatac ttacaggtt gataataatc tccatagtta tttgaagtgg cttgaaaaag 120
gcaagattga cttttatgac attggataaa atctacaaat cagccctoga gttattcaat 180
gataactgac aaactaaatt atttccttag aaaggaagat gaaaggnagt ggagtgtggt 240

t 241

<210> SEQ ID NO 372
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 26, 27, 59
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 372

-continued

```

aggtacagca aagcgaccct tgggtgnata gatcagacgg aaattctctc cegtcttgnc      60
aatgctgatg acatccatga atccagcagg gtaggttata tcagttcgga ccttgccatc      120
gattttaatg aaccgctgca tgcaaatctt ctttacttca tctcctgtca gggcatactt      180
aagtctgttc ctcaggaaaa tgatgagggg gagacactct ctcaacttgt ggggaccggg      240
g                                                                           241

```

```

<210> SEQ ID NO 373
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 373

```

```

tactgaaaca gaaaaaatgt attcccacaa aagctgttac acagcggttt cccgtcccca      60
gaagcagtag aaaatcttag cattccaatg gaaggcatgt atttgtaaaa tattctaaaa      120
tcagctctat agtttccttg tcctctttga taagggatca gacagagggt gtgtccccct      180
tcagcagcta cccttcttga caaactggtc tccaataata cctttcagaa acttacaaga      240
c                                                                           241

```

```

<210> SEQ ID NO 374
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 374

```

```

cagggtactaa aacttacaat aaatatcaga gaagccgtta gtttttacag catcgtctgc      60
ttaaaagcta agttgaccag gtgcataatt tcccatcagt ctgtccttgt agtaggcagg      120
gcaatttctg ttttcatgat cggaatactc aaatatatcc aaacatcttt ttaaaacttt      180
gatttatagc tcctagaaaag ttatgttttt taatagtcac tctactctaa tcaggcctag      240
c                                                                           241

```

```

<210> SEQ ID NO 375
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 375

```

```

aggtacaaaag gaccagtatc cctacctgaa gtctgtgtgt gagatggcag agaacggtgt      60
gaagaccatc acctccgtgg ccatgaccag tgctctgccc atcatccaga agctagagcc      120
gcaaattgca gttgccaata cctatgcctg taaggggcta gacaggattg aggagagact      180
gcctattctg aatcagccat caactcagat tgttgccaat gccaaaggcg ctgtgactgg      240
g                                                                           241

```

```

<210> SEQ ID NO 376
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 376

```

```

ggtacatctt actttccttc tttcagaatg ctaataaaaa acttttgttt ataactaaaa      60
aaaccataaa tcagacaaaac aaaagaaacg attccaacat cacttctgtg atgagaaaag      120

```

-continued

aggcaatgga attcaacata agcaaagaaa actctacctg gaggaaagaa atcgatcagc 180
gaagaaacaa ctggggctg ctgccagact gcaggccatg cgaggaggag cctcctagag 240
g 241

<210> SEQ ID NO 377
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 234
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 377

tcctttctgt ccagggtgatt cacagactag acctttctta tcctcctcct agagttttga 60
cttgggactc tagtgtaag atgatgagcc cgtgcatcag gtccttctgc actttggtgg 120
aagtctccca gggtaggttt cctatttgaa acagtggaat catgtttcca gtgataaagt 180
ttaatgacct catccttttt ttttttttcc tcacttgcca tttgtgtgtc ttanatgggt 240
t 241

<210> SEQ ID NO 378
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 378

aggtcagcga tcaggtcctt tatgggcagc tgctgggcag cccacaagc ccagggccag 60
ggcactatct ccgctgcgac tccactcagc ccctcttggc gggcctcacc cccagcccca 120
agtccatga gaacctctgg ttccaggcca gcccttggg gacctggta accccagccc 180
caagccagga ggacgactgt gtcttgggc cactgctcaa cttccccctc ctgcagggga 240
t 241

<210> SEQ ID NO 379
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 379

tacggagcaa tcgaagagcc atatccacac ttgggggtggc tatagggtctg gaaaatgctg 60
aagatgactg ctttactga ggtcaaggat tgtaatatgt ccagctttgt aaagccatta 120
aagcagaagt ttcttcagt atcttctctc taagaaacac catcacctcc atgtgcctta 180
cagaggcccc ctgcttctg ctgcattgct tttgcgcaat cccttgatga tgaagatggt 240
c 241

<210> SEQ ID NO 380
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 24, 25, 26, 34, 36, 56, 113, 129, 137, 184, 185, 208,
210, 237, 240
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 380

-continued

acgtacacgc agaccgacat gggnnnttca ggcntnagat caaactcaaa acctgnaatg 60
atatccactc tcttttttctt aagctcaggg aaatattcca agtagaagtc canaaagtca 120
tcggctaana tgcttcngaa tttgaattca tgcacatagg ccttgaaaaa actgtcaaac 180
tgannctgat caccacacaa gtgggccntn tatgacacaa agcagaaaacc tttctcntan 240
g 241

<210> SEQ ID NO 381
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 381

agggtacaact taatggatta gcttttgggt ttaactgaat atatgaagaa attgggtctg 60
tctaagaga gggatatttca tatggctttt agttcacttg tttgtatttc atcttgattt 120
ttttctttgg aaaataaagc attctatttg gttcagattt ctcagatttg aaaaaggctc 180
tatctcagat gtagtaaaatt atttcctttc agtttgtgaa agcaggattt gactctgaaa 240
g 241

<210> SEQ ID NO 382
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 382

gtactgctat aatcaatacg tctgatagac aggtttatcc actatattga ccctacctct 60
aaaaggattg tcataattta tatgctttat gtttacacct atgatacagt tgccttgga 120
cacaaaattt ttcattgtaa ttaaaaaaag aagagttgtg cagacagaag aaatcaaadc 180
taagaaaatc acaggagtag ataaatactc tagaattcat atacccttg aagatgggtt 240
t 241

<210> SEQ ID NO 383
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 383

ggcaggtaaa aagtcttctc tttgcttttt ataattttta agcaaataac acatttaact 60
gtattttaagt ctgtgcaaat aatccttcag aagaaatadc caagattctg tttgcagagg 120
tcattttgtc tctcaaagat gattaaatga gtttgccttc agataaagtg ctccgtgtcca 180
gcagaactca aaaggccttc aagctgttca gtaagtgtag ttcagataag actccgtcat 240
a 241

<210> SEQ ID NO 384
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 384

ggtacacaaa atacacttgc aagcttgctt acagagacct gttaaacaaa gaacagacag 60
attctataaa atcagttata tcaacatata aaggagtgtg attttcagtt tgttttttta 120

-continued

agtaaatatg accaaactga ctaaataaga aggcaaaaca aaaaattatg cttccttgac 180
aaggcctttg gagtaaacaa aatgctttaa ggctcctggg gaatgggggt gcaaggatga 240
a 241

<210> SEQ ID NO 385
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 385

ggcaggtcta caatggtctt gtcccttctg tggaaatcgtt acaccaagag gtctcagtcc 60
tggtccctga cccacacagt agctgttttag atgacccctt acatcttctt gatcaactgg 120
aagacactcc aatcctcagt gaagactctc tggagccctt caactctctg gcaccaggta 180
ggtttggagg ctatgtccct ttaacttatc catgcagagt agccaaactt tacctgaaag 240
a 241

<210> SEQ ID NO 386
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 386

aggtaccttt ttcctctcca aaggaacagt ttctaaagt ttctgggggg aaaaaaaact 60
tacatcaaat ttaaaccata tgtaaaactg catattagtt gtgttacacc aaaaaattgc 120
ctcagctgat ctacacaagt ttcaaagtca ttaatgcttg atataaattt actcaacatt 180
aaattatctt aaattattaa ttaaaaaaaa aactttctaa gggaaaaata aacaaatgta 240
g 241

<210> SEQ ID NO 387
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 387

acccactggt ccgtgtgga gtatctccac tctcccctcg tgaggggcgc tcccaccgac 60
cagtcgaact ttcgtaaatg gagttaatgt gttccactc cccttttccc ctttctggcc 120
ttttgtcca gaatttctg gccttcggc atactctggg agtcctcgac ttccaggaaa 180
gccaatgct ccccgatcac cttaagacc cggaggacct attggacctg gaaatcctcg 240
t 241

<210> SEQ ID NO 388
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 388

ttgtactct tgtccacagc agagacattg agtataccat tggcatcaat gtcaaaagtg 60
acttcaatct gaggaacacc tcgggggtgca ggaggtatgc ctgtgagttc aaacttgcca 120
agcaggttgt tatcctttgt catggcacgc tcgccttcat aaacctgaat aagtacacca 180
ggctggttgt cagaataggt agtgaaggtc tgtgtctgct tggtaggaat ggtggtatta 240

-continued

c 241

<210> SEQ ID NO 389
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 6, 28, 38, 43
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 389

tacctntgtt agtgagcacc ttgtcttntg tgcttatntc ttnaagataa atacatggaa 60
ggatgtgaaa atcggaacac caactatgtg tctcactgca tctaagttaa gcagccacag 120
ctgtgagagt tttcaaaagca gaaagatgct gatgtgacct ctggaattca gacatactga 180
gctatgggtc agaagtgttt tacttataaaa gcaaacatc cccaggaaat actgaatagg 240

a 241

<210> SEQ ID NO 390
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 390

gcaggtacat ccacatgttc ctccaaatga cgtttggggt cctgcttgcc aacattcttt 60
attgccagct gttcagggtg catcttatct tcttcttcta cagccttatt gtaattcttg 120
gctaattcca acatctcttt taccactgat tcattgctt tacaatgttc actgtagtcc 180
tgaagtgtca aaccttccat ccaactcttc ttatgcaaat ttagcaacat cttctgttcc 240

a 241

<210> SEQ ID NO 391
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 2, 10, 14, 22, 23, 25, 40, 50, 57, 59, 65, 71, 72, 73,
76, 77, 78, 82, 83, 84, 95, 98, 100, 101, 102, 107, 148, 152,
155, 158, 163, 169, 170, 172, 180, 182, 192, 193, 198, 200,
202, 203, 206, 207, 208, 213, 214, 218, 220, 224, 225
<223> OTHER INFORMATION: n = A,T,C or G
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 235, 236
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 391

cnggcacaan ctntgtttt tnntntttt ttttttttn tctttattn tttttantnt 60
taaaaaaaa nnntannnaa annngggttt aaatnctntn nncagancat taaaactgaa 120
ggggaaaaaa aaacaaaaa cgagcttntt anttnacntg ggnttggggn gntgctgatn 180
tnaagaagca anntttanan cnngcnnnat ganngagnn tcannttgaa atttnnacc 240

t 241

<210> SEQ ID NO 392
<211> LENGTH: 241
<212> TYPE: DNA

-continued

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 392

gagggtactaa atgggtatcct tagattaaaa tttgtgtcct gataacagct gttttttcta	60
cattagaaat aagatgccac acaagggaact acattccaga tttaaagaaa tgaaaggata	120
ccattagtgt gtataacaga ttattgttca tacttgtaaa gcattcttatg tcattgagaa	180
tataaagaac agtgccttag aagacagtga aaggtaagct ctagcttaat gtctatgatt	240
t	241

<210> SEO ID NO 393

<211> LENGTH: 241

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

```
<221> NAME/KEY: misc_feature
```

<222> LOCATION: 57, 75, 224

<223> OTHER INFORMATION: n = A, T, C or G

<400> SEQUENCE: 393

ggcaggtaca taagcataat cagttatgga cagcttcttg tataaattgc tattcancaa	60
tacataaact gcctnaaaga tttatgctta caggtagaca ttcaatttac caataaaaca	120
gcattgtctg aaaatatggg cacattttaa aacatattaa gacagttctg ttaaccataa	180
tagtcccaca gtatgactga gtaataagaa tctacttcaa aagnaaaaaa aaaattaatc	240
a	241

<210> SEQ ID NO 394

<211> LENGTH: 241

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 394

aggtacagca gcagtagatg gctgcaacaa ccttcctcct accccagccc agaaaaatatt	60
tctgccccac cccaggatcc gggacaaaa taaagagcaa gcaggcccc ttcactgagg	120
tgctgggtag ggctcagtgc cacattactg tgctttgaga aagaggaagg ggatttgttt	180
ggcactttaa aaatagagga gtaagcagga ctggagaggc cagagaagat accaaaattg	240
g	241

<210> SEO ID NO 395

<211> LENGTH: 241

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

```
<221> NAME/KEY: misc feature
```

<222> LOCATION: 1, 5, 8, 9, 14, 24, 26, 28, 32, 42, 54

<223> OTHER INFORMATION: n = A, T, C or G

<400> SEQUENCE: 395

nggcngggnnc caanatatga aatntnanta tnatacatga tnaaaagctt tatntatttt	60
agtgagtaat taagtttaca ctgtgaataa ggattaatto ccagatgacc atctacagtt	120
actaccacat agaggggata cacggatgga tcgattacaa gaatataaaa cttattttcc	180
ttcctgtatc cacatttctt tgcaatgtga atttgcaggc cctctcaaga agtggagtct	240
a	241

-continued

<210> SEQ ID NO 396
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 26
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 396

gagggtacacc ttgaatgaca atgctnnggag cccccctgtg gtcacgcgacg cctccactgc 60
cattgatgca ccatccaacc tgcgtttcct ggccaccaca cccaattcct tgctgggtatc 120
atggcagccg ccacgtgccg ggattaccgg ctacatcatc aagtatgaga agcctgggtc 180
tcctcccaga gaagtgtgcc ctgcggccccg ccctgggtgc acagaggcta ctattactgg 240
c 241

<210> SEQ ID NO 397
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 90
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 397

ggcaggtacc agcaggggga tgtgtttctg gggaattgtg gctctggaag cttcacggtt 60
tcccagaatg tggaataat atctgtgcan gatagaaatc ctgccagag gctgtttctg 120
tctcatttga gctctccttc atgtggcaga gctgactgtg gcggtttagg agcctacatt 180
ttagaaaagc ttacctcaaa gttctgcatt gagcctgagc actggaaagg agataaaata 240
a 241

<210> SEQ ID NO 398
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 3, 11, 22, 27, 38, 41, 53, 59, 63, 69, 77, 78, 94, 131,
133, 137, 149, 154, 162, 166, 167, 172, 175, 176, 179, 191, 230
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 398

gangtgacca ngacatcacc tnacacntgg aaagcganga nttgaatggt gcntacaang 60
ccntaccnt tgccannac ctgaacgcgc cttntgattg ggacagccgt ggggaaggaca 120
gttatgaaac nantcanctg gatgaccana gtgntgaaac cnacannac angcnntcna 180
cattatataa ncggaaagct aatgatgaga gcaatgatca ttccgatgtn attgatagtc 240
a 241

<210> SEQ ID NO 399
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 212, 226
<223> OTHER INFORMATION: n = A,T,C or G

-continued

<400> SEQUENCE: 399

cagagtgaga tgggagtggg agggccaatc tgatacagaa ggggggtgaag ggtagggccc 60
ctgagcagcc caccctctac cctgacgaag gcaatcctcc tctggaatgt ctcttccttc 120
ttcagtctgg gttctgcctc agccacgaac tgggaaggag tgaggaacat cccaacggca 180
atgagagtat cccagtgact ccaaacagga angaatcagt gttcanaaag tcaggggcct 240
t 241

<210> SEQ ID NO 400

<211> LENGTH: 241

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 400

ggtactcttg ctcttttagc tagagtgtat gtgaaaataa agaaatacat cattgtattc 60
acaacctagt gtcttcattt ataacttttt gtttaaaaaa tttttagttc aagtttagtt 120
cattgatatt atcctctgaa tgcagttaag gctgggcaga aattctactc atgtgacatc 180
tgccacaggt ctattttgaa gcttttcttc taatgggcaa tgtttgcctt taccaggatt 240
t 241

<210> SEQ ID NO 401

<211> LENGTH: 241

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 1, 2

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 401

nncaggtact ttgtagagca gagagaggct ttggttcctc ctttcttcaa tcacgtggag 60
atgtgtcatc acctgggatt tcactctggc cgccttttct gggccaacag ccaacacatg 120
ctggtaatga cggatggtat gtaagcgatc tttgttctca gcacggacat aacgccgtaa 180
ggcctggaga atgcgatgag gccgtggcgg gtcagactgc aaggcagcca ggtagttctc 240
c 241

<210> SEQ ID NO 402

<211> LENGTH: 241

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 26, 27

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 402

ggcaggtcca aaaaaaacct aaaaanngtt tcaggaatgt agagaaatat ccaacttaaa 60
tagcgaaaaa gtgcaccata attactgctg cactgcagtc atttctgcaa ttcccatgtt 120
tcttaataaa ctatcttgtc agataacaca caatataaag agcaattatg aaaaacagac 180
atttacatat acttctaaag tcttattggg aatatcctgt ttggccattg ggataaccaa 240
t 241

-continued

<210> SEQ ID NO 403
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 49
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 403

aggtgttaac taccgcctcc gagacgggat tgatgacgag tcctatgang ccattttcaa 60
gccggtcacg tccaaagtaa tggagatggt ccagcctagt gcggtggtct tacagtgtgg 120
ctcagactcc ctatctgggg atcgggttagg ttgcttcaat ctaactatca aaggacacgc 180
caagtgtgtg gaatttgtca agagctttaa cctgcctatg ctgatgctgg gaggcgggtg 240
t 241

<210> SEQ ID NO 404
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 404

cagggtactgc aaccataaa atactgtttc ctcatttttc accttcctta atttggagtt 60
ttctgtcttc ttttcacggc attcaaagta ggaataaact ttgcttgtgt tgggtggata 120
ttgtttatag tgagtaacct tgtaggagtc ggtggccagg aggatgttga actcggcttc 180
tgccgcagga ttcattctcg gccggaggac aaggggcccg cgcgccgcga gctccctgac 240
c 241

<210> SEQ ID NO 405
<211> LENGTH: 266
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 405

ttctgggctg gggagtggag agaaagaagt tgcagggttt acaggaaatc ccagagcctg 60
aggtttttct ccagatttga gaactotaga ttctgcatca ttatctttga gtctatattc 120
tcttgggctg taagaagatg aggaatgtaa taggtctgcc ccaagccttt catgccttct 180
gtaccaagct tgtttccttg tgcctccttc ccaggctctg gctgcccttt attggagaat 240
gtgatttcca agacaatcaa tccaca 266

<210> SEQ ID NO 406
<211> LENGTH: 231
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 406

ttggtgaaga accattcctc ggcctccttg cggttctttt ctgccattct ctcatactgg 60
tcacgcatct cgttcagaat gcggtcagg tccacgccag gtgcagcgtc catctccaca 120
ttgacatctc caccacctg gcctctcagg gcattcatct cctcctcgtg gttctctctc 180
aggtaggccca gctcctcctt caggctctca atctgcatct ccaggtcagc t 231

<210> SEQ ID NO 407
<211> LENGTH: 266

-continued

<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 407

```
cagcatcatt gtttataatc agaaactctg gtccttctgt ctggtggcac ttagagtctt    60
ttgtgccata atgcagcagt atggagggag gattttatgg agaaatgggg atagtcttca    120
tgaccacaaa taaataaagg aaaactaagc tgcattgtgg gttttgaaaa ggttattata    180
cttcttaaca attctttttt tcagggaactt ttctagctgt atgactgtta cttgaccttc    240
ttgaaaagc attcccaaaa tgctct                                     266
```

<210> SEQ ID NO 408
<211> LENGTH: 261
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 408

```
ctgtgtcagc gagcctcggg acactgattt cccgatcaaaa gaatcatcat ctttaccttg    60
acttttcagg gaattactga actttcttct cagaagatag ggcacagcca ttgccttggc    120
ctcacttgaa gggctgcgat ttgggtcctc tggctctctg ccaagtttcc cagccactcg    180
agggagtaat atctggaggg caaagaagag acttatgtta ttgttgaacc tccagccaca    240
gggaggagca tgggcatggg t                                     261
```

<210> SEQ ID NO 409
<211> LENGTH: 266
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 409

```
gctgacagta atacactgcc acatcttcag cctgcaggct gctgatggtg agagtgaaat    60
ctgtcccaga cccgctgccg ctgaatcggg cagggatccc ggattcccgg gtagatgccc    120
agtaaatgag cagtttagga ggctgtcctg gtttctgctg gtaccaagct aagtagttct    180
tattgttgga gctgtctaaa acactctggc tggctcttga gttgatggtg gccctctcgc    240
ccagagacac agccagggag tgtgga                                     266
```

<210> SEQ ID NO 410
<211> LENGTH: 181
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 9, 17, 24, 26, 65, 97, 98, 99, 100, 103, 105, 106, 107,
108, 120, 121, 123, 142, 145, 149, 162, 177
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 410

```
caaaaggtn cttttgntca aaancnattt ttattccttg atatttttct tttttttttt    60
tttgnngatg gggacttgtg aatttttcta aaggggnnnn ttnannnngg aagaaaaccn    120
ngntccgggt ccagccaaac cngtngctna ctttccacct tntttccacc tccctcnggt    180
t                                     181
```

<210> SEQ ID NO 411
<211> LENGTH: 261
<212> TYPE: DNA

-continued

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 411

```

gccctgcag tacttggccg atgtggacac ctctgatgag gaaagcatcc gggctcacgt    60
gatggcctcc caccattcca agcggagagg ccgggctct tctgagagtc aggggtctagg    120
tgctggagtg cgcacggagg ccgatgtaga ggaggaggcc ctgaggagga agctggagga    180
gctggccagc aacgtcagtg accaggagac ctcgtccgag gaggaggaag ccaaggacga    240
aaaggcagag cccaacaggg a                                         261

```

<210> SEQ ID NO 412

<211> LENGTH: 171

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 1, 6, 53, 79, 91, 96, 114, 132

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 412

```

ntttntctt tacaattcag tcttcaacaa cttgagagct ttcttcatgt tgncaagcaa    60
cagagctgta tctgcaggnt cgtaagcata nagacngttt gaatatcttc cagngatata    120
ggctctaact gncagagatg ggtcaacaaa cataatcctg gggacatact g          171

```

<210> SEQ ID NO 413

<211> LENGTH: 266

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 413

```

ttaggaccaa agatagcatc aactgtatth gaaggaactg tagtttgccg attttatgac    60
atttttataa agtactgtaa ttctttcatt gaggggctat gtgatggaga cagactaact    120
cattttgtta ttgcatthaa aattatthtg ggtctctgth caaatgagth tggagaatgc    180
ttgacttgth ggtctgtgta aatgtgtata tatatatacc tgaatacagg aacatcgagg    240
acctattcac tcccacacac tctgct                                         266

```

<210> SEQ ID NO 414

<211> LENGTH: 266

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 86, 153, 162, 178, 184, 205

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 414

```

tttgccataa ttgagtgaag agtggcagat ggcattaaact ctgctccgct tcaagctggc    60
tccatgacca ctcaaggcct cccancctg ttcgtcaagt tgcctcaag tccaagcaat    120
ggaatccatg tgthttgcaa aaaagtgtgc tanttttaag gnttttcgta taagaatnaa    180
tganacaatt ttcctaccaa aggangaaca aaaggataaa tataatacaa aatatatgta    240
tatggttgth tgacaaatta tataac                                         266

```

<210> SEQ ID NO 415

<211> LENGTH: 266

<212> TYPE: DNA

-continued

<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 37, 103, 223
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 415

```
cctccatcca gtctattaat tgttgccggg aagctanagt aagtagttcg ccagttaata    60
gtttgcgcaa cgttgttgcc attgctacag gcacgtgggt gtnacgctcg tcgattggta    120
tgggttcatt cagctccggg tcccaacgat caaggcgagt tacatgatcc cccatgttgt    180
gcaaaaaagc ggtagctcc ttcggtcctc cgatcggtgt canaagtaag ttggccgcag    240
tgttatcact catggttatg gcagca                                         266
```

<210> SEQ ID NO 416
<211> LENGTH: 878
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 416

```
cctgacgata gccatggctg taccacttaa ctatgattct attccaactg ttcagaatca    60
tatcacaaaa tgactgtgac acagtagttt acaacgactc ccaagagagg aaaaaaaaaa    120
aaaaagacgc ctcaaaattc actcaacttt tgagacagca atggcaatag gcagcagaga    180
agctatgctg caactgaggg cacatatcat tgaagatgtc acaggagttt aagagacagg    240
ctggaaaaaa tctcatacta agcaaacagt agtatctcat accaagcaaa accaagtagt    300
atctgctcag cctgccgcta acagatctca caatcaccaa ctgtgcttta ggactgtcac    360
caaagtcaga ttcgggtgcta accagggtggc atctatgata aacgtcgccc ctcttattta    420
acaaagggct ctgaaggagg tgtttctcaa gcaacaagga gactgcttca gtacaagact    480
ttgcaccttg aattcaattg catcaagtgt ggatagcaaa ataagtatct taccattgaa    540
atatgtgttc agcctaagat tttaccacac agcagaacaa aagtgaagggt gagagggatg    600
ggccagttag gggatggggg agaaaaaaaa atcacaggat taccaccaaa gccttgtttt    660
aaaagggtc ccttactat tcaggaaggg aagtgaagg agaaattaac caattcctgc    720
cacagcagcc ctttttggtt gttccacaa tagatacttt atggagtggc acagccaacc    780
ctatctgtga cctgcctg cggataaacac agccaagcag gtttaattag atcaaagaca    840
caaagggtc ttcctctctt tcataacaac gcagacct                               878
```

<210> SEQ ID NO 417
<211> LENGTH: 514
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 417

```
ttctgacttc tagaagacta aggtggtct gtgtttgctt gtttgccac ctttggtga    60
taccagaga acctgggac ttgctgctg atgccaccc ctgccagtca ttcctccatt    120
caccagcgg gaggtgggat gtgagacagc ccacattgga aaatccagaa aaccgggaac    180
agggatttgc cttcacaaat tctactcccc agatcctctc ccctggacac aggagacca    240
cagggcagga ccctaagatc tggggaagg aggtcctgag aaccttgagg tacccttaga    300
tccttttcta cccactttcc tatggaggat tocaagtcac cacttctctc accggcttct    360
```

-continued

accaggggtcc aggactaagg cgttttctcc atagcctcaa ctttttggga atcttccctt	420
aatcacccctt gctcctcctg ggtgcctgga agatggactg gcagagacct ctttgtgtcg	480
ttttgtgctt tgatgccagg aatgccgcct agtt	514

<210> SEQ ID NO 418
 <211> LENGTH: 352
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 418

ctgcaccagc gattaccagt ggcattcaaa tactgtgtga ctaaggattt tgtatgctcc	60
ccagtagaac cagaatcaga caggtagtag ctagtcaaca gcaagtcttt gttggattcg	120
agtaggctca ggatctgctg aaggctggag gagttagtcc ccgcaatcaa gagcctgtct	180
tcctgaagcc cttggtgata ttttgccact cagccaagaa tgaggatgca tccttcagat	240
tctctatgtc ccgaacctgg aaccatcca cgccagcttg cagccaaaac tccagagcat	300
ccttcacctt ggtggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa	352

<210> SEQ ID NO 419
 <211> LENGTH: 344
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 419

ctggacacca taatcccttt taagtggctg gatggtcaca cctctcccat tgacaagctg	60
ggttaagtca ataggttgac taggatcaac acgacccaaa tcaataagat actgcagtct	120
attgagactc aaaggcttat actggcgtct gaaactatgt ccttcgttaa acccgatttt	180
tgggattcgg atgtaaaatg gagtctggcc tccctcaaag cccaagcggg gccgggttcc	240
tctttgcctt tctcctttat ggccctctgc acattttcta cctcttctcc gacctcttg	300
tcttctctcc ggtttcttg agccgggatt cggctttaag ttgg	344

<210> SEQ ID NO 420
 <211> LENGTH: 935
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 420

cgaaagtcaa cgtaaagggg ctgaggtgaa ccatgatgat gaccttctgt tgactttgaa	60
atattggctc ttgtgggtga caaaagccag acaagctgtg gctgtggtcc gattttaaga	120
cgaggttctc aaagatccaa aggagggaaa gggatttga aacactgtgt atcatctgag	180
acacacgtgt cctcatgatc ttaaatgcct actttaaaag cacctaatac tgcccttcac	240
tgtggtcaga agagatttct acaaaagcac tcagaattct ggaggcagtt gtgattttgc	300
catgtggcag ttggtttgtg gagttgggca ggtgtgaaag ggtaaaactc cacttctgaa	360
tgctgcttct gcccctggg acccagcaca ttgttagacc atcttcttga ctgaaaattc	420
tctcctgatg ctgagccctg caccaccacc ttccttttcc taactatgaa ttgatggcaa	480
agtccactca aaacaaccag ttaagtgtc acgagagagt agtcaagcac ctccagaaag	540
aaaccgggtt tttgttcaca tagcaggaag tgactccctg ggtggttaatt tatcttgaa	600
acacaggtag attggcagaa aaacgggaac atgtaggtag cgcgatgttg gtgcatgtcc	660

-continued

attacttttg gataggcttt ctcaagtcttt cctcaaatga tagttgagcc agttttccag	720
tggaattctt gactgacttg cgcttgcttt atggtgtggt caagggacgt tcagaactac	780
ggaaaacttt tactgaaaca gcgaagcaga gtataccggc atgagaggga agatgaacac	840
tcacctatgt accactcttt gacaataaat atagtatttc tcaaaaaaaaa aaaaaaaaaa	900
agtaaaaaaa ctgaaatcgc aagtcaaaaa atcca	935

<210> SEQ ID NO 421

<211> LENGTH: 745

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 421

ggcttcgagc ggccgcccgg gcaggtccta gatgtcattt gggacccttc acaaccattt	60
tgaagccctg tttgagtcctc tgggatatgt gagctgtttc tatgcataat ggatattcgg	120
ggttaacaac agtcccctgc ttggcttcta ttctgaatcc ttttctttca ccatggggtg	180
cctgaagggt ggctgatgca tatggtacaa tggcaccagc tgtaaagcag ctacaattag	240
gagtggatgt gttctgtagc atcctattta aataagccta ttttatcctt tggcccgtca	300
actctgttat ctgctgcttg tactggtgcc tgtacttttc tgactctcat tgacctatt	360
ccacgacctt ggtgtgctgc cattaactga tcctacttta catgtctagt ctgtgtggtt	420
ggtggtgaat aggccttctt ttacatggtg ctgccagccc agctaattaa tgggtgcacgt	480
ggacttttag caagcgggct cactggaaga gactgaacct ggcatggaat tcctgaagat	540
gtttggggtt tttttctttc ttaatcgaaa gttaacattg tctgaaaagt tttgttagaa	600
ctactgcgga acctcaaaat cagtagattt ggaagtgatt caaagctaaa ctttttcctt	660
ggccctcctt gtgttcta atgtctgcaag tgtaatacta ggatgtccaa gatgccagtt	720
tttgcttctt tgttagttgt cagac	745

<210> SEQ ID NO 422

<211> LENGTH: 764

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 422

gagttcagta gcaaagtcac acctgtccaa ttccctgagc tttgctcact cagctaattg	60
gatggcaaa ggtgtgtgct tttcatcttc aggcagaagc ctctgcccac cccctcaag	120
ggctgcaggc ccagttctca tgctgccctt ggggtggcat ctgttaacag aggagaacgt	180
ctgggtggcg gcagcagctt tgctctgagt gcctacaaag ctaatgcttg gtgctagaaa	240
catcatcatt attaaacttc agaaaagcag cagccatggt cagtcaggct catgctgcct	300
cactgcttaa gtgcctgcag gagccgcctg ccaagctccc cttcctacac ctggcacact	360
gggtgtgca caaggtttt tcaaccaaag acagcttccc ccttttgatt gcctgtagac	420
tttgagacca agaaacactc tgtgtgactc tacacacact tcagggtggt tgtgcttcaa	480
agtcattgat gcaacttgaa aggaacagc ttaatggtgg aaatgaacta ccatttataa	540
cttctgtttt ttatttgaga aaatgattca cgaattccaa atcagattgc caggaagaaa	600
taggacgtga cggtagctgg ccctgtgatt ctcccagccc ttgcagtcgg ctaggtgaga	660
ggaaaagctc ttacttccg cccctggcag ggacttctgg gttatgggag aaaccagaga	720

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tggaatgag gaaaatatga actacagcag aagcccctgg gcag	764
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<210> SEQ ID NO 423
 <211> LENGTH: 1041
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 423

ctcagagagg ttgaaagatt tgcctacgaa agggacagtg atgaagctaa gctctagatc	60
caggatgtct gacttcaaat tgaaactccc aaagtaatga gtttgggaagg gtgggggtgtg	120
gcctttccag gatgggggtc ttttctgtc ccagcggata gtgaaacccc tgtctgcacc	180
tggttgggcg tgttgcttcc ccaaagggtt tttttttagg tccgtcgtcg tcttgtggat	240
taggcattat tatctttact ttgtctccaa ataacctgga gaatggagag agtagtgacc	300
agctcagggc cacagtgcga tgaggacat cttctcacct ctctaaatgc aggaagaaac	360
gcagagtaac gtggaagtgg tccacaccta ccgccagcac attgtgaatg acatgaaccc	420
cggcaacctg cacctgttca tcaatgccta caacaggtat tgggatgtag ttcagccaca	480
tcattgctat ttatgaggtg tcttctgtag atccgaaatg tgggacagat gagagggaga	540
gtataaaatg agcgggaagag gcaggctctg agtttgagca aatagattaa taggacaggt	600
gtccccagga aggacacctg gcctgtaagc tggttcctgg cattcagctc gccttgcagg	660
gatctgaaca aacactccag accactgggg gtgcagacgt gagagggacg cagtcgcaca	720
ctcagagggg tgagagtaaa tatgtgtgcc cgctgctgac cttcacgaaa ggccaaatgt	780
aagaagagct aagttagaga gcagcaaagc actcctggag gccggggata atccaggcag	840
gcttctggga gtttgtcatt ccaaggataa ggaggacctg aacatggcct ttgcctaagg	900
cgtggccctc tcaaccagca ctagggtgct atctggagct cagctagggg aggagacagc	960
tcagggccat tgggtgcagc cagagactct gtaatcttcc agggagctcg ctcaacctgc	1020
tgagctcgct ctgccacgca c	1041

<210> SEQ ID NO 424
 <211> LENGTH: 1288
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 424

ctaagaactg agacttgtga cacaaggcca acgacctaa attagcccag ggttgtagct	60
ggaagacctc caaccaagg atggaaggcc cctgtcaca agcctacct gatggataga	120
ggaccaagc gaaaaaggta tctcaagact aacggccgga atctggaggc ccatgacca	180
gaaccagga aggatagaag cttgaagacc tggggaaatc ccaagatgag aacctaaac	240
cctacctctt ttctattgtt tacacttctt actcttagat atttccagtt ctctgttta	300
tctttaagcc tgattctttt gagatgtact ttttgatgtt gccggttacc tttagattga	360
cagtattatg cctgggcccag tcttgagcca gctttaaatc acagctttta cctatttgtt	420
aggctatagt gttttgtaaa cttctgttcc tattcacatc ttctccactt gagagagaca	480
ccaaaatcca gtcagtatct aatctggcct ttgttaactt ccctcaggag cagacattca	540
tataggtgat actgtatttc agtcctttct tttgacccca gaagccctag actgagaaga	600
taaaatggtc aggttgttgg ggaaaaaaa gtgccaggct ctctagagaa aaatgtgaag	660

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agatgctcca ggccaatgag aagaattaga caagaaatac acagatgtgc cagacttctg 720
agaagcacct gccagcaaca gcttccttct ttgagcttag tccatccctc atgaaaaatg 780
actgaccact gctgggcagc aggagggatg atgaccaact aattcccaaa ccccgagtctc 840
attggtacca gccttgggga accacctaca cttgagccac aattggtttt gaagtgcatt 900
tacaagtttc tggcatcact accactactg attaaacaag aataagagaa cattttatca 960
tcattctgctt tattcacata aatgaagttg tgatgaataa atctgctttt atgcagacac 1020
aaggaattaa gtggcttcgt cattgtcctt ctacctcaa gataatttat tccaaaagct 1080
aagataaatg gaagactcct gaacttgtga actgatgtga aatgcagaat ctcttttgag 1140
tctttgctgt ttggaagatt gaaaaatatt gttcagcatg ggtgaccacc agaaagtaat 1200
cttaagccat ctagatgtca caattgaaac aaactgggga gttggttgct attgtaaaat 1260
aaaatatact gttttgaaaa aaaaaaac 1288

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<210> SEQ ID NO 425
<211> LENGTH: 446
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 425
ccacttaaag ggtgcctctg ccaactgggt gaatcatcgc cacttcagc accacgcaa 60
gcctaacatc ttccacaagg atcccgatgt gaacatgctg cacgtgtttg ttctgggcga 120
atggcagccc atcgagtacg gcaagaagaa gctgaaatac ctgccctaca atcaccagca 180
cgaataacttc ttctgattg ggccgccgct gctcatcccc atgtatttcc agtaccagat 240
catcatgacc atgatcgtcc ataagaactg ggtggacctg gcctgggccg tcagctacta 300
catccggttc ttcatcacct acatcccttt ctacggcatc ctgggagccc tccttttcct 360
caacttcac aggttccttg agagccactg gtttgtgtgg gtcacacaga tgaatcacat 420
cgctatggag attgaccagg aggacc 446

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<210> SEQ ID NO 426
<211> LENGTH: 874
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 426
tttttttttt tttttttttt ttttttcaat taaagatttg atttattcaa gtatgtgaaa 60
acattctaca atggaaactt ttattaaatg ctgcatgtac tgtgctatgg accacgcaca 120
tacagccatg ctgtttcaga agacttgaaa tgccattgat agtttaaaaa ctctacaccc 180
gatggagaat cgaggaagac aatttaatgt ttcatctgaa tccagagggt catcaaatta 240
aatgacagct ccacttggca aataatagct gttacttgat ggatccaag aagaaatggt 300
tggtgatgga taaattcaga aatgcttccc caaagggtgg tggtttttta aaagttttca 360
ggtcacaacc cttgcagaaa aactgatgc ccaacacact gattcgcggt ccaggaaaca 420
cgggtcttcc aagttccaag gggctggggt tccccaacga tcaagttcct gtgctgtaat 480
caagagggtc ctttgactg gatagggagc acttgggagc tgtacaccat cagtcataat 540
ggatggcagt gtaaaagatg atccaaatga cctgagatgc tcctgaggag tggatgcacca 600
gaccaggag tgccactgta gggctgcttc tttgctttag tcatcacaca cacacacagc 660

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tccagagcag caatggcctt tcctgtaaca ggaaaaaagc ctctgtctat tcccaagaac	720
cctcgtaatg gcaaaactcc ccaaatagaca cccaggacca cagcaatgat ctgtcggaac	780
cagtagatca catctaaaaa ttcactcctta tcctcccagg ccgcgtcgct ccgcagcacc	840
ttactccaga cggagacttt gagggccccg ttgg	874

<210> SEQ ID NO 427
 <211> LENGTH: 638
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 427

acttgtaatt agcacttggt gaaagctgga aggaagataa ataacactaa actatgctat	60
ttgatTTTTT ttcttgaaag agtaaggTTT acctgttaca ttttcaagtt aattcatgta	120
aaaaatgata gtgattttga tgtaatttat ctctgtttg aatctgtcat tcaaaggcca	180
ataatttaag ttgctatcag ctgatattag tagctttgca accctgatag agtaaaaaa	240
ttttatgggc gggtgccaaa tactgctgtg aatctatttg tatagtatcc atgaatgaat	300
ttatggaaat agatattttgt gcagctcaat ttatgcagag attaatgac atcataatac	360
tggtgaaaa ctgcataga attctgatta aatagtgggt ctgtttcaca tgtgcagttt	420
gaagtattta aataaccact cctttcacag tttattttct tctcaagcgt tttcaagatc	480
tagcatgtgg atttttaaag atttgccctc attaacaaga ataacattta aaggagattg	540
tttcaaaata tttttgcaaa ttgagataag gacagaaaaga ttgagaaaaca ttgtatatTT	600
tgcaaaaaca agatgtttgt agctgtttca gagagagt	638

<210> SEQ ID NO 428
 <211> LENGTH: 535
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 428

acaagatgat tcttcctcct caatttgaca gatcaaagaa gtatcccttg ctaattcaag	60
tgtatggtgg tccctgcagt cagagtgtaa ggtctgtatt tgctgttaat tggatatctt	120
atcttgcaag taaggaagg atggtcattg ccttggtgga tggtcgagga acagctttcc	180
aaggtgacaa actcctctat gcagtgtatc gaaagctggg tgtttatgaa gttgaagacc	240
agattacagc tgtcagaaaa ttcatagaaa tgggtttcat tgatgaaaaa agaatagcc	300
tatggggctg gtcctatgga ggatacgttt catcactggc ccttgcatct ggaactggtc	360
ttttcaaatg tggatatgca gtggctccag tctccagctg ggaatattac gcgtctgtct	420
acacagagag attcatgggt ctccaacaa aggatgataa tcttgagcac tataagaatt	480
caactgtgat ggcaagagca gaattattca gaaatgtaga ctatcttctc atcca	535

<210> SEQ ID NO 429
 <211> LENGTH: 675
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 429

actattttca accctgagca ttaacactgc ataccaaggg ggggtgggtc aagaagctgg	60
ttagatcgaa gcacaagcac aagccactga tattctctat gtgatcaggt ttttcaaaa	120

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aaatacatag ttttcaataa ataatgctta attttacaac ttgatacag caatgtcata 180
caccgtttca acacactaca ctctgcatgc tagatagtct acgagaagac gaaactttgc 240
catgcatttt ctttcccccc tagtgctatc aaacacttca tcctccagcg cactgcctca 300
ggtagcttta ctttctctct gtttcacagc aataggccgt gcgctggcat gcaaactcta 360
aaaaagggtcc cccccacaaa ccactcagac ttctacacaa aagggttttt cagcttttct 420
gctcccaaac ctggagtggtc taagaaagta agtttcatgt ggccttgga aatacacact 480
tgtaaacagt gtcattgtga aaactgctct aaaacatcag gtggttctgt cctggtggcc 540
gtcacgaagc attatgggat gccataacca ctaggagtcc caaaccggaa aaaataggcc 600
tccgttttaa aacagtcaat tcaaaaaagg tgtcacagaa caaatgcaa agactcttaa 660
acccacaaca tatgt 675

```

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<210> SEQ ID NO 430
<211> LENGTH: 434
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 430

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```

acctctgcc aaggtccagc gagaggacct cacagtagag cacaggccac tccgggagtg 60
catcagaaga ttcattctca tggaggaaga aggtctcaaa cgtgaatggg taggagaagt 120
gagccacctt gtccattgcc agggacttgg tggcgaggt ctgtgttact cctgagagct 180
gttggaatgc tgggcttgac cagttagcag ttggcaattc tacaagaag tggacgtaga 240
gattgtcata ctcatagcct tgggtgaaa cgacctctcc atttacaag agccggaggg 300
cacctgggac agtcattctc aagtcggtgc ctacgaggct gctgagatac tccttggtgc 360
ggccataaag atccttgaac actcgccgtt cccgctctc ctctccggc tgtgcgtggg 420
gggaaacatt gtcg 434

```

```

<210> SEQ ID NO 431
<211> LENGTH: 581
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```

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<400> SEQUENCE: 431

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```

acacaagcct ccagcccgac ccagcggcct aatgaaactc tggcaaccta tcctgggcgt 60
ggccacgagt atccagctcc aagcccaagt gaggcgggga gtcaacttcc ccatgattgc 120
caagtgacca agaccagaag cagggacgat taggctagtt ctgcggcaag gtgaactgga 180
gaccctgtct ctgccctctc tccctggcct gtcccacaga catcccggtt ttaacccac 240
tgcccttgca aggacctgct ctgtccactc caaatcaaag gatacttgca tccttcttac 300
acagactccc atctctctgc tcatagtggc ccagggtgc ccgagaaaaa gaaacttggg 360
tcagtagaag gtcattagt gtgaaggagt gagaggccag gccttcctgt gacataatgc 420
ttctatgctt gtttcctaaa cacttggtcc acacacaata cctgggcagg aagagagAAC 480
caagcaccac tggatggctc tggagccagg ggacttctat gcacatacaa ccaacatcac 540
cccactctgc tcatctgtgc ctccaccctg aacagcagag t 581

```

```

<210> SEQ ID NO 432
<211> LENGTH: 532
<212> TYPE: DNA

```

-continued

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 432

```
actccaactc aagtttataa gttacacctt tgccacagcc ttggctaaat cttgaactag    60
tgcagaattc agctgtggtg gagtgcctgt cttagcatgc ttcgatgtgg catacttggt    120
cttgacagtc atgtgctttg taagtccctg atttaccatg actacattct tagccagggtg    180
ctgcataact ggaagaagag attcttcagt atatgacagg taatgttgta gagttgggtg    240
ccattcacca ttatccagaa ttttcagtgc taagcaaaaa gtcctctgtg caatttgaga    300
aggaggaaa gtcacatgt catagtccaa catagttagt tccatcaggt atttggccaa    360
agtatgttg tgcacatcaa cctctccaat cttagatgct ctccgaagga agtgcaaaag    420
tagaggccga ccagaccaa agtttaaaag tcttagaatc ttcatttcca tctgtctgat    480
ttggtgctta gtataagtgt tgtcagtcac aaaagcaaag tcaccaatth ct          532
```

<210> SEQ ID NO 433

<211> LENGTH: 531

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 433

```
acttggtttt acagctcctt tgaaaactct gtgtttggaa tatctctaaa aacatagaaa    60
acactacagt ggtttagaaa ttactaatth tacttctaag tcattcataa accttgctta    120
tgaaatgact tcttaaatat ttagttagata gactgctaca ggtaataggg acttagcaag    180
ctcttttata tgctaaagga gcatctatca gattaagtta gaacatttgc tgcagccac    240
atattgagat gacactaggt gcaatagcag ggatagatth tgttggtgag tagtctcatg    300
ccttgagatc tgtggtggtc ttcaaatgg tggccagcca gatcaaggat gtagtatctc    360
atagtcccc ggtgatatth ttcttattag aaaaatatta taactcatth gttgtttgac    420
acttatagat tgaaatttcc taatttattc taaattttta gtggttctth ggttccagtg    480
ctttatgttg ttgttggtth tggatggtgt tacatattat atgttctaga a          531
```

<210> SEQ ID NO 434

<211> LENGTH: 530

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 434

```
acaagagaaa acccctaaaa aaaggatggc tttagatgac aagctctacc agagagactt    60
agaagttgca ctagctttat cagtgaagga acttccaaca gtcaccacta atgtgcagaa    120
ctctcaagat aaaagcattg aaaaacatgg cagttagtaa atagaaacaa tgaataagtc    180
tcctcatatc tctaattgca gtgtagccag tgattattta gatttgata agattactgt    240
ggaagatgat gttggtggtg ttcaagggaa aagaaaagca gcatctaaag ctgcagcaca    300
gcagagggaag attcttcttg aaggcagtga tggatgagat gctaatgaca ctgaaccaga    360
ctttgcacct ggtgaagatt ctgaggatga ttctgattth tgtgagagtg aggataatga    420
cgaagacttc tctatgagaa aaagtaaagt taaagaaatt aaaaagaaag aagtgaaggt    480
aaaatcccc gtagaaaaga aagagaagaa atctaatacc aatgtaatg          530
```

<210> SEQ ID NO 435

-continued

<211> LENGTH: 677

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 435

```
accttatgat ctaattaata gatattagaa acagtagaaa gacaagttac acgtcaatgc      60
ccaatgacta gagtcaacat taaagagttg taatttaagt aatccaaact gacatctaata    120
tccaaaatca ttataaaaat gtatttggtc ttggaatcca caggacttca aacaagcaaaa    180
gtttcactgc agatagtcac aaagatgcag atacactgaa atacttaaga gccttatttaa    240
tgatttttgt tattttggat cttctgtttt tttcttatta tggccgaag cctccttaata    300
accaatttat cagacagaag catgtcatct tgttgttcaa gataatccag taaatttttca    360
gtccattcaa gtgccgtttt atggctaata cgcttctctg gattcagttc tgttttttcta    420
ctcttactgg aaggcttttg ctcagcagcc ttggtctggt cctcagcact ttcactgtca    480
gtcagcacct gacagcttga gtcactgctc cgagagtcga accactgata aatattctca    540
atgtcaacat gttcacattc ttctgtgttc tgtaaaactg ttgctaaatt agctgctaaa    600
atggctcctt catcaatggt catacctgaa ttctcttcat tgccagggaa aagttttttc    660
catgctttgg ttatggt                                     677
```

<210> SEQ ID NO 436

<211> LENGTH: 573

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 436

```
acctcttagg gtgggagaaa tgggaagag ttgttcctac aacttgctaa cctagtggac      60
agggtagtag attagcatca tccggataga tgtgaagagg acggctgttt ggataataat    120
taaggataaa atttggccag ttgacagatt ctgtttccag cagtttttac agcaacagtg    180
gagtgtctca gtattgtgtt cctgtaaatt taattttgat ccgcaatcat ttggtataca    240
atgctgtttt aagttttgtc ctattggaaa agtcttgtgt tgcaggggtg cagttaagat    300
ctttgtgatg aggaatggga tgggctaatt ttttgccgtt ttcttggaat tgggggcatg    360
gcaaatacag tagggtagtt tagttcttta cacagaacat gataaactac acctgttgat    420
gtcaccgtct gtcaatgaat attatagaag gtatgaaggt gtaattacca taataacaaa    480
acaccctgtc tttagggctg acctttcgtc ctttgacctc ctcagcctcc attcccatct    540
tcgctcagac tgcaagtatg tttgtattaa tgt                                     573
```

<210> SEQ ID NO 437

<211> LENGTH: 645

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: 605

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 437

```
acaattggta tccatatctt gttgaaattg taatgggaaa acaatatatt tcaatctcta    60
tgtagatagt ggggtttttg tttcataata tattctttta gtttactgta tgagttttgc    120
aggactgcat aatagatcac cacaatcata acatcttagg accacagaca tttatgagat    180
```

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catggcttct gtgggttaga agtatgtca tgtcttaact gggtcctctg ctcaagtctta	240
tctggctgca atcaagggtg cagctgggct gaattttcat ttggaatctt gactgggaaa	300
gagtctgctt ccaaggctcat gaagtttgct ggcaaaatgt atgtttttat gacagtatga	360
ctgaaatccc aagctatctc ctgactttta gctgggtaat ctcaggccct aaatgttgcc	420
tacagttcct agaggctggt cacagttctt agccatgtgg atttcctcaa catggctgct	480
tgcttcatca agtcagcaag aatagcctgt catatcagtg tatatcaggc tcaactcagga	540
taatttccct actgatgagc caaacactaa ctgatttttag agcttaacta catctgcaaa	600
attcngttca ccagaggcaa gtcattttca ggggaaggaga agtgt	645

<210> SEQ ID NO 438
 <211> LENGTH: 485
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 438

acagaattga gagacaagat tgcttgaat ggagatgctt ctactctca gataatacat	60
atttctgatg aaaatgaagg aaaagaaatg tgtgttctgc gaatgactcg agctagacgt	120
tcccaggtag aacagcagca gctcatcact gttgaaaagg ctttggcaat tctttctcag	180
cctacaccct cacttgttgt ggatcatgag cgattaaaaa atcttttgaa gactgttgtt	240
aaaaaaagtc aaactacaa catatttcag ttggaaaatt tgtatgcagt aatcagccaa	300
tgtatttata ggcatcgcaa ggaccatgat aaaacatcac ttattcagaa aatggagcaa	360
gaggtagaaa acttcagttg ttccagatga tgatgtcatg gtatcgagta ttctttatat	420
tcagttccta tttaagtcata ttttgtcatg tccgcctaata tgatgtagta tgaaaccctg	480
catct	485

<210> SEQ ID NO 439
 <211> LENGTH: 533
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 439

acagcagttt cctcatccct gcagctgtgt ttgaacaggt catttaccat actgtcctcc	60
aggttcaaca gtatggctcc aatgatgaa atttcattct gattttcttg ctgaagacta	120
ttctgtttgt gtatgtccac cacagttact ttatcccttc atctgtggat gggcagaatg	180
aaacatatat ggaaatgttc tgtgcaataa aaacagcagt ggtaacacag atgtaggctc	240
tgagtgtctc actggagact gaagtcaca gatatgcaac aaagcctttg tctccctgat	300
gtttttgcct cctgctggtc atgtgcttcc acacatcaag agaggacatt taacatttga	360
gccacagtgt catttgctgt tgtctgatgg ttggttgga gagaatttga actggagatg	420
aactttatta tccagagcgc tgagagtata acatgcatga cagagctttt agagcactgt	480
gatgtaacat gtcaagcaga aataggagc atgtttacag ccatttctatg aaa	533

<210> SEQ ID NO 440
 <211> LENGTH: 341
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 440

-continued

catggggtag gggggtcggg gattcattga attgtggttg gcaggagcaa gccctgctca	60
cactctcaca ctgcaccca gaattgtcaa agatacagat tgtaaaaatc tacgatccct	120
cagtctcact cacaaaaaat aaaatctcat gtccccaacg aaccagagt cagacgacag	180
ctggagcatt ggcagggaca gtcagaaaagg agacaagtga aaacggtcag atggacacag	240
gcggaggaga aaagacagag ggagagagac catcgggaac aatcagaggg gccgagacga	300
tcagaaaagg gtcagcccga gacaggctga gccagagttt c	341

<210> SEQ ID NO 441
 <211> LENGTH: 572
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 53, 84, 132, 138, 148
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 441

aagtttgggg ataatttatt atgcagcaag agataataca caggacttct canagcactt	60
aatatgttaa tataaatctc caanaaaaaa gatatacaat gaaacattcc tcttagttat	120
ctggccaagg anactttntt tttttganaa tattcttcaa aaagctgac taatgatatg	180
gctctggtcc tacaattcca tgtaacttct aaccttgatt ttatctcatg agcaaactat	240
ttatccttcc agaacctcaa cttttccctt ttacaaagta gaaataaacc atctgccttt	300
acataaatca ttaatacagc cctggatggg cagattctga gctatttttg gctggggggg	360
gggaaatagc ctgtggaggt cctaaaaaga tctacggggc tcgagatggg tctctgcaag	420
gtagcagggt ggctcagggc ccatttcagt cttgttccc caggccattt ccacaaaatg	480
gtgagaaata gtgtcttctt ttagcttgct cataactcaa agatgggggg catggacctg	540
ggcctttcta ggctagggca tgaacctcct cc	572

<210> SEQ ID NO 442
 <211> LENGTH: 379
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 34, 67
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 442

tcccagctgc actgcttaca cgtcttcctt cgtnttcacc taccocgagg ctgactcctt	60
ccccagntgt gcagctgcc accgcaagg cagcagcagc aatgagcctt cctctgactc	120
gctcagctca cccacgctgc tggccctgtg agggggcagg gaaggggagg cagccggcac	180
ccacaagtgc cactgcccga gctgggtgat tacagagagg agaaacacat cttccctaga	240
gggttcctgt agacctaggg aggaccttat ctgtgcgtga aacacaccag gctgtgggcc	300
tcaaggactt gaaagcatcc atgtgtggac tcaagtcctt acctcttcg gagatgtagc	360
aaaacgcatg gagtgtgta	379

<210> SEQ ID NO 443
 <211> LENGTH: 511
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:

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<221> NAME/KEY: misc_feature
 <222> LOCATION: 444
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 443

```

acatgcccc aaaggtctgc ttcattgcta cgattctcta cttaaatacca cattcacagc      60
tattgcctca gaccctctgg aggaggggcc aggggttagc tggctttgaa tagcatgtag      120
agcacaggca gtgtggccac aaatgtcaca caggtgacca gggtgctata gatgggtgttc      180
ctgttgactt gggcttctag tctctgtccc gtgtctgaca gtgccaagat catgctcccc      240
tgctccagca agaagctggg catagccccg tctgtctggt ccaccaggcc tgggtgtgct      300
gcagacttta caagctgaac cccccagcc atttggctac aagtcttttc taggccatca      360
agctgctctc gtaagccttc tagacatgaa tggacttgcc tggaatgact aagctgctct      420
ttcaaggcag ctgaaaggac atcnacatct ctgtctctgg tcgggggact acctgcctgt      480
gaccagagat cctgccttgg cccagcagca t                                     511

```

<210> SEQ ID NO 444
 <211> LENGTH: 612
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 547
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 444

```

acaggaagaa ttctacagtt aatctatcac agtgttcag caaagcatat gttgaaaact      60
acagttttca atctaacatc taaattttaa aaagtagcat ttcagcaaca aacaagctca      120
gagaggctca tggcaaaagt gaaataacag aactattgct cagatgtctg caaagtcaag      180
ctgtgccctc cagctccgcc cacttgaagg cttaggcaga cacgtaaggt ggcgggtggt      240
ccttggcagc accattcaca gtggcatcat catacggagg tagcagcacc gtagtgtcat      300
tgctggtaac ataaaccagg acatcagagg agttcctacc attgatgtat cggtagcagt      360
tccaaacaca gctaatacaag taacccttaa aagtcaagat aatgctaata aacagaagaa      420
taataaggac caaacaggta ggattcactg acatgacatc atctctgtag ggaaaattag      480
gaggcagttg ccgtatgtat tcctgaatgg agtttgata aataagcaca gtgattgcaa      540
ccaacancctt cagggcгааг tcaaagatct ggtaacagaa gaatgggatg atccaggctg      600
cgcgttgctt gt                                     612

```

<210> SEQ ID NO 445
 <211> LENGTH: 708
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 643, 676
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 445

```

accatcctgt tccaacagag ccattgccta ttcctaaatt gaatctgact ggggtgtgcc      60
ctcctcggaa cacaacagta gaccttaata gtggaacat cgatgtgcct cccaacatga      120
caagctgggc cagctttcat aatgggtgtgg ctgctggcct gaagatagct cctgcctccc      180

```

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agatcgactc agcttggtt gtttacaata agcccaagca tgctgagttg gccaatgagt	240
atgctggcctt tctcatggct ctgggtttga atgggcacct taccaagctg gcgactctca	300
atatccatga ctacttgacc aagggccatg aaatgacaag cattggactg ctacttggtg	360
ttctgctgc aaaactaggc accatggata tgtctattac tcggcttggt agcattcgca	420
ttcctgctct cttaccccca acgtccacag agttggatgt tcctcacaat gtccaagtgg	480
ctgcagtggg tggcattggc cttgtatatc aagggcacgc tcacagacat actgcagaag	540
tcctgttggc tgagatagga cggcctcctg gtcctgaaat ggaatactgc actgacagag	600
agtcatactc cttagctgct ggcttggccc tgggcacatg ctncttgggg catggcagca	660
atgtgatagg tatgtntgat ctcaatgtgc ctgagcagct ctatcagt	708

<210> SEQ ID NO 446

<211> LENGTH: 612

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 446

acaagcaacg cgcagcctgg atcatcccat tcttctgtta ccagatcttt gactttgccc	60
tgaacatggt ggttgcaatc actgtgctta tttatccaaa ctccattcag gaatacatatc	120
ggcaactgcc tcctaatttt ccctacagag atgatgtcat gtcagtgaat cctacctgtt	180
tggctcctat tattcttctg tttattagca ttatcttgac ttttaagggt tacttgatta	240
gctgtgtttt gaactgctac cgatacatca atggttaggaa ctctctgat gtcctggttt	300
atgttaccag caatgacact acggtgctgc taccctcgta tgatgatgcc actgtgaatg	360
gtgctgcca ggagccaccg ccaccttacg tgtctgccta agccttcaag tgggcggagc	420
tgagggcagc agcttgactt tgcagacatc tgagcaatag ttctgttatt tcacttttgc	480
catgagcctc tctgagcttg tttgttgctg aaatgctact ttttaaaatt tagatgttag	540
attgaaaact gtagttttca acatatgctt tgctggaaca ctgtgataga ttaactgtag	600
aattcttcct gt	612

<210> SEQ ID NO 447

<211> LENGTH: 642

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 447

actgaaagaa ttaaagtcag aagtcttccc aaaacaaaaa gaactgcca cagagaaaat	60
cctttctgat acttttcatt gctaaaataa aacaggcggg aaatgtggaa aagaaattca	120
acaaaataat gtagcaccag aagaacaagt cctagatgat tcaagttcaa aaggaagct	180
ccagcaatgt ggaagaggta aagaccaatg tagacaagct gacgaggaat atcttctttt	240
ttggttttct ggaagtagag ttcaggaaaa gcatgaagcc agtaagccag ctgtgatatg	300
tagaaaaact tcatttgaaa tgtcatcagg ttatggggat aagccctcca taagatagtt	360
gggtctgaga ttagttttcc agagatgaga atgaatgtgc cccaaacaca ggcaaaaagg	420
tagaacgcac taagctgacc agattcatta aacttgctgt gttttgtttt ggagaagtgc	480
attcgctgt taattttatc caacatatac tottgaatta cggcatgaat aattatcgcc	540
actagcatgt agaagaaaac agtagccaaa totttgatgc catagtaata aaggacact	600

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gattcagtag cttgttcttc tggtgctggg aggtgacat tg 642

<210> SEQ ID NO 448
<211> LENGTH: 394
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 66
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 448

accagaagac cttagaaaaa ggaggaaagg aggagaggca gataatttgg atgaattcct 60
caaaagnttt gaaaaatccag aggttccttag agaggaccag caacagcagc atcagcagcg 120
tgatgtttatc gatgagccca ttattgaaga gccaaagccgc ctccaggagt cagtgatgga 180
ggccagcaga acaaacatag atgagtcagc tatgcctcca ccaccacctc agggagttaa 240
gcgaaaagct ggacaaattg acccagagcc tgtgatgcct cctcagcagg tagagcagat 300
ggaaatacca cctgtagagc ttccccaga agaacctcca aatatctgtc agctaatacc 360
agagttagaa cttctgccag aaaaagagaa ggag 394

<210> SEQ ID NO 449
<211> LENGTH: 494
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 66
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 449

acaaaaaaca caaggaatac aaccaatag aaaatagtcc tgggaatgtg gtcagaagca 60
aaggcntgag tgtctttctc aacctgcaa aagccgtgtt cttcccgga aaccaggaaa 120
aggatccgct actcaaaaac caagaattta aaggagtctt ttaaatttcg acctgtttc 180
tgaagctcac ttttcagtgc cattgatgtg agatgtgctg gagtggctat taacctttt 240
ttcctaaaga ttattgttaa atagatattg tggtttggg aagtgaatt ttttataggt 300
taaatgtcat tttagagatg gggagaggga ttatactgca ggcagcttca gccatgttgt 360
gaaactgata aaagcaactt agcaaggctt cttttcatta tttttatgt ttcacttata 420
aagtcttagg taactagtag gatagaaaca ctgtgtccc agagtaagga gagaagctac 480
tattgattag agcc 494

<210> SEQ ID NO 450
<211> LENGTH: 547
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 450

actttgggct ccagacttca ctgtccttag gcattgaaac catcacctgg tttgcattct 60
tcatgactga ggtaaactta aaacaaaaat ggtaggaaag ctttcctatg cttcggttaa 120
gagacaaatt tgcttttcta gaattggtgg ctgagaaagg cagacagggc ctgattaaag 180
aagacatttg tcaccactag ccaccaagtt aagttgtgga acccaaaggt gacggccatg 240
gaaacgtaga tcatcagctc tgctaagtag ttaggggaag aaacatattc aaaccagtct 300

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ccaaatggga tcctgtggtt acagtgaatg gccactcctg ctttattttt cctgagattg	360
ccgagaataa catggcactt atactgatgg gcagatgacc agatgaacat catcatccca	420
agaatatgga accaccgtgc ttgcatcaat agatttttcc ctgttatgta ggcatcctctg	480
ccatccattg gcacttggct cagcacagtt aggccaacaa ggacataata gacaagtcca	540
aaacagt	547

<210> SEQ ID NO 451
 <211> LENGTH: 384
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 8, 9, 19, 41
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 451

actacttnnt ggttaaaang ccactggtag agtcatctga ntgtaaacaa tgtccctgca	60
ctgctggaaa aatccactgg ctccaagaa aagaaaatgg tctgaagcct ctgttggtggc	120
tctcacaact catctttccc taagtcatca agctccacat cactgaggtc aatgtcatcc	180
tccacgggaa gctcgccatc cctgccgtcc caaggctctc tctcaacgat ggtagggaaa	240
gccccgcctc ctacagggtgc cgtggagcca cgcccaaaag agagctccct gagaaactcg	300
ttgatgcctt gctcactgaa ggagcctttt agcagagcaa atttcatctt gcgtgcattg	360
atggcgggcca tggcggggta ccca	384

<210> SEQ ID NO 452
 <211> LENGTH: 381
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 291, 341, 368
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 452

actctaaagt tgccactctc acaggggtca gtgataccca ctgaacctgg caggaaacagt	60
cctgcagcca gaatctgcaa gcagcgcctg tatgcaacgt ttagggccaa aggctgtctg	120
gtggggttgt tcatcacagc ataatggcct agtaggtcaa ggatccaggg tgtgaggggc	180
tcaaagccag gaaaacgaat cctcaagtcc ttcagtagtc tgatgagaac tttactgtg	240
gactgagaag ctttttctc gaaccagcgg gcattgtcga tggctgctaa ngcactctgc	300
aatactttga tatccaaatg gagttctgga tccagttttc naagattggg tggcactgtt	360
gtaatganaa tcttctactgt a	381

<210> SEQ ID NO 453
 <211> LENGTH: 455
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 453

actgtgctaa acagcctata gccaaagttt aaagagttac aggaacaact gctacacatt	60
caaagaacag gcattcactg cagcctcctg atttgacctg atgggaggga caggagaatg	120
agtcactctg ccaccacttt tcctgccttg gatttgtaga ggatttggtt tgctctaatt	180

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tgtttttctt atatctgccc tactaaggta cacagtctgg gcactttgaa aatgttaaag	240
tttttaacgt ttgactgaca gaagcagcac ttaaaggctt catgaatcta ttttccaaaa	300
aaagtatgct ttcagtaaaa cattttacca ttttatctaa ctatgcactg acatttttgt	360
tcttcctgaa aaggggattt atgctaacac tgtattttta atgtaaaaat atacgtgtag	420
agatatttta acttcctgag tgacttatac ctcaa	455

<210> SEQ ID NO 454
 <211> LENGTH: 383
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 9
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 454

acagagcanc ttacaagtt gtcacatttc tttataaatt tttttaaaagc tacagttaa	60
tacaaaaatga attgcggttt tattacatta ataaccttc acctcagggt tttatgaaga	120
ggaaagggtt ttatgcaaaa gaaagtgcta caattcctaa tcattttaga cacttttaga	180
gggggtgaag ttgtatgata aagcagatat ttaattatt tggtatcttt ttgtattgca	240
agaaatttct tgctagttaa tcaagaaaac atccagattg acagtctaaa atggctactg	300
gtattttagt taattcaaaa atgaaacttt tcagtgttc actttactaa cattctattt	360
gagaaggctt attggtaaag ttt	383

<210> SEQ ID NO 455
 <211> LENGTH: 383
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 10
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 455

actcctttan gacaaggaaa caggtatcag catgatggta gcagaaacct taccaccaag	60
gtgcaggagc tgacttcttc caaagagttg tggttccggg cagcggcat tgccgtgccc	120
attgctggag ggctgatttt agtgttgctt attatgttgg ccctgaggat gcttcgaagt	180
gaaaataaga ggctgcagga tcagcggcaa cagatgctct cccgtttgca ctacagcttt	240
cacggacacc attccaaaaa ggggcaggtt gcaaagttag acttggaatg catggtgccg	300
gtcagtgggc acgagaactg ctgtctgacc tgtgataaaa tgagacaagc agacctcagc	360
aacgataaga tcctctcgct tgt	383

<210> SEQ ID NO 456
 <211> LENGTH: 543
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 64
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 456

acaaacattt tacaaaaaag aacattacca atatcagtgg cagtaagggc aagctgaaga	60
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atangtagac tgagtttccg ggcaatgtct gtcctcaaag acatccaaac tgcgttcagg	120
cagctgaaac aggccttcttt cccagtgaca agcatatgtg gtcagtaata caaacgatgg	180
taaatgaggc tactacatag gcccggttaa caaactcctc ttctcctcgg gtagggccatg	240
atacaagtgg aactcatcaa ataattttaa cccaaggcga taacaacact atttcccatc	300
taaactcatt taagccttca caatgtcgca atggattcag ttacttgcaa acgatcccgg	360
gtgtgcatac agatacttgt tttttacaca taacgctgtg ccatcccttc cttcactgcc	420
ccagtcaggt ttctctgtgt tggaccgaaa ggggatacat tttagaaatg cttccctcaa	480
gacagaagtg agaaagaaa gagaccctga ggccaggatc tattaaacct ggtgtgtgcg	540
caa	543

<210> SEQ ID NO 457
 <211> LENGTH: 544
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 17
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 457

actggtgcc aatattgnat ggtgagctcc tctctaattgt cttccagggc accaatatct	60
gcccattgtc cattagggac agtgacaaaag ccttcccttt tggcagaggg ttggactgag	120
gatagagcaa caatgaaatc attcagttca atgcacagtc cttgcactctg ctcctctgag	180
aggggatctt ggtctcttag caacccagc agcctttgta attcatcctg tgtttcagaa	240
gtgggctcag ttccagcct ttctcctcgg actccttttag atggcaaatc ttccatttca	300
ggatttttct tctgtgttcc ctgtagcttc attaagactc tattgactgc acacattgct	360
gcctctcggc acagtgccat gagatcagca ccaacaaagc ctggagttag gtgtgctaag	420
tgacagaaat caaaagcttg aggaagcctc agttttctgc acaatgtttg aagtattctt	480
tccttgatg cttcatctgg gatacctagg catatttctc ggtcgaacct tccgcacgt	540
ctca	544

<210> SEQ ID NO 458
 <211> LENGTH: 382
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 5, 23
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 458

acctntaggc tcaacggcag aancttcacc acaaaagcga aatgggcaca ccacagggag	60
aaaaactggt gtctctgatg ttgaaaagt tggctgtgt catggtgtgt tacttcatcc	120
tatctatcat taactccatg gcacaaagt atgccaaagc aatccagcag cggttgaact	180
cagaggagaa aactaaataa gtagagaaag ttttaaactg cagaaattgg agtggatggg	240
ttctgcotta aattgggagg actccaagcc gggaaggaaa attccctttt ccaacctgta	300
tcaattttta caactttttt cctgaaagca gtttagtcca tactttgcac tgacatactt	360
tttcttctg tgctaaggta ag	382

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<210> SEQ ID NO 459
<211> LENGTH: 168
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 459

```
ctcgtactct agccaggcac gaaaccatga agtagcctga tccttcttag ccatcctggc    60
cgcccttagcg gtagtaactt tgtgttatga atcacatgaa agcatggaat cttatgaa    120
taatcccttc attaacagga gaaatgcaaa taccttcata tccccctca    168
```

<210> SEQ ID NO 460
<211> LENGTH: 190
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 4
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 460

```
acantgcta ccaggagacc gagagctgac tatcccagcc tcggctaatag tattctacgc    60
catggatgga gcttcacacg atttcctcct gcggcagcgg cgaaggctcct ctactgctac    120
acctggcgct accagtggcc cgtctgcctc aggaactcct ccgagtgagg gaggaggggg    180
ctcctttccc    190
```

<210> SEQ ID NO 461
<211> LENGTH: 495
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 461

```
acagacaggc ttctctgcta tcctccagcc agtgtaatag tcaaggaaaa gggcaacagt    60
attggatcat tccttagaca ctaatcagct ggggaaagag ttcatggca aaagtgtcct    120
cccaagaatg gtttacacca agcagagagg acatgtcact gaatggggaa agggaacccc    180
cgtatccaca gtcactgtaa gcatccagta ggcaggaaga tggctttggg cagtggctgg    240
atgaaagcag atttgagata ccagctccg gaacgaggtc atcttctaca ggttcttcct    300
tcactgagac aatgaattca gggatgatcat tctctgaggg gctgagaggt gcttcctcga    360
ttttcactac cacattagct tggctctctg tctcagaggg tatctctaag actaggggct    420
tggtatatat gtggtcaaaa cgaattagtt cattaatggc ttccagcttg gctgatgacg    480
tcccactga cagag    495
```

<210> SEQ ID NO 462
<211> LENGTH: 493
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: 68
<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 462

```
acactgaaac ataatccgc aagtcaccac acatacaaca cccggcagga aaaaaacaaa    60
aacaggngt ttacatgac cctgtaacag ccatgggtctc aaactcagat gcttcctcca    120
```

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tctgccaaagt gtgttttggg tacagagcac atcgtggctt ctgggggtcac actcagctta	180
ggctgtgggt ccacagagca ctcatctggc tgggctatgg tgggtgtggc tctactcaag	240
aagcaaaagca gttaccagca cattcaaaca gtgtattgaa catcttttaa atatcaaagt	300
gagaaacaag aaggcaacat aataatgtta tcagaaagat gttaggaagt aaggacagct	360
gtgtaaagct tgaggctgaa aagtagcttg ccagcttcat ttctttggtt tcttggttag	420
tggggcccg aacagcaaga tgtgaggttc tggttcatgg atcatataat ggacccatcc	480
ctgactctgc tga	493

<210> SEQ ID NO 463

<211> LENGTH: 3681

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 463

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ctagctggcc ctgtgggcat ttattagtaa agttttaatg acaaaagctt tgagtcaaca	120
caccctgtgg taattaacct ggtcatcccc accctggaga gccatcctgc ccatgggtga	180
tcaaagaagg aacatctgca ggaacacctg atgaggctgc acccttggcg gaaagaacac	240
ctgacacagc tgaaagcttg gtgaaaaaa cacctgatga ggctgcaccc ttggtggaaa	300
gaacacctga cacggctgaa agcttgggtg aaaaaacacc tgatgaggct gcatccttg	360
tggagggaac atctgacaaa attcaatgtt tggagaaagc gacatctgga aagttcgaac	420
agtcagcaga agaaacacct agggaaatta cgagtcctgc aaaagaaaca tctgagaaat	480
ttacgtggcc agcaaaagga agacctagga agatcgcatg ggagaaaaa gaagacacac	540
ctagggaaat tatgagtcgc gcaaaagaaa catctgagaa atttacgtgg gcagcaaaag	600
gaagacctag gaagatcgca tgggagaaaa aagaaacacc tgtaaagact ggatgcgtgg	660
caagagtaac atctaataaa actaaagttt tggaaaaagg aagatctaag atgattgcat	720
gtcctacaaa agaatacatc acaaaagcaa gtgccaatga tcagaggttc ccatcagaat	780
caaacaaga ggaagatgaa gaataattct gtgattctcg gagtctcttt gagagttctg	840
caaagattca agtgtgtata cctgagtcta tataatcaaaa agtaattggag ataaatagag	900
aagtagaaga gcctcctaag aagccatctg ccttcaagcc tgccattgaa atgcaaaact	960
ctgttccaaa taaagccttt gaattgaaga atgaacaaac attgagagca gatccgatgt	1020
tcccaccaga atccaaacaa aaggactatg aagaaaattc ttgggattct gagagtctct	1080
gtgagactgt ttacagaaag gatgtgtgtt tacccaaggc tacacatcaa aaagaaatag	1140
ataaaataaa tggaaaatta gaagagtctc ctaataaaga tggctctctg aaggctacct	1200
gcggaatgaa agtttctatt ccaactaaag ccttagaatt gaaggacatg caaactttca	1260
aagcagagcc tccggggaag catctgcct tcgagcctgc cactgaaatg caaaagtctg	1320
tcccaataaa agccttgtaa ttgaaaaatg aacaacatt gagagcagat gagatactcc	1380
catcagaatc caaacaaga gactatgaag aaagtcttg ggattctgag agtctctgtg	1440
agactgtttc acagaaggat gtgtgtttac ccaaggctrc rcatcaaaaa gaaatagata	1500
aaataaatgg aaaattagaa gggctctcctg ttaaagatgg tcttctgaag gctaactgcg	1560
gaatgaaagt ttctattcca actaaagcct tagaattgat ggacatgcaa actttcaaag	1620

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cagagcctcc	cgagaagcca	tctgccttcg	agcctgccat	tgaaatgcaa	aagtctgttc	1680
caataaaagc	cttggaattg	aagaatgaac	aaacattgag	agcagatgag	atactcccat	1740
cagaatccaa	acaaaaggac	tatgaagaaa	gttcttgga	ttctgagagt	ctctgtgaga	1800
ctgtttcaca	gaaggatgtg	tgtttaccca	aggctrccca	tcaaaaagaa	atagataaaa	1860
taaatggaaa	attagaagag	tctcctgata	atgatggttt	tctgaaggct	ccctgcagaa	1920
tgaaagtttc	tattccaact	aaagccttag	aattgatgga	catgcaaact	ttcaaagcag	1980
agcctcccg	gaagccatct	gccttcgagc	ctgccattga	aatgcaaaag	tctgttccaa	2040
ataaagcctt	ggaattgaag	aatgaacaaa	cattgagagc	agatcagatg	ttcccttcag	2100
aatcaaaaca	aaagaasgtt	gaagaaaatt	cttgggattc	tgagagtctc	cgtgagactg	2160
tttcacagaa	ggatgtgtgt	gtacccaagg	ctacacatca	aaaagaaatg	gataaaataa	2220
gtggaaaatt	agaagattca	actagcctat	caaaaatcct	ggatacagtt	cattcttgtg	2280
aaagagcaag	ggaacttcaa	aaagatcact	gtgaacaacg	tacaggaaaa	atggaacaaa	2340
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agttagagaa	ccaaaagtt	aatgggaac	aagagctctg	cagtgtgagg	tttctcacac	2460
tcatgaaaat	gaaaattatc	tcttacatga	aaattgcatg	ttgaaaaagg	aaattgccat	2520
gctaaaactg	gaaatagcca	cactgaaaca	ccaataccag	gaaaaggaaa	ataaatactt	2580
tgaggacatt	aagattttta	aagaaaagaa	tgctgaactt	cagatgaccc	taaaactgaa	2640
agaggaatca	ttaactaaaa	gggcatctca	atatagtggg	cagcttaaag	ttctgatagc	2700
tgagaacaca	atgctcactt	ctaaattgaa	ggaaaaacaa	gacaaagaaa	tactagaggc	2760
agaaattgaa	tcacaccatc	ctagactggc	ttctgctgta	caagaccatg	atcaaattgt	2820
gacatcaaga	aaaagtcaag	aacctgcttt	ccacattgca	ggagatgctt	gtttgcaaag	2880
aaaaatgaat	gttgatgtga	gtagtacgat	atataacaat	gaggtgctcc	atcaaccact	2940
ttctgaagct	caaaggaaat	ccaaaagcct	aaaaattaat	ctcaattatg	cmggagatgc	3000
tctaagagaa	aatacattgg	tttcagaaca	tgacaaaaga	gaccaacgtg	aaacacagtg	3060
tcaaatagaag	gaagctgaac	acatgtatca	aaacgaacaa	gataatgtga	acaaacacac	3120
tgaacagcag	gagtctctag	atcagaaaatt	atttcaacta	caaagcaaaa	atatgtggct	3180
tcaacagcaa	ttagttcatg	cacataagaa	agctgacaac	aaaagcaaga	taacaattga	3240
tattcatttt	cttgagagga	aaatgcaaca	tcattctccta	aaagagaaaa	atgaggagat	3300
atttaattac	aataaccatt	taaaaaaccg	tatatatcaa	tatgaaaaag	agaaagcaga	3360
aacagaaaac	tcatgagaga	caagcagtaa	gaaacttctt	ttggagaaac	aacagaccag	3420
atctttactc	acaactcatg	ctaggaggcc	agtcctagca	tcaccttatg	ttgaaatct	3480
taccaatagt	ctgtgtcaac	agaatactta	ttttagaaga	aaaattcatg	atttcttcct	3540
gaagcctaca	gacataaaat	aacagtgtga	agaattactt	gttcacgaat	tgcataaagc	3600
tgacagggat	tcccctctac	cctgatgatg	cagcagacat	cattcaatcc	aaccagaatc	3660
tcgctctgtc	actcaggctg	g				3681

<210> SEQ ID NO 464

<211> LENGTH: 1424

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 464

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tccgagctga ttacagacac caaggaagat gctgtaaaga gtcagcagcc acagccctgg      60
ctagctggcc ctgtgggcat ttattagtaa agttttaatg acaaaagctt tgagtcaaca      120
caccctgtgg taattaacct ggtcatcccc accctggaga gccatcctgc ccatgggtga      180
tcaaagaagg aacatctgca ggaacacctg atgaggctgc acccttggcg gaaagaacac      240
ctgacacagc tgaagccttg gtggaaaaaa cacctgatga ggctgcaccc ttggtggaaa      300
gaacacctga caccgctgaa agcttgggtg aaaaaacacc tgatgaggct gcatccttgg      360
tggagggaac atctgacaaa attcaatgtt tggagaaaag gacatctgga aagttcgaac      420
agtcagcaga agaaacacct agggaaatta cgagtcctgc aaaagaaaca tctgagaaat      480
ttacgtggcc agcaaaagga agacctagga agatcgcatg ggagaaaaaa gaagacacac      540
ctagggaaat tatgagctcc gcaaaagaaa catctgagaa atttacgtgg gcagcaaaag      600
gaagacctag gaagatcgca tgggagaaaa aagaaacacc tgtaaagact ggatgcgtgg      660
caagagtaac atctaataaa actaaagttt tggaaaaagg aagatctaag atgattgcat      720
gtcctacaaa agaatcatct acaaaagcaa gtgccaatga tcagagggtc ccatcagaat      780
caaacaaga ggaagatgaa gaatatctt gtgattctcg gagtctcttt gagagttctg      840
caaagattca agtgtgtata cctgagtcta tatatcaaaa agtaatggag ataaatagag      900
aagtagaaga gcctcctaag aagccatctg cttcaagcc tgccattgaa atgcaaaact      960
ctgttccaaa taaagccttt gaattgaaga atgaacaaac attgagagca gatccgatgt      1020
tcccaccaga atccaaacaa aaggactatg aagaaaattc ttgggattct gagagtctct      1080
gtgagactgt ttcacagaag gatgtgtgtt tacccaaggc tacacatcaa aaagaaatag      1140
ataaaataaa tggaataaata gaaggtaaga accgtttttt atttaaaaat cagttgaccg      1200
aatattttct taaactgatg agggaggata tcctctagta gctgaagaaa attacctcct      1260
aaatgcaaac catggaaaaa aagagaagtg caatggtcgt aagttgtatg tctcatcagg      1320
tgttggaac agactatatt gagagtgtcg aaaaggagct gaattattag tttgaattca      1380
agatattgca agacctgaga gaaaaaaaaa aaaaaaaaaa aaaa                        1424

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<210> SEQ ID NO 465

<211> LENGTH: 674

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 465

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attccgagct gattacagac accaaggaag atgctgtaaa ggtcagcag ccacagccct      60
ggctagctgg ccctgtgggc atttattagt aaagttttaa tgacaaaagc tttgagtcaa      120
cacaccctgt ggtaattaac ctggtcatcc ccaccctgga gagccatcct gcccatgggt      180
gatcaaaaga ggaacatctg caggaacacc tgatgaggct gcacccttgg cggaaagAAC      240
acctgacaca gctgaaagct tgggtggaaa aacacctgat gaggtgcac ccttggtgga      300
aagaacacct gacacggctg aaagcttggg ggaaaaaaca cctgatgagg ctgcatcctt      360
ggtggaggga acatctgaca aaattcaatg tttggagaaa gcgacatctg gaaagttcga      420
acagtcagca gaagaacac ctagggaat tacgagtcct gcaaaagaaa catctgagaa      480
atttacgtgg ccagcaaaag gaagacctag gaagatcgca tgggagaaaa aagatgactc      540

```

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agttaaggca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	600
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	660
aaaaaaaaaa aaaa	674

<210> SEQ ID NO 466
 <211> LENGTH: 1729
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 11, 1128
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 466

gaaagttcga ncagtcagca gaagaacac ctagggaat tacgagtcct gcaaaagaaa	60
catctgagaa atttactgtg ccagcaaaag gaagacctag gaagatcgca tgggagaaaa	120
aagaagacac acctaggga attatgagtc ccgcaaaaga aacatctgag aaatttacgt	180
gggcagcaaa aggaagacct aggaagatcg catgggagaa aaaagaaaca cctgtaaaga	240
ctggatgcgt ggcaagagta acatctaata aaactaaagt tttggaaaaa ggaagatcta	300
agatgattgc atgtcttaca aaagaatcat ctacaaaagc aagtgccaat gatcagagggt	360
tcccatcaga atccaaacaa gaggaagatg aagaatatc ttgtgattct cggagtctct	420
ttgagagttc tgcaagatt caagtgtgta tacctgagtc tatatatcaa aaagtaatgg	480
agataaatag agaagtagaa gagcttccta agaagccatc tgccttcaag cctgccattg	540
aaatgcaaaa ctctgttcca aataaagcct ttgaattgaa gaatgaacaa acattgagag	600
cagatccgat gttcccacca gaatccaaac aaaaggacta tgaagaaaat tcttgggatt	660
ctgagagtct ctgtgagact gtttcacaga aggatgtgtg tttacccaag gctacacatc	720
aaaaagaaat agataaaata aatggaaaat tagaagagtc tcctaataaa gatggtcttc	780
tgaaggctac ctgcggaatg aaagtttcta ttccaactaa agccttagaa ttgaaggaca	840
tgcaaaacttt caaagcagag cctccgggga agccatctgc cttcgagcct gccactgaaa	900
tgcaaaagtc tgtcccaaat aaagccttg aattgaaaaa tgaacaaaca ttgagagcag	960
atgagatact cccatcagaa tccaacaaaa aggactatga agaaaattct tgggatactg	1020
agagtctctg tgagactgtt tcacagaagg atgtgtgttt acccaaggct gcgcatacaa	1080
aagaaataga taaaataaat ggaaaattag aagggtctcc tggtaaanat ggtcttctga	1140
aggctaactg cggaatgaaa gtttctattc caactaaagc cttagaattg atggacatgc	1200
aaactttcaa agcagagcct cccgagaagc catctgcctt cagcctgcc attgaaatgc	1260
aaaagtctgt tccaaataaa gccttggaat tgaagaatga acaaacattg agagcagatg	1320
agatactccc atcagaatcc aaacaaaagg actatgaaga aagttcttgg gattctgaga	1380
gtctctgtga gactgtttca cagaaggatg tgtgtttacc caaggctgcg catcaaaaag	1440
aaatagataa aataaatgga aaattagaag gtaagaaccg ttttttattt aaaaatcatt	1500
tgaccaaata tttctctaaa ttgatgagga aggatatcct ctagtagctg aagaaaatta	1560
cctcctaaat gcaaaccatg gaaaaaaga gaagtgcaat ggtcataagc tatgtgtctc	1620
atcaggcatt ggcaacagac tatattgtga gtgctgaaga ggagctgaat tactagttaa	1680
aattcaagat attccaagac gtgaggaaaa tgagaaaaaa aaaaaaaaaa	1729

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<210> SEQ ID NO 467

<211> LENGTH: 1337

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 467

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aaaaagaaat agataaaata aatggaaaat tagaagggtc tcctgttaaa gatggctctc    60
tgaaggctaa ctgcggaatg aaagtttcta ttccaactaa agccttagaa ttgatggaca    120
tgcaaaacttt caaagcagag cctcccgaga agccatctgc cttcgagcct gccattgaaa    180
tgcaaaagtc tgttccaaat aaagccttgg aattgaagaa tgaacaaaca ttgagagcag    240
atgagatact cccatcagaa tccaaacaaa aggactatga agaaagtctt tgggattctg    300
agagtctctg tgagactgtt tcacagaagg atgtgtgttt acccaaggct gcgcatcaaa    360
aagaaataga taaaataaat ggaaaattag aagagtctcc tgataatgat ggttttctga    420
aggctccctg cagaatgaaa gtttctattc caactaaagc cttagaattg atggacatgc    480
aaactttcaa agcagagcct cccgagaagc catctgcctt cgagcctgcc attgaaatgc    540
aaaagtctgt tccaaataaa gccttggaat tgaagaatga acaaacattg agagcagatc    600
agatgttccc ttcagaatca aaacaaaaga aggttgaaga aaattcttgg gattctgaga    660
gtctccgtga gactgtttca cagaaggatg tgtgtgtacc caaggctaca catcaaaaag    720
aaatggataa aataagtgga aaattagaag attcaactag cctatcaaaa atcttgata    780
cagttcattc ttgtgaaaga gcaagggaac ttcaaaaaga tcaactgtga caacgtacag    840
gaaaaatgga acaaatgaaa aagaagtttt gtgtactgaa aaagaaactg tcagaagcaa    900
aagaaataaa atcacagtta gagaacccaa aagttaaag ggaacaagag ctctgcagtg    960
tgagattgac tttaaaccaa gaagaagaga agagaagaaa tgccgatata ttaaatgaaa   1020
aaattagggg agaattagga agaatcgaag agcagcatag gaaagagtta gaagtgaac   1080
aacaacttga acaggctctc agaatacaag atatagaatt gaagagtgtg gaaagtaatt   1140
tgaatcaggt ttctcacact catgaaaatg aaaattatct cttacatgaa aattgcatgt   1200
tgaaaaagga aattgccatg ctaaaactgg aaatagccac actgaaacac caataccagg   1260
aaaaggaaaa taaatacttt gaggacatta agatttttaa agaaaagaat gctgaacttc   1320
agatgacccc tcgtgcc                                     1337
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<210> SEQ ID NO 468

<211> LENGTH: 2307

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 468

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ttgggattct gagagtctct gtgagactgt ttcacagaag gatgtgtgtt tacccaaggc    120
tacacatcaa aaagaaatag ataaaaataa tggaaaatta gaagggtctc ctgttaaaga    180
tggtcttctg aaggctaact gcggaatgaa agtttctatt ccaactaaag ccttagaatt    240
gatggacatg caaactttca aagcagagcc tcccgagaag ccactctgct tcgagcctgc    300
cattgaaatg caaaagtctg ttccaaataa agccttgga ttgaagaatg aacaaacatt    360
gagagcagat gagatactcc catcagaatc caaacaaaag gactatgaag aaagttcttg    420
```

-continued

ggattctgag agtctctgtg agactgttcc acagaaggat gtgtgtttac ccaaggctac	480
acatcaaaaa gaaatagata aaataaatgg aaaattagaa gagtctcctg ataattgatg	540
ttttctgaag tctccctgca gaataaaagt ttctattcca actaaagcct tagaattgat	600
ggacatgcaa actttc aaag cagagcctcc cgagaagcca tctgccttcg agcctgccat	660
tgaaatgcaa aagtctgttc caaataaaagc cttggaattg aagaatgaac aaacattgag	720
agcagatcag atgttccctt cagaatcaaa acaaaagaac gttgaagaaa attccttgga	780
ttctgagagt ctccgtgaga ctgtttcaca gaaggatgtg tgtgtaccca aggctacaca	840
tcaaaaagaa atggataaaa taagtggaaa attagaagat tcaactagcc tatcaaaaat	900
cttgataca gttcattctt gtgaaagagc aagggaactt caaaaagatc actgtgaaca	960
acgtacagga aaaatggaac aaatgaaaaa gaagttttgt gtactgaaaa agaaactgtc	1020
agaagcaaaa gaaataaaat cacagttaga gaacccaaaa gttaaattggg aacaagagct	1080
ctgcagtgtg aggtttctca cactcatgaa aatgaaaatt atctcttaca tgaaaattgc	1140
atgttgaaaa aggaaattgc catgctaaaa ctggaaatag ccacactgaa acaccaatac	1200
caggaaaagg aaaataaata ctttgaggac attaagattt taaaagaaaa gaatgctgaa	1260
cttcagatga ccctaaaact gaaagaggaa tcattaacta aaagggcatc tcaatatagt	1320
gggcagctta aagttctgat agctgagaac acaatgctca cttctaaatt gaaggaaaaa	1380
caagacaaag aaatactaga ggcagaaatt gaatcacacc atcctagact ggcttctgct	1440
gtacaagacc atgatcaa atgtgacatca agaaaaagtc aagaacctgc ttccacatt	1500
gcaggagatg cttgtttgca aagaaaaatg aatgttgatg tgagtagtac gatataaac	1560
aatgaggtgc tccatcaacc actttctgaa gctcaaagga aatccaaaag cctaaaaatt	1620
aatctcaatt atgcaggaga tgctctaaga gaaaatacat tggtttcaga acatgcacaa	1680
agagaccaac gtgaaacaca gtgtcaaatg aaggaagctg aacacatgta tcaaaacgaa	1740
caagataatg tgaacaaaca cactgaacag caggagtctc tagatcagaa attatttcaa	1800
ctacaaagca aaaatatgtg gcttcaacag caattagttc atgcacataa gaaagctgac	1860
aacaaaagca agataacaat tgatattcat tttcttgaga ggaaaatgca acatcatctc	1920
ctaaaagaga aaaatgagga gatattttaat tacaataacc atttaaaaaa ccgtatatat	1980
caatatgaaa aagagaaaagc agaaacagaa aactcatgag agacaagcag taagaaactt	2040
cttttgagga aacaacagac cagatcttta ctcaactc atgctaggag gccagtccta	2100
gcatcacctt atgttgaaaa tcttaccat agtctgtgtc aacagaatac ttattttaga	2160
agaaaaattc atgatttctt cctgaagcct acagacataa aataacagtg tgaagaatta	2220
ctgtttcacg aattgcataa agctgcacag gattcccatc taccctgatg atgcagcaga	2280
catcattcaa tccaaccaga atctcgc	2307

<210> SEQ ID NO 469

<211> LENGTH: 650

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: VARIANT

<222> LOCATION: 310, 429, 522

<223> OTHER INFORMATION: Xaa = Any Amino Acid

<400> SEQUENCE: 469

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Met	Ser	Pro	Ala	Lys	Glu	Thr	Ser	Glu	Lys	Phe	Thr	Trp	Ala	Ala	Lys
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Gly	Arg	Pro	Arg	Lys	Ile	Ala	Trp	Glu	Lys	Lys	Glu	Thr	Pro	Val	Lys
			20					25					30		
Thr	Gly	Cys	Val	Ala	Arg	Val	Thr	Ser	Asn	Lys	Thr	Lys	Val	Leu	Glu
		35					40					45			
Lys	Gly	Arg	Ser	Lys	Met	Ile	Ala	Cys	Pro	Thr	Lys	Glu	Ser	Ser	Thr
	50					55					60				
Lys	Ala	Ser	Ala	Asn	Asp	Gln	Arg	Phe	Pro	Ser	Glu	Ser	Lys	Gln	Glu
65					70				75					80	
Glu	Asp	Glu	Glu	Tyr	Ser	Cys	Asp	Ser	Arg	Ser	Leu	Phe	Glu	Ser	Ser
				85					90					95	
Ala	Lys	Ile	Gln	Val	Cys	Ile	Pro	Glu	Ser	Ile	Tyr	Gln	Lys	Val	Met
			100					105					110		
Glu	Ile	Asn	Arg	Glu	Val	Glu	Glu	Pro	Pro	Lys	Lys	Pro	Ser	Ala	Phe
		115					120					125			
Lys	Pro	Ala	Ile	Glu	Met	Gln	Asn	Ser	Val	Pro	Asn	Lys	Ala	Phe	Glu
	130					135					140				
Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Pro	Met	Phe	Pro	Pro	Glu
145					150				155						160
Ser	Lys	Gln	Lys	Asp	Tyr	Glu	Glu	Asn	Ser	Trp	Asp	Ser	Glu	Ser	Leu
			165						170					175	
Cys	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Thr	His
		180						185					190		
Gln	Lys	Glu	Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asn
		195					200					205			
Lys	Asp	Gly	Leu	Leu	Lys	Ala	Thr	Cys	Gly	Met	Lys	Val	Ser	Ile	Pro
	210					215				220					
Thr	Lys	Ala	Leu	Glu	Leu	Lys	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro
225					230					235				240	
Pro	Gly	Lys	Pro	Ser	Ala	Phe	Glu	Pro	Ala	Thr	Glu	Met	Gln	Lys	Ser
			245						250					255	
Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala
			260					265					270		
Asp	Glu	Ile	Leu	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Asp	Tyr	Glu	Glu	Ser
		275				280					285				
Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val
	290					295					300				
Cys	Leu	Pro	Lys	Ala	Xaa	His	Gln	Lys	Glu	Ile	Asp	Lys	Ile	Asn	Gly
305					310					315				320	
Lys	Leu	Glu	Gly	Ser	Pro	Val	Lys	Asp	Gly	Leu	Leu	Lys	Ala	Asn	Cys
			325						330					335	
Gly	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala	Leu	Glu	Leu	Met	Asp	Met
		340						345					350		
Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu	Lys	Pro	Ser	Ala	Phe	Glu	Pro
		355					360					365			
Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys
	370					375					380				
Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Glu	Ile	Leu	Pro	Ser	Glu	Ser	Lys
385					390					395				400	
Gln	Lys	Asp	Tyr	Glu	Glu	Ser	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu

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405					410					415					
Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Xaa	His	Gln	Lys
			420					425					430		
Glu	Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asp	Asn	Asp
		435					440					445			
Gly	Phe	Leu	Lys	Ala	Pro	Cys	Arg	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys
		450					455					460			
Ala	Leu	Glu	Leu	Met	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu
		465					470					475			480
Lys	Pro	Ser	Ala	Phe	Glu	Pro	Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro
			485						490					495	
Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Gln
			500					505					510		
Met	Phe	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Xaa	Val	Glu	Glu	Asn	Ser	Trp
			515				520					525			
Asp	Ser	Glu	Ser	Leu	Arg	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Val
		530					535					540			
Pro	Lys	Ala	Thr	His	Gln	Lys	Glu	Met	Asp	Lys	Ile	Ser	Gly	Lys	Leu
		545					550					555			560
Glu	Asp	Ser	Thr	Ser	Leu	Ser	Lys	Ile	Leu	Asp	Thr	Val	His	Ser	Cys
			565						570					575	
Glu	Arg	Ala	Arg	Glu	Leu	Gln	Lys	Asp	His	Cys	Glu	Gln	Arg	Thr	Gly
			580					585					590		
Lys	Met	Glu	Gln	Met	Lys	Lys	Lys	Phe	Cys	Val	Leu	Lys	Lys	Lys	Leu
		595					600					605			
Ser	Glu	Ala	Lys	Glu	Ile	Lys	Ser	Gln	Leu	Glu	Asn	Gln	Lys	Val	Lys
		610					615					620			
Trp	Glu	Gln	Glu	Leu	Cys	Ser	Val	Arg	Phe	Leu	Thr	Leu	Met	Lys	Met
		625					630					635			640
Lys	Ile	Ile	Ser	Tyr	Met	Lys	Ile	Ala	Cys						
			645						650						

<210> SEQ ID NO 470

<211> LENGTH: 228

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 470

Met	Ser	Pro	Ala	Lys	Glu	Thr	Ser	Glu	Lys	Phe	Thr	Trp	Ala	Ala	Lys
1				5					10					15	
Gly	Arg	Pro	Arg	Lys	Ile	Ala	Trp	Glu	Lys	Lys	Glu	Thr	Pro	Val	Lys
		20					25						30		
Thr	Gly	Cys	Val	Ala	Arg	Val	Thr	Ser	Asn	Lys	Thr	Lys	Val	Leu	Glu
		35					40					45			
Lys	Gly	Arg	Ser	Lys	Met	Ile	Ala	Cys	Pro	Thr	Lys	Glu	Ser	Ser	Thr
		50					55				60				
Lys	Ala	Ser	Ala	Asn	Asp	Gln	Arg	Phe	Pro	Ser	Glu	Ser	Lys	Gln	Glu
		65				70				75					80
Glu	Asp	Glu	Glu	Tyr	Ser	Cys	Asp	Ser	Arg	Ser	Leu	Phe	Glu	Ser	Ser
			85						90					95	
Ala	Lys	Ile	Gln	Val	Cys	Ile	Pro	Glu	Ser	Ile	Tyr	Gln	Lys	Val	Met
			100					105					110		

-continued

Glu Ile Asn Arg Glu Val Glu Glu Pro Pro Lys Lys Pro Ser Ala Phe
 115 120 125

Lys Pro Ala Ile Glu Met Gln Asn Ser Val Pro Asn Lys Ala Phe Glu
 130 135 140

Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Pro Met Phe Pro Pro Glu
 145 150 155 160

Ser Lys Gln Lys Asp Tyr Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu
 165 170 175

Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His
 180 185 190

Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Lys Asn Arg
 195 200 205

Phe Leu Phe Lys Asn Gln Leu Thr Glu Tyr Phe Ser Lys Leu Met Arg
 210 215 220

Arg Asp Ile Leu
 225

<210> SEQ ID NO 471
 <211> LENGTH: 154
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: 148
 <223> OTHER INFORMATION: Xaa = Any Amino Acid

<400> SEQUENCE: 471

Met Arg Leu His Pro Trp Arg Lys Glu His Leu Thr Gln Leu Lys Ala
 1 5 10 15

Trp Trp Lys Lys His Leu Met Arg Leu His Pro Trp Trp Lys Glu His
 20 25 30

Leu Thr Arg Leu Lys Ala Trp Trp Lys Lys His Leu Met Arg Leu His
 35 40 45

Pro Trp Trp Arg Glu His Leu Thr Lys Phe Asn Val Trp Arg Lys Arg
 50 55 60

His Leu Glu Ser Ser Asn Ser Gln Gln Lys Lys His Leu Gly Lys Leu
 65 70 75 80

Arg Val Leu Gln Lys Lys His Leu Arg Asn Leu Arg Gly Gln Gln Lys
 85 90 95

Glu Asp Leu Gly Arg Ser His Gly Arg Lys Lys Met Thr Gln Leu Arg
 100 105 110

Gln Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
 115 120 125

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
 130 135 140

Lys Lys Lys Xaa Lys Lys Lys Lys Lys Lys
 145 150

<210> SEQ ID NO 472
 <211> LENGTH: 466
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: 329
 <223> OTHER INFORMATION: Xaa = Any Amino Acid

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<400> SEQUENCE: 472

Met	Ser	Pro	Ala	Lys	Glu	Thr	Ser	Glu	Lys	Phe	Thr	Trp	Ala	Ala	Lys
1				5					10					15	
Gly	Arg	Pro	Arg	Lys	Ile	Ala	Trp	Glu	Lys	Lys	Glu	Thr	Pro	Val	Lys
			20					25					30		
Thr	Gly	Cys	Val	Ala	Arg	Val	Thr	Ser	Asn	Lys	Thr	Lys	Val	Leu	Glu
		35					40					45			
Lys	Gly	Arg	Ser	Lys	Met	Ile	Ala	Cys	Pro	Thr	Lys	Glu	Ser	Ser	Thr
	50					55					60				
Lys	Ala	Ser	Ala	Asn	Asp	Gln	Arg	Phe	Pro	Ser	Glu	Ser	Lys	Gln	Glu
65					70					75					80
Glu	Asp	Glu	Glu	Tyr	Ser	Cys	Asp	Ser	Arg	Ser	Leu	Phe	Glu	Ser	Ser
				85					90					95	
Ala	Lys	Ile	Gln	Val	Cys	Ile	Pro	Glu	Ser	Ile	Tyr	Gln	Lys	Val	Met
			100					105					110		
Glu	Ile	Asn	Arg	Glu	Val	Glu	Glu	Pro	Pro	Lys	Lys	Pro	Ser	Ala	Phe
		115					120					125			
Lys	Pro	Ala	Ile	Glu	Met	Gln	Asn	Ser	Val	Pro	Asn	Lys	Ala	Phe	Glu
	130					135					140				
Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Pro	Met	Phe	Pro	Pro	Glu
145					150					155					160
Ser	Lys	Gln	Lys	Asp	Tyr	Glu	Glu	Asn	Ser	Trp	Asp	Ser	Glu	Ser	Leu
				165					170					175	
Cys	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Thr	His
			180					185					190		
Gln	Lys	Glu	Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asn
		195					200					205			
Lys	Asp	Gly	Leu	Leu	Lys	Ala	Thr	Cys	Gly	Met	Lys	Val	Ser	Ile	Pro
	210					215					220				
Thr	Lys	Ala	Leu	Glu	Leu	Lys	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro
225					230					235					240
Pro	Gly	Lys	Pro	Ser	Ala	Phe	Glu	Pro	Ala	Thr	Glu	Met	Gln	Lys	Ser
				245					250					255	
Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala
				260				265					270		
Asp	Glu	Ile	Leu	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Asp	Tyr	Glu	Glu	Asn
		275					280					285			
Ser	Trp	Asp	Thr	Glu	Ser	Leu	Cys	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val
	290					295					300				
Cys	Leu	Pro	Lys	Ala	Ala	His	Gln	Lys	Glu	Ile	Asp	Lys	Ile	Asn	Gly
305					310					315					320
Lys	Leu	Glu	Gly	Ser	Pro	Gly	Lys	Xaa	Gly	Leu	Leu	Lys	Ala	Asn	Cys
				325					330					335	
Gly	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala	Leu	Glu	Leu	Met	Asp	Met
			340					345					350		
Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu	Lys	Pro	Ser	Ala	Phe	Glu	Pro
			355				360					365			
Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys
	370					375					380				
Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Glu	Ile	Leu	Pro	Ser	Glu	Ser	Lys
385					390					395					400

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Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu
 405 410 415

Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys
 420 425 430

Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Lys Asn Arg Phe Leu
 435 440 445

Phe Lys Asn His Leu Thr Lys Tyr Phe Ser Lys Leu Met Arg Lys Asp
 450 455 460

Ile Leu
 465

<210> SEQ ID NO 473
 <211> LENGTH: 445
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 473

Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser Pro Val Lys
 1 5 10 15

Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr
 20 25 30

Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro
 35 40 45

Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val
 50 55 60

Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp
 65 70 75 80

Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser
 85 90 95

Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys
 100 105 110

Leu Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys
 115 120 125

Leu Glu Glu Ser Pro Asp Asn Asp Gly Phe Leu Lys Ala Pro Cys Arg
 130 135 140

Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln
 145 150 155 160

Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala
 165 170 175

Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn
 180 185 190

Glu Gln Thr Leu Arg Ala Asp Gln Met Phe Pro Ser Glu Ser Lys Gln
 195 200 205

Lys Lys Val Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu Arg Glu Thr
 210 215 220

Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala Thr His Gln Lys Glu
 225 230 235 240

Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser Thr Ser Leu Ser Lys
 245 250 255

Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala Arg Glu Leu Gln Lys
 260 265 270

Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met Lys Lys Lys

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275	280	285
Phe Cys Val Leu Lys Lys Lys Leu Ser Glu Ala Lys Glu Ile Lys Ser 290 295 300		
Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu Cys Ser Val 305 310 315 320		
Arg Leu Thr Leu Asn Gln Glu Glu Glu Lys Arg Arg Asn Ala Asp Ile 325 330 335		
Leu Asn Glu Lys Ile Arg Glu Glu Leu Gly Arg Ile Glu Glu Gln His 340 345 350		
Arg Lys Glu Leu Glu Val Lys Gln Gln Leu Glu Gln Ala Leu Arg Ile 355 360 365		
Gln Asp Ile Glu Leu Lys Ser Val Glu Ser Asn Leu Asn Gln Val Ser 370 375 380		
His Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn Cys Met Leu 385 390 395 400		
Lys Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His 405 410 415		
Gln Tyr Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu 420 425 430		
Lys Glu Lys Asn Ala Glu Leu Gln Met Thr Pro Arg Ala 435 440 445		

<210> SEQ ID NO 474

<211> LENGTH: 3865

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 474

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tccgagctga ttacagacac caaggaagat gctgtaaaga gtcagcagcc acagccctgg      60
ctagctggcc ctgtgggcat ttattagtaa agttttaatg acaaaagctt tgagtcaaca      120
caccctgggg taattaacct ggtcatcccc accctggaga gccatcctgc ccatgggtga      180
tcaaagaagg aacatctgca ggaacacctg atgaggctgc acccttggcg gaaagaacac      240
ctgacacagc tgaaagcttg gtggaaaaaa cacctgatga ggctgcaccc ttggtggaaa      300
gaacacctga cacggctgaa agcttggtgg aaaaaacacc tgatgaggct gcatccttgg      360
tggagggaac atctgacaaa attcaatgtt tggagaaagc gacatctgga aagttcgaac      420
agtcagcaga agaaacacct agggaaatta cgagtcctgc aaaagaaaca tctgagaaat      480
ttacgtggcc agcaaaagga agacctagga agatcgcatg ggagaaaaaa gaagacacac      540
ctagggaaat tatgagtcct gcaaaagaaa catctgagaa atttacgtgg gcagcaaaag      600
gaagacctag gaagatcgca tgggagaaaa aagaaacacc tgtaaagact ggatgcgtgg      660
caagagtaac atctaataaa actaaagttt tggaaaaagg aagatctaag atgattgcat      720
gtcctacaaa agaatacatc acaaaagcaa gtgccaatga tcagagggtc ccatcagaat      780
caaacaaga ggaagatgaa gaataattct gtgattctcg gagtctcttt gagagttctg      840
caaagattca agtgtgtata cctgagtcta tatatcaaaa agtaatggag ataaatagag      900
aagtagaaga gcctcctaag aagccatctg ccttcaagcc tgccattgaa atgcaaaact      960
ctgttccaaa taaagccttt gaattgaaga atgaacaaac attgagagca gatccgatgt     1020
tcccaccaga atccaaacaa aaggactatg aagaaaattc ttgggattct gagagtctct     1080

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gtgagactgt ttcacagaag gatgtgtgtt tacccaaggc tacacatcaa aaagaaatag	1140
ataaaataaa tggaaaatta gaagagtctc ctaataaaga tggctctctg aaggctacct	1200
gcggaatgaa agtttctatt ccaactaaag ccttagaatt gaaggacatg caaactttca	1260
aagcagagcc tccggggaag ccctctgcct tcgagcctgc cactgaaatg caaaagtctg	1320
tcccaaataa agccttgga ttgaaaaatg aacaaacatt gagagcagat gagatactcc	1380
catcagaatc caaacaaaag gactatgaag aaagtctctg ggattctgag agtctctgtg	1440
agactgtttc acagaaggat gtgtgtttac ccaaggctrc rcacaaaaa gaaatagata	1500
aaataaatgg aaaattagaa gggctctcctg ttaaagatgg tcttctgaag gctaactgcg	1560
gaatgaaagt ttctattcca actaaagcct tagaattgat ggacatgcaa actttcaaa	1620
cagagcctcc cgagaagcca tctgccttcg agcctgccat tgaatgcaa aagtctgttc	1680
caataaaagc cttggaattg aagaatgaac aaacattgag agcagatgag atactcccat	1740
cagaatccaa acaaaaggac tatgaagaaa gttcttgga ttctgagagt ctctgtgaga	1800
ctgtttcaca gaaggatgtg tgtttaccca aggctrcrca tcaaaaagaa atagataaaa	1860
taaatggaaa attagaagag tctcctgata atgatggttt tctgaaggct ccctgcagaa	1920
tgaaagtttc tattccaact aaagccttag aattgatgga catgcaaact ttcaaagcag	1980
agcctcccg gaagccatct gccttcgagc ctgccattga aatgcaaaag tctgttccaa	2040
ataaagcctt ggaattgaag aatgaacaaa cattgagagc agatcagatg ttcccttcag	2100
aatcaaaaca aaagaasgtt gaagaaaatt cttgggattc tgagagtctc cgtgagactg	2160
tttcacagaa ggatgtgtgt gtacccaagg ctacacatca aaaagaaatg gataaaataa	2220
gtggaaaatt agaagattca actagcctat caaaaatctt ggatacagtt cattcttgtg	2280
aaagagcaag ggaacttcaa aaagatcact gtgaacaacg tacaggaaaa atggaacaaa	2340
tgaaaaagaa gttttgtgta ctgaaaaaga aactgtcaga agcaaaagaa ataaatcac	2400
agttagagaa ccaaaaagtt aaatgggaac aagagctctg cagtgtgaga ttgactttaa	2460
accaagaaga agagaagaga agaaatgccg atatattaaa tgaaaaaatt agggaagaat	2520
taggaagaat cgaagagcag cataggaaa agttagaagt gaaacaacaa cttgaacagg	2580
ctctcagaat acaagatata gaattgaaga gtgtagaag taatttgaat caggtttctc	2640
acactcatga aaatgaaaat tatctcttac atgaaaattg catgttgaaa aaggaaattg	2700
ccatgctaaa actggaaata gccacactga aacaccaata ccaggaaaag gaaaataaat	2760
actttgagga cattaagatt ttaaagaaa agaattgctga acttcagatg accctaaaac	2820
tgaaagagga atcattaact aaaagggcat ctcaatatag tgggcagctt aaagttctga	2880
tagctgagaa cacatgtctc acttctaata tgaaggaaaa acaagacaaa gaaatactag	2940
aggcagaaat tgaatcacac catcctagac tggcttctgc tgtacaagac catgatcaaa	3000
ttgtgacatc aagaaaaagt caagaacctg ctttcacat tgcaggagat gcttgtttgc	3060
aaagaaaaat gaatgttgat gtgagtagta cgatatataa caatgaggtg ctccatcaac	3120
cactttctga agctcaaag aaatccaaaa gcctaaaaat taatctcaat tatgcmggag	3180
atgctctaag agaaaatata ttggtttcag aacatgcaca aagagaccaa cgtgaaacac	3240
agtgtaaat gaaggagct gaacacatgt atcaaacga acaagataat gtgaacaaac	3300
acactgaaca gcaggagtct ctagatcaga aattatttca actacaaagc aaaaatatgt	3360

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ggcttcaaca gcaattagtt catgcacata agaaagctga caacaaaagc aagataacaa 3420
ttgatattca ttttcttgag aggaaaatgc aacatcatct cctaaaagag aaaaatgagg 3480
agatatattaa ttacaataac cattaataaa accgtatata tcaatatgaa aaagagaaaag 3540
cagaaacaga aaactcatga gagacaagca gtaagaaact tcttttggag aaacaacaga 3600
ccagatcttt actcacaact catgctagga ggccagtcct agcatcacct tatgttgaaa 3660
atcttaccaa tagtctgtgt caacagaata cttatttttag aagaaaaatt catgatttct 3720
tcctgaagcc tacagacata aaataacagt gtgaagaatt acttggtcac gaattgcata 3780
aagctgcaca ggattcccat ctaccctgat gatgcagcag acatcattca atccaaccag 3840
aatctcgctc tgtcactcag gctgg 3865

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<210> SEQ ID NO 475
<211> LENGTH: 1002
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 310, 429, 522
<223> OTHER INFORMATION: Xaa = Any Amino Acid

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<400> SEQUENCE: 475

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Met Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Ala Ala Lys
 1           5           10          15
Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Thr Pro Val Lys
          20          25          30
Thr Gly Cys Val Ala Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu
          35          40          45
Lys Gly Arg Ser Lys Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr
          50          55          60
Lys Ala Ser Ala Asn Asp Gln Arg Phe Pro Ser Glu Ser Lys Gln Glu
          65          70          75          80
Glu Asp Glu Glu Tyr Ser Cys Asp Ser Arg Ser Leu Phe Glu Ser Ser
          85          90          95
Ala Lys Ile Gln Val Cys Ile Pro Glu Ser Ile Tyr Gln Lys Val Met
          100         105         110
Glu Ile Asn Arg Glu Val Glu Glu Pro Pro Lys Lys Pro Ser Ala Phe
          115         120         125
Lys Pro Ala Ile Glu Met Gln Asn Ser Val Pro Asn Lys Ala Phe Glu
          130         135         140
Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Pro Met Phe Pro Pro Glu
          145         150         155         160
Ser Lys Gln Lys Asp Tyr Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu
          165         170         175
Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His
          180         185         190
Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asn
          195         200         205
Lys Asp Gly Leu Leu Lys Ala Thr Cys Gly Met Lys Val Ser Ile Pro
          210         215         220
Thr Lys Ala Leu Glu Leu Lys Asp Met Gln Thr Phe Lys Ala Glu Pro
          225         230         235         240
Pro Gly Lys Pro Ser Ala Phe Glu Pro Ala Thr Glu Met Gln Lys Ser

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245								250					255				
Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala		
			260				265						270				
Asp	Glu	Ile	Leu	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Asp	Tyr	Glu	Glu	Ser		
		275				280					285						
Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val		
		290				295					300						
Cys	Leu	Pro	Lys	Ala	Xaa	His	Gln	Lys	Glu	Ile	Asp	Lys	Ile	Asn	Gly		
			305	310						315			320				
Lys	Leu	Glu	Gly	Ser	Pro	Val	Lys	Asp	Gly	Leu	Leu	Lys	Ala	Asn	Cys		
			325				330						335				
Gly	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala	Leu	Glu	Leu	Met	Asp	Met		
			340				345						350				
Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu	Lys	Pro	Ser	Ala	Phe	Glu	Pro		
			355				360						365				
Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys		
			370	375						380							
Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Glu	Ile	Leu	Pro	Ser	Glu	Ser	Lys		
			385	390						395			400				
Gln	Lys	Asp	Tyr	Glu	Glu	Ser	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu		
			405				410						415				
Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Xaa	His	Gln	Lys		
			420				425						430				
Glu	Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asp	Asn	Asp		
			435	440						445							
Gly	Phe	Leu	Lys	Ala	Pro	Cys	Arg	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys		
			450	455						460							
Ala	Leu	Glu	Leu	Met	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu		
			465	470						475			480				
Lys	Pro	Ser	Ala	Phe	Glu	Pro	Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro		
			485				490						495				
Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Gln		
			500				505						510				
Met	Phe	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Xaa	Val	Glu	Glu	Asn	Ser	Trp		
			515				520			525							
Asp	Ser	Glu	Ser	Leu	Arg	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Val		
			530	535						540							
Pro	Lys	Ala	Thr	His	Gln	Lys	Glu	Met	Asp	Lys	Ile	Ser	Gly	Lys	Leu		
			545	550						555			560				
Glu	Asp	Ser	Thr	Ser	Leu	Ser	Lys	Ile	Leu	Asp	Thr	Val	His	Ser	Cys		
			565				570						575				
Glu	Arg	Ala	Arg	Glu	Leu	Gln	Lys	Asp	His	Cys	Glu	Gln	Arg	Thr	Gly		
			580				585						590				
Lys	Met	Glu	Gln	Met	Lys	Lys	Lys	Phe	Cys	Val	Leu	Lys	Lys	Lys	Leu		
			595				600			605							
Ser	Glu	Ala	Lys	Glu	Ile	Lys	Ser	Gln	Leu	Glu	Asn	Gln	Lys	Val	Lys		
			610	615						620							
Trp	Glu	Gln	Glu	Leu	Cys	Ser	Val	Arg	Leu	Thr	Leu	Asn	Gln	Glu	Glu		
			625	630						635			640				
Glu	Lys	Arg	Arg	Asn	Ala	Asp	Ile	Leu	Asn	Glu	Lys	Ile	Arg	Glu	Glu		
			645				650						655				

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Leu Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln
 660 665 670
 Gln Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val
 675 680 685
 Glu Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr
 690 695 700
 Leu Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys
 705 710 715 720
 Leu Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys
 725 730 735
 Tyr Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln
 740 745 750
 Met Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln
 755 760 765
 Tyr Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr
 770 775 780
 Ser Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile
 785 790 795 800
 Glu Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln
 805 810 815
 Ile Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly
 820 825 830
 Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Ile
 835 840 845
 Tyr Asn Asn Glu Val Leu His Gln Pro Leu Ser Glu Ala Gln Arg Lys
 850 855 860
 Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg
 865 870 875 880
 Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg Asp Gln Arg Glu Thr
 885 890 895
 Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr Gln Asn Glu Gln Asp
 900 905 910
 Asn Val Asn Lys His Thr Glu Gln Glu Ser Leu Asp Gln Lys Leu
 915 920 925
 Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln Gln Leu Val His
 930 935 940
 Ala His Lys Lys Ala Asp Asn Lys Ser Lys Ile Thr Ile Asp Ile His
 945 950 955 960
 Phe Leu Glu Arg Lys Met Gln His His Leu Leu Lys Glu Lys Asn Glu
 965 970 975
 Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile Tyr Gln Tyr
 980 985 990
 Glu Lys Glu Lys Ala Glu Thr Glu Asn Ser
 995 1000

<210> SEQ ID NO 476

<211> LENGTH: 356

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 476

aggtctgccc gaaatgtag gcacccaac tcaagtccca ggcccaggc atctttctg

60

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ccctgccttg cttggcccat ccagtcacagg cgcctggagc aagtgtctcag ctactttctcc	120
tgcactttga aagacccctc ccaactcctgg cctcacattt ctctgtgtga tccccactt	180
ctgggctctg ccaccccaca gtgggaaagg ccaccctaga aagaagtccg ctggcaccca	240
taggaagggg cctcaggagc aggaagggcc aggaccagaa ccttgcccac ggcaactgcc	300
ttcctgcctc tcccccttct cctctgtctt tgatctgtgt ttcaataaat taatgt	356

<210> SEQ ID NO 477

<211> LENGTH: 1876

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 477

atgacctgcg gatcaggatt tgggtgggccc gccttcagct gcatctcggc ctgcggggccg	60
cgcggggccc gctgtgcat caccgcccgc ccctaccgtg gcatctcctg ctaccgcccgc	120
ctcaccgggg gcttcggcag ccacagcgtg tgcggaggct ttcggggccg ctccctgcgga	180
cgcagcttcg gctaccgctc cgggggctg tgcgggccc gtcgcccatg catcaccacc	240
gtgtcgggta acgagagcct cctcacgccc ctcaacctgg agatcgaccc caacgcgcag	300
tgcgtgaagc aggagagaa ggagcagatc aagtcctca acagcagggt cgcggccttc	360
atcgacaagg tgcgcttctt ggagcagcag aacaaactgc tggagacaaa gctgcagttc	420
taccagaacc gcgaggtgtt ccagagcaac ctggagcccc tgtttgaggg ctacatcgag	480
actctgcggc gggaggccga gtgcgtggag gccgacagcg ggaggctggc ctcagagctt	540
aaccacgtgc aggaggtgct ggagggtac aagaagaagt atgaggagga ggtttctctg	600
agagcaacag ctgagaacga gtttgtggct ctgaagaagg atgtggactg cgcctacctc	660
cgcagtcag acctggaggc caacgtggag gccctgatcc aggagatcga ctctctgagg	720
cggctgtatg aggagagat ccgcattctc cagtcgcaca tctcagacac ctccgtgggt	780
gtcaagctgg acaacagccg ggacctgaac atggactgca tcattgccga gattaaggca	840
cagtatgacg acattgtcac ccgcagcccg gccgaggccg agtcctggta ccgcagcaag	900
tgtgaggaga tgaagccac ggtgatcagg cacggggaga ccctgcgccg caccaaggag	960
gagatcaatg agctgaaccg catgatccaa aggctgacgg ccgagggtga gaatgccaag	1020
tgccagaact ccaagctgga ggccgcgggtg gctcagtctg agcagcaggg tgaggcagcc	1080
ctcagtgatg ccgctgcaa gctggccgag ctggaggcg ccctgcagaa ggccaagcag	1140
gacatggcct gcctgatcag ggagtaccag gaggtgatga actccaagct gggcctggac	1200
atcgagatcg ccacctacag gcgcctgctg gagggcgagg agcagaggct atgtgaaggc	1260
attggggctg tgaatgtctg tgtcagcagc tcccggggcg gggctgtgtg cggggacctc	1320
tgcgtgtcag gctcccggcc agtgactggc agtgtctgca gcgctccgtg caacgggaac	1380
gtggcggtga gcaccggcct gtgtgcgccc tgcggccaat tgaacaccac ctgcggaggg	1440
ggttcctgcg gcgtgggctc ctgtgggtatc agtcacctgg gtgtggggtc ttgcggcagc	1500
agctgccgga aatgttaggc accccaactc aagtcacagg cccagggcat ctttcctgcc	1560
ctgccttgct tggcccatcc agtcacggcg cctggagcaa gtgctcagct acttctctctg	1620
cactttgaaa gaccctctcc actcctggcc tcacatttct ctgtgtgatc ccccacttct	1680
gggctctgcc accccacagt gggaaaggcc accctagaaa gaagtccgct ggcaccata	1740

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ggaaggggcc tcaggagcag gaagggccag gaccagaacc ttgcccacgg caactgcctt 1800
ctgcctctc cccttctctc tctgtcttg atctgtgttt caataaatta atgtagccaa 1860
aaaaaaaaa aaaaaa 1876

```

<210> SEQ ID NO 478

<211> LENGTH: 505

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 478

```

Met Thr Cys Gly Ser Gly Phe Gly Gly Arg Ala Phe Ser Cys Ile Ser
 1          5          10          15
Ala Cys Gly Pro Arg Pro Gly Arg Cys Cys Ile Thr Ala Ala Pro Tyr
 20          25          30
Arg Gly Ile Ser Cys Tyr Arg Gly Leu Thr Gly Gly Phe Gly Ser His
 35          40          45
Ser Val Cys Gly Gly Phe Arg Ala Gly Ser Cys Gly Arg Ser Phe Gly
 50          55          60
Tyr Arg Ser Gly Gly Val Cys Gly Pro Ser Pro Pro Cys Ile Thr Thr
 65          70          75          80
Val Ser Val Asn Glu Ser Leu Leu Thr Pro Leu Asn Leu Glu Ile Asp
 85          90          95
Pro Asn Ala Gln Cys Val Lys Gln Glu Glu Lys Glu Gln Ile Lys Ser
100          105          110
Leu Asn Ser Arg Phe Ala Ala Phe Ile Asp Lys Val Arg Phe Leu Glu
115          120          125
Gln Gln Asn Lys Leu Leu Glu Thr Lys Leu Gln Phe Tyr Gln Asn Arg
130          135          140
Glu Cys Cys Gln Ser Asn Leu Glu Pro Leu Phe Glu Gly Tyr Ile Glu
145          150          155          160
Thr Leu Arg Arg Glu Ala Glu Cys Val Glu Ala Asp Ser Gly Arg Leu
165          170          175
Ala Ser Glu Leu Asn His Val Gln Glu Val Leu Glu Gly Tyr Lys Lys
180          185          190
Lys Tyr Glu Glu Glu Val Ser Leu Arg Ala Thr Ala Glu Asn Glu Phe
195          200          205
Val Ala Leu Lys Lys Asp Val Asp Cys Ala Tyr Leu Arg Lys Ser Asp
210          215          220
Leu Glu Ala Asn Val Glu Ala Leu Ile Gln Glu Ile Asp Phe Leu Arg
225          230          235          240
Arg Leu Tyr Glu Glu Glu Ile Arg Ile Leu Gln Ser His Ile Ser Asp
245          250          255
Thr Ser Val Val Val Lys Leu Asp Asn Ser Arg Asp Leu Asn Met Asp
260          265          270
Cys Ile Ile Ala Glu Ile Lys Ala Gln Tyr Asp Asp Ile Val Thr Arg
275          280          285
Ser Arg Ala Glu Ala Glu Ser Trp Tyr Arg Ser Lys Cys Glu Glu Met
290          295          300
Lys Ala Thr Val Ile Arg His Gly Glu Thr Leu Arg Arg Thr Lys Glu
305          310          315          320
Glu Ile Asn Glu Leu Asn Arg Met Ile Gln Arg Leu Thr Ala Glu Val

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325					330					335					
Glu	Asn	Ala	Lys	Cys	Gln	Asn	Ser	Lys	Leu	Glu	Ala	Ala	Val	Ala	Gln
			340					345					350		
Ser	Glu	Gln	Gln	Gly	Glu	Ala	Ala	Leu	Ser	Asp	Ala	Arg	Cys	Lys	Leu
		355						360					365		
Ala	Glu	Leu	Glu	Gly	Ala	Leu	Gln	Lys	Ala	Lys	Gln	Asp	Met	Ala	Cys
		370						375					380		
Leu	Ile	Arg	Glu	Tyr	Gln	Glu	Val	Met	Asn	Ser	Lys	Leu	Gly	Leu	Asp
				385				390					395		400
Ile	Glu	Ile	Ala	Thr	Tyr	Arg	Arg	Leu	Leu	Glu	Gly	Glu	Glu	Gln	Arg
				405					410					415	
Leu	Cys	Glu	Gly	Ile	Gly	Ala	Val	Asn	Val	Cys	Val	Ser	Ser	Ser	Arg
			420					425						430	
Gly	Gly	Val	Val	Cys	Gly	Asp	Leu	Cys	Val	Ser	Gly	Ser	Arg	Pro	Val
			435					440					445		
Thr	Gly	Ser	Val	Cys	Ser	Ala	Pro	Cys	Asn	Gly	Asn	Val	Ala	Val	Ser
			450					455					460		
Thr	Gly	Leu	Cys	Ala	Pro	Cys	Gly	Gln	Leu	Asn	Thr	Thr	Cys	Gly	Gly
				465				470					475		480
Gly	Ser	Cys	Gly	Val	Gly	Ser	Cys	Gly	Ile	Ser	Ser	Leu	Gly	Val	Gly
				485					490					495	
Ser	Cys	Gly	Ser	Ser	Cys	Arg	Lys	Cys							
			500					505							

<210> SEQ ID NO 479
 <211> LENGTH: 221
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 22
 <223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 479

```

ggtccattcc tttcctcgcg tnggggtttc tctgtgtcag cgagcctcgg tacactgatt      60
tccgatcaaa agaatcatca tctttacctt gacttttcag ggaattactg aactttcttc      120
tcagaagata gggcacagcc attgccttgg cctcacttga aggggtctgca tttgggtcct      180
ctggtctctt gccaaagtct ccagccactc gagggagaaa t                             221
  
```

<210> SEQ ID NO 480
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: PCR primer

<400> SEQUENCE: 480

```

cggcgaattc accatgggaa caagagctct gcagtg                                36
  
```

<210> SEQ ID NO 481
 <211> LENGTH: 62
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: PCR primer

<400> SEQUENCE: 481

-continued

 cggcaagctt ttaatggtga tggatgatgt gtataacttc tgtttctgct ttctcttttt 60

ca 62

<210> SEQ ID NO 482

<211> LENGTH: 972

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 482

atgggaacaa gagctctgca gtgtgaggtt tctcacactc atgaaaatga aaattatctc 60

ttacatgaaa attgcatgtt gaaaaaggaa attgccatgc taaaactgga aatagccaca 120

ctgaaacacc aataccagga aaaggaaaat aaatactttg aggacattaa gatttttaaaa 180

gaaaagaatg ctgaacttca gatgacccta aaactgaaag aggaatcatt aactaaaagg 240

gcatctcaat atagtgggca gcttaaaagt ctgatagctg agaacacaat gctcacttct 300

aaattgaagg aaaaacaaga caaagaaata ctagaggcag aaattgaatc acaccatcct 360

agactggctt ctgctgtaca agaccatgat caaattgtga catcaagaaa aagtcaagaa 420

cctgctttcc acattgcagg agatgcttgt ttgcaaagaa aaatgaatgt tgatgtgagt 480

agtagcatat ataacaatga ggtgctccat caaccacttt ctgaagctca aaggaaatcc 540

aaaagcctaa aaattaatct caattatgcc ggagatgctc taagagaaaa tacattgggt 600

tcagaacatg cacaaagaga ccaacgtgaa acacagtgtc aaatgaagga agctgaacac 660

atgtatcaaa acgaacaaga taatgtgaac aaacacactg aacagcagga gtctctagat 720

cagaaattat ttcaactaca aagcaaaaat atgtgggttc aacagcaatt agttcatgca 780

cataagaaa ctgacaacaa aagcaagata acaattgata ttcattttct tgagaggaaa 840

atgcaacatc atctcctaaa agagaaaaat gaggagatat ttaattacaa taaccattta 900

aaaaaccgta tatatcaata tgaaaaagag aaagcagaaa cagaagttat acatcatcac 960

catcaccatt aa 972

<210> SEQ ID NO 483

<211> LENGTH: 323

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 483

Met Gly Thr Arg Ala Leu Gln Cys Glu Val Ser His Thr His Glu Asn
1 5 10 15Glu Asn Tyr Leu Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala
20 25 30Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys
35 40 45Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala
50 55 60Glu Leu Gln Met Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg
65 70 75 80Ala Ser Gln Tyr Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr
85 90 95Met Leu Thr Ser Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu
100 105 110

-continued

Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp
115 120 125

His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His
130 135 140

Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser
145 150 155 160

Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Ser Glu Ala
165 170 175

Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp
180 185 190

Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg Asp Gln
195 200 205

Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr Gln Asn
210 215 220

Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu Ser Leu Asp
225 230 235 240

Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln Gln
245 250 255

Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser Lys Ile Thr Ile
260 265 270

Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu Leu Lys Glu
275 280 285

Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile
290 295 300

Tyr Gln Tyr Glu Lys Glu Lys Ala Glu Thr Glu Val Ile His His His
305 310 315 320

His His His

<210> SEQ ID NO 484

<211> LENGTH: 1518

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 484

```

atgacctgcg gatcaggatt tgggtggcgc gccttcgct gcatctcggc ctgcgggccg      60
cgccccggcc gctgtgcat caccgccgcc cctaccgtg gcatctcctg ctaccgcggc      120
ctcaccgggg gcttcggcag ccacagcgtg tgcggaggct ttcgggccgg ctccctgcgga      180
cgcagcttcg gctaccgctc cgggggcgtg tgcgggccca gtcccccattg catcaccacc      240
gtgtcgggtca acgagagcct cctcacgccc ctcaacctgg agatcgaccc caacgcgcag      300
tgctgaagc aggaggagaa ggagcagatc aagtcctca acagcagggt cgcggccttc      360
atcgacaagg tgcgttctct ggagcagcag aacaaactgc tggagacaaa gctgcagttc      420
taccagaacc gcgagtgttg ccagagcaac ctggagcccc tgtttgaggg ctacatcgag      480
actctgcggc gggaggccga gtgcgtggag gccgacagcg ggaggctggc ctcagagcct      540
aaccacgtgc aggaggtgct ggagggttac aagaagaagt atgaggagga ggtttctctg      600
agagcaacag ctgagaacga gtttgtggct ctgaagaagg atgtggactg cgcctacctc      660
cgcaagtcag acctggaggc caacgtggag gccctgatcc aggagatcga ctctctgagg      720
cggctgtatg aggaggagat ccgcattctc cagtgcaca tctcagacac ctccgtggtt      780
gtcaagctgg acaacagccg ggacctgaac atggactgca tcattgccga gattaaggca      840

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cagtatgacg acattgtcac ccgcagccgg gccgaggccg agtcctggta ccgcagcaag    900
tgtgaggaga tgaagggcac ggtgatcagg cacggggaga ccctgcgccg caccaaggag    960
gagatcaatg agctgaaccg catgatccaa aggctgacgg ccgagggtgga gaatgccaag   1020
tgccagaact ccaagctgga ggccgcggtg gcccagtctg agcagcaggg tgaggcagcc   1080
ctcagtgatg cccgctgcaa gctggccgag ctggagggcg ccctgcagaa ggccaagcag   1140
gacatggcct gcctgatcag ggagtaccag gaggtgatga actccaagct gggcctggac   1200
atcgagatcg ccacctacag gcgcctgctg gagggcgagg agcagaggct atgtgaaggc   1260
attggggctg tgaatgtctg tgtcagcagc tcccggggcg gggtcgtgtg cggggacctc   1320
tgcgtgtcag gctcccgccc agtgactggc agtgtctgca gcgtccgtg caacgggaac   1380
gtggcggtga gcaccggcct gtgtgcgccc tgcggccaat tgaacaccac ctgcggaggg   1440
ggttcctgcg gcgtgggctc ctgtggtatc agctccctgg gtgtggggtc ttgcggcagc   1500
agctgccgga aatgttag                                     1518

```

<210> SEQ ID NO 485

<211> LENGTH: 505

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 485

```

Met Thr Cys Gly Ser Gly Phe Gly Gly Arg Ala Phe Arg Cys Ile Ser
 1          5          10          15
Ala Cys Gly Pro Arg Pro Gly Arg Cys Cys Ile Thr Ala Ala Pro Tyr
 20          25          30
Arg Gly Ile Ser Cys Tyr Arg Gly Leu Thr Gly Gly Phe Gly Ser His
 35          40          45
Ser Val Cys Gly Gly Phe Arg Ala Gly Ser Cys Gly Arg Ser Phe Gly
 50          55          60
Tyr Arg Ser Gly Gly Val Cys Gly Pro Ser Pro Pro Cys Ile Thr Thr
 65          70          75          80
Val Ser Val Asn Glu Ser Leu Leu Thr Pro Leu Asn Leu Glu Ile Asp
 85          90          95
Pro Asn Ala Gln Cys Val Lys Gln Glu Glu Lys Glu Gln Ile Lys Ser
100          105          110
Leu Asn Ser Arg Phe Ala Ala Phe Ile Asp Lys Val Arg Phe Leu Glu
115          120          125
Gln Gln Asn Lys Leu Leu Glu Thr Lys Leu Gln Phe Tyr Gln Asn Arg
130          135          140
Glu Cys Cys Gln Ser Asn Leu Glu Pro Leu Phe Glu Gly Tyr Ile Glu
145          150          155          160
Thr Leu Arg Arg Glu Ala Glu Cys Val Glu Ala Asp Ser Gly Arg Leu
165          170          175
Ala Ser Glu Leu Asn His Val Gln Glu Val Leu Glu Gly Tyr Lys Lys
180          185          190
Lys Tyr Glu Glu Glu Val Ser Leu Arg Ala Thr Ala Glu Asn Glu Phe
195          200          205
Val Ala Leu Lys Lys Asp Val Asp Cys Ala Tyr Leu Arg Lys Ser Asp
210          215          220
Leu Glu Ala Asn Val Glu Ala Leu Ile Gln Glu Ile Asp Phe Leu Arg

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225	230	235	240
Arg Leu Tyr Glu Glu Glu Ile Arg Ile Leu Gln Ser His Ile Ser Asp	245	250	255
Thr Ser Val Val Val Lys Leu Asp Asn Ser Arg Asp Leu Asn Met Asp	260	265	270
Cys Ile Ile Ala Glu Ile Lys Ala Gln Tyr Asp Asp Ile Val Thr Arg	275	280	285
Ser Arg Ala Glu Ala Glu Ser Trp Tyr Arg Ser Lys Cys Glu Glu Met	290	295	300
Lys Ala Thr Val Ile Arg His Gly Glu Thr Leu Arg Arg Thr Lys Glu	305	310	315
Glu Ile Asn Glu Leu Asn Arg Met Ile Gln Arg Leu Thr Ala Glu Val	325	330	335
Glu Asn Ala Lys Cys Gln Asn Ser Lys Leu Glu Ala Ala Val Ala Gln	340	345	350
Ser Glu Gln Gln Gly Glu Ala Ala Leu Ser Asp Ala Arg Cys Lys Leu	355	360	365
Ala Glu Leu Glu Gly Ala Leu Gln Lys Ala Lys Gln Asp Met Ala Cys	370	375	380
Leu Ile Arg Glu Tyr Gln Glu Val Met Asn Ser Lys Leu Gly Leu Asp	385	390	395
Ile Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu Gly Glu Glu Gln Arg	405	410	415
Leu Cys Glu Gly Ile Gly Ala Val Asn Val Cys Val Ser Ser Ser Arg	420	425	430
Gly Gly Val Val Cys Gly Asp Leu Cys Val Ser Gly Ser Arg Pro Val	435	440	445
Thr Gly Ser Val Cys Ser Ala Pro Cys Asn Gly Asn Val Ala Val Ser	450	455	460
Thr Gly Leu Cys Ala Pro Cys Gly Gln Leu Asn Thr Thr Cys Gly Gly	465	470	475
Gly Ser Cys Gly Val Gly Ser Cys Gly Ile Ser Ser Leu Gly Val Gly	485	490	495
Ser Cys Gly Ser Ser Cys Arg Lys Cys	500	505	

<210> SEQ ID NO 486

<211> LENGTH: 827

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 486

gcattctcca gtcgcacatc tcagacacct ccgtggttgt caagctggac aacagccggg	60
acctgaacat ggactgcacg attgcccaga ttaaggcaca gtatgacgac attgtcacc	120
gcagccgggc cgaggccgag tcctggtacc gcagcaagtg tgaggagatg aaggccacgg	180
tgatcaggca cggggagacc ctgcgccgca ccaaggagga gatcaatgag ctgaaccgca	240
tgatccaaag gctgacggcc gaggtggaga atgccaagtg ccagaactcc aagctggagg	300
ccgcggtggc ccagtctgag cagcagggtg aggcagccct cagtgatgcc cgctgcaagc	360
tgcccgagct ggaggcgcc ctgcagaagg ccaagcagga catggcctgc ctgatcagg	420
agtaccagga ggtgatgaac tccaagctgg gcctggacat cgagatcgcc acctacaggc	480

-continued

```
gcctgctgga gggcgaggag cagaggctat gtgaaggcat tggggctgtg aatgtctgtg 540
tcagcagctc ccggggcggg gtcgtgtgcg gggacctctg cgtgtcaggc tcccggccag 600
tgactggcag tgtctgcagc gctccgtgca acgggaacgt ggcggtgagc accggcctgt 660
gtgcgccctg cggccaattg aacaccacct gcggaggggg ttcctgcggc gtgggctcct 720
gtggtatcag ctcccgggt gtggggctct gcggcagcag ctgccggaaa tgttaggcac 780
cccaactcaa gtcccaggcc ccaggcatct ttcctgccct gccttgc 827
```

<210> SEQ ID NO 487

<211> LENGTH: 235

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 487

```
Met Asp Cys Ile Ile Ala Glu Ile Lys Ala Gln Tyr Asp Asp Ile Val
  1           5           10          15
Thr Arg Ser Arg Ala Glu Ala Glu Ser Trp Tyr Arg Ser Lys Cys Glu
          20          25          30
Glu Met Lys Ala Thr Val Ile Arg His Gly Glu Thr Leu Arg Arg Thr
          35          40          45
Lys Glu Glu Ile Asn Glu Leu Asn Arg Met Ile Gln Arg Leu Thr Ala
          50          55          60
Glu Val Glu Asn Ala Lys Cys Gln Asn Ser Lys Leu Glu Ala Ala Val
          65          70          75          80
Ala Gln Ser Glu Gln Gln Gly Glu Ala Ala Leu Ser Asp Ala Arg Cys
          85          90          95
Lys Leu Ala Glu Leu Glu Gly Ala Leu Gln Lys Ala Lys Gln Asp Met
          100         105         110
Ala Cys Leu Ile Arg Glu Tyr Gln Glu Val Met Asn Ser Lys Leu Gly
          115         120         125
Leu Asp Ile Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu Gly Glu Glu
          130         135         140
Gln Arg Leu Cys Glu Gly Ile Gly Ala Val Asn Val Cys Val Ser Ser
          145         150         155         160
Ser Arg Gly Gly Val Val Cys Gly Asp Leu Cys Val Ser Gly Ser Arg
          165         170         175
Pro Val Thr Gly Ser Val Cys Ser Ala Pro Cys Asn Gly Asn Val Ala
          180         185         190
Val Ser Thr Gly Leu Cys Ala Pro Cys Gly Gln Leu Asn Thr Thr Cys
          195         200         205
Gly Gly Gly Ser Cys Gly Val Gly Ser Cys Gly Ile Ser Ser Leu Gly
          210         215         220
Val Gly Ser Cys Gly Ser Ser Cys Arg Lys Cys
          225         230         235
```

<210> SEQ ID NO 488

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 488

```
Ser Leu Thr Lys Arg Ala Ser Gln Tyr
  1           5
```

-continued

<210> SEQ ID NO 489
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 489

tcattaacta aaagggcatc tcaatat 27

<210> SEQ ID NO 490
<211> LENGTH: 3288
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 490

atgaagttgc tgaatgtcct catgctggcg gccctctccc agcactgcta cgcaggctct 60
ggctgcccc tattggagaa tgtgatttcc aagacaatca atccacaagt gtctaagact 120
gaatacaaa aacttcttca agagttcata gacgacaatg ccactacaaa tgccatagat 180
gaattgaagg aatgttttct taaccaaacc gatgaaactc tgagcaatgt tgaggtgttt 240
atgcaattaa tatatgacag cagtctttgt gatttattta tgagtcccg aaagaaaca 300
tctgagaaat ttacgtgggc agcaaaagga agacctagga agatcgcatg ggagaaaaa 360
gaaacacctg taaagactgg atgctgggca agagtaacat ctaataaaac taaagttttg 420
gaaaaggaa gatctaagat gattgcatgt cctacaaaag aatcatctac aaaagcaagt 480
gccaatgac agaggttccc atcagaatcc aaacaagagg aagatgaaga atattcttgt 540
gattctcgga gtctctttga gagttctgca aagattcaag tgtgtatacc tgagtctata 600
tatcaaaaag taatggagat aaatagagaa gtagaagagc ctcctaagaa gccatctgcc 660
ttcaagcctg ccattgaaat gcaaaactct gttccaaata aagccttga attgaagaat 720
gaacaaacat tgagagcaga tccgatgttc ccaccagaat ccaacaaaa ggactatgaa 780
gaaaattctt gggattctga gagtctctgt gagactgttt cacagaagga tgtgtgttta 840
cccaaggcta cacatcaaaa agaaatagat aaaataaatg gaaaattaga agagtctcct 900
aataaagatg gtcttctgaa ggctacctgc ggaatgaaag tttctattcc aactaaagcc 960
ttagaattga aggacatgca aactttcaaa gcagagcctc cggggaagcc atctgccttc 1020
gagcctgcca ctgaaatgca aaagtctgtc ccaataaag ccttggaatt gaaaaatgaa 1080
caaacattga gagcagatga gatactccca tcagaatcca aacaaaagga ctatgaagaa 1140
agttcttggg attctgagag tctctgtgag actgtttcac agaaggatgt gtgtttaccc 1200
aaggctrcrc atcaaaaaga aatagataaa ataaatggaa aattagaagg gtctcctgtt 1260
aaagatggtc ttctgaaggc taactgcgga atgaaagttt ctattccaac taaagcotta 1320
gaattgatgg acatgcaaac tttcaaagca gagcctcccg agaagccatc tgccttcgag 1380
cctgccattg aaatgcaaaa gtctgttcca aataaagcct tgggaattgaa gaatgaacaa 1440
acattgagag cagatgagat actcccatca gaatccaaac aaaaggacta tgaagaaagt 1500
tcttgggatt ctgagagtct ctgtgagact gtttcacaga aggatgtgtg tttacccaag 1560
gctrcrcatc aaaaagaaat agataaaata aatggaaaat tagaagagtc tcctgataat 1620
gatggttttc tgaagctcc ctgcagaatg aaagtttcta ttccaactaa agccttagaa 1680
ttgatggaca tgcaaaactt caaagcagag cctcccgaga agccatctgc ctctgagcct 1740

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gccattgaaa tgcaaaagtc tgttccaaat aaagccttgg aattgaagaa tgaacaaaca 1800
ttgagagcag atcagatgtt cccttcagaa tcaaaacaaa agaasgttga agaaaattct 1860
tggtgattctg agagtctccg tgagactgtt tcacagaagg atgtgtgtgt acccaaggct 1920
acacatcaaa aagaaatgga taaaataagt ggaaaattag aagattcaac tagcctatca 1980
aaaaatcttg atacagtcca ttcttgtgaa agagcaaggg aacttcaaaa agatcactgt 2040
gaacaacgta caggaaaaat ggaacaaatg aaaaagaagt tttgtgtact gaaaaagaaa 2100
ctgtcagaag caaaagaaat aaaatcacag ttagagaacc aaaaagttaa atgggaacaa 2160
gagctctgca gtgtgagatt gactttaaac caagaagaag agaagagaag aaatgccgat 2220
atattaaatg aaaaaattag ggaagaatta ggaagaatcg aagagcagca taggaaagag 2280
ttagaagtga aacaacaact tgaacaggct ctcagaatac aagatataga attgaagagt 2340
gtagaaagta atttgaatca ggtttctcac actcatgaaa atgaaaatta tctcttacat 2400
gaaaattgca tgttgaaaaa ggaaattgcc atgctaaac tggaaatagc cactactgaaa 2460
caccaatacc aggaaaagga aaataaatatc tttgaggaca ttaagatttt aaaagaaaag 2520
aatgtctgaac ttcagatgac cctaaaactg aaagaggaat cattaactaa aagggcatct 2580
caatatagtg ggcagcttaa agttctgata gctgagaaca caatgctcac ttctaaattg 2640
aaggaaaaac aagacaaaga aatactagag gcagaaattg aatcacacca tcctagactg 2700
gcttctgctg tacaagacca tgatcaaatt gtgacatcaa gaaaaagtca agaacctgct 2760
ttccacattg caggagatgc ttgtttgcaa agaaaaatga atgttgatgt gagtagtacg 2820
atatataaca atgaggtgct ccatcaacca ctttctgaag ctcaaaggaa atccaaaagc 2880
ctaaaaatta atctcaatta tgcmggagat gctctaagag aaaatacatt ggtttcagaa 2940
catgcacaaa gagaccaacg tgaaacacag tgtcaaatga aggaagctga acacatgtat 3000
caaacgaac aagataatgt gaacaaacac actgaacagc aggagtctct agatcagaaa 3060
ttattttcaac tacaaagcaa aaatatgttg cttcaacagc aattagttca tgcacataag 3120
aaagctgaca acaaaagcaa gataacaatt gatattcatt ttcttgagag gaaaatgcaa 3180
catcatctcc taaaagagaa aatgaggag atatttaatt acaataacca tttaaaaaac 3240
cgtatatatc aatatgaaaa agagaaagca gaaacagaaa actcatga 3288

```

<210> SEQ ID NO 491

<211> LENGTH: 2232

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 491

```

atgaagtgc tgatgttct catgctggcg gccctctccc agcactgcta cgcaggctct 60
ggctgccct tattggagaa tgtgatttcc aagacaatca atccacaagt gtctaagact 120
gaatacaaa aacttcttca agagttcata gacgacaatg ccactacaaa tgccatagat 180
gaattgaag aatgttttct taaccaaagc gatgaaactc tgagcaatgt tgaggtgttt 240
atgcaattaa tatatgacag cagtctttgt gatttattta tgagtccgcg aaaagaaaca 300
tctgagaaat ttacgtgggc agcaaaagga agacctagga agatcgcatg ggagaaaaaa 360
gaaacacctg taaagactgg atgctgggca agagtaacat ctaataaaac taaagttttg 420
gaaaagga gatctaagat gattgcatgt cctacaaaag aatcatctac aaaagcaagt 480

```

-continued

```

gccaatgatac agagggtccc atcagaatcc aaacaagagg aagatgaaga atattcttgt 540
gattctcggga gtctcttttga gagttctgca aagattcaag tgtgtataacc tgagtctata 600
tatcaaaaag taatggagat aaatagagaa gtagaagagc ctcctaagaa gccatctgcc 660
ttcaagcctg ccattgaaat gcaaaactct gttccaaata aagcctttga attgaagaat 720
gaacaaacat tgagagcaga tccgatgttc ccaccagaat ccaacaaaaa ggactatgaa 780
gaaaattctt gggattctga gagtctctgt gagactgttt cacagaagga tgtgtgttta 840
cccaaggcta cacatcaaaa agaaatagat aaaataaatg gaaaattaga agagtctcct 900
aataaagatg gtcttctgaa ggctacctgc ggaatgaaag tttctattcc aactaaagcc 960
ttagaattga aggacatgca aactttcaaa gcagagcctc cggggaagcc atctgccttc 1020
gagcctgcca ctgaaatgca aaagtctgtc ccaataaag ccttggaatt gaaaaatgaa 1080
caaacattga gagcagatga gatactccca tcagaatcca acaaaaagga ctatgaagaa 1140
agttcttggg attctgagag tctctgtgag actgtttcac agaaggatgt gtgtttacc 1200
aaggctrcrc atcaaaaaga aatagataaa ataatggaa aattagaagg gtctcctgtt 1260
aaagatggtc ttctgaaggc taactgcgga atgaaagttt ctattccaac taaagcctta 1320
gaattgatgg acatgcaaac tttcaaagca gagcctcccg agaagccatc tgccttcgag 1380
cctgccattg aaatgcaaaa gtctgttcca aataaagcct tgggaattgaa gaatgaacaa 1440
acattgagag cagatgagat actcccata gaatccaaac aaaaggacta tgaagaaagt 1500
tcttgggatt ctgagagtct ctgtgagact gtttcacaga aggatgtgtg tttacccaag 1560
gctrcrcatc aaaaagaaat agataaaata aatggaaat tagaagagtc tctgtataat 1620
gatgtttttc tgaaggctcc ctgcagaatg aaagtttcta ttccaactaa agccttagaa 1680
ttgatggaca tgcaaaacttt caaagcagag cctcccaga agccatctgc cttcgagcct 1740
gccattgaaa tgcaaaagtc tgttccaaat aaagccttgg aattgaagaa tgaacaaaca 1800
ttgagagcag atcagatgtt cccttcagaa tcaaaacaaa agaasgttga agaaaattct 1860
tggtgattctg agagtctccg tgagactgtt tcacagaagg atgtgtgtgt acccaaggct 1920
acacatcaaa aagaaatgga taaaataagt ggaaaattag aagattcaac tagcctatca 1980
aaaaatcttg atacagtcca ttctgtgtaa agagcaaggg aacttcaaaa agatcactgt 2040
gaacaacgta caggaaaaat ggaacaaatg aaaaagaagt tttgtgtact gaaaaagaaa 2100
ctgtcagaag caaaagaaat aaaatcacag ttagagaacc aaaaagttaa atgggaacaa 2160
gagctctgca gtgtgaggtt tctcacactc atgaaaatga aaattatctc ttacatgaaa 2220
attgcatggt ga 2232

```

<210> SEQ ID NO 492

<211> LENGTH: 1233

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 492

```

atgaagttgc tgatgttct catgtggcg gccctctccc agcactgcta cgcaggctct 60
ggctgcccc tattggagaa tgtgatttcc aagacaatca atccacaagt gtctaagact 120
gaatacaaa aacttcttca agagttcata gacgacaatg ccactacaaa tgccatagat 180
gaattgaagg aatgttttct taaccaaagc gatgaaactc tgagcaatgt tgaggtgttt 240

```

-continued

```

atgcaattaa tatatgacag cagtctttgt gatttattta tgggaacaag agctctgcag    300
tgtgagggtt ctcacactca tgaaaatgaa aattatctct tacatgaaaa ttgcatgttg    360
aaaaaggaaa ttgccatgct aaaactggaa atagccacac tgaaacacca ataccaggaa    420
aaggaaaata aatactttga ggacattaag attttaaaag aaaagaatgc tgaacttcag    480
atgaccctaa aactgaaaga ggaatcatta actaaaaggg catctcaata tagtgggcag    540
cttaaagttc tgatagctga gaacacaatg ctcacttcta aattgaagga aaaacaagac    600
aaagaaatac tagaggcaga aattgaatca caccatccta gactggcttc tgctgtacaa    660
gaccatgac aaattgtgac atcaagaaaa agtcaagaac ctgctttcca cattgcagga    720
gatgcttggt tgcaaagaaa aatgaatggt gatgtgagta gtacgatata taacaatgag    780
gtgctccatc aaccactttc tgaagctcaa aggaaatcca aaagcctaaa aattaatctc    840
aattatgccg gagatgctct aagagaaaaat acattgggtt cagaacatgc acaaagagac    900
caacgtgaaa cacagtgtca aatgaaggaa gctgaacaca tgtatcaaaa cgaacaagat    960
aatgtgaaca aacacactga acagcaggag tctctagatc agaaattatt tcaactacaa   1020
agcaaaaata tgtggcttca acagcaatta gttcatgcac ataagaaagc tgacaacaaa   1080
agcaagataa caattgatat tcattttctt gagaggaaaa tgcaacatca tctcctaaaa   1140
gagaaaaaat aggagatatt taattacaat aaccatttaa aaaaccgtat atatcaatat   1200
gaaaaagaga aagcagaaac agaagttata taa                                1233

```

```

<210> SEQ ID NO 493
<211> LENGTH: 1095
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 403, 522, 615
<223> OTHER INFORMATION: Xaa = Any Amino Acid

```

```

<400> SEQUENCE: 493

```

```

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

```

-continued

Ala	Asn	Asp	Gln	Arg	Phe	Pro	Ser	Glu	Ser	Lys	Gln	Glu	Glu	Asp	Glu	165	170	175
Glu	Tyr	Ser	Cys	Asp	Ser	Arg	Ser	Leu	Phe	Glu	Ser	Ser	Ala	Lys	Ile	180	185	190
Gln	Val	Cys	Ile	Pro	Glu	Ser	Ile	Tyr	Gln	Lys	Val	Met	Glu	Ile	Asn	195	200	205
Arg	Glu	Val	Glu	Glu	Pro	Pro	Lys	Lys	Pro	Ser	Ala	Phe	Lys	Pro	Ala	210	215	220
Ile	Glu	Met	Gln	Asn	Ser	Val	Pro	Asn	Lys	Ala	Phe	Glu	Leu	Lys	Asn	225	230	235
Glu	Gln	Thr	Leu	Arg	Ala	Asp	Pro	Met	Phe	Pro	Pro	Glu	Ser	Lys	Gln	245	250	255
Lys	Asp	Tyr	Glu	Glu	Asn	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu	Thr	260	265	270
Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Thr	His	Gln	Lys	Glu	275	280	285
Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asn	Lys	Asp	Gly	290	295	300
Leu	Leu	Lys	Ala	Thr	Cys	Gly	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala	305	310	315
Leu	Glu	Leu	Lys	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Gly	Lys	325	330	335
Pro	Ser	Ala	Phe	Glu	Pro	Ala	Thr	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn	340	345	350
Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Glu	Ile	355	360	365
Leu	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Asp	Tyr	Glu	Glu	Ser	Ser	Trp	Asp	370	375	380
Ser	Glu	Ser	Leu	Cys	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	385	390	395
Lys	Ala	Xaa	His	Gln	Lys	Glu	Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	405	410	415
Gly	Ser	Pro	Val	Lys	Asp	Gly	Leu	Leu	Lys	Ala	Asn	Cys	Gly	Met	Lys	420	425	430
Val	Ser	Ile	Pro	Thr	Lys	Ala	Leu	Glu	Leu	Met	Asp	Met	Gln	Thr	Phe	435	440	445
Lys	Ala	Glu	Pro	Pro	Glu	Lys	Pro	Ser	Ala	Phe	Glu	Pro	Ala	Ile	Glu	450	455	460
Met	Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	465	470	475
Thr	Leu	Arg	Ala	Asp	Glu	Ile	Leu	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Asp	485	490	495
Tyr	Glu	Glu	Ser	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu	Thr	Val	Ser	500	505	510
Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Xaa	His	Gln	Lys	Glu	Ile	Asp	515	520	525
Lys	Ile	Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asp	Asn	Asp	Gly	Phe	Leu	530	535	540
Lys	Ala	Pro	Cys	Arg	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala	Leu	Glu	545	550	555

-continued

Leu	Met	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu	Lys	Pro	Ser	565	570	575
Ala	Phe	Glu	Pro	Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	580	585	590
Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Gln	Met	Phe	Pro	595	600	605
Ser	Glu	Ser	Lys	Gln	Lys	Xaa	Val	Glu	Glu	Asn	Ser	Trp	Asp	Ser	Glu	610	615	620
Ser	Leu	Arg	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Val	Pro	Lys	Ala	625	630	635
Thr	His	Gln	Lys	Glu	Met	Asp	Lys	Ile	Ser	Gly	Lys	Leu	Glu	Asp	Ser	645	650	655
Thr	Ser	Leu	Ser	Lys	Ile	Leu	Asp	Thr	Val	His	Ser	Cys	Glu	Arg	Ala	660	665	670
Arg	Glu	Leu	Gln	Lys	Asp	His	Cys	Glu	Gln	Arg	Thr	Gly	Lys	Met	Glu	675	680	685
Gln	Met	Lys	Lys	Lys	Phe	Cys	Val	Leu	Lys	Lys	Lys	Leu	Ser	Glu	Ala	690	695	700
Lys	Glu	Ile	Lys	Ser	Gln	Leu	Glu	Asn	Gln	Lys	Val	Lys	Trp	Glu	Gln	705	710	715
Glu	Leu	Cys	Ser	Val	Arg	Leu	Thr	Leu	Asn	Gln	Glu	Glu	Glu	Lys	Arg	725	730	735
Arg	Asn	Ala	Asp	Ile	Leu	Asn	Glu	Lys	Ile	Arg	Glu	Glu	Leu	Gly	Arg	740	745	750
Ile	Glu	Glu	Gln	His	Arg	Lys	Glu	Leu	Glu	Val	Lys	Gln	Gln	Leu	Glu	755	760	765
Gln	Ala	Leu	Arg	Ile	Gln	Asp	Ile	Glu	Leu	Lys	Ser	Val	Glu	Ser	Asn	770	775	780
Leu	Asn	Gln	Val	Ser	His	Thr	His	Glu	Asn	Glu	Asn	Tyr	Leu	Leu	His	785	790	795
Glu	Asn	Cys	Met	Leu	Lys	Lys	Glu	Ile	Ala	Met	Leu	Lys	Leu	Glu	Ile	805	810	815
Ala	Thr	Leu	Lys	His	Gln	Tyr	Gln	Glu	Lys	Glu	Asn	Lys	Tyr	Phe	Glu	820	825	830
Asp	Ile	Lys	Ile	Leu	Lys	Glu	Lys	Asn	Ala	Glu	Leu	Gln	Met	Thr	Leu	835	840	845
Lys	Leu	Lys	Glu	Glu	Ser	Leu	Thr	Lys	Arg	Ala	Ser	Gln	Tyr	Ser	Gly	850	855	860
Gln	Leu	Lys	Val	Leu	Ile	Ala	Glu	Asn	Thr	Met	Leu	Thr	Ser	Lys	Leu	865	870	875
Lys	Glu	Lys	Gln	Asp	Lys	Glu	Ile	Leu	Glu	Ala	Glu	Ile	Glu	Ser	His	885	890	895
His	Pro	Arg	Leu	Ala	Ser	Ala	Val	Gln	Asp	His	Asp	Gln	Ile	Val	Thr	900	905	910
Ser	Arg	Lys	Ser	Gln	Glu	Pro	Ala	Phe	His	Ile	Ala	Gly	Asp	Ala	Cys	915	920	925
Leu	Gln	Arg	Lys	Met	Asn	Val	Asp	Val	Ser	Ser	Thr	Ile	Tyr	Asn	Asn	930	935	940
Glu	Val	Leu	His	Gln	Pro	Leu	Ser	Glu	Ala	Gln	Arg	Lys	Ser	Lys	Ser	945	950	955
Leu	Lys	Ile	Asn	Leu	Asn	Tyr	Ala	Gly	Asp	Ala	Leu	Arg	Glu	Asn	Thr			

-continued

965					970					975					
Leu	Val	Ser	Glu	His	Ala	Gln	Arg	Asp	Gln	Arg	Glu	Thr	Gln	Cys	Gln
			980					985					990		
Met	Lys	Glu	Ala	Glu	His	Met	Tyr	Gln	Asn	Glu	Gln	Asp	Asn	Val	Asn
		995					1000					1005			
Lys	His	Thr	Glu	Gln	Gln	Glu	Ser	Leu	Asp	Gln	Lys	Leu	Phe	Gln	Leu
	1010					1015					1020				
Gln	Ser	Lys	Asn	Met	Trp	Leu	Gln	Gln	Gln	Leu	Val	His	Ala	His	Lys
1025					1030					1035					1040
Lys	Ala	Asp	Asn	Lys	Ser	Lys	Ile	Thr	Ile	Asp	Ile	His	Phe	Leu	Glu
			1045						1050					1055	
Arg	Lys	Met	Gln	His	His	Leu	Leu	Lys	Glu	Lys	Asn	Glu	Glu	Ile	Phe
			1060					1065						1070	
Asn	Tyr	Asn	Asn	His	Leu	Lys	Asn	Arg	Ile	Tyr	Gln	Tyr	Glu	Lys	Glu
		1075					1080					1085			
Lys	Ala	Glu	Thr	Glu	Asn	Ser									
	1090					1095									

<210> SEQ ID NO 494
 <211> LENGTH: 743
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: 403, 522, 615
 <223> OTHER INFORMATION: Xaa = Any Amino Acid

<400> SEQUENCE: 494

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

-continued

Arg	Glu	Val	Glu	Glu	Pro	Pro	Lys	Lys	Pro	Ser	Ala	Phe	Lys	Pro	Ala	210	215	220
Ile	Glu	Met	Gln	Asn	Ser	Val	Pro	Asn	Lys	Ala	Phe	Glu	Leu	Lys	Asn	225	230	235
Glu	Gln	Thr	Leu	Arg	Ala	Asp	Pro	Met	Phe	Pro	Pro	Glu	Ser	Lys	Gln	245	250	255
Lys	Asp	Tyr	Glu	Glu	Asn	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu	Thr	260	265	270
Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Thr	His	Gln	Lys	Glu	275	280	285
Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asn	Lys	Asp	Gly	290	295	300
Leu	Leu	Lys	Ala	Thr	Cys	Gly	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala	305	310	315
Leu	Glu	Leu	Lys	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Gly	Lys	325	330	335
Pro	Ser	Ala	Phe	Glu	Pro	Ala	Thr	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn	340	345	350
Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Glu	Ile	355	360	365
Leu	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Asp	Tyr	Glu	Glu	Ser	Ser	Trp	Asp	370	375	380
Ser	Glu	Ser	Leu	Cys	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	385	390	395
Lys	Ala	Xaa	His	Gln	Lys	Glu	Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	405	410	415
Gly	Ser	Pro	Val	Lys	Asp	Gly	Leu	Leu	Lys	Ala	Asn	Cys	Gly	Met	Lys	420	425	430
Val	Ser	Ile	Pro	Thr	Lys	Ala	Leu	Glu	Leu	Met	Asp	Met	Gln	Thr	Phe	435	440	445
Lys	Ala	Glu	Pro	Pro	Glu	Lys	Pro	Ser	Ala	Phe	Glu	Pro	Ala	Ile	Glu	450	455	460
Met	Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	465	470	475
Thr	Leu	Arg	Ala	Asp	Glu	Ile	Leu	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Asp	485	490	495
Tyr	Glu	Glu	Ser	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu	Thr	Val	Ser	500	505	510
Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Xaa	His	Gln	Lys	Glu	Ile	Asp	515	520	525
Lys	Ile	Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asp	Asn	Asp	Gly	Phe	Leu	530	535	540
Lys	Ala	Pro	Cys	Arg	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala	Leu	Glu	545	550	555
Leu	Met	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu	Lys	Pro	Ser	565	570	575
Ala	Phe	Glu	Pro	Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	580	585	590
Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Gln	Met	Phe	Pro	595	600	605

-continued

Ser Glu Ser Lys Gln Lys Xaa Val Glu Glu Asn Ser Trp Asp Ser Glu
 610 615 620
 Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala
 625 630 635 640
 Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser
 645 650 655
 Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala
 660 665 670
 Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu
 675 680 685
 Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser Glu Ala
 690 695 700
 Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln
 705 710 715 720
 Glu Leu Cys Ser Val Arg Phe Leu Thr Leu Met Lys Met Lys Ile Ile
 725 730 735
 Ser Tyr Met Lys Ile Ala Cys
 740

<210> SEQ ID NO 495

<211> LENGTH: 410

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 495

Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Ser Gln His Cys
 1 5 10 15
 Tyr Ala Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr
 20 25 30
 Ile Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu
 35 40 45
 Phe Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu
 50 55 60
 Cys Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe
 65 70 75 80
 Met Gln Leu Ile Tyr Asp Ser Ser Leu Cys Asp Leu Phe Met Gly Thr
 85 90 95
 Arg Ala Leu Gln Cys Glu Val Ser His Thr His Glu Asn Glu Asn Tyr
 100 105 110
 Leu Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys
 115 120 125
 Leu Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys
 130 135 140
 Tyr Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln
 145 150 155 160
 Met Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln
 165 170 175
 Tyr Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr
 180 185 190
 Ser Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile
 195 200 205
 Glu Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln
 210 215 220

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Ile Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly
225                230                235                240

Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Ile
                245                250                255

Tyr Asn Asn Glu Val Leu His Gln Pro Leu Ser Glu Ala Gln Arg Lys
                260                265                270

Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg
                275                280                285

Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg Asp Gln Arg Glu Thr
                290                295                300

Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr Gln Asn Glu Gln Asp
305                310                315                320

Asn Val Asn Lys His Thr Glu Gln Gln Glu Ser Leu Asp Gln Lys Leu
                325                330                335

Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln Gln Leu Val His
                340                345                350

Ala His Lys Lys Ala Asp Asn Lys Ser Lys Ile Thr Ile Asp Ile His
                355                360                365

Phe Leu Glu Arg Lys Met Gln His His Leu Leu Lys Glu Lys Asn Glu
                370                375                380

Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile Tyr Gln Tyr
385                390                395                400

Glu Lys Glu Lys Ala Glu Thr Glu Val Ile
                405                410

```

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<210> SEQ ID NO 496
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 496

```

```

Ile Asp Glu Leu Lys Glu Cys Phe Leu Asn Gln Thr Asp Glu Thr Leu
  1              5              10              15

Ser Asn Val Glu
              20

```

```

<210> SEQ ID NO 497
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 497

```

```

Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu Cys Phe Leu Asn Gln
  1              5              10              15

```

```

<210> SEQ ID NO 498
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 498

```

```

Ser Gln His Cys Tyr Ala Gly Ser Gly Cys Pro Leu Leu Glu Asn Val
  1              5              10              15

Ile Ser Lys Thr Ile
              20

```

-continued

<210> SEQ ID NO 499
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 499

Glu Tyr Lys Glu Leu Leu Gln Glu Phe Ile Asp Asp Asn Ala Thr Thr
1 5 10 15

Asn Ala Ile Asp
20

<210> SEQ ID NO 500
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 500

Lys Leu Leu Met Val Leu Met Leu Ala
1 5

<210> SEQ ID NO 501
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 501

Gln Glu Phe Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile
1 5 10

<210> SEQ ID NO 502
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 502

Leu Lys Glu Cys Phe Leu Asn Gln Thr Asp Glu Thr Leu
1 5 10

<210> SEQ ID NO 503
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 503

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

Tyr Ala Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr
20 25 30

Ile Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu
35 40 45

Phe Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu
50 55 60

Cys Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe
65 70 75 80

Met Gln Leu Ile Tyr Asp Ser Ser Leu Cys Asp Leu Phe
85 90

<210> SEQ ID NO 504
<211> LENGTH: 1964

-continued

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 504

```

gcatgctcga cgccccatgt gctgaaaggg cgaggagcct cctgcggcgg ccctgtgtc      60
cctgcctcta cctgcgcacc tgcattgttt caacccccgg gagaacacct ggcggccct      120
gaccaggtg cccgaggagg ccccgcttcg gggctgcggt ctctgcacca tgcacaacta      180
cctgtttctg gcggggggca tccgtggctc cggtgccaag gccgtctgct ccaacgaggt      240
cttctgctac aacctcttga ccaacatctg gagccaggtt cgcccatgc agcaggcccg      300
agccagctc aagctggttg ccctggacgg gctgctctat gccatcggtg gcgaatgcct      360
gtacagcatg gagtgtctac acccgcgaa acacgccttg accccacgcg cgccactccc      420
cgaggcacc ttccctgttg cccacgaggg tgtggcctgc cgtggggaca tctacgtcac      480
cgggggtcac ctctcttacc gcctgctcag gtacagcccc gtgaaggatg cttgggacga      540
gtgcccatac agtgccagcc accggcgctc cagcgacatc gttgcaactg ggggcttcct      600
gtaccgcttc gacctgctgc ggggcgtggg cgccgcccgt atcgctaca acacagtgc      660
cggctccttg agcagggtg cctccctgcc cctgcccgcc cccgccccac tgcgtgcac      720
caccctgggc aacaccattt actgcctcaa ccccaggtc actgccacct tcacggtctc      780
tggggggact gcccagttcc aggccaaagg gctgcagccc ttccccttg ggagcaccgg      840
ggtcctcagt ccattcatcc tgaactctgc ccctgaggac cggctgcaga cctcaactctg      900
agtggcaggc agagaaccaa agctgcttcg ctgctctcca gggagacct cctgggatgg      960
gcctgagagg ccggggctca ggaaggggc tgggatcgga acttcctgct cttgtttctg      1020
gacaactttc cccttctgct ttaaagggtg tcgattattt tgaagcccag actccctcag      1080
cctctttctg ccctcactc cacaccaga ctgtttcctg actcaattcc gtacctactt      1140
acagaccctc tcagcttgct gacaccccc tgtctgtggg actccctatt ccttagagcc      1200
agggactgat gcgtctccac agacaaggac ttggctcgtc ggagctctgc tgagccgaga      1260
gaggaggggg tagaaaacat tcacacttcc tatgctctgt cagcaggaca gggagcaaaa      1320
acgtccccag gcaacgccct cgctctggg actttctgcc tgtcctaagg cctcccagg      1380
taccaccccc gtagctatct gggctgtttt ggcactgtgg attctcaagg gcctagaacc      1440
cttgctctg aaactggtcc gctggtgag ccctgctgtc tgcagctcct gcccataccc      1500
ccagcccaca ccaggccagg cccactccgg gctcaccacc ctctgcagcc ttgtggggct      1560
ctccagccc ctccagaagc ccaccocact tctcgccaac ccccgatctc taaatgaggc      1620
ctgagcgtca ccctagtctt gccccttttt agctgtgtag acttgacga gacatttgac      1680
ttccctttct ccttgtctat aaaatgtgga cagtggacgt ctgtcaccca agagagttgt      1740
gggagacaag atcacagcta tgagcacctc gcacggtgtc caggatgcac agcacaatcc      1800
atgatgcgtt ttctccctt acgcactttg aaacccatgc tagaaaagtg aatacatctg      1860
actgtgctcc actccaacct ccagcctgga tgtccctgtc tgggcccttt ttctgttttt      1920
tattctatgt tcagaccac tggcacaaa tacatttta ttca                        1964

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<210> SEQ ID NO 505

<211> LENGTH: 732

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

-continued

<400> SEQUENCE: 505

```

atgcacaact acctgtttct ggcggggggc atccgtggct ccggtgccaa ggccgtctgc    60
tccaacgagg tcttctgcta caaccctctg accaaccatct ggagccaggt tcggcccatg   120
cagcaggccc gagcccagct caagctgggt gccctggacg ggctgctcta tgccatcggg   180
ggcgaatgcc tgtacagcat ggagtgtac gacccgcgaa cagacgcctg gacccacgc    240
gcgcactcc ccgcaggcac cttccctgtg gccacgagg ctgtggcctg ccgtggggac    300
atctacgtca ccgggggtca cctcttctac cgcctgtctc ggtacagccc cgtgaaggat   360
gcttgggacg agtgccata cagtgcacg caccggcgtt ccagcgacat cgttgactg    420
gggggcttcc tgtaccgctt cgacctgtg cggggcgctg gcgccgcctg gatgcgctac   480
aacacagtga ccggctcctg gagcagggt gcctccctgc ccctgccgcg ccccgcccca   540
ctgcgtgca ccacctggg caacaccatt tactgcctca accccaggt cactgccacc    600
ttcacggtct ctggggggac tgcccagttc caggccaagg agctgcagcc cttccccttg   660
gggagcaccg gggtcctcag tccattcatc ctgactctgc cccctgagga ccggctgcag   720
acctcactct ga                                     732

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<210> SEQ ID NO 506

<211> LENGTH: 729

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 506

```

atgcacaact acctgtttct ggcggggggc atccgtggct ccggtgccaa ggccgtctgc    60
tccaacgagg tcttctgcta caaccctctg accaaccatct ggagccaggt tcggcccatg   120
cagcaggccc gagcccagct caagctgggt gccctggacg ggctgctcta tgccatcggg   180
ggcgaatgcc tgtacagcat ggagtgtac gacccgcgaa cagacgcctg gacccacgc    240
gcgcactcc ccgcaggcac cttccctgtg gccacgagg ctgtggcctg ccgtggggac    300
atctacgtca ccgggggtca cctcttctac cgcctgtctc ggtacagccc cgtgaaggat   360
gcttgggacg agtgccata cagtgcacg caccggcgtt ccagcgacat cgttgactg    420
gggggcttcc tgtaccgctt cgacctgtg cggggcgctg gcgccgcctg gatgcgctac   480
aacacagtga ccggctcctg gagcagggt gcctccctgc ccctgccgcg ccccgcccca   540
ctgcgtgca ccacctggg caacaccatt tactgcctca accccaggt cactgccacc    600
ttcacggtct ctggggggac tgcccagttc caggccaagg agctgcagcc cttccccttg   660
gggagcaccg gggtcctcag tccattcatc ctgactctgc cccctgagga ccggctgcag   720
acctcactc                                     729

```

<210> SEQ ID NO 507

<211> LENGTH: 243

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 507

```

Met His Asn Tyr Leu Phe Leu Ala Gly Gly Ile Arg Gly Ser Gly Ala
 1         5         10        15
Lys Ala Val Cys Ser Asn Glu Val Phe Cys Tyr Asn Pro Leu Thr Asn
 20        25        30

```

-continued

```

Ile Trp Ser Gln Val Arg Pro Met Gln Gln Ala Arg Ala Gln Leu Lys
   35                40                45
Leu Val Ala Leu Asp Gly Leu Leu Tyr Ala Ile Gly Gly Glu Cys Leu
   50                55                60
Tyr Ser Met Glu Cys Tyr Asp Pro Arg Thr Asp Ala Trp Thr Pro Arg
   65                70                75                80
Ala Pro Leu Pro Ala Gly Thr Phe Pro Val Ala His Glu Ala Val Ala
                85                90                95
Cys Arg Gly Asp Ile Tyr Val Thr Gly Gly His Leu Phe Tyr Arg Leu
   100               105               110
Leu Arg Tyr Ser Pro Val Lys Asp Ala Trp Asp Glu Cys Pro Tyr Ser
   115               120               125
Ala Ser His Arg Arg Ser Ser Asp Ile Val Ala Leu Gly Gly Phe Leu
   130               135               140
Tyr Arg Phe Asp Leu Leu Arg Gly Val Gly Ala Ala Val Met Arg Tyr
   145               150               155               160
Asn Thr Val Thr Gly Ser Trp Ser Arg Ala Ala Ser Leu Pro Leu Pro
   165               170               175
Ala Pro Ala Pro Leu Arg Cys Thr Thr Leu Gly Asn Thr Ile Tyr Cys
   180               185               190
Leu Asn Pro Gln Val Thr Ala Thr Phe Thr Val Ser Gly Gly Thr Ala
   195               200               205
Gln Phe Gln Ala Lys Glu Leu Gln Pro Phe Pro Leu Gly Ser Thr Gly
   210               215               220
Val Leu Ser Pro Phe Ile Leu Thr Leu Pro Pro Glu Asp Arg Leu Gln
   225               230               235               240
Thr Ser Leu

```

<210> SEQ ID NO 508

<211> LENGTH: 158

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 508

```

Met His Asn Tyr Leu Phe Leu Ala Gly Gly Ile Arg Gly Ser Gly Ala
   1                5                10                15
Lys Ala Val Cys Ser Asn Glu Val Phe Cys Tyr Asn Pro Leu Thr Asn
                20                25                30
Ile Trp Ser Gln Val Arg Pro Met Gln Gln Ala Arg Ala Gln Leu Lys
   35                40                45
Leu Val Ala Leu Asp Gly Leu Leu Tyr Ala Ile Gly Gly Glu Cys Leu
   50                55                60
Tyr Ser Met Glu Cys Tyr Asp Pro Arg Thr Asp Ala Trp Thr Pro Arg
   65                70                75                80
Ala Pro Leu Pro Ala Gly Thr Phe Pro Val Ala His Glu Ala Val Ala
                85                90                95
Cys Arg Gly Asp Ile Tyr Val Thr Gly Gly His Leu Phe Tyr Arg Leu
   100               105               110
Leu Arg Tyr Ser Pro Val Lys Asp Ala Trp Asp Glu Cys Pro Tyr Ser
   115               120               125
Ala Ser His Arg Arg Ser Ser Asp Ile Val Ala Leu Gly Gly Phe Leu
   130               135               140

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-continued

Tyr Arg Phe Asp Leu Leu Arg Gly Val Gly Ala Ala Val Met
145 150 155

<210> SEQ ID NO 509
<211> LENGTH: 85
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 509

Arg Tyr Asn Thr Val Thr Gly Ser Trp Ser Arg Ala Ala Ser Leu Pro
1 5 10 15
Leu Pro Ala Pro Ala Pro Leu Arg Cys Thr Thr Leu Gly Asn Thr Ile
20 25 30
Tyr Cys Leu Asn Pro Gln Val Thr Ala Thr Phe Thr Val Ser Gly Gly
35 40 45
Thr Ala Gln Phe Gln Ala Lys Glu Leu Gln Pro Phe Pro Leu Gly Ser
50 55 60
Thr Gly Val Leu Ser Pro Phe Ile Leu Thr Leu Pro Pro Glu Asp Arg
65 70 75 80
Leu Gln Thr Ser Leu
85

<210> SEQ ID NO 510
<211> LENGTH: 732
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 510

atgcgacccc agggccccgc cgcctccccg cagcggctcc gcggcctcct gctgctcctg 60
ctgctgcagc tgccccgcgc gtcgagcgcc tctgagatcc ccaaggggaa gcaaaaggcg 120
cagctccggc agagggaggt ggtggacctg tataatggaa tgtgcttaca agggccagca 180
ggagtgcttg gtcgagacgg gagccctggg gccaatgtta ttccgggtac acctgggatc 240
ccaggtcggg atggattcaa aggagaaaag ggggaatgtc tgagggaaag ctttgaggag 300
tcctggacac ccaactacaa gcagtgttca tggagtccat tgaattatgg catagatctt 360
gggaaaattg cggagtgtac atttacaag atgcgttcaa atagtgtctt aagagttttg 420
ttcagtggct cacttcggct aaaatgcaga aatgcatgct gtcagcgttg gtatttcaca 480
ttcaatggag ctgaatgttc aggacctctt cccattgaag ctataattta ttggaccaa 540
ggaagccctg aaatgaattc aacaattaat attcatcgca cttcttctgt ggaaggactt 600
tgtgaaggaa ttggtgctgg attagtggat gttgctatct gggttggcac ttgttcagat 660
tacccaaaag gagatgcttc tactggatgg aattcagttt ctgcacatcat tattgaagaa 720
ctaccaaatt aa 732

<210> SEQ ID NO 511
<211> LENGTH: 729
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 511

atgcgacccc agggccccgc cgcctccccg cagcggctcc gcggcctcct gctgctcctg 60
ctgctgcagc tgccccgcgc gtcgagcgcc tctgagatcc ccaaggggaa gcaaaaggcg 120

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cagctccggc agagggaggt ggtggacctg tataatggaa tgtgcttaca agggccagca	180
ggagtgcctg gtcgagacgg gagccctggg gccaatgtta ttccgggtac acctgggatc	240
ccaggtcggg atggattcaa aggagaaaag ggggaatgtc tgagggaaag ctttgaggag	300
tcctggacac ccaactacaa gcagtgttca tggagtcat tgaattatgg catagatctt	360
gggaaaattg cggagtgtac atttacaag atgcgttcaa atagtgtctt aagagttttg	420
ttcagtggct cacttcggct aaaatgcaga aatgcatgct gtcagcgttg gtatttcaca	480
ttcaatggag ctgaatgttc aggacctctt cccattgaag ctataattta ttggaccaaa	540
ggaagccctg aaatgaattc aacaattaat attcatcgca cttcttctgt ggaaggactt	600
tgtgaaggaa ttggtgctgg attagtggat gttgctatct gggttgccac ttgttcagat	660
tacccaaaag gagatgcttc tactggatgg aattcagttt ctcgcatcat tattgaagaa	720
ctacaaaaa	729

<210> SEQ ID NO 512

<211> LENGTH: 837

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 512

atgcagcctg cggcggcctc ggagcggcgg ggagcagacg ctgaccacgt tcctctcctc	60
ggtctcctcc gcctccagct ccgcgctgcc cggcagccgg gagccatgcg accccagggc	120
cccgcgcct ccccgagcgg gctccgcggc ctctgctgc tcctgctgct gcagctgccc	180
gcgcgctcga gcgcctctga gatccccaag gggaaagcaa aggcgcagct ccggcagagg	240
gaggtggtgg acctgtataa tggaatgtgc ttacaagggc cagcaggagt gcctggtcga	300
gacgggagcc ctggggccaa tgttattccg ggtacacctg ggatcccagg tcgggatgga	360
ttcaaaggag aaaaggggga atgtctgagg gaaagctttg aggagtcttg gacacccaac	420
tacaagcagt gtcatggag ttcattgaat tatggcatag atcttgggaa aattgcggag	480
tgtacattta caaagatgcg ttcaaatagt gctctaagag ttttgttcag tggctcactt	540
cggctaaaat gcagaaatgc atgctgtcag cgttggtatt tcacattcaa tggagctgaa	600
tgttcaggac ctcttcccat tgaagctata atttatttgg accaaggaag ccctgaaatg	660
aattcaacaa ttaatatcca tcgcacttct tctgtggaag gactttgtga aggaattggt	720
gctgatttag tggatgttgc tatctgggtt ggcacttggt cagattaccc aaaaggagat	780
gcttctactg gatggaattc agtttctcgc atcattattg aagaactacc aaaataa	837

<210> SEQ ID NO 513

<211> LENGTH: 837

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 513

atgcagcctg cggcggcctc ggagcggcgg ggagcagacg ctgaccacgt tcctctcctc	60
ggtctcctcc gcctccagct ccgcgctgcc cggcagccgg gagccatgcg accccagggc	120
cccgcgcct ccccgagcgg gctccgcggc ctctgctgc tcctgctgct gcagctgccc	180
gcgcgctcga gcgcctctga gatccccaag gggaaagcaa aggcgcagct ccggcagagg	240
gaggtggtgg acctgtataa tggaatgtgc ttacaagggc cagcaggagt gcctggtcga	300

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gacgggagcc ctggggccaa tgttattccg ggtacacctg ggatcccagg tcgggatgga 360
ttcaaaggag aaaaggggga atgtctgagg gaaagctttg aggagtcctg gacacccaac 420
tacaagcagt gttcatggag ttcatatgaat tatggcatag atcttgggaa aattgcggag 480
tgtacattta caaagatgcg ttcaaatagt gctctaagag ttttggtcag tggetcactt 540
cggctaaaaat gcagaaatgc atgctgtcag cgttggtatt tcacattcaa tggagctgaa 600
tgttcaggac ctcttcccat tgaagctata atttatttgg accaaggaag ccctgaaatg 660
aattcaacaa ttaatatattca tcgcacttct tctgtggaag gactttgtga aggaattggt 720
gctggattag tggatgttgc tatctgggtt ggcacttggt cagattaccc aaaaggagat 780
gcttctactg gatggaattc agtttctcgc atcattattg aagaactacc aaaataa 837

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<210> SEQ ID NO 514

<211> LENGTH: 243

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 514

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Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly Leu
 1             5             10             15
Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala Ser Glu
 20             25             30
Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg Glu Val Val
 35             40             45
Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val Pro Gly
 50             55             60
Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro Gly Thr Pro Gly Ile
 65             70             75             80
Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu Arg Glu
 85             90             95
Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser Trp Ser
100            105            110
Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys Thr Phe
115            120            125
Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser Gly Ser
130            135            140
Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr
145            150            155            160
Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile
165            170            175
Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His
180            185            190
Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu
195            200            205
Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly
210            215            220
Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
225            230            235            240
Leu Pro Lys

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<210> SEQ ID NO 515

<211> LENGTH: 278

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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 515

Met Gln Pro Ala Ala Ala Ser Glu Arg Gly Gly Ala Asp Ala Asp His
 5 10 15

Val Pro Leu Leu Gly Leu Leu Arg Leu Gln Leu Arg Ala Ala Arg Gln
 20 25 30

Pro Gly Ala Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu
 35 40 45

Arg Gly Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser
 50 55 60

Ala Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 65 70 75 80

Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly
 85 90 95

Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro Gly Thr
 100 105 110

Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys
 115 120 125

Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys
 130 135 140

Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu
 145 150 155 160

Cys Thr Phe Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe
 165 170 175

Ser Gly Ser Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp
 180 185 190

Tyr Phe Thr Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu
 195 200 205

Ala Ile Ile Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile
 210 215 220

Asn Ile His Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly
 225 230 235 240

Ala Gly Leu Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr
 245 250 255

Pro Lys Gly Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile
 260 265 270

Ile Glu Glu Leu Pro Lys
 275

<210> SEQ ID NO 516
<211> LENGTH: 197
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 516

Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly Leu
 5 10 15

Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala Ser Glu
 20 25 30

Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg Glu Val Val
 35 40 45

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Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val Pro Gly
  50          55          60

Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro Gly Thr Pro Gly Ile
  65          70          75          80

Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu Arg Glu
          85          90          95

Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser Trp Ser
          100          105          110

Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys Thr Phe
          115          120          125

Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser Gly Ser
          130          135          140

Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr
          145          150          155          160

Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile
          165          170          175

Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His
          180          185          190

Arg Thr Ser Ser Val
          195

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<210> SEQ ID NO 517

<211> LENGTH: 232

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 517

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Met Gln Pro Ala Ala Ala Ser Glu Arg Gly Gly Ala Asp Ala Asp His
          5          10          15

Val Pro Leu Leu Gly Leu Leu Arg Leu Gln Leu Arg Ala Ala Arg Gln
          20          25          30

Pro Gly Ala Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu
          35          40          45

Arg Gly Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser
          50          55          60

Ala Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
          65          70          75          80

Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly
          85          90          95

Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro Gly Thr
          100          105          110

Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys
          115          120          125

Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys
          130          135          140

Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu
          145          150          155          160

Cys Thr Phe Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe
          165          170          175

Ser Gly Ser Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp
          180          185          190

Tyr Phe Thr Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu
          195          200          205

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Ala Ile Ile Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile
210 215 220

Asn Ile His Arg Thr Ser Ser Val
225 230

<210> SEQ ID NO 518
<211> LENGTH: 46
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 518

Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp Val Ala Ile
5 10 15

Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp Ala Ser Thr Gly
20 25 30

Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu Leu Pro Lys
35 40 45

<210> SEQ ID NO 519
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 519

Cys Ser Asp Tyr Pro Lys Gly Asp Ala Ser Thr Gly Trp Asn Ser Val
5 10 15

Ser Arg Ile Ile Ile Glu Glu Leu Pro Lys
20 25

<210> SEQ ID NO 520
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 520

aaaaatgagg agatatttaa ttacaataac catttaaaaa accgtatata tcaatatgaa 60

<210> SEQ ID NO 521
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 521

atgcaacatc atctcctaaa agagaaaaat gaggagatat ttaattacaa taaccattta 60

<210> SEQ ID NO 522
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 522

gacaacaaaa gcaagataac aattgatatt cattttcttg agaggaaaat gcaacatcat 60

<210> SEQ ID NO 523
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 523

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aaaaatatgt ggcttcaaca gcaattagtt catgcacata agaaagctga caacaaaagc 60

<210> SEQ ID NO 524
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 524

gatcagaaat tatttcaact acaaagcaaa aatatgtggc ttcaacagca attagttcat 60

gca 63

<210> SEQ ID NO 525
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 525

actgaacagc aggagtctct agatcagaaa ttatttcaac taaaagcaa aaatatgtgg 60

<210> SEQ ID NO 526
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 526

gctcaaagga aatccaaaag ctaaaaatt aatctcaatt atgccggaga tgctctaaga 60

gaa 63

<210> SEQ ID NO 527
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 527

agtacgatat ataacaatga ggtgctccat caaccacttt ctgaagctca aaggaaatcc 60

<210> SEQ ID NO 528
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 528

agaaaaatga atgttgatgt gagtagtacg atatataaca atgaggtgct ccatcaacca 60

<210> SEQ ID NO 529
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 529

attgcaggag atgcttggtt gcaaagaaaa atgaatgttg atgtgagtag tacgatatat 60

<210> SEQ ID NO 530
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 530

aaaagtcaag aacctgcttt ccacattgca ggagatgctt gtttgcaaag aaaaatgaat 60

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<210> SEQ ID NO 531
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 531

gaaaataaat actttgagga cattaagatt ttaaaagaaa agaatgctga acttcagatg 60

<210> SEQ ID NO 532
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 532

ctgaaacacc aataccagga aaaggaaaat aaatactttg aggacattaa gatttttaaaa 60

<210> SEQ ID NO 533
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 533

aattgcatgt tgaaaaagga aattgccatg ctaaaactgg aaatagccac actgaaacac 60

caa 63

<210> SEQ ID NO 534
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 534

Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala
5 10 15

Thr Leu Lys His Gln
20

<210> SEQ ID NO 535
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 535

Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile
5 10 15

Lys Ile Leu Lys
20

<210> SEQ ID NO 536
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 536

Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala
5 10 15

Glu Leu Gln Met
20

<210> SEQ ID NO 537

-continued

<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 537
Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln
 5 10 15

Arg Lys Met Asn
 20

<210> SEQ ID NO 538
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 538
Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser
 5 10 15

Ser Thr Ile Tyr
 20

<210> SEQ ID NO 539
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 539
Arg Lys Met Asn Val Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val
 5 10 15

Leu His Gln Pro
 20

<210> SEQ ID NO 540
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 540
Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Ser Glu Ala
 5 10 15

Gln Arg Lys Ser
 20

<210> SEQ ID NO 541
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 541
Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly
 5 10 15

Asp Ala Leu Arg Glu
 20

<210> SEQ ID NO 542
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 542

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Thr Glu Gln Gln Glu Ser Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser
5 10 15

Lys Asn Met Trp
20

<210> SEQ ID NO 543
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 543

Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln
5 10 15

Gln Leu Val His Ala
20

<210> SEQ ID NO 544
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 544

Lys Asn Met Trp Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala
5 10 15

Asp Asn Lys Ser
20

<210> SEQ ID NO 545
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 545

Asp Asn Lys Ser Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys
5 10 15

Met Gln His His
20

<210> SEQ ID NO 546
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 546

Met Gln His His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr
5 10 15

Asn Asn His Leu
20

<210> SEQ ID NO 547
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 547

Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile
5 10 15

Tyr Gln Tyr Glu
20

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<210> SEQ ID NO 548

<211> LENGTH: 3045

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 548

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aaatttacgt gggcagcaaa aggaagacct aggaagatcg catgggagaa aaaagaaca    120
cctgtaaaga ctggatgcgt ggcaagagta acatctaata aaactaaagt ttggaaaaa    180
ggaagatcta agatgattgc atgtcctaca aaagaatcat ctacaaaagc aagtgccaat    240
gatcagaggt tcccacaga atccaaacaa gaggaagatg aagaatatc ttgtgattct    300
cggagtctct ttgagagttc tgcaaagatt caagtgtgta tacctgagtc tatatatcaa    360
aaagtaatgg agataaatag agaagtagaa gagcctccta agaagccatc tgccttcaag    420
cctgccattg aaatgcaaaa ctctgttcca aataaagcct ttgaattgaa gaatgaacaa    480
acattgagag cagatccgat gttcccacca gaatccaaac aaaaggacta tgaagaaaat    540
tcttgggatt ctgagagtct ctgtgagact gtttcacaga aggatgtgtg tttacccaag    600
gctacacatc aaaaaaagat agataaaata aatggaaaat tagaagagtc tcctaataaa    660
gatggtcttc tgaaggctac ctgcggaatg aaagtttcta ttccaactaa agccttagaa    720
ttgaaggaca tgcaaaacttt caaagcagag cctccgggga agccatctgc cttegagcct    780
gccactgaaa tgcaaaagtc tgtcccaaat aaagccttgg aattgaaaaa tgaacaaaca    840
ttgagagcag atgagatact cccatcagaa tccaaacaaa aggactatga agaaaattct    900
tgggatactg agagtctctg tgagactgtt tcacagaagg atgtgtgttt acccaaggct    960
gcgcacataa aagaaataga taaaataaat ggaaaattag aagggtctcc tggtaaagat   1020
ggtcttctta aggctaactg cggaatgaaa gtttctattc caactaaagc cttagaattg   1080
atggacatgc aaactttcaa agcagagcct cccgagaagc catctgcctt cgagcctgcc   1140
attgaaatgc aaaagtctgt tccaaataaa gccttggaat tgaagaatga acaaacattg   1200
agagcagatg agatactccc atcagaatcc aaacaaaagg actatgaaga aagttcttgg   1260
gattctgaga gtctctgtga gactgtttca cagaaggatg tgtgtttacc caaggctgcg   1320
catcaaaaag aaatagataa aataaatgga aaattagaag agtctcctga taatgatggt   1380
tttctgaagt ctccctgcag aatgaaagtt tctattccaa ctaaagcctt agaattgatg   1440
gacatgcaaa ctttcaaagc agagcctccc gagaagccat ctgccttcga gcctgccatt   1500
gaaatgcaaa agtctgttcc aaataaagcc ttggaattga agaatgaaca aacattgaga   1560
gcagatcaga tgttcccttc agaatcaaaa caaaagaacg ttgaagaaaa ttcttgggat   1620
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caaaaagaaa tggataaaat aagtggaaaa ttagaagatt caactagcct atcaaaaatc   1740
ttggatacac ttcattcttg tgaaagagca agggaacttc aaaaagatca ctgtgaacaa   1800
cgtacaggaa aaatggaaca aatgaaaaag aagttttgtg tactgaaaaa gaaactgtca   1860
gaagcaaaag aaataaaatc acagttagag aaccaaaaag ttaaatggga acaagagctc   1920
tgcagtgtga gattgacttt aaaccaagaa gaagagaaga gaagaaatgc cgatatatta   1980
aatgaaaaaa ttagggaaga attaggaaga atcgaagagc agcataggaa agagttagaa   2040
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gtgaaacaac aacttgaaca ggctctcaga atacaagata tagaattgaa gagtgtagaa	2100
agtaatttaa atcaggtttc tcacactcat gaaaatgaaa attatctctt acatgaaaat	2160
tgcatgttga aaaagaaaat tgccatgcta aaactggaaa tagccacact gaaacaccaa	2220
taccaggaaa aggaaaaata atactttgag gacattaaga ttttaaaaga aaagaatgct	2280
gaacttcaga tgaccctaaa actgaaagag gaatcattaa ctaaaagggc atctcaatat	2340
agtgggcagc ttaaagtctt gatagctgag aacacaatgc tcacttctaa attgaaggaa	2400
aaacaagaca aagaaatact agaggcagaa attgaatcac accatcctag actggcttct	2460
gctgtacaag accatgatca aattgtgaca tcaagaaaaa gtcaagaacc tgctttccac	2520
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caactacaaa gcaaaaatat gtggcttcaa cagcaattag ttcatgcaca taagaaagct	2880
gacaacaaaa gcaagataac aattgatatt cttttcttg agaggaaaat gcaacatcat	2940
ctcctaaaaa agaaaaatga ggagatattt aattacaata accatttaaa aaaccgtata	3000
tatcaatatg aaaaagagaa agcagaaaca gaagttatat aatag	3045

<210> SEQ ID NO 549
 <211> LENGTH: 1953
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: 985
 <223> OTHER INFORMATION: n = A,T,C or G
 <400> SEQUENCE: 549

atgagtcccg caaaagaaac atctgagaaa ttacgtggg cagcaaaagg aagacctagg	60
aagatcgcat gggagaaaaa agaaacacct gtaaagactg gatgcgtggc aagagtaaca	120
tctaataaaa ctaaagtttt ggaaaaagga agatctaaga tgattgcatg tcctacaaaa	180
gaatcatcta caaaagcaag tgccaatgat cagaggttcc catcagaatc caaacaagag	240
gaagatgaag aatattcttg tgattctcgg agtctctttg agagtcttgc aaagattcaa	300
gtgtgtatac ctgagtctat atatcaaaaa gtaatggaga taaatagaga agtagaagag	360
cctcctaaga agccatctgc cttcaagcct gccattgaaa tgcaaaactc tgttccaaat	420
aaagcctttg aattgaagaa tgaacaaaca ttgagagcag atccgatgtt cccaccagaa	480
tccaaacaaa aggactatga agaaaattct tgggattctg agagtctctg tgagactgtt	540
tcacagaagg atgtgtgttt acccaaggct acacatcaaa aagaaataga taaaataaat	600
ggaaatttag aagagtctcc taataaagat ggtcttctga aggctacctg cggaatgaaa	660
gtttctattc caactaaagc cttagaattg aaggacatgc aaactttcaa agcagagcct	720
ccggggaagc catctgcctt cgagcctgcc actgaaatgc aaaagtctgt cccaaataaa	780
gccttggaat tgaaaaatga acaaacattg agagcagatg agatactccc atcagaatcc	840
aaacaaaagg actatgaaga aaattcttgg gatactgaga gtctctgtga gactgtttca	900

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cagaaggatg tgtgtttacc caaggctgcg catcaaaaag aaatagataa aataaatgga	960
aaattagaag ggtctcctgg taaanatggt cttctgaagg ctaactgcgg aatgaaagtt	1020
tctattccaa ctaaagcctt agaattgatg gacatgcaa ctttcaaagc agagcctccc	1080
gagaagccat ctgccttcga gcctgccatt gaaatgcaa agtctgttcc aaataaagcc	1140
ttggaattga agaatgaaca aacattgaga gcagatgaga tactcccatc agaatccaaa	1200
caaaaggact atgaagaaag ttcttgggat tctgagagtc tctgtgagac tgtttcacag	1260
aaggatgtgt gtttaccctaa ggctgcgcat caaaaagaaa tagataaaat aaatggaaaa	1320
ttagaagagt ctctgataa tgatggtttt ctgaagtctc cctgcagaat gaaagtttct	1380
attccaacta aagccttaga attgatggac atgcaaactt tcaaagcaga gcctcccgag	1440
aagccatctg ccttcgagcc tgccattgaa atgcaaaagt ctgttccaaa taaagccttg	1500
gaattgaaga atgaacaaac attgagagca gatcagatgt tcccttcaga atcaaaacaa	1560
aagaacgttg aagaaaattc ttgggattct gagagtctcc gtgagactgt ttcacagaag	1620
gatgtgtgtg tacccaaggc tacacatcaa aaagaaatgg ataaaataag tggaaaatta	1680
gaagattcaa ctagcctatc aaaaatcttg gatacagttc attcttgtga aagagcaagg	1740
gaacttcaaa aagatcactg tgaacaacgt acaggaaaaa tggaacaaat gaaaaagaag	1800
ttttgtgtac tgaaaaagaa actgtcagaa gcaaaagaaa taaaatcaca gttagagAAC	1860
caaaaagtta aatgggaaca agagctctgc agtgtgaggt ttctcacact catgaaaatg	1920
aaaattatct cttacatgaa aattgcatgt tga	1953

<210> SEQ ID NO 550

<211> LENGTH: 978

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 550

atgcagcatc accaccatca ccacggcaca agagctctgc agtgtgaggt ttctcacact	60
catgaaaatg aaaattatct cttacatgaa aattgcatgt tgaaaaagga aattgccatg	120
ctaaaactgg aaatagccac actgaaacac caataccagg aaaaggaaaa taaatacttt	180
gaggacatta agatttttaa agaaaagaat gctgaacttc agatgaccct aaaactgaaa	240
gaggaatcat taactaaaag ggcattctca tatagtgggc agcttaaagt tctgatagct	300
gagaacacaa tgctcacttc taaattgaag gaaaaacaag acaagaaat actagaggca	360
gaaattgaat cacaccatcc tagactggct tctgctgtac aagaccatga tcaaattgtg	420
acatcaagaa aaagtcaaga acctgctttc cacattgcag gagatgcttg ttgcaaaga	480
aaaatgaatg ttgatgtgag tagtacgata tataacaatg aggtgctcca tcaaccactt	540
tctgaagctc aaaggaaatc caaaagccta aaaattaatc tcaattatgc cggagatgct	600
ctaagagaaa atacattggt ttcagaacat gcacaaagag accaacgtga aacacagtgt	660
caaatgaagg aagctgaaca catgtatcaa aacgaacaag ataatgtgaa caaacacact	720
gaacagcagg agtctctaga tcagaaatta tttcaactac aaagcaaaaa tatgtggctt	780
caacagcaat tagttcatgc acataagaaa gctgacaaca aaagcaagat aacaattgat	840
attcattttc ttgagaggaa aatgcaacat catctcctaa aagagaaaaa tgaggagata	900
tttaattaca ataaccattt aaaaaaccgt atatatcaat atgaaaaaga gaaagcagaa	960

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acagaagtta tataatag

978

<210> SEQ ID NO 551

<211> LENGTH: 324

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 551

Met Gln His His His His His His Gly Thr Arg Ala Leu Gln Cys Glu
5 10 15

Val Ser His Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn Cys
20 25 30

Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala Thr Leu
35 40 45

Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile Lys
50 55 60

Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met Thr Leu Lys Leu Lys
65 70 75 80

Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr Ser Gly Gln Leu Lys
85 90 95

Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser Lys Leu Lys Glu Lys
100 105 110

Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu Ser His His Pro Arg
115 120 125

Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg Lys
130 135 140

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

Lys Met Asn Val Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val Leu
165 170 175

His Gln Pro Leu Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile
180 185 190

Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg Glu Asn Thr Leu Val Ser
195 200 205

Glu His Ala Gln Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys Glu
210 215 220

Ala Glu His Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr
225 230 235 240

Glu Gln Gln Glu Ser Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys
245 250 255

Asn Met Trp Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala Asp
260 265 270

Asn Lys Ser Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met
275 280 285

Gln His His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr Asn
290 295 300

Asn His Leu Lys Asn Arg Ile Tyr Gln Tyr Glu Lys Glu Lys Ala Glu
305 310 315 320

Thr Glu Val Ile

<210> SEQ ID NO 552

<211> LENGTH: 661

<212> TYPE: PRT

-continued

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 552

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Met Gln His His His His His Val Gly Ser Met Ser Pro Ala Lys
      5              10              15

Glu Thr Ser Glu Lys Phe Thr Trp Ala Ala Lys Gly Arg Pro Arg Lys
      20              25              30

Ile Ala Trp Glu Lys Lys Glu Thr Pro Val Lys Thr Gly Cys Val Ala
      35              40              45

Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu Lys Gly Arg Ser Lys
      50              55              60

Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr Lys Ala Ser Ala Asn
      65              70              75              80

Asp Gln Arg Phe Pro Ser Glu Ser Lys Gln Glu Glu Asp Glu Glu Tyr
      85              90              95

Ser Cys Asp Ser Arg Ser Leu Phe Glu Ser Ser Ala Lys Ile Gln Val
      100             105             110

Cys Ile Pro Glu Ser Ile Tyr Gln Lys Val Met Glu Ile Asn Arg Glu
      115             120             125

Val Glu Glu Pro Pro Lys Lys Pro Ser Ala Phe Lys Pro Ala Ile Glu
      130             135             140

Met Gln Asn Ser Val Pro Asn Lys Ala Phe Glu Leu Lys Asn Glu Gln
      145             150             155             160

Thr Leu Arg Ala Asp Pro Met Phe Pro Pro Glu Ser Lys Gln Lys Asp
      165             170             175

Tyr Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser
      180             185             190

Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu Ile Asp
      195             200             205

Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asn Lys Asp Gly Leu Leu
      210             215             220

Lys Ala Thr Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu
      225             230             235             240

Leu Lys Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Gly Lys Pro Ser
      245             250             255

Ala Phe Glu Pro Ala Thr Glu Met Gln Lys Ser Val Pro Asn Lys Ala
      260             265             270

Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro
      275             280             285

Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Asn Ser Trp Asp Thr Glu
      290             295             300

Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala
      305             310             315             320

Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser
      325             330             335

Pro Gly Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser
      340             345             350

Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala
      355             360             365

Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln
      370             375             380

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Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu
 385 390 395 400
 Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu
 405 410 415
 Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys
 420 425 430
 Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile
 435 440 445
 Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly Phe Leu Lys Ser
 450 455 460
 Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met
 465 470 475 480
 Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe
 485 490 495
 Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu
 500 505 510
 Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met Phe Pro Ser Glu
 515 520 525
 Ser Lys Gln Lys Asn Val Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu
 530 535 540
 Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala Thr His
 545 550 555 560
 Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser Thr Ser
 565 570 575
 Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala Arg Glu
 580 585 590
 Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met
 595 600 605
 Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser Glu Ala Lys Glu
 610 615 620
 Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu
 625 630 635 640
 Cys Ser Val Arg Phe Leu Thr Leu Met Lys Met Lys Ile Ile Ser Tyr
 645 650 655
 Met Lys Ile Ala Cys
 660

<210> SEQ ID NO 553

<211> LENGTH: 1013

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 553

Met Gln His His His His His His Val Gly Ser Met Ser Pro Ala Lys
 5 10 15
 Glu Thr Ser Glu Lys Phe Thr Trp Ala Ala Lys Gly Arg Pro Arg Lys
 20 25 30
 Ile Ala Trp Glu Lys Lys Glu Thr Pro Val Lys Thr Gly Cys Val Ala
 35 40 45
 Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu Lys Gly Arg Ser Lys
 50 55 60
 Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr Lys Ala Ser Ala Asn
 65 70 75 80

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Asp	Gln	Arg	Phe	Pro	Ser	Glu	Ser	Lys	Gln	Glu	Glu	Asp	Glu	Glu	Tyr	85	90	95
Ser	Cys	Asp	Ser	Arg	Ser	Leu	Phe	Glu	Ser	Ser	Ala	Lys	Ile	Gln	Val	100	105	110
Cys	Ile	Pro	Glu	Ser	Ile	Tyr	Gln	Lys	Val	Met	Glu	Ile	Asn	Arg	Glu	115	120	125
Val	Glu	Glu	Pro	Pro	Lys	Lys	Pro	Ser	Ala	Phe	Lys	Pro	Ala	Ile	Glu	130	135	140
Met	Gln	Asn	Ser	Val	Pro	Asn	Lys	Ala	Phe	Glu	Leu	Lys	Asn	Glu	Gln	145	150	155
Thr	Leu	Arg	Ala	Asp	Pro	Met	Phe	Pro	Pro	Glu	Ser	Lys	Gln	Lys	Asp	165	170	175
Tyr	Glu	Glu	Asn	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu	Thr	Val	Ser	180	185	190
Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Thr	His	Gln	Lys	Glu	Ile	Asp	195	200	205
Lys	Ile	Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asn	Lys	Asp	Gly	Leu	Leu	210	215	220
Lys	Ala	Thr	Cys	Gly	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala	Leu	Glu	225	230	235
Leu	Lys	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Gly	Lys	Pro	Ser	245	250	255
Ala	Phe	Glu	Pro	Ala	Thr	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	260	265	270
Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Glu	Ile	Leu	Pro	275	280	285
Ser	Glu	Ser	Lys	Gln	Lys	Asp	Tyr	Glu	Glu	Asn	Ser	Trp	Asp	Thr	Glu	290	295	300
Ser	Leu	Cys	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	305	310	315
Ala	His	Gln	Lys	Glu	Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	Gly	Ser	325	330	335
Pro	Gly	Lys	Asp	Gly	Leu	Leu	Lys	Ala	Asn	Cys	Gly	Met	Lys	Val	Ser	340	345	350
Ile	Pro	Thr	Lys	Ala	Leu	Glu	Leu	Met	Asp	Met	Gln	Thr	Phe	Lys	Ala	355	360	365
Glu	Pro	Pro	Glu	Lys	Pro	Ser	Ala	Phe	Glu	Pro	Ala	Ile	Glu	Met	Gln	370	375	380
Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	385	390	395
Arg	Ala	Asp	Glu	Ile	Leu	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Asp	Tyr	Glu	405	410	415
Glu	Ser	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu	Thr	Val	Ser	Gln	Lys	420	425	430
Asp	Val	Cys	Leu	Pro	Lys	Ala	Ala	His	Gln	Lys	Glu	Ile	Asp	Lys	Ile	435	440	445
Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asp	Asn	Asp	Gly	Phe	Leu	Lys	Ser	450	455	460
Pro	Cys	Arg	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala	Leu	Glu	Leu	Met	465	470	475

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Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu	Lys	Pro	Ser	Ala	Phe
				485					490					495	
Glu	Pro	Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu
			500					505					510		
Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Gln	Met	Phe	Pro	Ser	Glu
		515					520					525			
Ser	Lys	Gln	Lys	Asn	Val	Glu	Glu	Asn	Ser	Trp	Asp	Ser	Glu	Ser	Leu
	530					535					540				
Arg	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Val	Pro	Lys	Ala	Thr	His
545					550					555					560
Gln	Lys	Glu	Met	Asp	Lys	Ile	Ser	Gly	Lys	Leu	Glu	Asp	Ser	Thr	Ser
				565					570					575	
Leu	Ser	Lys	Ile	Leu	Asp	Thr	Val	His	Ser	Cys	Glu	Arg	Ala	Arg	Glu
			580					585					590		
Leu	Gln	Lys	Asp	His	Cys	Glu	Gln	Arg	Thr	Gly	Lys	Met	Glu	Gln	Met
		595					600					605			
Lys	Lys	Lys	Phe	Cys	Val	Leu	Lys	Lys	Lys	Leu	Ser	Glu	Ala	Lys	Glu
	610					615					620				
Ile	Lys	Ser	Gln	Leu	Glu	Asn	Gln	Lys	Val	Lys	Trp	Glu	Gln	Glu	Leu
625					630					635					640
Cys	Ser	Val	Arg	Leu	Thr	Leu	Asn	Gln	Glu	Glu	Glu	Lys	Arg	Arg	Asn
			645					650						655	
Ala	Asp	Ile	Leu	Asn	Glu	Lys	Ile	Arg	Glu	Glu	Leu	Gly	Arg	Ile	Glu
		660					665						670		
Glu	Gln	His	Arg	Lys	Glu	Leu	Glu	Val	Lys	Gln	Gln	Leu	Glu	Gln	Ala
		675					680					685			
Leu	Arg	Ile	Gln	Asp	Ile	Glu	Leu	Lys	Ser	Val	Glu	Ser	Asn	Leu	Asn
	690				695						700				
Gln	Val	Ser	His	Thr	His	Glu	Asn	Glu	Asn	Tyr	Leu	Leu	His	Glu	Asn
705					710					715					720
Cys	Met	Leu	Lys	Lys	Glu	Ile	Ala	Met	Leu	Lys	Leu	Glu	Ile	Ala	Thr
			725					730						735	
Leu	Lys	His	Gln	Tyr	Gln	Glu	Lys	Glu	Asn	Lys	Tyr	Phe	Glu	Asp	Ile
		740					745						750		
Lys	Ile	Leu	Lys	Glu	Lys	Asn	Ala	Glu	Leu	Gln	Met	Thr	Leu	Lys	Leu
	755					760						765			
Lys	Glu	Glu	Ser	Leu	Thr	Lys	Arg	Ala	Ser	Gln	Tyr	Ser	Gly	Gln	Leu
	770				775						780				
Lys	Val	Leu	Ile	Ala	Glu	Asn	Thr	Met	Leu	Thr	Ser	Lys	Leu	Lys	Glu
785					790					795					800
Lys	Gln	Asp	Lys	Glu	Ile	Leu	Glu	Ala	Glu	Ile	Glu	Ser	His	His	Pro
			805					810						815	
Arg	Leu	Ala	Ser	Ala	Val	Gln	Asp	His	Asp	Gln	Ile	Val	Thr	Ser	Arg
		820					825						830		
Lys	Ser	Gln	Glu	Pro	Ala	Phe	His	Ile	Ala	Gly	Asp	Ala	Cys	Leu	Gln
	835					840					845				
Arg	Lys	Met	Asn	Val	Asp	Val	Ser	Ser	Thr	Ile	Tyr	Asn	Asn	Glu	Val
	850				855						860				
Leu	His	Gln	Pro	Leu	Ser	Glu	Ala	Gln	Arg	Lys	Ser	Lys	Ser	Leu	Lys
865				870					875						880
Ile	Asn	Leu	Asn	Tyr	Ala	Gly	Asp	Ala	Leu	Arg	Glu	Asn	Thr	Leu	Val

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885										890										895										
Ser	Glu	His	Ala	Gln	Arg	Asp	Gln	Arg	Glu	Thr	Gln	Cys	Gln	Met	Lys															
			900						905					910																
Glu	Ala	Glu	His	Met	Tyr	Gln	Asn	Glu	Gln	Asp	Asn	Val	Asn	Lys	His															
		915					920					925																		
Thr	Glu	Gln	Gln	Glu	Ser	Leu	Asp	Gln	Lys	Leu	Phe	Gln	Leu	Gln	Ser															
	930					935					940																			
Lys	Asn	Met	Trp	Leu	Gln	Gln	Gln	Leu	Val	His	Ala	His	Lys	Lys	Ala															
945					950					955					960															
Asp	Asn	Lys	Ser	Lys	Ile	Thr	Ile	Asp	Ile	His	Phe	Leu	Glu	Arg	Lys															
				965					970					975																
Met	Gln	His	His	Leu	Leu	Lys	Glu	Lys	Asn	Glu	Glu	Ile	Phe	Asn	Tyr															
			980				985						990																	
Asn	Asn	His	Leu	Lys	Asn	Arg	Ile	Tyr	Gln	Tyr	Glu	Lys	Glu	Lys	Ala															
		995				1000						1005																		
Glu	Thr	Glu	Val	Ile																										
	1010																													

<210> SEQ ID NO 554
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: PCR primer

<400> SEQUENCE: 554

gtcggctcca tgagtccgc aaaag

25

<210> SEQ ID NO 555
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: PCR primer

<400> SEQUENCE: 555

cgagaattca atacttaaga agaccatctt taccag

36

<210> SEQ ID NO 556
 <211> LENGTH: 31
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: PCR primer

<400> SEQUENCE: 556

cataagctta aggctaactg cggaatgaaa g

31

<210> SEQ ID NO 557
 <211> LENGTH: 35
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: PCR primer

<400> SEQUENCE: 557

cccgagaat tcaacatgca attttcatgt aagag

35

<210> SEQ ID NO 558

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer

<400> SEQUENCE: 558

ctaaatgccg gcacaagagc tctgc

25

<210> SEQ ID NO 559
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer

<400> SEQUENCE: 559

cgcgcagaat tctattatat aacttctgtt tctgc

35

<210> SEQ ID NO 560
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer

<400> SEQUENCE: 560

ggggaattgt gagcggataa caattc

26

<210> SEQ ID NO 561
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer

<400> SEQUENCE: 561

cgtagaattc aacctgattt aaattacttt ctacac

36

<210> SEQ ID NO 562
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer

<400> SEQUENCE: 562

gaaagtaatt taaatcaggt ttctcacact c

31

<210> SEQ ID NO 563
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer

<400> SEQUENCE: 563

gaggcccaa ggggttatgc tag

23

<210> SEQ ID NO 564
<211> LENGTH: 4458
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

-continued

<400> SEQUENCE: 564

ctagtctata ccagcaacga ctcctacatc gtccactctg gggatcttag aaagatccat	60
aaagctgcct cccggggaca agtccggaag ctggagaaga tgacaaagag gaagaagacc	120
atcaacctta atatacaaga cgcccagaag aggactgctc tacactgggc ctgtgtcaat	180
ggccatgagg aagtagtaac atttctggta gacagaaagt gccagcttga cgtccttgat	240
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<210> SEQ ID NO 565

<211> LENGTH: 1341

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 565

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Val Thr Phe Leu Val Asp Arg Lys Cys Gln Leu Asp Val Leu Asp Gly
35 40 45

Glu His Arg Thr Pro Leu Met Lys Ala Leu Gln Cys His Gln Glu Ala
50 55 60

Cys Ala Asn Ile Leu Ile Asp Ser Gly Ala Asp Ile Asn Leu Val Asp
65 70 75 80

Val Tyr Gly Asn Met Ala Leu His Tyr Ala Val Tyr Ser Glu Ile Leu
85 90 95

Ser Val Val Ala Lys Leu Leu Ser His Gly Ala Val Ile Glu Val His
100 105 110

Asn Lys Ala Ser Leu Thr Pro Leu Leu Leu Ser Ile Thr Lys Arg Ser
115 120 125

Glu Gln Ile Val Glu Phe Leu Leu Ile Lys Asn Ala Asn Ala Asn Ala
130 135 140

Val Asn Lys Tyr Lys Cys Thr Ala Leu Met Leu Ala Val Cys His Gly
145 150 155 160

Ser Ser Glu Ile Val Gly Met Leu Leu Gln Gln Asn Val Asp Val Phe
165 170 175

Ala Ala Asp Ile Cys Gly Val Thr Ala Glu His Tyr Ala Val Thr Cys
180 185 190

Gly Phe His His Ile His Glu Gln Ile Met Glu Tyr Ile Arg Lys Leu
195 200 205

Ser Lys Asn His Gln Asn Thr Asn Pro Glu Gly Thr Ser Ala Gly Thr
210 215 220

Pro Asp Glu Ala Ala Pro Leu Ala Glu Arg Thr Pro Asp Thr Ala Glu
225 230 235 240

Ser Leu Val Glu Lys Thr Pro Asp Glu Ala Ala Pro Leu Val Glu Arg
245 250 255

Thr Pro Asp Thr Ala Glu Ser Leu Val Glu Lys Thr Pro Asp Glu Ala
260 265 270

Ala Ser Leu Val Glu Gly Thr Ser Asp Lys Ile Gln Cys Leu Glu Lys
275 280 285

Ala Thr Ser Gly Lys Phe Glu Gln Ser Ala Glu Glu Thr Pro Arg Glu
290 295 300

Ile Thr Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Pro Ala
305 310 315 320

Lys Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Asp Thr Pro
325 330 335

Arg Glu Ile Met Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp
340 345 350

Ala Ala Lys Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Thr
355 360 365

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Pro	Val	Lys	Thr	Gly	Cys	Val	Ala	Arg	Val	Thr	Ser	Asn	Lys	Thr	Lys	370	375	380
Val	Leu	Glu	Lys	Gly	Arg	Ser	Lys	Met	Ile	Ala	Cys	Pro	Thr	Lys	Glu	385	390	395
Ser	Ser	Thr	Lys	Ala	Ser	Ala	Asn	Asp	Gln	Arg	Phe	Pro	Ser	Glu	Ser	405	410	415
Lys	Gln	Glu	Glu	Asp	Glu	Glu	Tyr	Ser	Cys	Asp	Ser	Arg	Ser	Leu	Phe	420	425	430
Glu	Ser	Ser	Ala	Lys	Ile	Gln	Val	Cys	Ile	Pro	Glu	Ser	Ile	Tyr	Gln	435	440	445
Lys	Val	Met	Glu	Ile	Asn	Arg	Glu	Val	Glu	Glu	Pro	Pro	Lys	Lys	Pro	450	455	460
Ser	Ala	Phe	Lys	Pro	Ala	Ile	Glu	Met	Gln	Asn	Ser	Val	Pro	Asn	Lys	465	470	475
Ala	Phe	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Pro	Met	Phe	485	490	495
Pro	Pro	Glu	Ser	Lys	Gln	Lys	Asp	Tyr	Glu	Glu	Asn	Ser	Trp	Asp	Ser	500	505	510
Glu	Ser	Leu	Cys	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	515	520	525
Ala	Thr	His	Gln	Lys	Glu	Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	Glu	530	535	540
Ser	Pro	Asn	Lys	Asp	Gly	Leu	Leu	Lys	Ala	Thr	Cys	Gly	Met	Lys	Val	545	550	555
Ser	Ile	Pro	Thr	Lys	Ala	Leu	Glu	Leu	Lys	Asp	Met	Gln	Thr	Phe	Lys	565	570	575
Ala	Glu	Pro	Pro	Gly	Lys	Pro	Ser	Ala	Phe	Glu	Pro	Ala	Thr	Glu	Met	580	585	590
Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	595	600	605
Trp	Arg	Ala	Asp	Glu	Ile	Leu	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Asp	Tyr	610	615	620
Glu	Glu	Asn	Ser	Trp	Asp	Thr	Glu	Ser	Leu	Cys	Glu	Thr	Val	Ser	Gln	625	630	635
Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Ala	His	Gln	Lys	Glu	Ile	Asp	Lys	645	650	655
Ile	Asn	Gly	Lys	Leu	Glu	Gly	Ser	Pro	Val	Lys	Asp	Gly	Leu	Leu	Lys	660	665	670
Ala	Asn	Cys	Gly	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala	Leu	Glu	Leu	675	680	685
Met	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu	Lys	Pro	Ser	Ala	690	695	700
Phe	Glu	Pro	Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	705	710	715
Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Glu	Ile	Leu	Pro	Ser	725	730	735
Glu	Ser	Lys	Gln	Lys	Asp	Tyr	Glu	Glu	Ser	Ser	Trp	Asp	Ser	Glu	Ser	740	745	750
Leu	Cys	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Thr	755	760	765

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His	Gln	Lys	Glu	Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro
770						775					780				
Asp	Asn	Asp	Gly	Phe	Leu	Lys	Ala	Pro	Cys	Arg	Met	Lys	Val	Ser	Ile
785					790					795				800	
Pro	Thr	Lys	Ala	Leu	Glu	Leu	Met	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu
				805					810					815	
Pro	Pro	Glu	Lys	Pro	Ser	Ala	Phe	Glu	Pro	Ala	Ile	Glu	Met	Gln	Lys
			820					825					830		
Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg
		835					840					845			
Ala	Asp	Gln	Met	Phe	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Lys	Val	Glu	Glu
	850					855					860				
Asn	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Arg	Glu	Thr	Val	Ser	Gln	Lys	Asp
865					870					875				880	
Val	Cys	Val	Pro	Lys	Ala	Thr	His	Gln	Lys	Glu	Met	Asp	Lys	Ile	Ser
				885					890					895	
Gly	Lys	Leu	Glu	Asp	Ser	Thr	Ser	Leu	Ser	Lys	Ile	Leu	Asp	Thr	Val
		900						905					910		
His	Ser	Cys	Glu	Arg	Ala	Arg	Glu	Leu	Gln	Lys	Asp	His	Cys	Glu	Gln
		915					920					925			
Arg	Thr	Gly	Lys	Met	Glu	Gln	Met	Lys	Lys	Lys	Phe	Cys	Val	Leu	Lys
	930					935					940				
Lys	Lys	Leu	Ser	Glu	Ala	Lys	Glu	Ile	Lys	Ser	Gln	Leu	Glu	Asn	Gln
945					950					955				960	
Lys	Val	Lys	Trp	Glu	Gln	Glu	Leu	Cys	Ser	Val	Arg	Leu	Thr	Leu	Asn
			965						970					975	
Gln	Glu	Glu	Glu	Lys	Arg	Arg	Asn	Ala	Asp	Ile	Leu	Asn	Glu	Lys	Ile
		980					985						990		
Arg	Glu	Glu	Leu	Gly	Arg	Ile	Glu	Glu	Gln	His	Arg	Lys	Glu	Leu	Glu
	995						1000					1005			
Val	Lys	Gln	Gln	Leu	Glu	Gln	Ala	Leu	Arg	Ile	Gln	Asp	Ile	Glu	Leu
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Lys	Ser	Val	Glu	Ser	Asn	Leu	Asn	Gln	Val	Ser	His	Thr	His	Glu	Asn
1025					1030					1035				1040	
Glu	Asn	Tyr	Leu	Leu	His	Glu	Asn	Cys	Met	Leu	Lys	Lys	Glu	Ile	Ala
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Met	Leu	Lys	Leu	Glu	Ile	Ala	Thr	Leu	Lys	His	Gln	Tyr	Gln	Glu	Lys
		1060						1065					1070		
Glu	Asn	Lys	Tyr	Phe	Glu	Asp	Ile	Lys	Ile	Leu	Lys	Glu	Lys	Asn	Ala
	1075					1080						1085			
Glu	Leu	Gln	Met	Thr	Leu	Lys	Leu	Lys	Glu	Glu	Ser	Leu	Thr	Lys	Arg
	1090					1095					1100				
Ala	Ser	Gln	Tyr	Ser	Gly	Gln	Leu	Lys	Val	Leu	Ile	Ala	Glu	Asn	Thr
1105					1110					1115				1120	
Met	Leu	Thr	Ser	Lys	Leu	Lys	Glu	Lys	Gln	Asp	Lys	Glu	Ile	Leu	Glu
			1125						1130					1135	
Ala	Glu	Ile	Glu	Ser	His	His	Pro	Arg	Leu	Ala	Ser	Ala	Val	Gln	Asp
		1140						1145					1150		
His	Asp	Gln	Ile	Val	Thr	Ser	Arg	Lys	Ser	Gln	Glu	Pro	Ala	Phe	His
	1155						1160					1165			
Ile	Ala	Gly	Asp	Ala	Cys	Leu	Gln	Arg	Lys	Met	Asn	Val	Asp	Val	Ser

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1170	1175	1180
Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Ser Glu Ala		
1185	1190	1195 1200
Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp		
	1205	1210 1215
Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg Asp Gln		
	1220	1225 1230
Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr Gln Asn		
	1235	1240 1245
Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu Ser Leu Asp		
	1250	1255 1260
Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln Gln		
1265	1270	1275 1280
Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser Lys Ile Thr Ile		
	1285	1290 1295
Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu Leu Lys Glu		
	1300	1305 1310
Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile		
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Tyr Gln Tyr Glu Lys Glu Lys Ala Glu Thr Glu Asn Ser		
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<210> SEQ ID NO 566

<211> LENGTH: 4047

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 566

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ataaatcac agttagagaa ccaaaaagt aaatgggaac aagagctctg cagtgtgaga	2940
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agggaagaat taggaagaat cgaagagcag cataggaaag agttagaagt gaaacaacaa	3060
cttgaacagg ctctcagaat acaagatata gaattgaaga gtgtagaaag taatttgaat	3120
cagggtttctc acactcatga aaatgaaaat tatctcttac atgaaaattg catgttgaaa	3180
aaggaaaattg ccatgctaaa actggaaata gccacactga aacaccaata ccaggaaaag	3240
gaaaataaat actttgagga cattaagatt ttaaaagaaa agaagctga acttcagatg	3300
accctaaaac tgaaagagga atcattaact aaaagggcac ctcaatatag tgggcagctt	3360

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aaagttctga tagctgagaa cacaatgctc acttctaaat tgaaggaaaa acaagacaaa	3420
gaaatactag aggcagaaat tgaatcacac catcctagac tggcttctgc tgtacaagac	3480
catgatcaaa ttgtgacatc aagaaaaagt caagaacctg ctttccacat tgcaggagat	3540
gcttgtttgc aaagaaaaat gaatgttgat gtgagtagta cgatatataa caatgaggtg	3600
ctccatcaac cactttctga agctcaaagg aaatccaaaa gcctaaaaat taatctcaat	3660
tatgcaggag atgctctaag agaaaataca ttggtttcag aacatgcaca aagagaccaa	3720
cgtgaaacac agtgtcaaat gaaggaagct gaacacatgt atcaaacga acaagataat	3780
gtgaacaaac aactgaaca gcaggagtct ctagatcaga aattatttca actacaaagc	3840
aaaaatatgt ggcttcaaca gcaattagtt catgcacata agaaagctga caacaaaagc	3900
aagataacaa ttgatattca ttttcttgag aggaaaatgc aacatcatct cctaaaagag	3960
aaaaatgagg agatatttaa ttacaataac catttaaaaa accgtatata tcaatatgaa	4020
aaagagaaag cagaaacaga agttata	4047

<210> SEQ ID NO 567

<211> LENGTH: 1199

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 567

acaaagagga agaagacat caacctaat atacaagacg cccagaagag gactgctcta	60
cactgggcct gtgtcaatgg ccatgaggaa gtagtaacat ttctggtaga cagaaagtgc	120
cagcctgacg tccttgatgg cgaacacagg acacctctga tgaaggctct acaatgccat	180
caggaggctt gtgcaaatat tctgatagat tctggtgccg atataaatct cgtagatgtg	240
tatggcaaca tggctctcca ttatgctgtt tatagtga ttttgtcagt ggtggcaaaa	300
ctgctgtccc atggtgcagt catcgaagtg cacaacaagg ctgacctcac accactttta	360
ctatccataa cgaagaag tgagcaaatt gtggaatttt tgctgataaa aaatgcaaat	420
gcgaatgcag ttaataagta taaatgcaca gccctcatgc ttgctgtatg tcatggatta	480
tcagagatag ttggcatgct tcttcagcaa aatgttgacg tctttgctgc agatatatgt	540
ggagtaactg cagaacatta tgctgttact tgtggatttc atcacattca tgaacaaatt	600
atggaatata tacgaaaatt atctaaaaat catcaaaata ccaatccaga aggaacatct	660
gcaggaacac ctgatgaggc tgcaccttg gcgaaagaa cacctgacac agctgaaagc	720
ttggtggaaa aaacacctga tgaggctgca cccttggtgg aaagaacacc tgacacggct	780
gaaagcttg tggaaaaaac acctgatgag gctgcatcct tggaggagg aacatctgac	840
aaaattcaat gtttgagaa agcgacatct ggaaagtgc aacagtcagc agaagaaca	900
cctagggaaa ttacgagtcc tgcaaaagaa acatctgaga aatttacgtg gccagcaaaa	960
ggaagacct ggaagatgc atgggagaaa aaagaagaca cacctaggga aattatgagt	1020
cccgcataag aaacatctga gaaatttacg tgggcagcaa aaggaagacc taggaagatc	1080
gcatgggaga aaaaagaaac acctgtaaag actggatgcg tggcaagagt aacatcta	1140
aaaactaaag ttttgaaaa aggaagatct aagatgattg catgtcctac aaaagaatc	1199

<210> SEQ ID NO 568

<211> LENGTH: 1199

<212> TYPE: DNA

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 568

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acaaagagga agaagaccat caaccttaat atacaagacg cccagaagag gactgctcta    60
cactgggcct gtgtcaatgg ccatgaggaa gtagtaacat ttctggtaga cagaaagtgc    120
cagcttgacg tccttgatgg cgaacacagg acacctctga tgaaggctct acaatgccat    180
caggaggcct gtgcaaatat tctgatatag tctgggtgccg atataaatct cgtagatgtg    240
tatgacaaca cggtctctcca ttatgctgtt tatagtgaga ttttgtcagt ggtggcaaaa    300
ctgctgtccc atgggtgcagt catctaagcg cacaacaagg ctagcctcac accactttta    360
ctatccataa cgaagaagag tgagcaaat gtggaatddd tgctgataaa aaatgcaaat    420
gcgaatgcag ttaataagta taaatgcaca gccctcatgc ttgctgtatg tcatggatca    480
tcagagatag ttggcatgct tcttcagcaa aatgttgacg tctttgctgc agatatatgt    540
ggagtaactg cagaacatta tgctgttact tgtggatttc atcacattca tgaacaaatt    600
atggaatata tacgaaaatt atctaaaaat catcaaaata ccaatccaga aggaacatct    660
gcaggaacac ctgatgagcg tgcacccttg gcggaagaa cacctgacac agctgaaagc    720
ttggtggaaa aaacacctga tgaggctgca cccttggtgg aaagaacacc tgacacggct    780
gaaagcttgg tggaaaaaac acctgatgag gctgcacctt tggaggaggg aacatctgac    840
aaaattcaat gtttgagaaa agcgacatct ggaaagtctg aacagtcagc agaagaaca    900
cctagggaaa ttacgagtcc tgcaaaagaa acatctgaga aatttacgtg gccagcaaaa    960
ggaagaccta ggaagatcgc atgggagaaa aaagaagaca cacctaggga aattatgagt   1020
cccgcaaaaag aaacatctga gaaatttacg tgggcagcaa aaggaagacc taggaagatc   1080
gcatgggaga aaaaaaaaac acctgtaaag actggatgcg tggcaagagt aacatctaatt   1140
aaaactaaag ttttgaaaaa aggaagatct aagatgattg catgtcctac aaaagaatc   1199

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<210> SEQ ID NO 569

<211> LENGTH: 1199

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 569

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acaaagagga agaagaccat caaccttaat atacaagacg cccagaagag gactgctcta    60
cactgggcct gtgtcaatgg ccatgaggaa gtagtaacat ttctggtaga cagaaagtgc    120
cagcttgacg tccttgatgg cgaacacagg acacctctga tgaaggctct acaatgccat    180
caggaggcct gtgcaaatat tctgatatag tctgggtgccg atataaatct cgtagatgtg    240
tatggcaaca tggtctctcca ttatgctgtt tatagtgaga ttttgtcagt ggtggcaaaa    300
ctgctgtccc atgggtgcagt catcgaagtg cacaacaagg ctagcctcac accactttta    360
ctatccataa cgaagaagag tgagcaaat gtggaatddd tgctgataaa aaatgcaaat    420
gcgaatgcag ttaataagta taaatgcaca gccctcatgc ttgctgtatg tcatggatca    480
tcagagatag ttggcatgct tcttcagcaa aatgttgacg tctttgctgc agatatatgt    540
ggagtaactg cagaacatta tgctgttact tgtggatttc atcacattca tgaacaaatt    600
atggaatata tacgaaaatt atctaaaaat catcaaaata ccaatccaga aggaacatct    660
gcaggaacac ctgatgagcg tgcacccttg gcggaagaa cacctgacac agctgaaagc    720

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ttggtggaaa aaacacctga tgaggctgca cccttggtgg aaagaacacc tgacacggct 780
gaaagcttgg tggaaaaaac acctgatgag gctgcatcct tggaggaggg aacatctgac 840
aaaaattcaat gtttgaggaa agcgacatct ggaaagttcg aacagtcagc agaagaaca 900
cctagggaaa ttacgagtcc tgcaaaagaa acatctgaga aatttacgtg gccagcaaaa 960
ggaagaccta ggaagatcgc atgggagaaa aaagaagaca cacctaggga aattatgagt 1020
cccgcaaaag aaacatctga gaaatttacg tgggcagcaa aaggaagacc taggaagatc 1080
gcatgggaga aaaaagaaac acctgtaaag actggatgcg tggcaagagt aacatctaata 1140
aaaactaaag ttttgaaaaa aggaagatct aagatgattg catgtcctac aaaagaatc 1199

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<210> SEQ ID NO 570

<211> LENGTH: 399

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 570

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Thr Lys Arg Lys Lys Thr Ile Asn Leu Asn Ile Gln Asp Ala Gln Lys
      5              10              15
Arg Thr Ala Leu His Trp Ala Cys Val Asn Gly His Glu Glu Val Val
      20              25              30
Thr Phe Leu Val Asp Arg Lys Cys Gln Leu Asp Val Leu Asp Gly Glu
      35              40              45
His Arg Thr Pro Leu Met Lys Ala Leu Gln Cys His Gln Glu Ala Cys
      50              55              60
Ala Asn Ile Leu Ile Asp Ser Gly Ala Asp Ile Asn Leu Val Asp Val
      65              70              75              80
Tyr Gly Asn Met Ala Leu His Tyr Ala Val Tyr Ser Glu Ile Leu Ser
      85              90              95
Val Val Ala Lys Leu Leu Ser His Gly Ala Val Ile Glu Val His Asn
      100             105             110
Lys Ala Ser Leu Thr Pro Leu Leu Leu Ser Ile Thr Lys Arg Ser Glu
      115             120             125
Gln Ile Val Glu Phe Leu Leu Ile Lys Asn Ala Asn Ala Asn Ala Val
      130             135             140
Asn Lys Tyr Lys Cys Thr Ala Leu Met Leu Ala Val Cys His Gly Ser
      145             150             155             160
Ser Glu Ile Val Gly Met Leu Leu Gln Gln Asn Val Asp Val Phe Ala
      165             170             175
Ala Asp Ile Cys Gly Val Thr Ala Glu His Tyr Ala Val Thr Cys Gly
      180             185             190
Phe His His Ile His Glu Gln Ile Met Glu Tyr Ile Arg Lys Leu Ser
      195             200             205
Lys Asn His Gln Asn Thr Asn Pro Glu Gly Thr Ser Ala Gly Thr Pro
      210             215             220
Asp Glu Ala Ala Pro Leu Ala Glu Arg Thr Pro Asp Thr Ala Glu Ser
      225             230             235             240
Leu Val Glu Lys Thr Pro Asp Glu Ala Ala Pro Leu Val Glu Arg Thr
      245             250             255
Pro Asp Thr Ala Glu Ser Leu Val Glu Lys Thr Pro Asp Glu Ala Ala
      260             265             270
Ser Leu Val Glu Gly Thr Ser Asp Lys Ile Gln Cys Leu Glu Lys Ala

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275	280	285
Thr Ser Gly Lys Phe Glu Gln Ser Ala Glu Glu Thr Pro Arg Glu Ile 290 295 300		
Thr Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Pro Ala Lys 305 310 315 320		
Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Asp Thr Pro Arg 325 330 335		
Glu Ile Met Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Ala 340 345 350		
Ala Lys Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Thr Pro 355 360 365		
Val Lys Thr Gly Cys Val Ala Arg Val Thr Ser Asn Lys Thr Lys Val 370 375 380		
Leu Glu Lys Gly Arg Ser Lys Met Ile Ala Cys Pro Thr Lys Glu 385 390 395		
<210> SEQ ID NO 571		
<211> LENGTH: 247		
<212> TYPE: PRT		
<213> ORGANISM: Homo sapiens		
<400> SEQUENCE: 571		
Met Leu Ala Val Cys His Gly Ser Ser Glu Ile Val Gly Met Leu Leu 5 10 15		
Gln Gln Asn Val Asp Val Phe Ala Ala Asp Ile Cys Gly Val Thr Ala 20 25 30		
Glu His Tyr Ala Val Thr Cys Gly Phe His His Ile His Glu Gln Ile 35 40 45		
Met Glu Tyr Ile Arg Lys Leu Ser Lys Asn His Gln Asn Thr Asn Pro 50 55 60		
Glu Gly Thr Ser Ala Gly Thr Pro Asp Glu Ala Ala Pro Leu Ala Glu 65 70 75 80		
Arg Thr Pro Asp Thr Ala Glu Ser Leu Val Glu Lys Thr Pro Asp Glu 85 90 95		
Ala Ala Pro Leu Val Glu Arg Thr Pro Asp Thr Ala Glu Ser Leu Val 100 105 110		
Glu Lys Thr Pro Asp Glu Ala Ala Ser Leu Val Glu Gly Thr Ser Asp 115 120 125		
Lys Ile Gln Cys Leu Glu Lys Ala Thr Ser Gly Lys Phe Glu Gln Ser 130 135 140		
Ala Glu Glu Thr Pro Arg Glu Ile Thr Ser Pro Ala Lys Glu Thr Ser 145 150 155 160		
Glu Lys Phe Thr Trp Pro Ala Lys Gly Arg Pro Arg Lys Ile Ala Trp 165 170 175		
Glu Lys Lys Glu Asp Thr Pro Arg Glu Ile Met Ser Pro Ala Lys Glu 180 185 190		
Thr Ser Glu Lys Phe Thr Trp Ala Ala Lys Gly Arg Pro Arg Lys Ile 195 200 205		
Ala Trp Glu Lys Lys Glu Thr Pro Val Lys Thr Gly Cys Val Ala Arg 210 215 220		
Val Thr Ser Asn Lys Thr Lys Val Leu Glu Lys Gly Arg Ser Lys Met 225 230 235 240		

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Ile Ala Cys Pro Thr Lys Glu
245

<210> SEQ ID NO 572

<211> LENGTH: 399

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 572

Thr Lys Arg Lys Lys Thr Ile Asn Leu Asn Ile Gln Asp Ala Gln Lys
5 10 15

Arg Thr Ala Leu His Trp Ala Cys Val Asn Gly His Glu Glu Val Val
20 25 30

Thr Phe Leu Val Asp Arg Lys Cys Gln Pro Asp Val Leu Asp Gly Glu
35 40 45

His Arg Thr Pro Leu Met Lys Ala Leu Gln Cys His Gln Glu Ala Cys
50 55 60

Ala Asn Ile Leu Ile Asp Ser Gly Ala Asp Ile Asn Leu Val Asp Val
65 70 75 80

Tyr Gly Asn Met Ala Leu His Tyr Ala Val Tyr Ser Glu Ile Leu Ser
85 90 95

Val Val Ala Lys Leu Leu Ser His Gly Ala Val Ile Glu Val His Asn
100 105 110

Lys Ala Ser Leu Thr Pro Leu Leu Leu Ser Ile Thr Lys Arg Ser Glu
115 120 125

Gln Ile Val Glu Phe Leu Leu Ile Lys Asn Ala Asn Ala Asn Ala Val
130 135 140

Asn Lys Tyr Lys Cys Thr Ala Leu Met Leu Ala Val Cys His Gly Leu
145 150 155 160

Ser Glu Ile Val Gly Met Leu Leu Gln Gln Asn Val Asp Val Phe Ala
165 170 175

Ala Asp Ile Cys Gly Val Thr Ala Glu His Tyr Ala Val Thr Cys Gly
180 185 190

Phe His His Ile His Glu Gln Ile Met Glu Tyr Ile Arg Lys Leu Ser
195 200 205

Lys Asn His Gln Asn Thr Asn Pro Glu Gly Thr Ser Ala Gly Thr Pro
210 215 220

Asp Glu Ala Ala Pro Leu Ala Glu Arg Thr Pro Asp Thr Ala Glu Ser
225 230 235 240

Leu Val Glu Lys Thr Pro Asp Glu Ala Ala Pro Leu Val Glu Arg Thr
245 250 255

Pro Asp Thr Ala Glu Ser Leu Val Glu Lys Thr Pro Asp Glu Ala Ala
260 265 270

Ser Leu Val Glu Gly Thr Ser Asp Lys Ile Gln Cys Leu Glu Lys Ala
275 280 285

Thr Ser Gly Lys Phe Glu Gln Ser Ala Glu Glu Thr Pro Arg Glu Ile
290 295 300

Thr Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Pro Ala Lys
305 310 315 320

Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Asp Thr Pro Arg
325 330 335

Glu Ile Met Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Ala
340 345 350

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Ala Lys Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Thr Pro
355 360 365

Val Lys Thr Gly Cys Val Ala Arg Val Thr Ser Asn Lys Thr Lys Val
370 375 380

Leu Glu Lys Gly Arg Ser Lys Met Ile Ala Cys Pro Thr Lys Glu
385 390 395

<210> SEQ ID NO 573
<211> LENGTH: 1349
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 573

Met Gln His His His His His His His Thr Lys Arg Lys Lys Thr Ile
5 10 15

Asn Leu Asn Ile Gln Asp Ala Gln Lys Arg Thr Ala Leu His Trp Ala
20 25 30

Cys Val Asn Gly His Glu Glu Val Val Thr Phe Leu Val Asp Arg Lys
35 40 45

Cys Gln Pro Asp Val Leu Asp Gly Glu His Arg Thr Pro Leu Met Lys
50 55 60

Ala Leu Gln Cys His Gln Glu Ala Cys Ala Asn Ile Leu Ile Asp Ser
65 70 75 80

Gly Ala Asp Ile Asn Leu Val Asp Val Tyr Gly Asn Met Ala Leu His
85 90 95

Tyr Ala Val Tyr Ser Glu Ile Leu Ser Val Val Ala Lys Leu Leu Ser
100 105 110

His Gly Ala Val Ile Glu Val His Asn Lys Ala Ser Leu Thr Pro Leu
115 120 125

Leu Leu Ser Ile Thr Lys Arg Ser Glu Gln Ile Val Glu Phe Leu Leu
130 135 140

Ile Lys Asn Ala Asn Ala Asn Ala Val Asn Lys Tyr Lys Cys Thr Ala
145 150 155 160

Leu Met Leu Ala Val Cys His Gly Leu Ser Glu Ile Val Gly Met Leu
165 170 175

Leu Gln Gln Asn Val Asp Val Phe Ala Ala Asp Ile Cys Gly Val Thr
180 185 190

Ala Glu His Tyr Ala Val Thr Cys Gly Phe His His Ile His Glu Gln
195 200 205

Ile Met Glu Tyr Ile Arg Lys Leu Ser Lys Asn His Gln Asn Thr Asn
210 215 220

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

Glu Arg Thr Pro Asp Thr Ala Glu Ser Leu Val Glu Lys Thr Pro Asp
245 250 255

Glu Ala Ala Pro Leu Val Glu Arg Thr Pro Asp Thr Ala Glu Ser Leu
260 265 270

Val Glu Lys Thr Pro Asp Glu Ala Ala Ser Leu Val Glu Gly Thr Ser
275 280 285

Asp Lys Ile Gln Cys Leu Glu Lys Ala Thr Ser Gly Lys Phe Glu Gln
290 295 300

Ser Ala Glu Glu Thr Pro Arg Glu Ile Thr Ser Pro Ala Lys Glu Thr

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305		310		315		320
Ser Glu Lys Phe Thr	Trp Pro Ala Lys Gly Arg Pro Arg Lys Ile Ala					
	325		330			335
Trp Glu Lys Lys Glu Asp Thr Pro Arg Glu Ile Met Ser Pro Ala Lys						
	340		345			350
Glu Thr Ser Glu Lys Phe Thr Trp Ala Ala Lys Gly Arg Pro Arg Lys						
	355		360		365	
Ile Ala Trp Glu Lys Lys Glu Thr Pro Val Lys Thr Gly Cys Val Ala						
	370		375		380	
Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu Lys Gly Arg Ser Lys						
	385		390		395	400
Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr Lys Ala Ser Ala Asn						
	405		410			415
Asp Gln Arg Phe Pro Ser Glu Ser Lys Gln Glu Glu Asp Glu Glu Tyr						
	420		425		430	
Ser Cys Asp Ser Arg Ser Leu Phe Glu Ser Ser Ala Lys Ile Gln Val						
	435		440		445	
Cys Ile Pro Glu Ser Ile Tyr Gln Lys Val Met Glu Ile Asn Arg Glu						
	450		455		460	
Val Glu Glu Pro Pro Lys Lys Pro Ser Ala Phe Lys Pro Ala Ile Glu						
	465		470		475	480
Met Gln Asn Ser Val Pro Asn Lys Ala Phe Glu Leu Lys Asn Glu Gln						
	485		490			495
Thr Leu Arg Ala Asp Pro Met Phe Pro Pro Glu Ser Lys Gln Lys Asp						
	500		505			510
Tyr Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser						
	515		520		525	
Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu Ile Asp						
	530		535		540	
Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asn Lys Asp Gly Leu Leu						
	545		550		555	560
Lys Ala Thr Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu						
	565		570			575
Leu Lys Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Gly Lys Pro Ser						
	580		585		590	
Ala Phe Glu Pro Ala Thr Glu Met Gln Lys Ser Val Pro Asn Lys Ala						
	595		600		605	
Leu Glu Leu Lys Asn Glu Gln Thr Trp Arg Ala Asp Glu Ile Leu Pro						
	610		615		620	
Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Asn Ser Trp Asp Thr Glu						
	625		630		635	640
Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala						
	645		650			655
Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser						
	660		665			670
Pro Val Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser						
	675		680		685	
Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala						
	690		695		700	
Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln						
	705		710		715	720

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Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu
				725					730					735	
Arg	Ala	Asp	Glu	Ile	Leu	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Asp	Tyr	Glu
			740					745					750		
Glu	Ser	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu	Thr	Val	Ser	Gln	Lys
		755				760						765			
Asp	Val	Cys	Leu	Pro	Lys	Ala	Thr	His	Gln	Lys	Glu	Ile	Asp	Lys	Ile
	770					775					780				
Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asp	Asn	Asp	Gly	Phe	Leu	Lys	Ala
785					790					795					800
Pro	Cys	Arg	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala	Leu	Glu	Leu	Met
			805						810						815
Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu	Lys	Pro	Ser	Ala	Phe
		820						825					830		
Glu	Pro	Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu
		835					840					845			
Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Gln	Met	Phe	Pro	Ser	Glu
	850					855					860				
Ser	Lys	Gln	Lys	Lys	Val	Glu	Glu	Asn	Ser	Trp	Asp	Ser	Glu	Ser	Leu
865					870					875					880
Arg	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Val	Pro	Lys	Ala	Thr	His
			885					890						895	
Gln	Lys	Glu	Met	Asp	Lys	Ile	Ser	Gly	Lys	Leu	Glu	Asp	Ser	Thr	Ser
		900						905					910		
Leu	Ser	Lys	Ile	Leu	Asp	Thr	Val	His	Ser	Cys	Glu	Arg	Ala	Arg	Glu
		915					920					925			
Leu	Gln	Lys	Asp	His	Cys	Glu	Gln	Arg	Thr	Gly	Lys	Met	Glu	Gln	Met
	930					935					940				
Lys	Lys	Lys	Phe	Cys	Val	Leu	Lys	Lys	Lys	Leu	Ser	Glu	Ala	Lys	Glu
945					950					955					960
Ile	Lys	Ser	Gln	Leu	Glu	Asn	Gln	Lys	Val	Lys	Trp	Glu	Gln	Glu	Leu
			965						970					975	
Cys	Ser	Val	Arg	Leu	Thr	Leu	Asn	Gln	Glu	Glu	Glu	Lys	Arg	Arg	Asn
		980						985					990		
Ala	Asp	Ile	Leu	Asn	Glu	Lys	Ile	Arg	Glu	Glu	Leu	Gly	Arg	Ile	Glu
		995					1000					1005			
Glu	Gln	His	Arg	Lys	Glu	Leu	Glu	Val	Lys	Gln	Gln	Leu	Glu	Gln	Ala
	1010					1015					1020				
Leu	Arg	Ile	Gln	Asp	Ile	Glu	Leu	Lys	Ser	Val	Glu	Ser	Asn	Leu	Asn
1025					1030					1035					1040
Gln	Val	Ser	His	Thr	His	Glu	Asn	Glu	Asn	Tyr	Leu	Leu	His	Glu	Asn
			1045						1050					1055	
Cys	Met	Leu	Lys	Lys	Glu	Ile	Ala	Met	Leu	Lys	Leu	Glu	Ile	Ala	Thr
		1060						1065					1070		
Leu	Lys	His	Gln	Tyr	Gln	Glu	Lys	Glu	Asn	Lys	Tyr	Phe	Glu	Asp	Ile
	1075					1080						1085			
Lys	Ile	Leu	Lys	Glu	Lys	Asn	Ala	Glu	Leu	Gln	Met	Thr	Leu	Lys	Leu
	1090					1095					1100				
Lys	Glu	Glu	Ser	Leu	Thr	Lys	Arg	Ala	Ser	Gln	Tyr	Ser	Gly	Gln	Leu
1105					1110					1115					1120

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Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser Lys Leu Lys Glu
 1125 1130 1135
 Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu Ser His His Pro
 1140 1145 1150
 Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg
 1155 1160 1165
 Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln
 1170 1175 1180
 Arg Lys Met Asn Val Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val
 1185 1190 1195 1200
 Leu His Gln Pro Leu Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys
 1205 1210 1215
 Ile Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg Glu Asn Thr Leu Val
 1220 1225 1230
 Ser Glu His Ala Gln Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys
 1235 1240 1245
 Glu Ala Glu His Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His
 1250 1255 1260
 Thr Glu Gln Gln Glu Ser Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser
 1265 1270 1275 1280
 Lys Asn Met Trp Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala
 1285 1290 1295
 Asp Asn Lys Ser Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys
 1300 1305 1310
 Met Gln His His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr
 1315 1320 1325
 Asn Asn His Leu Lys Asn Arg Ile Tyr Gln Tyr Glu Lys Glu Lys Ala
 1330 1335 1340
 Glu Thr Glu Val Ile
 1345

<210> SEQ ID NO 574
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: PCR primer

<400> SEQUENCE: 574

cacacaaaga ggaagaagac catc

24

<210> SEQ ID NO 575
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: PCR primer

<400> SEQUENCE: 575

gattcttttg taggacatgc aatcatc

27

<210> SEQ ID NO 576
 <211> LENGTH: 3720
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature

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<222> LOCATION: 1149

<223> OTHER INFORMATION: n = A,T,C or G

<400> SEQUENCE: 576

atggtggcaa cactgctgtc ctatggtgca gtcacgagg tgcaaaacaa ggctagcctc	60
acaccctttt tactggccat acagaaaaga agcaagcaaa ctgtggaatt ttactaaca	120
aaaaatgcaa atgcaaacgc atttaagtga tctaaatgca cagccctcat gcttgccata	180
tgtgaaggct catcagagat agtcggcatg cttcttcagc aaaatgttga cgtctttgct	240
gaagacatac atggaataac tgcagaacgt tatgctgctg ctcgtggagt taattacatt	300
catcaacaac ttttgaaca tatacgaaaa ttacctaaaa atcctcaaaa taccaatcca	360
gaaggaacat ctacaggaac acctgatgag gctgcaccct tggcggaaaag aacacctgac	420
acggctgaaa gcttgctgga aaaaacacct gacgaggctg cacgcttggt ggagggaacg	480
tctgccaaaa ttcaatgtct ggggaaagca acatctggaa agtttgaaca gtcaacagaa	540
gaaacaccta ggaaaatttt gaggcctaca aaagaaacat ctgagaaatt ttcattggcca	600
gcaaaagaaa gatctaggaa gatcacatgg gagaaaaag aaacatctgt aaagactgaa	660
tgcgtggcag gagtaacacc taataaaact gaagttttgg aaaaaggaac atctaatatg	720
attgcatgtc ctacaaaaga aacatctaca aaagcaagta caaatgtgga tgtgagttct	780
gtagagccta tattcagtct ttttggcaca cggactattg aaaattcaca gtgtacaaaa	840
gttgagggaag actttaatct tgctaccaag attatctcta agagtgtgtc acagaattat	900
acgtgtttac ctgatgtctac atatcaaaaa gatatcaaaa caataaatca caaaatagaa	960
gatcagatgt tcccatcaga atccaaacga gaggaagatg aagaatattc ttgggattct	1020
gggagtctct ttgagagttc tgcaaaagact caagtgtgta tacctgagtc tatgtatcag	1080
aaagtaatgg agataaatag agaagtagaa gagcttcctg agaagccatc tgccttcaag	1140
cctgccgtng aaatgcaaaa gactgttcca aataaagcct ttgaattgaa gaatgaacaa	1200
acattgagag cagctcagat gttcccatca gaatccaaac aaaaggacga tgaagaaaat	1260
tcttgggatt ctgagagtcc ctgtgagacg gtttcacaga aggatgtgta ttaccctaaa	1320
gctacacatc aaaaagaatt cgatacctta agtggaagaa tagaagagtc tctgtttaa	1380
gatggtcttc tgaagcctac ctgtggaagg aaagtttctc ttccaaataa agccttagaa	1440
ttaaaggaca gagaaacatt caaagcagag tctcctgata aagatgggtc tctgaagcct	1500
acctgtggaa ggaaagtctt tcttccaaat aaagccttag aattaaagga cagagaaaca	1560
ctcaaagcag agtctcctga taatgatggt cttctgaagc ctacctgtgg aaggaaagtt	1620
tctcttccaa ataaagcttt agaattgaag gacagagaaa cattcaaagc agctcagatg	1680
ttcccatcag aatccaaaca aaaggatgat gaagaaaatt cttgggattt tgagagtctc	1740
cttgagactc tcttacagaa tgatgtgtgt ttacccaagg ctacacatca aaaagaattc	1800
gataccttaa gtggaaaatt agaagagtct cctgataaag atggtcttct gaagcctacc	1860
tgtggaatga aaatttctct tccaaataaa gccttagaat tgaaggacag agaaacattc	1920
aaagcagagg atgtgagttc tgtagagtcc acattcagtc tttttggcaa accgactact	1980
gaaaattcac agtctacaaa agttgaggaa gactttaatc ttactaccaa ggaggagca	2040
acaaagacag taactggaca acaggaacgt gatattggca ttattgaacg agctccacaa	2100
gatcaaacaa ataagatgcc cacatcagaa ttaggaagaa aagaagatac aaaatcaact	2160

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tcagattctg agattatctc tgtgagtgat acacagaatt atgagtgttt acctgaggct 2220
acatatcaaa aagaaataaa gacaacaaat ggcaaaatag aagagtctcc tgaagagcct 2280
tctcactttg agcctgccac tgaatgcaa aactctgttc caaataaagg cttagaatgg 2340
aagaataaac aaacattgag agcagattca actaccctat caaaaatcctt ggatgcactt 2400
ccttcttgtg aaagaggaag ggaacttaaa aaagataact gtgaacaaat tacagcaaaa 2460
atggaacaaa tgaataataa gttttgtgta ctacaaaagg aactgtcaga agcgaaagaa 2520
ataaaatcac agttagagaa ccaaaaagct aaatgggaac aagagctctg cagtgtgaga 2580
ttgcctttaa atcaagaaga agagaagaga agaaatgtcg atatattaaa agaaaaaatt 2640
agacccgaag agcaacttag gaaaagtta gaagtgaac accaacttga acagactctc 2700
agaatacaag atatagaatt gaaaagtga acaagtaatt tgaatcaggt ttctcacact 2760
catgaaagtg aaaatgatct ctttcatgaa aattgcatgt tgaagaaagg aattgccatg 2820
ctaaaactgg aagtagccac actgaaacat caacaccagg tgaaggaaaa taaatacttt 2880
gaggacatta agattttaca agaaaagaat gctgaacttc aaatgaccct aaaactgaaa 2940
cagaaaaacag taacaaaaag ggcattctcag tatagagagc agcttaaagt tctgacggca 3000
gagaacacga tgctgacttc taaattgaag gaaaaacaag acaagaaat actggagaca 3060
gaaattgaat cacaccatcc tagactggct tctgctttac aagaccatga tcaaagtgtc 3120
acatcaagaa aaaaccaaga acttgctttc cacagtgcag gagatgctcc ttgcaagga 3180
ataatgaatg ttgatgtgag taatacaata tataacaatg aggtgctcca tcaaccactt 3240
tatgaagctc aaaggaaatc caaaagccca aaaattaatc tcaattatgc aggagatgat 3300
ctaagagaaa atgcattggt ttcagaacat gcacaaagag accgatgtga aacacagtgt 3360
caaatgaaga aagctgaaca catgtatcaa aatgaacaag ataatgtgga caaacacact 3420
gaacagcagg agtctctgga gcagaaatta tttcaactag aaagcaaaaa taggtggcct 3480
cgacagcaat tagttttatg acataagaaa gttaacaaaa gcaaggtaac aattaatatt 3540
cagtttcctg agatgaaaat gcaacgtcat ctaaaagaga aaaatgagga ggtattcaat 3600
tatggttaac atttaaaaga acgtatagat caatatgaaa aagagaaagc agaaagagaa 3660
gtaagtatca aaaaataata atacttttca aacttcctga aagaaagtgg ccttggtctaa 3720

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<210> SEQ ID NO 577

<211> LENGTH: 1239

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 577

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Met Val Ala Thr Leu Leu Ser Tyr Gly Ala Val Ile Glu Val Gln Asn
      5              10              15

Lys Ala Ser Leu Thr Pro Leu Leu Leu Ala Ile Gln Lys Arg Ser Lys
      20              25              30

Gln Thr Val Glu Phe Leu Leu Thr Lys Asn Ala Asn Ala Asn Ala Phe
      35              40              45

Asn Glu Ser Lys Cys Thr Ala Leu Met Leu Ala Ile Cys Glu Gly Ser
      50              55              60

Ser Glu Ile Val Gly Met Leu Leu Gln Gln Asn Val Asp Val Phe Ala
      65              70              75              80

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Glu	Asp	Ile	His	Gly	Ile	Thr	Ala	Glu	Arg	Tyr	Ala	Ala	Ala	Arg	Gly
				85					90					95	
Val	Asn	Tyr	Ile	His	Gln	Gln	Leu	Leu	Glu	His	Ile	Arg	Lys	Leu	Pro
			100					105					110		
Lys	Asn	Pro	Gln	Asn	Thr	Asn	Pro	Glu	Gly	Thr	Ser	Thr	Gly	Thr	Pro
		115					120					125			
Asp	Glu	Ala	Ala	Pro	Leu	Ala	Glu	Arg	Thr	Pro	Asp	Thr	Ala	Glu	Ser
	130					135					140				
Leu	Leu	Glu	Lys	Thr	Pro	Asp	Glu	Ala	Ala	Arg	Leu	Val	Glu	Gly	Thr
145					150					155					160
Ser	Ala	Lys	Ile	Gln	Cys	Leu	Gly	Lys	Ala	Thr	Ser	Gly	Lys	Phe	Glu
			165						170					175	
Gln	Ser	Thr	Glu	Glu	Thr	Pro	Arg	Lys	Ile	Leu	Arg	Pro	Thr	Lys	Glu
		180						185					190		
Thr	Ser	Glu	Lys	Phe	Ser	Trp	Pro	Ala	Lys	Glu	Arg	Ser	Arg	Lys	Ile
		195				200						205			
Thr	Trp	Glu	Glu	Lys	Glu	Thr	Ser	Val	Lys	Thr	Glu	Cys	Val	Ala	Gly
	210					215					220				
Val	Thr	Pro	Asn	Lys	Thr	Glu	Val	Leu	Glu	Lys	Gly	Thr	Ser	Asn	Met
225					230					235					240
Ile	Ala	Cys	Pro	Thr	Lys	Glu	Thr	Ser	Thr	Lys	Ala	Ser	Thr	Asn	Val
			245						250					255	
Asp	Val	Ser	Ser	Val	Glu	Pro	Ile	Phe	Ser	Leu	Phe	Gly	Thr	Arg	Thr
		260						265					270		
Ile	Glu	Asn	Ser	Gln	Cys	Thr	Lys	Val	Glu	Glu	Asp	Phe	Asn	Leu	Ala
		275					280					285			
Thr	Lys	Ile	Ile	Ser	Lys	Ser	Ala	Ala	Gln	Asn	Tyr	Thr	Cys	Leu	Pro
	290					295					300				
Asp	Ala	Thr	Tyr	Gln	Lys	Asp	Ile	Lys	Thr	Ile	Asn	His	Lys	Ile	Glu
305					310					315					320
Asp	Gln	Met	Phe	Pro	Ser	Glu	Ser	Lys	Arg	Glu	Glu	Asp	Glu	Glu	Tyr
			325						330				335		
Ser	Trp	Asp	Ser	Gly	Ser	Leu	Phe	Glu	Ser	Ser	Ala	Lys	Thr	Gln	Val
		340					345						350		
Cys	Ile	Pro	Glu	Ser	Met	Tyr	Gln	Lys	Val	Met	Glu	Ile	Asn	Arg	Glu
		355					360					365			
Val	Glu	Glu	Leu	Pro	Glu	Lys	Pro	Ser	Ala	Phe	Lys	Pro	Ala	Val	Glu
	370					375					380				
Met	Gln	Lys	Thr	Val	Pro	Asn	Lys	Ala	Phe	Glu	Leu	Lys	Asn	Glu	Gln
385					390					395					400
Thr	Leu	Arg	Ala	Ala	Gln	Met	Phe	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Asp
			405						410					415	
Asp	Glu	Glu	Asn	Ser	Trp	Asp	Ser	Glu	Ser	Pro	Cys	Glu	Thr	Val	Ser
			420				425						430		
Gln	Lys	Asp	Val	Tyr	Leu	Pro	Lys	Ala	Thr	His	Gln	Lys	Glu	Phe	Asp
		435					440					445			
Thr	Leu	Ser	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Val	Lys	Asp	Gly	Leu	Leu
	450					455					460				
Lys	Pro	Thr	Cys	Gly	Arg	Lys	Val	Ser	Leu	Pro	Asn	Lys	Ala	Leu	Glu
465					470					475					480
Leu	Lys	Asp	Arg	Glu	Thr	Phe	Lys	Ala	Glu	Ser	Pro	Asp	Lys	Asp	Gly

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485								490				495			
Leu	Leu	Lys	Pro	Thr	Cys	Gly	Arg	Lys	Val	Ser	Leu	Pro	Asn	Lys	Ala
			500					505				510			
Leu	Glu	Leu	Lys	Asp	Arg	Glu	Thr	Leu	Lys	Ala	Glu	Ser	Pro	Asp	Asn
			515				520				525				
Asp	Gly	Leu	Leu	Lys	Pro	Thr	Cys	Gly	Arg	Lys	Val	Ser	Leu	Pro	Asn
		530				535				540					
Lys	Ala	Leu	Glu	Leu	Lys	Asp	Arg	Glu	Thr	Phe	Lys	Ala	Ala	Gln	Met
545					550				555			560			
Phe	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Asp	Asp	Glu	Glu	Asn	Ser	Trp	Asp
			565						570			575			
Phe	Glu	Ser	Phe	Leu	Glu	Thr	Leu	Leu	Gln	Asn	Asp	Val	Cys	Leu	Pro
			580						585			590			
Lys	Ala	Thr	His	Gln	Lys	Glu	Phe	Asp	Thr	Leu	Ser	Gly	Lys	Leu	Glu
			595			600						605			
Glu	Ser	Pro	Asp	Lys	Asp	Gly	Leu	Leu	Lys	Pro	Thr	Cys	Gly	Met	Lys
		610			615						620				
Ile	Ser	Leu	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asp	Arg	Glu	Thr	Phe
625					630						635			640	
Lys	Ala	Glu	Asp	Val	Ser	Ser	Val	Glu	Ser	Thr	Phe	Ser	Leu	Phe	Gly
			645						650			655			
Lys	Pro	Thr	Thr	Glu	Asn	Ser	Gln	Ser	Thr	Lys	Val	Glu	Glu	Asp	Phe
			660						665			670			
Asn	Leu	Thr	Thr	Lys	Glu	Gly	Ala	Thr	Lys	Thr	Val	Thr	Gly	Gln	Gln
			675			680						685			
Glu	Arg	Asp	Ile	Gly	Ile	Ile	Glu	Arg	Ala	Pro	Gln	Asp	Gln	Thr	Asn
		690			695						700				
Lys	Met	Pro	Thr	Ser	Glu	Leu	Gly	Arg	Lys	Glu	Asp	Thr	Lys	Ser	Thr
705					710						715			720	
Ser	Asp	Ser	Glu	Ile	Ile	Ser	Val	Ser	Asp	Thr	Gln	Asn	Tyr	Glu	Cys
			725						730			735			
Leu	Pro	Glu	Ala	Thr	Tyr	Gln	Lys	Glu	Ile	Lys	Thr	Thr	Asn	Gly	Lys
			740						745			750			
Ile	Glu	Glu	Ser	Pro	Glu	Lys	Pro	Ser	His	Phe	Glu	Pro	Ala	Thr	Glu
			755			760						765			
Met	Gln	Asn	Ser	Val	Pro	Asn	Lys	Gly	Leu	Glu	Trp	Lys	Asn	Lys	Gln
		770			775						780				
Thr	Leu	Arg	Ala	Asp	Ser	Thr	Thr	Leu	Ser	Lys	Ile	Leu	Asp	Ala	Leu
785					790						795			800	
Pro	Ser	Cys	Glu	Arg	Gly	Arg	Glu	Leu	Lys	Lys	Asp	Asn	Cys	Glu	Gln
			805						810			815			
Ile	Thr	Ala	Lys	Met	Glu	Gln	Met	Lys	Asn	Lys	Phe	Cys	Val	Leu	Gln
			820						825			830			
Lys	Glu	Leu	Ser	Glu	Ala	Lys	Glu	Ile	Lys	Ser	Gln	Leu	Glu	Asn	Gln
			835			840						845			
Lys	Ala	Lys	Trp	Glu	Gln	Glu	Leu	Cys	Ser	Val	Arg	Leu	Pro	Leu	Asn
		850			855						860				
Gln	Glu	Glu	Glu	Lys	Arg	Arg	Asn	Val	Asp	Ile	Leu	Lys	Glu	Lys	Ile
865					870						875			880	
Arg	Pro	Glu	Glu	Gln	Leu	Arg	Lys	Lys	Leu	Glu	Val	Lys	His	Gln	Leu
			885						890			895			

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Glu Gln Thr Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Thr Ser
 900 905 910
 Asn Leu Asn Gln Val Ser His Thr His Glu Ser Glu Asn Asp Leu Phe
 915 920 925
 His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu Glu
 930 935 940
 Val Ala Thr Leu Lys His Gln His Gln Val Lys Glu Asn Lys Tyr Phe
 945 950 955 960
 Glu Asp Ile Lys Ile Leu Gln Glu Lys Asn Ala Glu Leu Gln Met Thr
 965 970 975
 Leu Lys Leu Lys Gln Lys Thr Val Thr Lys Arg Ala Ser Gln Tyr Arg
 980 985 990
 Glu Gln Leu Lys Val Leu Thr Ala Glu Asn Thr Met Leu Thr Ser Lys
 995 1000 1005
 Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Thr Glu Ile Glu Ser
 1010 1015 1020
 His His Pro Arg Leu Ala Ser Ala Leu Gln Asp His Asp Gln Ser Val
 1025 1030 1035 1040
 Thr Ser Arg Lys Asn Gln Glu Leu Ala Phe His Ser Ala Gly Asp Ala
 1045 1050 1055
 Pro Leu Gln Gly Ile Met Asn Val Asp Val Ser Asn Thr Ile Tyr Asn
 1060 1065 1070
 Asn Glu Val Leu His Gln Pro Leu Tyr Glu Ala Gln Arg Lys Ser Lys
 1075 1080 1085
 Ser Pro Lys Ile Asn Leu Asn Tyr Ala Gly Asp Asp Leu Arg Glu Asn
 1090 1095 1100
 Ala Leu Val Ser Glu His Ala Gln Arg Asp Arg Cys Glu Thr Gln Cys
 1105 1110 1115 1120
 Gln Met Lys Lys Ala Glu His Met Tyr Gln Asn Glu Gln Asp Asn Val
 1125 1130 1135
 Asp Lys His Thr Glu Gln Gln Glu Ser Leu Glu Gln Lys Leu Phe Gln
 1140 1145 1150
 Leu Glu Ser Lys Asn Arg Trp Leu Arg Gln Gln Leu Val Tyr Ala His
 1155 1160 1165
 Lys Lys Val Asn Lys Ser Lys Val Thr Ile Asn Ile Gln Phe Pro Glu
 1170 1175 1180
 Met Lys Met Gln Arg His Leu Lys Glu Lys Asn Glu Glu Val Phe Asn
 1185 1190 1195 1200
 Tyr Gly Asn His Leu Lys Glu Arg Ile Asp Gln Tyr Glu Lys Glu Lys
 1205 1210 1215
 Ala Glu Arg Glu Val Ser Ile Lys Lys Tyr Lys Tyr Phe Ser Asn Phe
 1220 1225 1230
 Leu Lys Glu Ser Gly Leu Gly
 1235

<210> SEQ ID NO 578

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 578

Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile

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	5	10	15
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Tyr Gln Tyr Glu
20

<210> SEQ ID NO 579
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 579

Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu Ser Leu Asp			
	5	10	15

Gln Lys Leu Phe
20

<210> SEQ ID NO 580
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 580

Thr Glu Gln Gln Glu Ser Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser			
	5	10	15

Lys Asn Met Trp
20

<210> SEQ ID NO 581
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 581

Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr Ser Gly Gln Leu			
	5	10	15

Lys Val Leu Ile
20

<210> SEQ ID NO 582
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 582

Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser			
	5	10	15

Ser Thr Ile Tyr
20

<210> SEQ ID NO 583
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 583

Arg Lys Met Asn Val Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val			
	5	10	15

Leu His Gln Pro
20

-continued

<210> SEQ ID NO 584
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 584

Met Gly Thr Arg Ala Leu Gln Cys Glu Val Ser His Thr His Glu Asn
 5 10 15

Glu Asn Tyr Leu
 20

<210> SEQ ID NO 585
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 585

Glu Val Ser His Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn
 5 10 15

Cys Met Leu Lys
 20

<210> SEQ ID NO 586
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 586

Glu Asn Tyr Leu Leu His Glu Asn Leu Met Leu Lys Lys Glu Ile Ala
 5 10 15

Met Leu Lys Leu
 20

<210> SEQ ID NO 587
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 587

Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala
 5 10 15

Thr Leu Lys His Gln
 20

<210> SEQ ID NO 588
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 588

Met Leu Thr Ser Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu
 5 10 15

Ala Glu Ile Glu
 20

<210> SEQ ID NO 589
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 589

-continued

Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu Ser His His Pro
5 10 15

Arg Leu Ala Ser
20

<210> SEQ ID NO 590
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 590

Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp
5 10 15

His Asp Gln Ile
20

<210> SEQ ID NO 591
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 591

Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg
5 10 15

Lys Ser Gln Glu
20

<210> SEQ ID NO 592
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 592

His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His
5 10 15

Ile Ala Gly Asp
20

<210> SEQ ID NO 593
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 593

Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln
5 10 15

Arg Lys Met Asn
20

<210> SEQ ID NO 594
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 594

Met Gly Thr Arg Ala Leu Gln Cys Glu Val Ser His Thr His Glu Asn
1 5 10 15

Glu Asn Tyr Leu
20

-continued

<210> SEQ ID NO 595
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 595

Ser His Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn Cys Met
1 5 10 15

Leu Lys Lys Glu
20

<210> SEQ ID NO 596
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 596

Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu
1 5 10 15

Glu Ile Ala Thr
20

<210> SEQ ID NO 597
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 597

Ile Ala Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His Gln Tyr Gln
1 5 10 15

Glu Lys Glu Asn
20

<210> SEQ ID NO 598
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 598

Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile
1 5 10 15

Lys Ile Leu Lys
20

<210> SEQ ID NO 599
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 599

Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu
1 5 10 15

Gln Met Thr Leu
20

<210> SEQ ID NO 600
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

-continued

<400> SEQUENCE: 600

Glu Lys Asn Ala Glu Leu Gln Met Thr Leu Lys Leu Lys Glu Glu Ser
1 5 10 15

Leu Thr Lys Arg
20

<210> SEQ ID NO 601

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 601

Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr Ser Gly
1 5 10 15

Gln Leu Lys Val
20

<210> SEQ ID NO 602

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 602

Ala Ser Gln Tyr Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr
1 5 10 15

Met Leu Thr Ser
20

<210> SEQ ID NO 603

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 603

Leu Ile Ala Glu Asn Thr Met Leu Thr Ser Lys Leu Lys Glu Lys Gln
1 5 10 15

Asp Lys Glu Ile
20

<210> SEQ ID NO 604

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 604

Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu
1 5 10 15

Ser His His Pro
20

<210> SEQ ID NO 605

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 605

Leu Glu Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser Ala Val
1 5 10 15

-continued

Gln Asp His Asp
20

<210> SEQ ID NO 606
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 606

Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg
1 5 10 15

Lys Ser Gln Glu
20

<210> SEQ ID NO 607
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 607

Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile
1 5 10 15

Ala Gly Asp Ala Cys Leu
20

<210> SEQ ID NO 608
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 608

Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn
1 5 10 15

Val Asp Val Ser
20

<210> SEQ ID NO 609
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 609

Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Ile Tyr Asn Asn
1 5 10 15

Glu Val Leu His
20

<210> SEQ ID NO 610
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 610

Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Ser Glu Ala
1 5 10 15

Gln Arg Lys Ser
20

<210> SEQ ID NO 611
<211> LENGTH: 21

-continued

<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 611

His Gln Pro Leu Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile
1 5 10 15

Asn Leu Asn Tyr Ala
20

<210> SEQ ID NO 612
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 612

Lys Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg Glu
1 5 10 15

Asn Thr Leu Val
20

<210> SEQ ID NO 613
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 613

Gly Asp Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg
1 5 10 15

Asp Gln Arg Glu
20

<210> SEQ ID NO 614
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 614

Ser Glu His Ala Gln Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys
1 5 10 15

Glu Ala Glu His
20

<210> SEQ ID NO 615
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 615

Thr Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr Gln Asn Glu Gln
1 5 10 15

Asp Asn Val Asn
20

<210> SEQ ID NO 616
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 616

Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln

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1	5	10	15
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Glu Ser Leu Asp
20

<210> SEQ ID NO 617
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 617

Lys His Thr Glu Gln Gln Glu Ser Leu Asp Gln Lys Leu Phe Gln Leu
1 5 10 15

Gln Ser Lys Asn
20

<210> SEQ ID NO 618
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 618

Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln
1 5 10 15

Gln Leu Val His Ala
20

<210> SEQ ID NO 619
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 619

Met Trp Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala Asp Asn
1 5 10 15

Lys Ser Lys Ile
20

<210> SEQ ID NO 620
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 620

His Lys Lys Ala Asp Asn Lys Ser Lys Ile Thr Ile Asp Ile His Phe
1 5 10 15

Leu Glu Arg Lys
20

<210> SEQ ID NO 621
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 621

Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu Leu
1 5 10 15

Lys Glu Lys Asn
20

-continued

<210> SEQ ID NO 622
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 622

Met Gln His His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr
1 5 10 15

Asn Asn His Leu
20

<210> SEQ ID NO 623
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 623

Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile Tyr Gln
1 5 10 15

Tyr Glu Lys Glu
20

<210> SEQ ID NO 624
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 624

Asn His Leu Lys Asn Arg Ile Tyr Gln Tyr Glu Lys Glu Lys Ala Glu
1 5 10 15

Thr Glu Val Ile
20

<210> SEQ ID NO 625
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 625

Leu Thr Leu Asn Gln Glu Glu Glu Lys Arg Arg Asn Ala Asp Ile Leu
1 5 10 15

Asn Glu Lys Ile Arg Glu Glu Leu Gly Cys Gly
20 25

<210> SEQ ID NO 626
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 626

Ile Arg Glu Glu Leu Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu
1 5 10 15

Glu Val Lys Gln Gln Leu Glu Gln Ala Leu Gly Cys Gly
20 25

<210> SEQ ID NO 627
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 627

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Leu	Glu	Gln	Ala	Leu	Arg	Ile	Gln	Asp	Ile	Glu	Leu	Lys	Ser	Val	Glu
1				5				10						15	
Ser	Asn	Leu	Asn	Gln	Gly	Cys	Gly								
			20												

What is claimed:

1. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

- (d) sequences set forth in SEQ ID NO:594-627;
- (e) sequences having at least 70% identity to a sequence set forth in SEQ ID NO:594-627; and
- (f) sequences having at least 90% identity to a sequence set forth in SEQ ID NO:594-627.

2. An expression vector comprising a polynucleotide encoding a polypeptide of claim 1 operably linked to an expression control sequence.

3. A host cell transformed or transfected with an expression vector according to claim 2.

4. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 1.

5. A method for detecting the presence of a cancer in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with a binding agent that binds to a polypeptide of claim 1;
- (c) detecting in the sample an amount of polypeptide that binds to the binding agent; and
- (d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of a cancer in the patient.

6. A fusion protein comprising at least one polypeptide according to claim 1.

7. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

- (a) polypeptides according to claim 1;
- (b) polynucleotides encoding a polypeptide according to claim 1;
- (c) antibodies according to claim 4;
- (d) fusion proteins according to claim 6;
- (e) antigen presenting cells that express a polypeptide according to claim 1.

8. A method for stimulating an immune response in a patient, comprising administering to the patient a composition of claim 7.

9. A method for the treatment of a cancer in a patient, comprising administering to the patient a composition of claim 7.

10. A diagnostic kit comprising at least one antibody according to claim 4 and a detection reagent, wherein the detection reagent comprises a reporter group.

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