

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
29 November 2001 (29.11.2001)

PCT

(10) International Publication Number
WO 01/90358 A2

(51) International Patent Classification⁷: **C12N 15/12**,
C07K 14/715, 16/18, G01N 33/53, C12N 5/10

(21) International Application Number: PCT/US01/16767

(22) International Filing Date: 23 May 2001 (23.05.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/206,862 24 May 2000 (24.05.2000) US

(71) Applicant: **SCHERING CORPORATION** [US/US];
2000 Galloping Hill Road, Kenilworth, NJ 07033-0530
(US).

(72) Inventor: **GORMAN, Daniel, M.**; 6371 Central Avenue,
Newark, CA 94560 (US).

(74) Agent: **ZARADIC, Sandy**; Schering-Plough Corpora-
tion, Patent Department, K-6-1, 1990, 2000 Galloping Hill
Road, Kenilworth, NJ 07033-0530 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CZ,
DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, HR, HU,
ID, IL, IN, IS, JP, KG, KR, KZ, LC, LK, LR, LT, LU, LV,
MA, MD, MG, MK, MN, MX, MZ, NO, NZ, PL, PT, RO,
RU, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UZ, VN,
YU, ZA.

(84) Designated States (*regional*): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:

— *as to the applicant's entitlement to claim the priority of the
earlier application (Rule 4.17(iii)) for all designations*

Published:

— *without international search report and to be republished
upon receipt of that report*

*For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.*

(54) Title: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS

(57) Abstract: Nucleic acids encoding mammalian, e.g., primate, receptors, purified receptor proteins and fragments thereof. Anti-
bodies, both polyclonal and monoclonal, are also provided. Methods of using the compositions for both diagnostic and therapeutic
utilities are described.



WO 01/90358 A2

5

MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS

10

FIELD OF THE INVENTION

The present invention relates to compositions and methods for affecting mammalian physiology, including immune system function. In particular, it provides methods to regulate development and/or the immune system. Diagnostic and therapeutic uses of these materials are also disclosed.

15

BACKGROUND OF THE INVENTION

Recombinant DNA technology refers generally to techniques of integrating genetic information from a donor source into vectors for subsequent processing, such as through introduction into a host, whereby the transferred genetic information is copied and/or expressed in the new environment. Commonly, the genetic information exists in the form of complementary DNA (cDNA) derived from messenger RNA (mRNA) coding for a desired protein product. The carrier is frequently a plasmid having the capacity to incorporate cDNA for later replication in a host and, in some cases, actually to control expression of the cDNA and thereby direct synthesis of the encoded product in the host. See, e.g., Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual, (2d ed.) vols. 1-3, CSH Press, NY.

25

30

35

For some time, it has been known that the mammalian immune response is based on a series of complex cellular interactions, called the "immune network". Recent research has provided new insights into the inner workings of this network. While it remains clear that much of the immune response does, in fact, revolve around the network-like interactions of lymphocytes, macrophages, granulocytes, and other cells, immunologists now generally hold the opinion that soluble proteins, known as lymphokines, cytokines, or monokines, play critical roles in controlling these cellular interactions. Thus, there is considerable interest in the isolation, characterization, and mechanisms of action of cell modulatory factors, an understanding of which will lead to significant advancements in the diagnosis and therapy of numerous medical abnormalities, e.g., immune system disorders.

The immune system of vertebrates consists of a number of organs and several different cell types. Two major cell types include the myeloid and lymphoid lineages. Among the lymphoid cell lineage are B cells, which were originally characterized as differentiating in fetal liver or adult bone marrow, and T cells, which were originally characterized as differentiating in the thymus. See, e.g., Paul (ed. 1998) Fundamental Immunology (4th ed.) Raven Press, New York; and Thomson (ed. 1994) The Cytokine Handbook 2d ed., Academic Press, San Diego. Lymphokines apparently mediate cellular activities in a variety of ways. They have been shown to support the proliferation, growth, and/or differentiation of cells, e.g., pluripotential hematopoietic stem cells, into vast numbers of progenitors comprising diverse cellular lineages which make up a complex immune system. Proper and balanced interactions between the cellular components are necessary for a healthy immune response. The different cellular lineages often respond in a different manner when lymphokines are administered in conjunction with other agents.

Cell lineages especially important to the immune response include two classes of lymphocytes: B-cells, which can produce and secrete immunoglobulins (proteins with the capability of recognizing and binding to foreign matter to effect its removal), and T-cells of various subsets that secrete lymphokines and induce or suppress the B-cells and various other cells (including other T-cells) making up the immune network. These lymphocytes interact with many other cell types.

Research to better understand and treat various immune disorders has been hampered by the general inability to maintain cells of the immune system in vitro. Immunologists have discovered that culturing many of these cells can be accomplished through the use of T-cell and other cell supernatants, which contain various growth factors, including many of the lymphokines.

Various growth and regulatory factors exist which modulate morphogenetic development. And many receptors for cytokines are also known. Often there are at least two critical subunits in the functional receptor. See, e.g., Gonda and D'Andrea (1997) Blood 89:355-369; Presky, et al. (1996) Proc. Nat'l Acad. Sci. USA 93:14002-14007; Drachman and Kaushansky (1995) Curr. Opin. Hematol. 2:22-28; Theze (1994) Eur. Cytokine Netw. 5:353-368; and Lemmon and Schlessinger (1994) Trends Biochem. Sci. 19:459-463.

From the foregoing, it is evident that the discovery and development of new soluble proteins and their receptors, including ones similar to lymphokines, should contribute to new therapies for a wide range of degenerative or abnormal conditions which directly or indirectly involve development, differentiation, or function, e.g., of the

immune system and/or hematopoietic cells. In particular, the discovery and understanding of novel receptors for lymphokine-like molecules which enhance or potentiate the beneficial activities of other lymphokines would be highly advantageous. However, the lack of understanding of how the immune system is regulated or differentiates has blocked the ability to advantageously modulate the normal defensive mechanisms to biological challenges. Medical conditions characterized by abnormal or inappropriate regulation of the development or physiology of relevant cells thus remain unmanageable. The discovery and characterization of specific cytokines and their receptors will contribute to the development of therapies for a broad range of degenerative or other conditions which affect the immune system, hematopoietic cells, as well as other cell types. The present invention provides new receptors for ligands exhibiting similarity to cytokine like compositions and related compounds, and methods for their use.

SUMMARY OF THE INVENTION

The present invention is directed to novel receptors related to cytokine receptors, e.g., primate, cytokine receptor like molecular structures, designated DNAX Cytokine Receptor Subunits (DCRS), and their biological activities. In particular, it provides description of various subunits, designated DCRS6, DCRS7, DCRS8, DCRS9, and DCRS10. Primate, e.g, human, and rodent, e.g., mouse, embodiments of the various subunits are provided. It includes nucleic acids coding for the polypeptides themselves and methods for their production and use. The nucleic acids of the invention are characterized, in part, by their homology to cloned complementary DNA (cDNA) sequences enclosed herein.

The present invention provides a composition of matter selected from: a substantially pure or recombinant polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 2, 5, 8, 11, 23, or 26; a substantially pure or recombinant polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 14; a substantially pure or recombinant polypeptide comprising at least two distinct nonoverlapping segments of at least five amino acids identical to segments of SEQ ID NO: 14; a natural sequence DCRS8 comprising mature SEQ ID NO: 14; a fusion polypeptide comprising DCRS8 sequence; a substantially pure or recombinant polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 17 or 20; a substantially pure or recombinant polypeptide comprising at least two distinct nonoverlapping segments of at least five amino acids identical to segments of SEQ ID NO: 17 or 20; a natural

sequence DCRS9 comprising mature SEQ ID NO: 17 or 20; or a fusion polypeptide comprising DCRS9 sequence. Preferably, wherein the distinct nonoverlapping segments of identity include: one of at least eight amino acids; one of at least four amino acids and a second of at least five amino acids; at least three segments of at least four, five, and six amino acids, or one of at least twelve amino acids. In other embodiments, the:

polypeptide: comprises a mature sequence of Tables 1, 2, 3, 4, or 5; is an unglycosylated form of DCRS8 or DCRS9; is from a primate, such as a human; comprises at least seventeen amino acids of SEQ ID NO: 14 or 17; exhibits at least four nonoverlapping segments of at least seven amino acids of SEQ ID NO: 14 or 17; is a natural allelic variant of DCRS8 or DCRS9; has a length at least about 30 amino acids; exhibits at least two non-overlapping epitopes which are specific for a primate DCRS8 or DCRS9; is glycosylated; has a molecular weight of at least 30 kD with natural glycosylation; is a synthetic polypeptide; is attached to a solid substrate; is conjugated to another chemical moiety; is a 5-fold or less substitution from natural sequence; or is a deletion or insertion variant from a natural sequence.

The invention further embraces a composition comprising: a substantially pure DCRS8 or DCRS9 and another cytokine receptor family member; a sterile DCRS8 or DCRS9 polypeptide; the DCRS8 or DCRS9 polypeptide and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration. Additional embodiments include a polypeptide comprising: mature protein sequence of Tables 1, 2, 3, 4, or 5; a detection or purification tag, including a FLAG, His6, or Ig sequence; or sequence of another cytokine receptor protein. Kit embodiments include ones comprising a described polypeptide, and: a compartment comprising the protein or polypeptide; or instructions for use or disposal of reagents in the kit.

Binding compositions are provided, e.g., comprising an antigen binding site from an antibody, which specifically binds to a natural DCRS8 or DCRS9 polypeptide, wherein: the binding compound is in a container; the DCRS8 or DCRS9 polypeptide is from a human; the binding compound is an Fv, Fab, or Fab2 fragment; the binding compound is conjugated to another chemical moiety; or the antibody: is raised against a peptide sequence of a mature polypeptide of Table 3 or 4; is raised against a mature DCRS8 or DCRS9; is raised to a purified human DCRS8 or DCRS9; is immunoselected; is a polyclonal antibody; binds to a denatured DCRS8 or DCRS9; exhibits a Kd to antigen of at least 30 μ M; is attached to a solid substrate, including a bead or plastic membrane; is in a sterile composition; or is detectably labeled, including a radioactive or fluorescent label. Kits include ones comprising such a binding compound, and: a compartment

comprising the binding compound; or instructions for use or disposal of reagents in the kit.

The invention also provides methods of producing an antigen:antibody complex, comprising contacting under appropriate conditions a primate DCRS8 or DCRS9

5 polypeptide with a described antibody, thereby allowing the complex to form. Preferred methods include ones wherein: the complex is purified from other cytokine receptors; the complex is purified from other antibody; the contacting is with a sample comprising an interferon; the contacting allows quantitative detection of the antigen; the contacting is with a sample comprising the antibody; or the contacting allows quantitative detection of
10 the antibody. Further compositions include those comprising: a sterile binding compound, as described, or the binding compound and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration.

Nucleic acid compositions include an isolated or recombinant nucleic acid
15 encoding a described polypeptide wherein the: DCRS8 or DCRS9 is from a human; or the nucleic acid: encodes an antigenic peptide sequence of Table 3 or 4; encodes a plurality of antigenic peptide sequences of Table 3 or 4; exhibits identity over at least thirteen nucleotides to a natural cDNA encoding the segment; is an expression vector; further comprises an origin of replication; is from a natural source; comprises a detectable label;
20 comprises synthetic nucleotide sequence; is less than 6 kb, preferably less than 3 kb; is from a primate; comprises a natural full length coding sequence; is a hybridization probe for a gene encoding the DCRS8 or DCRS9; or is a PCR primer, PCR product, or mutagenesis primer. Also provided are a cell or tissue comprising such a recombinant nucleic acid, e.g., where the cell is: a prokaryotic cell; a eukaryotic cell; a bacterial cell; a
25 yeast cell; an insect cell; a mammalian cell; a mouse cell; a primate cell; or a human cell.

Kit embodiments include those comprising a described nucleic acid and: a compartment comprising the nucleic acid; a compartment further comprising a primate DCRS8 or DCRS9 polypeptide; or instructions for use or disposal of reagents in the kit.

Other nucleic acids provided include ones which: hybridize under wash conditions
30 of 30 minutes at 30° C and less than 2M salt to the coding portion of SEQ ID NO: 13 or 16; or exhibit identity over a stretch of at least about 30 nucleotides to a primate DCRS8 or DCRS9. Preferably, such will be nucleic acids where: the wash conditions are: at 45° C and/or 500 mM salt; at 55° C and/or 150 mM salt; or the stretch is at least 55 or 75 nucleotides.

35 Also provided are methods of modulating physiology or development of a cell or tissue culture cells comprising contacting the cell with an agonist or antagonist of a

mammalian DCRS8 or DCRS9. Preferably, the cell is transformed with a nucleic acid encoding the DCRS8 or DCRS9 and another cytokine receptor subunit.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

5

OUTLINE

I. General

II. Activities

III. Nucleic acids

- 10 A. encoding fragments, sequence, probes
 B. mutations, chimeras, fusions
 C. making nucleic acids
 D. vectors, cells comprising

IV. Proteins, Peptides

- 15 A. fragments, sequence, immunogens, antigens
 B. muteins
 C. agonists/antagonists, functional equivalents
 D. making proteins

V. Making nucleic acids, proteins

- 20 A. synthetic
 B. recombinant
 C. natural sources

VI. Antibodies

- 25 A. polyclonals
 B. monoclonal
 C. fragments; Kd
 D. anti-idiotypic antibodies
 E. hybridoma cell lines

VII. Kits and Methods to quantify DCRSs

- 30 A. ELISA
 B. assay mRNA encoding
 C. qualitative/quantitative
 D. kits

VIII. Therapeutic compositions, methods

- 35 A. combination compositions
 B. unit dose
 C. administration

IX. Screening

X. Ligands

40

I. General

The present invention provides the amino acid sequence and DNA sequence of mammalian, herein primate, cytokine receptor-like subunit molecules, these designated DNAX Cytokine Receptor Subunits 6 (DCRS6), 7 (DCRS7), 8 (DCRS8), 9 (DCRS9),
 45 and 10 (DCRS10) having particular defined properties, both structural and biological.

Various cDNAs encoding these molecules were obtained from primate, e.g., human, and/or rodent, e.g., mouse, cDNA sequence libraries. Other primate or other mammalian counterparts would also be desired.

Some of the standard methods applicable are described or referenced, e.g., in
 5 Maniatis, et al. (1982) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor Press; Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual, (2d ed.), vols. 1-3, CSH Press, NY; Ausubel, et al., Biology, Greene Publishing Associates, Brooklyn, NY; or Ausubel, et al. (1987 and periodic supplements) Current Protocols in Molecular Biology, Greene/Wiley, New York; each of which is
 10 incorporated herein by reference.

Nucleotide (SEQ ID NO: 1) and corresponding amino acid sequence (SEQ ID NO: 2) of a primate, e.g., human, DCRS6 coding segment is shown in Table 1 along with reverse translation (SEQ ID NO: 3). Rodent, e.g., mouse, counterpart sequences are provided, e.g., SEQ ID NO: 4-6.

15 Similarly, nucleotide (SEQ ID NO: 7) and corresponding amino acid sequence (SEQ ID NO: 8) of a primate, e.g., human, DCRS7 coding segment is shown in Table 2 along with reverse translation (SEQ ID NO: 9). Rodent, e.g., mouse, counterpart sequences are provided, e.g., SEQ ID NO: 10-12. Nucleotide (SEQ ID NO: 13) and corresponding amino acid sequence (SEQ ID NO: 14) of a primate, e.g., human, DCRS8
 20 coding segment is shown in Table 3 along with reverse translation (SEQ ID NO: 15).

Nucleotide (SEQ ID NO: 16) and corresponding amino acid sequence (SEQ ID NO: 17) of a primate, e.g., human, DCRS9 coding segment is shown in Table 4 along with reverse translation (SEQ ID NO: 18). Rodent, e.g., mouse, counterpart sequences are provided, e.g., SEQ ID NO: 19-21. Nucleotide (SEQ ID NO: 22) and corresponding
 25 amino acid sequence (SEQ ID NO: 23) of a primate, e.g., human, DCRS10 coding segment is shown in Table 5 along with reverse translation (SEQ ID NO: 24). Rodent, e.g., mouse, counterpart sequences are provided, e.g., SEQ ID NO: 26-27.

30 Table 1: Nucleotide and polypeptide sequences of DNAX Cytokine Receptor Subunit like embodiments (DCRS6). Primate, e.g., human, embodiment (see SEQ ID NO: 1 and 2). Predicted signal sequence indicated, but may vary by a few positions and depending upon cell type.

35	gcg atg tcg ctc gtg ctg cta agc ctg gcc gcg ctg tgc agg agc gcc	48
	Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala	
	-10 -5 -1 1	
40	gta ccc cga gag ccg acc gtt caa tgt ggc tct gaa act ggg cca tct	96
	Val Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser	
	5 10 15	

	cca gag tgg atg cta caa cat gat cta atc ccg gga gac ttg agg gac	144
	Pro Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp	
	20 25 30	
5	ctc cga gta gaa cct gtt aca act agt gtt gca aca ggg gac tat tca	192
	Leu Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser	
	35 40 45	
10	att ttg atg aat gta agc tgg gta ctc cgg gca gat gcc agc atc cgc	240
	Ile Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg	
	50 55 60 65	
15	ttg ttg aag gcc acc aag att tgt gtg acg ggc aaa agc aac ttc cag	288
	Leu Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln	
	70 75 80	
20	tcc tac agc tgt gtg agg tgc aat tac aca gag gcc ttc cag act cag	336
	Ser Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln	
	85 90 95	
	acc aga ccc tct ggt ggt aaa tgg aca ttt tcc tat atc ggc ttc cct	384
	Thr Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro	
	100 105 110	
25	gta gag ctg aac aca gtc tat ttc att ggg gcc cat aat att cct aat	432
	Val Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn	
	115 120 125	
30	gca aat atg aat gaa gat ggc cct tcc atg tct gtg aat ttc acc tca	480
	Ala Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser	
	130 135 140 145	
35	cca ggc tgc cta gac cac ata atg aaa tat aaa aaa aag tgt gtc aag	528
	Pro Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys	
	150 155 160	
40	gcc gga agc ctg tgg gat ccg aac atc act gct tgt aag aag aat gag	576
	Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu	
	165 170 175	
	gag aca gta gaa gtg aac ttc aca acc act ccc ctg gga aac aga tac	624
	Glu Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr	
	180 185 190	
45	atg gct ctt atc caa cac agc act atc atc ggg ttt tct cag gtg ttt	672
	Met Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe	
	195 200 205	
50	gag cca cac cag aag aaa caa acg cga gct tca gtg gtg att cca gtg	720
	Glu Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val	
	210 215 220 225	
55	act ggg gat agt gaa ggt gct acg gtg cag ctg act cca tat ttt cct	768
	Thr Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro	
	230 235 240	

	act tgt ggc agc gac tgc atc cga cat aaa gga aca gtt gtg ctc tgc	816
	Thr Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys	
	245 250 255	
5	cca caa aca ggc gtc cct ttc cct ctg gat aac aac aaa agc aag ccg	864
	Pro Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro	
	260 265 270	
10	gga ggc tgg ctg cct ctc ctc ctg ctg tct ctg ctg gtg gcc aca tgg	912
	Gly Gly Trp Leu Pro Leu Leu Leu Ser Leu Leu Val Ala Thr Trp	
	275 280 285	
15	gtg ctg gtg gca ggg atc tat cta atg tgg agg cac gaa agg atc aag	960
	Val Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys	
	290 295 300 305	
20	aag act tcc ttt tct acc acc aca cta ctg ccc ccc att aag gtt ctt	1008
	Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu	
	310 315 320	
	gtg gtt tac cca tct gaa ata tgt ttc cat cac aca att tgt tac ttc	1056
	Val Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe	
	325 330 335	
25	act gaa ttt ctt caa aac cat tgc aga agt gag gtc atc ctt gaa aag	1104
	Thr Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys	
	340 345 350	
30	tgg cag aaa aag aaa ata gca gag atg ggt cca gtg cag tgg ctt gcc	1152
	Trp Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala	
	355 360 365	
35	act caa aag aag gca gca gac aaa gtc gtc ttc ctt ctt tcc aat gac	1200
	Thr Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp	
	370 375 380 385	
40	gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag ggc agt ccc	1248
	Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro	
	390 395 400	
	agt gag aac tct caa gac ctc ttc ccc ctt gcc ttt aac ctt ttc tgc	1296
	Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys	
	405 410 415	
45	agt gat cta aga agc cag att cat ctg cac aaa tac gtg gtg gtc tac	1344
	Ser Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr	
	420 425 430	
50	ttt aga gag att gat aca aaa gac gat tac aat gct ctc agt gtc tgc	1392
	Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys	
	435 440 445	
55	ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt gca gaa ctt	1440
	Pro Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu	
	450 455 460 465	

ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca caa gcc tgc 1488
 Leu His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys
 470 475 480

5 cac gat ggc tgc tgc tcc ttg tagccaccc atgagaagca agagacctta 1539
 His Asp Gly Cys Cys Ser Leu
 485

10 aaggcttcct atcccaccaa ttacagggaa aaaacgtgtg atgatcctga agcttactat 1599
 gcagcctaca aacagcctta gtaattaaaa cattttatac caataaaaatt ttcaaataatt 1659
 gctaactaat gtagcattaa ctaacgattg gaaactacat ttacaacttc aaagctgttt 1719

15 tatacataga aatcaattac agctttaatt gaaaactgta accattttga taatgcaaca 1779
 ataaagcatc ttcagcc 1796

20 MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIIPGDLRLDLRVEPVTTSVATGDYSILMNVSWVL
 RADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIPNA
 NMNEDGPSMSVNFTSPGCLDHIMKYKKKCKVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQHSTI
 IGFSQVFEHPHQKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPOQTGVFPFLDNNKSKPG
 GWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFLQNHCR
 SEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLSNDVNSVCDGTCGKSEGPSSENSQDLFPLAFNLFCS
 DLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELHVKQQVSAGKRSQACHDGCCSL.

25

Reverse translation of primate, e.g., human, DCRS6 (SEQ ID NO: 3):

30 atgwsnytnng tnytnytnws nytngcngcn ytntgymgnw sngcngtncc nmngngarccn 60
 acngtncart gyggngwsnga racngngccn wsncngart ggatgytnca rcaygayytn 120

35 athccnggng ayytnmnga yytnmngtn garccngtna cnacnwsngt ngcnacnggn 180
 gaytaywsna thytnatgaa ygtnwsntgg gtnytnmngn cngaygcnws nathmgnyn 240
 ytnaargcna cnaarathtg ygtnacnggn aarwsnaayt tycarwsnta ywsntgygtn 300

40 mgntgyaayt ayacngargc nttycaracn caracnmgnc cnwsnggngg naartggacn 360
 ttywsntaya thggnttycc ngtngarytn aayacngtn aytyathgg ngcnayaay 420

45 athccnaayg cnaayatgaa ygargayggn ccnwsnatgw sngtnaaytt yacnwsnccn 480
 ggntgyytnng aycayathat gaartayaar aaraartgyg tnaargcngg nwsnytnng 540
 gayccnaaya thacngcntg yaaraaraay gargaracng tngargtnaa ytyacnacn 600

50 acnccnytnng gnaaymgnta yatggcnyn athcarcayw snacnathat hggnttywsn 660
 cargtnntyg arccncayca raaraarc arcnmgngcnw sngtnngtnat hccngtnacn 720

55 ggngaywsng arggngcnac ngtnarytn acnccntayt tyccnacntg yggngwsngay 780
 tgyathmgnc ayaarggnac ngtnngtnytn tgyccncara cnggngtncc nttyccnytn 840
 gayaayaaya arwsnaarcc ngngngntgg ytnccnytn tnytnytnws nytnytnngtn 900

gcnacntggg tnytngtngc nggnathtay ytnatgtggm gncaygarmg nathaaraar 960
 acnwsnttyw snacnacnac nytnytnccn ccnathaarg tnytngtngt ntayccnwsn 1020
 5 garathhtgyt tycaycayac nathtgytay ttyacngart tyytncaraa ycaytgymgn 1080
 wsnrgargtna thytngaraa rtggcaraar aaraarathg cngaratggg nccngtncar 1140
 10 tgggytngcna cncaraaraa rgcngcngay aargtngtnt tyytnytnws naaygaygtn 1200
 aaywsngtnt gygayggnac ntgyggnaar wsnrgarggnw snccnwsnga raaywsncar 1260
 gayytnnttyc cnytngcntt yaayytnntty tgywsngayy tnmgnwsnca rathcayytn 1320
 15 cayaartayg tngtngtnta yttymngnar athgayacna argaygayta yaaygcnytn 1380
 wsngtntgyt cnaartayca yytnatgaar gaygcnacng cnttytgygc ngarytnytn 1440
 20 caygtnaarc arcargtnws ngcnggnaar mgnwsncarg cntgycayga yggntgytgy 1500
 wsnytn 1506

25 Rodent, e.g., mouse embodiment (see SEQ ID NO: 4 and 5).

gat ttc agc agc cag acg cat ctg cac aaa tac ctg gag gtc tat ctt 48
 Asp Phe Ser Ser Gln Thr His Leu His Lys Tyr Leu Glu Val Tyr Leu
 1 5 10 15
 30 ggg gga gca gac ctc aaa ggc gac tat aat gcc ctg agt gtc tgc ccc 96
 Gly Gly Ala Asp Leu Lys Gly Asp Tyr Asn Ala Leu Ser Val Cys Pro
 20 25 30
 35 caa tat cat ctc atg aag gac gcc aca gct ttc cac aca gaa ctt ctc 144
 Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu
 35 40 45
 40 aag gct acg cag agc atg tca gtg aag aaa cgc tca caa gcc tgc cat 192
 Lys Ala Thr Gln Ser Met Ser Val Lys Lys Arg Ser Gln Ala Cys His
 50 55 60
 gat agc tgt tca ccc ttg tagtccaccc gggggaatag agactctgaa 240
 Asp Ser Cys Ser Pro Leu
 45 65 70
 gccttcctac tctcccttcc agtgacaaat gctgtgtgac gactctgaaa tgtgtgggag 300
 aggctgtgtg gaggtagtgc tatgtacaaa cttgctttta aactggagtt tgcaaagtca 360
 50 acctgagcat acacgcctga ggctagtcac ttggtggatt tatgaagaca acacagttac 420
 agacaataat gagtgggacc tacatttggg atatacccaa agctgggtaa tgattatcac 480
 55 tgagaaccac gcactctggc catgaggtaa taoggcactt ccctgtcagg ctgtctgtca 540
 ggttgggtct gtcttgact gcccatgctc tatgtgtcac gtagaccgtt ttgtaacatt 600
 ttaatctgtt aatgaataat ccgtttggga ggctctc 637

DFSSQTHLHKYLEVYLGGADLKG DYNALSVCPQYHLMKDATAFHTELLKATQSMSVKKRSQACHDSCSPL.

5 Reverse translation of rodent, e.g., mouse, DCRS6 (SEQ ID NO: 6):

gayttywsnw sncaracnca yytncayaar tayytnngarg tntayytnngg nggngcngay 60
 ytnaarggng aytayaaygc nytnwsngtn tgyccncart aycayytnat gaargaygcn 120
 10 acngcnttyc ayacngaryt nytnaargcn acncarwsna tgwsngtnaa raarmgnwsn 180
 cargcntgyc aygaywsntg ywsnccnytn 210

15

Table 2: Nucleotide and polypeptide sequences of DNAX Cytokine Receptor Subunit like
 embodiments (DCRS7). Primate, e.g., human, embodiment (see SEQ ID NO: 7 and 8).
 Predicted signal sequence indicated, but may vary by a few positions and depending upon cell
 type.

20

gagtcaggac tcccaggaca gagagtgcac aaactaccca gcacagcccc ctccgcccc 60
 tctggagggt gaagagggat tccagcccct gccaccacaca gacacgggct gactgggggtg 120

25

tctgcccccc ttggggggcan ccacagggcc tcaggcctgg gtgccacctg gcactagaag 180

atg cct gtg ccc tgg ttc ttg ctg tcc ttg gca ctg ggc cga agc cag 228
 Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser Gln
 -20 -15 -10 -5

30

tgg atc ctt tct ctg gag agg ctt gtg ggg cct cag gac gct acc cac 276
 Trp Ile Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala Thr His
 -1 1 5 10

35

tgc tct ccg ggc ctc tcc tgc cgc ctc tgg gac agt gac ata ctc tgc 324
 Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys
 15 20 25

40

ctg cct ggg gac atc gtg cct gct ccg ggc ccc gtg ctg gcg cct acg 372
 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
 30 35 40

45

cac ctg cag aca gag ctg gtg ctg agg tgc cag aag gag acc gac tgt 420
 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
 45 50 55 60

50

gac ctc tgt ctg cgt gtg gct gtc cac ttg gcc gtg cat ggg cac tgg 468
 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
 65 70 75

gaa gag cct gaa gat gag gaa aag ttt gga gga gca gct gac tta ggg 516
 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Leu Gly
 80 85 90

55

gtg gag gag cct agg aat gcc tct ctc cag gcc caa gtc gtg ctc tcc 564
 Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
 95 100 105

	ttc cag gcc tac cct act gcc cgc tgc gtc ctg ctg gag gtg caa gtg	612
	Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val	
	110 115 120	
5	cct gct gcc ctt gtg cag ttt ggt cag tct gtg ggc tct gtg gta tat	660
	Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr	
	125 130 135 140	
10	gac tgc ttc gag gct gcc cta ggg agt gag gta cga atc tgg tcc tat	708
	Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr	
	145 150 155	
15	act cag ccc agg tac gag aag gaa ctc aac cac aca cag cag ctg cct	756
	Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro	
	160 165 170	
20	gac tgc agg ggg ctc gaa gtc tgg aac agc atc ccg agc tgc tgg gcc	804
	Asp Cys Arg Gly Leu Glu Val Trp Asn Ser Ile Pro Ser Cys Trp Ala	
	175 180 185	
25	ctg ccc tgg ctc aac gtg tca gca gat ggt gac aac gtg cat ctg gtt	852
	Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu Val	
	190 195 200	
30	ctg aat gtc tct gag gag cag cac ttc ggc ctc tcc ctg tac tgg aat	900
	Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp Asn	
	205 210 215 220	
35	cag gtc cag ggc ccc cca aaa ccc cgg tgg cac aaa aac ctg act gga	948
	Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr Gly	
	225 230 235	
40	ccg cag atc att acc ttg aac cac aca gac ctg gtt ccc tgc ctc tgt	996
	Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys	
	240 245 250	
45	att cag gtg tgg cct ctg gaa cct gac tcc gtt agg acg aac atc tgc	1044
	Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile Cys	
	255 260 265	
50	ccc ttc agg gag gac ccc cgc gca cac cag aac ctc tgg caa gcc gcc	1092
	Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala Ala	
	270 275 280	
55	cga ctg cga ctg ctg acc ctg cag agc tgg ctg ctg gac gca ccg tgc	1140
	Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro Cys	
	285 290 295 300	
50	tcg ctg ccc gca gaa gcg gca ctg tgc tgg cgg gct ccg ggt ggg gac	1188
	Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly Asp	
	305 310 315	
55	ccc tgc cag cca ctg gtc cca ccg ctt tcc tgg gag aat gtc act gtg	1236
	Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr Val	
	320 325 330	
55	gac gtg aac agc tcg gag aag ctg cag ctg cag gag tgc ttg tgg gct	1284
	Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp Ala	
	335 340 345	

5	gac Asp	tcc Ser	ctg Leu	ggg Gly	cct Pro	ctc Leu	aaa Lys	gac Asp	gat Asp	gtg Val	cta Leu	ctg Leu	ttg Leu	gag Glu	aca Thr	cga Arg	1332
	350			355			360										
10	ggc Gly	ccc Pro	cag Gln	gac Asp	aac Asn	aga Arg	tcc Ser	ctc Leu	tgt Cys	gcc Ala	ttg Leu	gaa Glu	ccc Pro	agt Ser	ggc Gly	tgt Cys	1380
	365			370			375			380							
15	act Thr	tca Ser	cta Leu	ccc Pro	agc Ser	aaa Lys	gcc Ala	tcc Ser	acg Thr	agg Arg	gca Ala	gct Ala	cgc Arg	ctt Leu	gga Gly	gag Glu	1428
	385			390			395										
20	tac Tyr	tta Leu	cta Leu	caa Gln	gac Asp	ctg Leu	cag Gln	tca Ser	ggc Gly	cag Gln	tgt Cys	ctg Leu	cag Gln	cta Leu	tgg Trp	gac Asp	1476
	400			405			410										
25	gat Asp	gac Asp	ttg Leu	gga Gly	gcg Ala	cta Leu	tgg Trp	gcc Ala	tgc Cys	ccc Pro	atg Met	gac Asp	aaa Lys	tac Tyr	atc Ile	cac His	1524
	415			420			425										
30	aag Lys	cgc Arg	tgg Trp	gcc Ala	ctc Leu	gtg Val	tgg Trp	ctg Leu	gcc Ala	tgc Cys	cta Leu	ctc Leu	ttt Phe	gcc Ala	gct Ala	gcg Ala	1572
	430			435			440										
35	ctt Leu	tcc Ser	ctc Leu	atc Ile	ctc Leu	ctt Leu	ctc Leu	aaa Lys	aag Lys	gat Asp	cac His	gcg Ala	aaa Lys	ggg Gly	tgg Trp	ctg Leu	1620
	445			450			455										
40	agg Arg	ctc Leu	ttg Leu	aaa Lys	cag Gln	gac Asp	gtc Val	cgc Arg	tcg Ser	ggg Gly	gcg Ala	gcc Ala	gcc Ala	agg Arg	ggc Gly	cgc Arg	1668
	465			470										475			
45	gcg Ala	gct Ala	ctg Leu	ctc Leu	ctc Leu	tac Tyr	tca Ser	gcc Ala	gat Asp	gac Asp	tcg Ser	ggg Gly	ttc Phe	gag Glu	cgc Arg	ctg Leu	1716
	480			485			490										
50	gtg Val	ggc Gly	gcc Ala	ctg Leu	gcg Ala	tcg Ser	gcc Ala	ctg Leu	tgc Cys	cag Gln	ctg Leu	ccg Pro	ctg Leu	cgc Arg	gtg Val	gcc Ala	1764
	495			500			505										
55	gta Val	gac Asp	ctg Leu	tgg Trp	agc Ser	cgt Arg	cgt Arg	gaa Glu	ctg Leu	agc Ser	gcg Ala	cag Gln	ggg Gly	ccc Pro	gtg Val	gct Ala	1812
	510			515			520										
60	tgg Trp	ttt Phe	cac His	gcg Ala	cag Gln	cgg Arg	cgc Arg	cag Gln	acc Thr	ctg Leu	cag Gln	gag Glu	ggc Gly	ggc Gly	gtg Val	gtg Val	1860
	525			530			535										
65	gtc Val	ttg Leu	ctc Leu	ttc Phe	tct Ser	ccc Pro	ggg Gly	gcg Ala	gtg Val	gcg Ala	ctg Leu	tgc Cys	agc Ser	gag Glu	tgg Trp	cta Leu	1908
	545			550										555			
70	cag Gln	gat Asp	ggg Gly	gtg Val	tcc Ser	ggg Gly	ccc Pro	ggg Gly	gcg Ala	cac His	ggc Gly	ccg Pro	cac His	gac Asp	gcc Ala	ttc Phe	1956
	560			565										570			

	cgc gcc tcg ctc agc tgc gtg ctg ccc gac ttc ttg cag ggc cgg gcg	2004
	Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala	
	575 580 585	
5	ccc ggc agc tac gtg ggg gcc tgc ttc gac agg ctg ctc cac ccg gac	2052
	Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp	
	590 595 600	
10	gcc gta ccc gcc ctt ttc cgc acc gtg ccc gtc ttc aca ctg ccc tcc	2100
	Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe Thr Leu Pro Ser	
	605 610 615 620	
15	caa ctg cca gac ttc ctg ggg gcc ctg cag cag cct cgc gcc ccg cgt	2148
	Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg	
	625 630 635	
20	tcc ggg cgg ctc caa gag aga gcg gag caa gtg tcc cgg gcc ctt cag	2196
	Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln	
	640 645 650	
25	cca gcc ctg gat agc tac ttc cat ccc ccg ggg acn tcc gcg ccg gga	2244
	Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Xaa Ser Ala Pro Gly	
	655 660 665	
30	cgc ggg gtg gga cca ggg gcg gga cct ggg gcg ggg gac ggg act	2289
	Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly Thr	
	670 675 680	
35	taaataaagg cagacgctg	2308
40	MPVPWFLLSLALGRSQWILSLERLVLGVPQDATHCSPGLSCRLWSDILCLPGDIVPAPGPVLAPTHLQTELVL RCQKETDCLCLRVAVHLAVHGHWEPEDEEKFGGAADLGVEEPRNASLQAQVVLVSFQAYPTARCVLLEVQV PAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPDCRGLEVWNSIPSCWALPWLNVSA DGDNVHLVLNVSEEQHFGLSLYWNQVQGPVKPRWHKNLTGPGQIITLNTDLVPCLCIQVWPLEPDSVRTNIC PFREDPRAHQNLWQAARLRLTLQSWLLDAPCSLPAEAALCWRAPGGDPQCPLVPPLSWENVTVDVNSSEKL QLQECWLWADSLGFLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYLLQDLQSGQCLQLWD DDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLLKKDHAKGWLRLKQDVRSGAAARGRAALLLYSA DDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVFWFAQRRTLQEGGVVLLFSPGAVALCSEWL QDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLHHPDAVPALFRTVPVFTLPSQLPDFLGA LQQPRAPRSGRLQERAEQVSRAALQPALDSYFHPGTSAPGRGVGPGAGPGAGDGT.	

Reverse translation of primate, e.g., human, DCRS7 (SEQ ID NO: 9):

45	atgccngtnc cntggttyyt nytnwsnytn gcnytnngnm gnwsncartg gathytnwsn	60
	ytngarmgny tngtnggncc ncargaygcn acncaytgyw snccnggnytn nwsntgymgn	120
50	ytntgggayw sngayathyt ntgyytnccn ggngayathg tncngcncncc nggnccngtn	180
	ytngcncnca cncayytnca racngarytn gtynymgmt gycaraarga racngaytgy	240
	gayytnntgyy tnmngntngc ngtncayytn gcngtncayg gncaytggga rgarccngar	300
55	gaygargara arttyggngg ngcngcngay ytngngntng argarccnmg naaygcnwsn	360
	ytncargcnc argtngntnytn nwsnttycar gcntayccna cngcnmgntg ygtnytnytn	420
	gargtncarg tncngcngc nytngtncar ttyggncarw sngtnggnws ngtngtntay	480

5 gaytgyttyg argcngcnyt nggnwsngar gtnmgnatht ggwsntayac ncarccnmgn 540
 taygaraarg arytnaayca yacncarcarg ytncngayt gymgnggnyt ngargtntgg 600
 aaywsnathc cnwsntgytg ggcnytnccn tggytnaayg tnwsngcnga yggngayaay 660
 gtncayytng tnytnaaygt nwsngargar carcayttyg gnytnwsnyt ntaytggay 720
 10 cargtncarg gncncnca rccnmgttg cayaaraay tncnggncc ncarathath 780
 acnytnaayc ayacngayyt ngtnccntgy ytntgyathc argtntggcc nytngarccn 840
 15 gaywsngtnm gnacnaayat htgyccntty mgngargayc cnmgngcnca ycaraayyt 900
 tggcargcng cnmgnytnmg nytnytnacn ytncarwsnt ggytnytnga ygcncntgy 960
 wsnytnccng cngargcngc nytnytnytn mgngcncng gngngaycc ntgycarccn 1020
 20 ytngtnccnc cnytnwsntg ggaraaygt acngtngayg tnaaywsnw ngaraarytn 1080
 carytncarg artgyytnytn ggngaywsn ytnggncny tnaargayga ygtnytnytn 1140
 25 ytngaracnm gnggncnca rgayaaymgn wsnytnytnytn cnytngarcc nwsnggntgy 1200
 acnwsnytn cwnsnaargc nwsnacnmgn gcngcnmgny tngngarta yytnytnar 1260
 gayytnarw snggncartg yytnarytn tgggagayg ayytnggngc nytnytnytn 1320
 30 tgyccnatgg ayaartayat hcayaarmgn tgggcnytng tntggytnytn ntgyytnytn 1380
 ttygcngcng cnytnwsnyt nathytnytn ytnaaraarg aycaygcnaa rggntggytn 1440
 35 mgnytnytna arcargaygt nmgnwsngn gcngcngcnm gnggngmngc ngcnytnytn 1500
 ytntaywsng cngaygayws nggnttygar mgnytnytnytn gngcnytnytn nwsngcnytn 1560
 tgyarytn cnytnmgnt ngcngtnytn ytntggwsnm gnmngaryt nwsngcncar 1620
 40 gngcngntng cntggttyca ygcncarmgn mgncaracny tncargarg ngngntngtn 1680
 gtnytnytn tywsncngg ngcngtnytn ytntgywsng artggytnca rgayggngtn 1740
 45 wsnggncng gngcncaygg nccncaygay gcnttymgng cwnsnytnws ntgygtnytn 1800
 ccngayttyt tncarggmng ngcncnggn wsntaygtng gngcntgytt ygaymgnytn 1860
 ytncaycngc aygngtncc ngcnytnytn mgncngtn cngnttyac nytnccnwsn 1920
 50 carytnccng aytyytnytn ngcnytnar carccnmng cncnmgng nngnmnytn 1980
 cargarmng cngarcargt nwsnmngcn ytncarccng cnytnytnytn ntaytycay 2040
 55 ccncnggna cwnsngcnc nggngnggn gtnggncng gngcnggnc nggngcnggn 2100
 gayggnacn 2109

Rodent, e.g., mouse, embodiment (see SEQ ID NO: 10 and 11). Predicted signal sequence indicated, but may vary by a few positions and depending upon cell type.

5	ccaaatcgaa agcacgggag ctgatactgg gcctggagtc caggctcact ggagtgggga	60
	agcatggctg gagaggaatt ctagcccttg ctctctccca gggacacggg gctgattgtc	120
	agcagggggcg aggggtctgc ccccccttgg gggggcagga cggggcctca ggcctgggtg	180
10	ctgtccggca cctggaag atg cct gtg tcc tgg ttc ctg ctg tcc ttg gca	231
	Met Pro Val Ser Trp Phe Leu Leu Ser Leu Ala	
	-20 -15 -10	
15	ctg ggc cga aac cct gtg gtc gtc tct ctg gag aga ctg atg gag cct	279
	Leu Gly Arg Asn Pro Val Val Val Ser Leu Glu Arg Leu Met Glu Pro	
	-5 -1 1 5	
20	cag gac act gca cgc tgc tct cta ggc ctc tcc tgc cac ctc tgg gat	327
	Gln Asp Thr Ala Arg Cys Ser Leu Gly Leu Ser Cys His Leu Trp Asp	
	10 15 20	
	ggt gac gtg ctc tgc ctg cct gga agc ctc cag tct gcc cca ggc cct	375
	Gly Asp Val Leu Cys Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro	
	25 30 35	
25	gtg cta gtg cct acc cgc ctg cag acg gag ctg gtg ctg agg tgt cca	423
	Val Leu Val Pro Thr Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro	
	40 45 50 55	
30	cag aag aca gat tgc gcc ctc tgt gtc cgt gtg gtg gtc cac ttg gcc	471
	Gln Lys Thr Asp Cys Ala Leu Cys Val Arg Val Val Val His Leu Ala	
	60 65 70	
35	gtg cat ggg cac tgg gca gag cct gaa gaa gct gga aag tct gat tca	519
	Val His Gly His Trp Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser	
	75 80 85	
40	gaa ctc cag gag tct agg aac gcc tct ctc cag gcc cag gtg gtg ctc	567
	Glu Leu Gln Glu Ser Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu	
	90 95 100	
	tcc ttc cag gcc tac ccc atc gcc cgc tgt gcc ctg ctg gag gtc cag	615
	Ser Phe Gln Ala Tyr Pro Ile Ala Arg Cys Ala Leu Leu Glu Val Gln	
	105 110 115	
45	gtg ccc gct gac ctg gtg cag cct ggt cag tcc gtg ggt tct gcg gta	663
	Val Pro Ala Asp Leu Val Gln Pro Gly Gln Ser Val Gly Ser Ala Val	
	120 125 130 135	
50	ttt gac tgt ttc gag gct agt ctt ggg gct gag gta cag atc tgg tcc	711
	Phe Asp Cys Phe Glu Ala Ser Leu Gly Ala Glu Val Gln Ile Trp Ser	
	140 145 150	
55	tac acg aag ccc agg tac cag aaa gag ctc aac ctc aca cag cag ctg	759
	Tyr Thr Lys Pro Arg Tyr Gln Lys Glu Leu Asn Leu Thr Gln Gln Leu	
	155 160 165	

	cct gac tgc agg ggt ctt gaa gtc cgg gac agc atc cag agc tgc tgg	807
	Pro Asp Cys Arg Gly Leu Glu Val Arg Asp Ser Ile Gln Ser Cys Trp	
	170 175 180	
5	gtc ctg ccc tgg ctc aat gtg tct aca gat ggt gac aat gtc ctt ctg	855
	Val Leu Pro Trp Leu Asn Val Ser Thr Asp Gly Asp Asn Val Leu Leu	
	185 190 195	
10	aca ctg gat gtc tct gag gag cag gac ttt agc ttc tta ctg tac ctg	903
	Thr Leu Asp Val Ser Glu Glu Gln Asp Phe Ser Phe Leu Leu Tyr Leu	
	200 205 210 215	
15	cgt cca gtc ccg gat gct ctc aaa tcc ttg tgg tac aaa aac ctg act	951
	Arg Pro Val Pro Asp Ala Leu Lys Ser Leu Trp Tyr Lys Asn Leu Thr	
	220 225 230	
20	gga cct cag aac att act tta aac cac aca gac ctg gtt ccc tgc ctc	999
	Gly Pro Gln Asn Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu	
	235 240 245	
25	tgc att cag gtg tgg tcg cta gag cca gac tct gag agg gtc gaa ttc	1047
	Cys Ile Gln Val Trp Ser Leu Glu Pro Asp Ser Glu Arg Val Glu Phe	
	250 255 260	
30	tgc ccc ttc cgg gaa gat ccc ggt gca cac agg aac ctc tgg cac ata	1095
	Cys Pro Phe Arg Glu Asp Pro Gly Ala His Arg Asn Leu Trp His Ile	
	265 270 275	
35	gcc agg ctg cgg gta ctg tcc cca ggg gta tgg cag cta gat gcg cct	1143
	Ala Arg Leu Arg Val Leu Ser Pro Gly Val Trp Gln Leu Asp Ala Pro	
	280 285 290 295	
40	tgc tgt ctg ccg ggc aag gta aca ctg tgc tgg cag gca cca gac cag	1191
	Cys Cys Leu Pro Gly Lys Val Thr Leu Cys Trp Gln Ala Pro Asp Gln	
	300 305 310	
45	agt ccc tgc cag cca ctt gtg cca cca gtg ccc cag aag aac gcc act	1239
	Ser Pro Cys Gln Pro Leu Val Pro Pro Val Pro Gln Lys Asn Ala Thr	
	315 320 325	
50	gtg aat gag cca caa gat ttc cag ttg gtg gca ggc cac ccc aac ctc	1287
	Val Asn Glu Pro Gln Asp Phe Gln Leu Val Ala Gly His Pro Asn Leu	
	330 335 340	
55	tgt gtc cag gtg agc acc tgg gag aag gtt cag ctg caa gcg tgc ttg	1335
	Cys Val Gln Val Ser Thr Trp Glu Lys Val Gln Leu Gln Ala Cys Leu	
	345 350 355	
60	tgg gct gac tcc ttg ggg ccc ttc aag gat gat atg ctg tta gtg gag	1383
	Trp Ala Asp Ser Leu Gly Pro Phe Lys Asp Asp Met Leu Leu Val Glu	
	360 365 370 375	
65	atg aaa acc ggc ctc aac aac aca tca gtc tgt gcc ttg gaa ccc agt	1431
	Met Lys Thr Gly Leu Asn Asn Thr Ser Val Cys Ala Leu Glu Pro Ser	
	380 385 390	
70	ggc tgt aca cca ctg ccc agc atg gcc tcc acg aga gct gct cgc ctg	1479
	Gly Cys Thr Pro Leu Pro Ser Met Ala Ser Thr Arg Ala Ala Arg Leu	
	395 400 405	

5	gga gag gag ttg ctg caa gac ttc cga tca cac cag tgt atg cag ctg 1527															
	Gly	Glu	Glu	Leu	Leu	Gln	Asp	Phe	Arg	Ser	His	Gln	Cys	Met	Gln	Leu
			410					415					420			
10	tgg aac gat gac aac atg gga tgc cta tgg gcc tgc ccc atg gac aag 1575															
	Trp	Asn	Asp	Asp	Asn	Met	Gly	Ser	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys
			425				430					435				
15	tac atc cac agg cgc tgg gtc cta gta tgg ctg gcc tgc cta ctc ttg 1623															
	Tyr	Ile	His	Arg	Arg	Trp	Val	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Leu
	440					445					450					455
20	gct gcg gcg ctt ttc ttc ttc ctc ctt cta aaa aag gac cgc agg aaa 1671															
	Ala	Ala	Ala	Leu	Phe	Phe	Phe	Leu	Leu	Leu	Lys	Lys	Asp	Arg	Arg	Lys
				460						465					470	
25	gcg gcc cgt ggc tcc cgc acg gcc ttg ctc ctc cac tcc gcc gac gga 1719															
	Ala	Ala	Arg	Gly	Ser	Arg	Thr	Ala	Leu	Leu	Leu	His	Ser	Ala	Asp	Gly
				475					480					485		
30	gcg ggc tac gag cgc ctg gtg gga gca ctg gcg tcc gcg ttg agc cag 1767															
	Ala	Gly	Tyr	Glu	Arg	Leu	Val	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Ser	Gln
			490					495					500			
35	atg cca ctg cgc gtg gcc gtg gac ctg tgg agc cgc cgc gag ctg agc 1815															
	Met	Pro	Leu	Arg	Val	Ala	Val	Asp	Leu	Trp	Ser	Arg	Arg	Glu	Leu	Ser
		505					510					515				
40	gcg cac gga gcc cta gcc tgg ttc cac cac cag cga cgc cgt atc ctg 1863															
	Ala	His	Gly	Ala	Leu	Ala	Trp	Phe	His	His	Gln	Arg	Arg	Arg	Ile	Leu
	520					525					530					535
45	cag gag ggt ggc gtg gta atc ctt ctc ttc tgc ccc gcg gcc gtg gcg 1911															
	Gln	Glu	Gly	Gly	Val	Val	Ile	Leu	Leu	Phe	Ser	Pro	Ala	Ala	Val	Ala
				540						545					550	
50	cag tgt cag cag tgg ctg cag ctc cag aca gtg gag ccc ggg ccg cat 1959															
	Gln	Cys	Gln	Gln	Trp	Leu	Gln	Leu	Gln	Thr	Val	Glu	Pro	Gly	Pro	His
			555					560						565		
55	gac gcc ctc gcc gcc tgg ctc agc tgc gtg cta ccc gat ttc ctg caa 2007															
	Asp	Ala	Leu	Ala	Ala	Trp	Leu	Ser	Cys	Val	Leu	Pro	Asp	Phe	Leu	Gln
			570					575					580			
60	ggc cgg gcg acc ggc cgc tac gtc ggg gtc tac ttc gac ggg ctg ctg 2055															
	Gly	Arg	Ala	Thr	Gly	Arg	Tyr	Val	Gly	Val	Tyr	Phe	Asp	Gly	Leu	Leu
			585				590					595				
65	cac cca gac tct gtg ccc tcc ccg ttc cgc gtc gcc ccg ctc ttc tcc 2103															
	His	Pro	Asp	Ser	Val	Pro	Ser	Pro	Phe	Arg	Val	Ala	Pro	Leu	Phe	Ser
	600					605					610					615
70	ctg ccc tcg cag ctg ccg gct ttc ctg gat gca ctg cag gga ggc tgc 2151															
	Leu	Pro	Ser	Gln	Leu	Pro	Ala	Phe	Leu	Asp	Ala	Leu	Gln	Gly	Gly	Cys
				620						625					630	

tcc act tcc gcg ggg cga ccc gcg gac cgg gtg gaa cga gtg acc cag 2199
 Ser Thr Ser Ala Gly Arg Pro Ala Asp Arg Val Glu Arg Val Thr Gln
 635 640 645

5 gcg ctg cgg tcc gcc ctg gac agc tgt act tct agc tcg gaa gcc cca 2247
 Ala Leu Arg Ser Ala Leu Asp Ser Cys Thr Ser Ser Ser Glu Ala Pro
 650 655 660

10 ggc tgc tgc gag gaa tgg gac ctg gga ccc tgc act aca cta gaa 2292
 Gly Cys Cys Glu Glu Trp Asp Leu Gly Pro Cys Thr Thr Leu Glu
 665 670 675

taaaagccga tacagtattc ct 2314

15 MPVSWFLLSLALGRNPVVVSLERLMEPQDTARCSLGLSCHLWDGDVLCPLPGSLQSAPGPVLVPTRLQTELVL
 RCPQKTDICALCVRVVVHLAVHGHWAEEAGKSDSELQESRNASLQAQVVL SFQAYPIARCALLEVQVPADL
 VQPGQSVGSAVFDCFEASLGAEVQIWSYTKPRYQKELNLTQQLPDCRGLEVRDSIQSCWVLPWLNVDGDN
 VLLTLDVSEEQDFSFLLYLRPVPDALKSLWYKNLTGPQNITLNHTDLVPCLCTIQVWSLEPDSEVEFCPFRE
 DPGAHRNLWHIARLRVLSPGVWQLDAPCCLPKVTLCWQAPDQSPCQPLVPPVPQKNATVNEPQDFQLVAGH
 PNLCVQVSTWEKVQLQACLWADSLGPFKDDMLLVEMKTGLNNTSVCALEPSGCTPLPSMASTRAARLGEELL
 QDFRSHQCMQLWNDNMGSLWACPMCKYIHRRVVLVWLACLLLAALFFFLLLKKDRRKAARGSR TALLHS
 ADGAGYERLVGALASALSQMPLRVAVDLWSRRELSAHGALAWFHHQRRRILQEGGVVILLFSPAAVAQCQW
 LQLQTVEPGPHDALAAWLSCVLPDFLQGRATGRYVG VYFDGLLHPDSVPSPF RVAPLFS LPSQLPAFLDALQ
 GGCSTSAGR PADRVERVTQALRSALD SCTSSEAPGCCEEWDLGPCTTLE.

20

25

Reverse translation of rodent, e.g., mouse, DCRS7 (SEQ ID NO: 12):

30 atgcengtnw sntgggttyt nytnwsnytn gcnytnggnm gnaayccngt ngtnngtnwsn 60
 ytngarmgny tnatggarcc ncargayacn gcnmgntgyw snytnggnyt nwsntgy cay 120
 ytntgggag gngaygtnyt ntgyytnccn ggnwsnytn arwsngcncc nggncengtn 180

35 ytngtnccna cnmgnytnca racngarytn gtnytnmgnt gyccncaraa racngaytgy 240
 gcnytntgyg tnmngntngt ngtncayytn gcngtncayg gncaytgggc ngarccngar 300
 gargcnggna arwsngayws ngarytn car garwsnmgna aygcnwsnyt ncargcn car 360

40 gtngtnytnw snttycargc ntayccnath gcnmgntgyg cnytnytn ga rgtncargtn 420
 ccngcngayy tngtn carcc nggncarwsn gtnggnwsng cngtnnttyga ytgyttygar 480

45 gcnwsnytn gngcngargt ncarathtg wsntayacna arccnmngnta ycaraargar 540
 ytnaayytna cncarcaryt nccngaytgy mgnggnytn argtnmgnga ywsnathcar 600
 wsntgytggg tnytnccntg gytnaaytn wsnacngayg gngayaaygt nytnytnacn 660

50 ytngaygtw sngargarca rgayttywsn ttyytnytn ayytnmgnc ngtnccngay 720
 gcnytnaarw snytn tggta yaaraaytn acnggncnc araayathac nytnaaycay 780

55 acngayytn tncntgyt ntgyathcar gtntggwsny tngarccnga ywsngarmgn 840
 gtngarttyt gyccnttymg ngargayccn ggngcncaym gnaayytn g cayathgcn 900
 mgnytnmgng tnytnwsncc ngngntntgg carytngay cncntgyt yytnccnggn 960

aargtnacny tntgytggca rgcnccngay carwsnccnt gycarccnyt ngtnccnccn 1020
 gtnccncara araaygcnac ngtnaaygar ccncargayt tycarytngt ngcnggncay 1080
 5 ccnaayytnt gygtncargt nwsnacntgg garaargtnc arytnccargc ntgyytntgg 1140
 gcngaywsny tnggnccntt yaargaygay atgytnytng tngaratgaa racnggnytn 1200
 10 aayaayacnw sngtntgygc nytngarccn wsnggntgya cncnnytncc nwsnatggcn 1260
 wsnacnmng cngcnmngyt ngngngargar ytnytncarg ayttymgnws ncaycartgy 1320
 atgcarytnt ggaaygayga yaayatgggn wsnynttggg cntgyccnat ggayaartay 1380
 15 athcaymgnm gntgggntyt ngnttgggtn gcntgyytny tnytngcngc ngcnytnntty 1440
 ttyttyytny tnytnaaraa rgaymgnmgn aargcngcnm gnggnwsnmg nacngcnnytn 1500
 20 ytnytncayw sngcngaygg ngcnggntay garmgnytn tnggngcnytn ngcnwsngcn 1560
 ytnwsncara tgccnytnmg ngtngcngtn gayytnntggw snmgnmgnga rytnwsngcn 1620
 cayggngcny tngcntgggt ycaycaycar mgnmgnmgna thytnccarga rggnggngtn 1680
 25 gtnathytny tnttywsncc ngcngcngtn gcncartgyc arcartggyt ncarytnccar 1740
 acngtngarc cnggncnca ygaygcnytn gcngcntggy tnwsntgygt nytnccngay 1800
 30 ttyytncarg gnmngcncac nggngmntay gtnggngntnt ayttgyaygg nytnytncay 1860
 ccngaywsng tnccnwsncc nttymgngtn gcncnnytn tywsnytncc nwsncarytn 1920
 ccngcnttyy tngaygcnytn ncarggnggn tgywsnacnw sngcnggngm nccngcngay 1980
 35 mgngtngarm gngtnacnca rgcnymngn wsngcnytn aywsntgyac nwsnwsnwsn 2040
 gargcncng gntgytgyga rgartgggay ytnggncnt gyacnacnytn ngar 2094

40

Table 3: Nucleotide and polypeptide sequences of DNAX Cytokine Receptor Subunit like
 embodiments (DCRS8). Primate, e.g., human, embodiment (see SEQ ID NO: 13 and 14).
 Predicted signal sequence indicated, but may vary by a few positions and depending upon cell
 type.

45

cccacgcntc cgggccagca gcgggcggcc ggggcgagga gaacggcctg gctgggagag 60
 cgacgggcc atg gcc ccg tgg ctg cag ctc tgc tcc gtc ttc ttt acg gtc 111
 Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val
 50 -15 -10 -5

50

aac gcc tgc ctc aac ggc tcg cag ctg gct gtn gcc gct ggc ggg tcc 159
 Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Xaa Ala Ala Gly Gly Ser
 -1 1 5 10

55

ggc cgc gcg cng ggc gcc gac acc tgt agc tgg ang gga gtg ggg cca 207
 Gly Arg Ala Xaa Gly Ala Asp Thr Cys Ser Trp Xaa Gly Val Gly Pro
 15 20 25 30

5	gcc agc aga aac agt ggg ctg tac aac atc acc ttc aaa tat gac aat 255 Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn 35 40 45	
	tgt acc acc tac ttg aat cca gtg ggg aag cat gtg att gct gac gcc 303 Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala 50 55 60	
10	cag aat atc acc atc agc cag tat gct tgc cat gac caa gtg gca gtc 351 Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val 65 70 75	
15	acc att ctt tgg tcc cca ggg gcc ctc ggc atc gaa ttc ctg aaa gga 399 Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly 80 85 90	
20	ttt cgg gta ata ctg gag gag ctg aag tcg gag gga aga cag ngc caa 447 Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Xaa Gln 95 100 105 110	
25	caa ctg att cta aag gat ccg aag cag ntc aac agt agc ttc aaa aga 495 Gln Leu Ile Leu Lys Asp Pro Lys Gln Xaa Asn Ser Ser Phe Lys Arg 115 120 125	
	act gga atg gaa tct caa cct ttn ctg aat atg aaa ttt gaa acg gat 543 Thr Gly Met Glu Ser Gln Pro Xaa Leu Asn Met Lys Phe Glu Thr Asp 130 135 140	
30	tat ttc gta agg ttg tcc ttt tcc ttc att aaa aac gaa agc aat tac 591 Tyr Phe Val Arg Leu Ser Phe Ser Phe Ile Lys Asn Glu Ser Asn Tyr 145 150 155	
35	cac cct ttc ttc ttt aga acc cga gcc tgt gac ctg ttg tta cag ccg 639 His Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro 160 165 170	
40	gac aat cta gct tgt aaa ccc ttc tgg aag cct cgg aac ctg aac atc 687 Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile 175 180 185 190	
45	agc cag cat ggc tcg gac atg cag gtg tcc ttc gac cac gca ccg cac 735 Ser Gln His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His 195 200 205	
	aac ttc ggc ttc cgt ttc ttc tat ctt cac tac aag ctc aag cac gaa 783 Asn Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu 210 215 220	
50	gga cct ttc aag cga aag acc tgt aag cag gag caa act aca gag atg 831 Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Met 225 230 235	
55	acc agc tgc ctc ctt caa aat gtt tct cca ggg gat tat ata att gag 879 Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu 240 245 250	

	ctg gtg gat gac act aac aca aca aga aaa gtg atg cat tat gcc tta	927
	Leu Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu	
	255 260 265 270	
5	aag cca gtg cac tcc ccg tgg gcc ggg ccc atc aga gcc gtg gcc atc	975
	Lys Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile	
	275 280 285	
10	aca gtg cca ctg gta gtc ata tcg gca ttc gcg acg ctc ttc act gtg	1023
	Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val	
	290 295 300	
15	atg tgc cgc aag aag caa caa gaa aat ata tat tca cat tta gat gaa	1071
	Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu	
	305 310 315	
20	gag agc tct gag tct tcc aca tac act gca gca ctc cca aga gag agg	1119
	Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg	
	320 325 330	
	ctc cgg ccg cgg ccg aag gtc ttt ctc tgc tat tcc agt aaa gat ggc	1167
	Leu Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly	
	335 340 345 350	
25	cag aat cac atg aat gtc gtc cag tgt ttc gcc tac ttc ctc cag gac	1215
	Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp	
	355 360 365	
30	ttc tgt ggc tgt gag gtg gct ctg gac ctg tgg gaa gac ttc agc ctc	1263
	Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu	
	370 375 380	
35	tgt aga gaa ggg cag aga gaa tgg gtc atc cag aag atc cac gag tcc	1311
	Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser	
	385 390 395	
40	cag ttc atc att gtg gtt tgt tcc aaa ggt atg aag tac ttt gtg gac	1359
	Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp	
	400 405 410	
	aag aag aac tac aaa cac aaa gga ggt ggc cga ggc tcg ggg aaa gga	1407
	Lys Lys Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly	
	415 420 425 430	
45	gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa aag ctc cgc cag	1455
	Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln	
	435 440 445	
50	gcc aag cag agt tcg tcc gcg gcg ctc agc aag ttt atc gcc gtc tac	1503
	Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr	
	450 455 460	
	ttt gat tat tcc tgc gag gga gac gtc ccc ggt atc cta gac ctg agt	1551
	Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser	
	465 470 475	
55	acc aag tac aga ctc atg gac aat ctt cct cag ctc tgt tcc cac ctg	1599
	Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu	
	480 485 490	

	cac tcc cga gac cac ggc ctc cag gag ccg ggg cag cac acg cga cag	1647
	His Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln	
	495 500 505 510	
5	ggc agc aga agg aac tac ttc cgg agc aag tca ggc cgg tcc cta tac	1695
	Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr	
	515 520 525	
10	gtc gcc att tgc aac atg cac cag ttt att gac gag gag ccc gac tgg	1743
	Val Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp	
	530 535 540	
15	ttc gaa aag cag ttc gtt ccc ttc cat cct cct cca ctg cgc tac cgg	1791
	Phe Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg	
	545 550 555	
20	gag cca gtc ttg gag aaa ttt gat tgc ggc ttg gtt tta aat gat gtc	1839
	Glu Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val	
	560 565 570	
25	atg tgc aaa cca ggg cct gag agt gac ttc tgc cta aag gta gag gcg	1887
	Met Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala	
	575 580 585 590	
30	gct gtt ctt ggg gca acc gga cca gcc gac tcc cag cac gag agt cag	1935
	Ala Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln	
	595 600 605	
35	cat ggg ggc ctg gac caa gac ggg gag gcc cgg cct gcc ctt gac ggt	1983
	His Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly	
	610 615 620	
40	agc gcc gcc ctg caa ccc ctg ctg cac acg gtg aaa gcc ggc agc ccc	2031
	Ser Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro	
	625 630 635	
45	tcg gac atg ccg cgg gac tca ggc atc tat gac tcg tct gtg ccc tca	2079
	Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser	
	640 645 650	
50	tcc gag ctg tct ctg cca ctg atg gaa gga ctc tcg acg gac cag aca	2127
	Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr	
	655 660 665 670	
55	gaa acg tct tcc ctg acg gag agc gtg tcc tcc tct tca ggc ctg ggt	2175
	Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly	
	675 680 685	
55	gag gag gaa cct cct gcc ctt cct tcc aag ctc ctc tct tct ggg tca	2223
	Glu Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser	
	690 695 700	
55	tgc aaa gca gat ctt ggt tgc cgc agc tac act gat gaa ctc cac gcg	2271
	Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala	
	705 710 715	
	gtc gcc cct ttg taacaaaacg aaagagtcta agcattgccca ctttagctgc	2323
	Val Ala Pro Leu	
	720	

5 tgcctccctc tgattcccca gctcatctcc ctggttgcac ggcccacttg gagctgaggt 2383
 ctcatacaag gatatttggga gtgaaatgct ggccagtact tgttctccct tgccccaacc 2443
 ctttaccgga tatcttgaca aactctccaa ttttctaaaa tgatatggag ctctgaaagg 2503
 catgtccata aggtctgaca acagcttgcc aaatttgggt agtccttgga tcagagcctg 2563
 10 ttgtgggagg tagggaggaa atatgtaaag aaaaacagga agatacctgc actaatcatt 2623
 cagacttcat tgagctctgc aaactttgcc tgtttgctat tggctacctt gatttgaaat 2683
 gctttgtgaa aaaaggcact tttaacatca tagccacaga aatcaagtgc cagtctatct 2743
 15 ggaatccatg ttgtattgca gataatgttc tcatttatatt ttg 2786

20 MAPWLQLCSVFFTVNACLNGSQLAVAAGSGRAXGADTCSWXGVGPASRNSGLYNITFKYDNCTTYLNPVGK
 HVIADAQNITISQYACHDQVAVTILWSPGALGIEFLKGFRVILEELKSEGRQXQQLILKDPKQXNSSFKRTG
 MESQPXLNMKFETDYFVRLSFSFIKNESNYHFFFRTRACDLLLPDNLACKPFWKPRNLNISQHGSDMQVS
 FDHAPHNFGFRFFYLHYKLKHEGPFKRKTCKQEQTTEMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKP
 VHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLC
 YSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKK
 25 NYKHKGGGRSGSGKELFLVAVSAIAEKLQAKQSSAALSKEFIIVYFDYSCGDVPGILDSTKYRLMDNLP
 QLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKSGRSLYVAICNMHQFIDEEDWFEKQFVFPFHPPLRYREP
 VLEKFDGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAAALQPLLHT
 VKAGSPSDMPRDSGIYDSSVPSSLSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEPALPSKLLSSGSK
 ADLGRSYTDELHAVAPL.

30 Reverse translation of primate, e.g., human, DCRS8 (SEQ ID NO: 15):

atggcncnt ggytncaryt ntgywsngtn ttyttyacng tnaaygcntg yytnaayggn 60
 35 wsncarytng cngtngcngc ngngngnwsn ggnmgngcnn nngngngnga yacntgywsn 120
 tggnnngng tngngcngc nwsnmgnaay wsnggnytn ayaayathac nttyaartay 180
 40 gayaaytgya cnacntayyt naayccngtn ggnaarcayg tnathgcnga ygcncaraay 240
 athacnathw sncartaygc ntgycaygay cargtngcng tnacnathyt ntggwsnccn 300
 ggngcnytn gnatthgartt yytnaarggn ttmngntna thytnngarga rytnaarwsn 360
 45 gargngmnc arnnncarca rytnathyt aargayccna arcarnnnaa ywsnwsntty 420
 aarmgnacng gnatggarws ncarccnnnn ytnaayatga arttygarac ngaytaytty 480
 gtnmgnytnw snttywsntt yathaaraay garwsnaayt aycayccntt yttyttymgn 540
 50 acnmngncnt gygayytnyt nytnarccn gayaaytng cntgyaarcc nttytggaar 600
 ccnmgnaayy tnaayathws ncarcayggn wsngayatgc argtnwsntt ygaycaygcn 660
 55 ccncayaayt tyggnttymg nttyttytay ytncaytaya arytnaarca ygargngcncn 720
 ttyaarmgna aracntgyaa rcargarcar acnacngara tgacnwsntg yytnytnar 780
 aaygtnwsnc cngngayta yathathgar ytnngtayg ayacnaayac nacnmgnaar 840

gtnatgcayt aygcnytnaa rccngtncay wsnccntggg cnggnccnat hmgngcngtn 900
 5 gcnathacng tncnytngt ngtnathwsn gcnttygcna cnytnnttyac ngtnatgtgy 960
 mgnaraarc arcargaraa yathtaywsn cayytngayg argarwsnws ngarwsnwsn 1020
 acntayacng cngcnytncc nmngngarmgn ytnmgncnm gncnaargt nttyyntgy 1080
 10 taywsnwsna argayggnca raaycayatg aaygtngtnc artgyttygc ntayttyytn 1140
 cargayttyt gyggntgyga rgtngcnytn gayytntgga argayttyws nyntngymgn 1200
 garggncarm gngartgggt nathcaraar athcaygarw sncarttyat hathgtngtn 1260
 15 tgywsnaarg gnatgaarta yttygtngay aaraaraayt ayaarcayaa rggnggnggn 1320
 mgnggnwsng gnaarggnga rytnttyytn gtngcngtnw sngcnathgc ngaraarytn 1380
 20 mgncargcna arcarwsnws nwsngcngcn ytnwsnaart tyathgcngt ntayttygay 1440
 taywsntgyg arggngaygt nccnggnath ytngayytnw snacnaarta ymgnytnatg 1500
 gayaayytnc cncarytntg ywsncayytn caywsnmng ayayggnyt ncargarccn 1560
 25 ggncarcaya cnmgncargg nwsnmgnmgn aaytaytym gnwsnaarws nggnmgnwsn 1620
 ytntaygtng cnathtgyaa yatgcaycar ttyathgayg argarccnga ytggttygar 1680
 30 aarcarttyg tncnttyca yccnccnccn ytnmgntaym gngarccngt nytngaraar 1740
 ttygaywsng gnytngtnt naaygaygt atgtgyaarc cnggnccnga rwsngaytty 1800
 tgyytnaarg tngargcngc ngtnytnngn gcnacnggc cngcngayws ncarcaygar 1860
 35 wsncarcayg gnggnytnga ycargayggn gargcnmgnc cngcnytnga yggngwsngcn 1920
 gcnytncarc cnytnytnc yacngtnaar gcnggnwsnc cnwsngayat gccnmngay 1980
 40 wsnggnatht aygaywsnws ngtnccnwsn wsngarytnw snytnccnyt natggarggn 2040
 ytnwsnacng ayacaracnga racnwsnwsn ytnacngarw sngtnwsnws nwsnwsnggn 2100
 ytnngngarg argarccncc ngcnytnccn wsnaarytny tnwsnwsngg nwsntgyaar 2160
 45 gcngayytng gntgymgnws ntayacngay garytncayg cngtngcncc nytn 2214

50 Table 4: Nucleotide and polypeptide sequences of DNAX Cytokine Receptor Subunit like
 embodiments (DCRS9). Primate, e.g., human, embodiment (see SEQ ID NO: 16 and 17).
 Predicted signal sequence indicated, but may vary by a few positions and depending upon cell
 type.

55 atg ggg agc tcc aga ctg gca gcc ctg ctc ctg cct ctc ctc ctc ata 48
 Met Gly Ser Ser Arg Leu Ala Ala Leu Leu Leu Pro Leu Leu Leu Ile
 -20 -15 -10

	gtc atc gac ctc tct gac tct gct ggg att ggc ttt cgc cac ctg ccc	96
	Val Ile Asp Leu Ser Asp Ser Ala Gly Ile Gly Phe Arg His Leu Pro	
	-5 -1 1 5	
5	cac tgg aac acc cgc tgt cct ctg gcc tcc cac acg gaa gtt ctg cct	144
	His Trp Asn Thr Arg Cys Pro Leu Ala Ser His Thr Glu Val Leu Pro	
	10 15 20 25	
10	ata tcc ctt gcc gca cct ggt ggg ccc tct tct cca caa agc ctt ggt	192
	Ile Ser Leu Ala Ala Pro Gly Gly Pro Ser Ser Pro Gln Ser Leu Gly	
	30 35 40	
15	gtg tgc gag tct ggc act gtt ccc gct gtt tgt gcc agc atc tgc tgt	240
	Val Cys Glu Ser Gly Thr Val Pro Ala Val Cys Ala Ser Ile Cys Cys	
	45 50 55	
20	cag gtg gct cag gtc ttc aac ggg gcc tct tcc acc tcc tgg tgc aga	288
	Gln Val Ala Gln Val Phe Asn Gly Ala Ser Ser Thr Ser Trp Cys Arg	
	60 65 70	
25	aat cca aaa agt ctt cca cat tca agt tct ata gga gac aca aga tgc	336
	Asn Pro Lys Ser Leu Pro His Ser Ser Ser Ile Gly Asp Thr Arg Cys	
	75 80 85	
30	cag cac ctg ctc aga gga agc tgc tgc ctc gtc gtc acc tgt ctg aga	384
	Gln His Leu Leu Arg Gly Ser Cys Cys Leu Val Val Thr Cys Leu Arg	
	90 95 100 105	
35	aga gcc atc aca ttt cca tcc cct ccc cag aca tct ccc aca agg gac	432
	Arg Ala Ile Thr Phe Pro Ser Pro Pro Gln Thr Ser Pro Thr Arg Asp	
	110 115 120	
40	ttc gct cta aaa gga ccc aac ctt cgg atc cag aga cat ggg aaa gtc	480
	Phe Ala Leu Lys Gly Pro Asn Leu Arg Ile Gln Arg His Gly Lys Val	
	125 130 135	
45	ttc cca gat tgg act cac aaa ggc atg gag gtg ggc act ggg tac aac	528
	Phe Pro Asp Trp Thr His Lys Gly Met Glu Val Gly Thr Gly Tyr Asn	
	140 145 150	
50	agg aga tgg gtt cag ctg agt ggt gga ccc gag ttc tcc ttt gat ttg	576
	Arg Arg Trp Val Gln Leu Ser Gly Gly Pro Glu Phe Ser Phe Asp Leu	
	155 160 165	
55	ctg cct gag gcc cgg gct att cgg gtg acc ata tct tca ggc cct gag	624
	Leu Pro Glu Ala Arg Ala Ile Arg Val Thr Ile Ser Ser Gly Pro Glu	
	170 175 180 185	
60	gtc agc gtg cgt ctt tgt cac cag tgg gca ctg gag tgt gaa gag ctg	672
	Val Ser Val Arg Leu Cys His Gln Trp Ala Leu Glu Cys Glu Glu Leu	
	190 195 200	
65	agc agt ccc tat gat gtc cag aaa att gtg tct ggg ggc cac act gta	720
	Ser Ser Pro Tyr Asp Val Gln Lys Ile Val Ser Gly Gly His Thr Val	
	205 210 215	
70	gag ctg cct tat gaa ttc ctt ctg ccc tgt ctg tgc ata gag gca tcc	768
	Glu Leu Pro Tyr Glu Phe Leu Leu Pro Cys Leu Cys Ile Glu Ala Ser	
	220 225 230	

5	tac ctg caa gag gac act gtg agg cgc aaa aaa tgt ccc ttc cag agc 816
	Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser
	235 240 245
10	tgg cca gaa gcc tat ggc tcg gac ttc tgg aag tca gtg cac ttc act 864
	Trp Pro Glu Ala Tyr Gly Ser Asp Phe Trp Lys Ser Val His Phe Thr
	250 255 260 265
15	gac tac agc cag cac act cag atg gtc atg gcc ctg aca ctc cgc tgc 912
	Asp Tyr Ser Gln His Thr Gln Met Val Met Ala Leu Thr Leu Arg Cys
	270 275 280
20	cca ctg aag ctg gaa gct gcc ctc tgc cag agg cac gac tgg cat acc 960
	Pro Leu Lys Leu Glu Ala Ala Leu Cys Gln Arg His Asp Trp His Thr
	285 290 295
25	ctt tgc aaa gac ctc ccg aat gcc acg gct cga gag tca gat ggg tgg 1008
	Leu Cys Lys Asp Leu Pro Asn Ala Thr Ala Arg Glu Ser Asp Gly Trp
	300 305 310
30	tat gtt ttg gag aag gtg gac ctg cac ccc cag ctc tgc ttc aag gta 1056
	Tyr Val Leu Glu Lys Val Asp Leu His Pro Gln Leu Cys Phe Lys Val
	315 320 325
35	caa cca tgg ttc tct ttt gga aac agc agc cat gtt gaa tgc ccc cac 1104
	Gln Pro Trp Phe Ser Phe Gly Asn Ser Ser His Val Glu Cys Pro His
	330 335 340 345
40	cag act ggg tct ctc aca tcc tgg aat gta agc atg gat acc caa gcc 1152
	Gln Thr Gly Ser Leu Thr Ser Trp Asn Val Ser Met Asp Thr Gln Ala
	350 355 360
45	cag cag ctg att ctt cac ttc tcc tca aga atg cat gcc acc ttc agt 1200
	Gln Gln Leu Ile Leu His Phe Ser Ser Arg Met His Ala Thr Phe Ser
	365 370 375
50	gct gcc tgg agc ctc cca ggc ttg ggg cag gac act ttg gtg ccc ccc 1248
	Ala Ala Trp Ser Leu Pro Gly Leu Gly Gln Asp Thr Leu Val Pro Pro
	380 385 390
55	gtg tac act gtc agc cag gtg tgg cgg tca gat gtc cag ttt gcc tgg 1296
	Val Tyr Thr Val Ser Gln Val Trp Arg Ser Asp Val Gln Phe Ala Trp
	395 400 405
60	aag cac ctc ttg tgt cca gat gtc tct tac aga cac ctg ggg ctc ttg 1344
	Lys His Leu Leu Cys Pro Asp Val Ser Tyr Arg His Leu Gly Leu Leu
	410 415 420 425
65	atc ctg gca ctg ctg gcc ctc ctc acc cta ctg ggt gtt gtt ctg gcc 1392
	Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu Ala
	430 435 440
70	ctc acc tgc cgg cgc cca cag tca ggc ccg ggc cca gcg cgg cca gtg 1440
	Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro Val
	445 450 455

	ctc ctc ctg cac gcg gcg gac tcg gag gcg cag cgg cgc ctg gtg gga	1488
	Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly	
	460 465 470	
5	gcg ctg gct gaa ctg cta cgg gca gcg ctg ggc ggc ggg cgc gac gtg	1536
	Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp Val	
	475 480 485	
10	atc gtg gac ctg tgg gag ggg agg cac gtg gcg cgc gtg ggc ccg ctg	1584
	Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro Leu	
	490 495 500 505	
15	ccg tgg ctc tgg gcg gcg cgg acg cgc gta gcg cgg gag cag ggc act	1632
	Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly Thr	
	510 515 520	
20	gtg ctg ctg ctg tgg agc ggc gcc gac ctt cgc ccg gtc agc ggc ccc	1680
	Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly Pro	
	525 530 535	
	gac ccc cgc gcc gcg ccc ctg ctc gcc ctg ctc cac gct gcc ccg cgc	1728
	Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro Arg	
	540 545 550	
25	ccg ctg ctg ctg ctc gct tac ttc agt cgc ctc tgc gcc aag ggc gac	1776
	Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp	
	555 560 565	
30	atc ccc ccg ccg ctg cgc gcc ctg ccg cgc tac cgc ctg ctg cgc gac	1824
	Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp	
	570 575 580 585	
35	ctg ccg cgt ctg ctg cgg gcg ctg gac gcg cgg cct ttc gca gag gcc	1872
	Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu Ala	
	590 595 600	
40	acc agc tgg ggc cgc ctt ggg gcg cgg cag cgc agg cag agc cgc cta	1920
	Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg Leu	
	605 610 615	
	gag ctg tgc agc cgg ctc gaa cga gag gcc gcc cga ctt gca gac cta	1968
	Glu Leu Cys Ser Arg Leu Glu Arg Glu Ala Ala Arg Leu Ala Asp Leu	
	620 625 630	
45	ggt tgagcagagc tccaccgcag tcccgggtgt ctgcggccgc t	2012
	Gly	
50	MGSSRLAALLPLLLIVIDLSDSAGIGFRHLPHWNTRCPLASHTEVLPISLAAPGGPSSPQSLGVCESGTVP	
	AVCASICCCQVAQVFNGASSTSWCRNPKSLPHSSSIGDTRCQHLLRGSCCLVVTCLRRAITFPSPPTSPTRD	
	FALKGPNLRIQRHGKVFPDWITHKGMEVGTGYNRRWVQLSGGPEFSFDLLPEARAIRVTISSGPEVSVRLCHQ	
	WALECEELSSPYDVQKIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPFQSWPEAYGSDFWKSVHFT	
	DYSQHTQMVMALTLRCPLKLEAALCQRHDWHTLCKDLPNATARES DGWYVLEKVDLHPQLCFKVQPWFSFGN	
	SSHVECPHQTGSLTSWNVSMDTQAQQLILHFSSRMHATFSAAWSLPGLGQDTLVPPVYTVSQVWRSDVQFAW	
	KHLLCPDVSYRHLGLLILALLALLTLLGVVLALTCCR PQSGPGPARPVLLLHAADSEAQRRLVGALAE LLRA	
55	ALGGGRDIVDLWEGRHVARVGPLPWLWAARTVAREQGTVLLLWSGADLRPVSGPDPRAPLLALLHAAPR	
	PLLLLAYFSRLCAKGDIPPLRALPRYRLRLDLPRLLRALDARPF AEATSWGRLGARQRRQSRLELC SRLER	
	EAARLADLG.	

Reverse translation of primate, e.g., human, DCRS9 (SEQ ID NO: 18):

5 atgggnwsnw snmgnytnge ngcnytnytn ytnccnytny tnytnathgt nathgayytn 60
 wsngaywsng cnggnathgg nttymgncay ytnccncayt ggaayacnmg ntgyccnytn 120
 gcwnsnccaya cngargtnyt nccnathwsn ytnngcngcnc cnggnggncc nwsnwsnccn 180
 10 carwsnytnng gngtntgyga rwsnggnacn gtncngcng tntgygcwsw nathtgytgy 240
 cargtnngcnc argtnttyaa yggngcnwsn wsnacnwsnt ggtgymgnaa yccnaarwsn 300
 15 ytnccncayw snwsnwsnat hggngayacn mgntgyarc ayytnytnmg nggnwsntgy 360
 tgyytnngtn tnaentgyyt nmgnmgngcn athacnttyc cnwsnccncc ncaracnwsn 420
 ccnacnmng ayttygcnyt naarggnccn aayytnmgna thcarmgnca yggnaargtn 480
 20 ttyccngayt ggacncayaa rggnatggar gtnggnacng gntayaaymg nmngtgggtn 540
 carytnwsng gnggnccnga rttywsntty gayytnytn cngargcnmg ngcnathmgn 600
 gtnacnathw snwsnggncc ngargtnwsn gtnmgnytn gycaycartg ggcnynngar 660
 25 tgygargary tnwsnwsncc ntaygaygtn caraarathg tnwsnggngg ncayacngtn 720
 garytnccnt aygarttyyt nytnccntgy ytntgyathg argcnwsnta yytnccargar 780
 30 gayacngtnm gnmgnaaraa rtgyccntty carwsntggc cngargcnta yggngwsngay 840
 ttytggaarw sngtncaytt yacngaytay wsnarcaya cncaratggt natggcnyn 900
 acnytnmgnt gyccnytnaa rytngargcn gcnytnngyc armgncaayga ytggcayacn 960
 35 ytntgyaarg ayytnccnaa ygcncngcn mgngarwsng ayggntggta ygtnytnngar 1020
 aargtngayy tncayccnaa rytntgytty aargtnarc cntggtyws nttyggnaay 1080
 40 wsnwsncayg tngartgycc ncaycaracn ggnwsnytna cnwsntggaa ygtwnsnatg 1140
 gayacncarg cncarcaryt nathytnca ytywsnwsnm gnatgcaygc nacnttywsn 1200
 gcngcntggw snytnccngg nytnngncar gayacnytn tncncngnt ntayacngtn 1260
 45 wsnargtnnt ggmgnwsnga ygtncartty gcntggaarc ayytnytnng yccngaygtn 1320
 wsnaymgnc ayytnngny nytnathytn gcnytnytn cnytnytnac nytnytnngn 1380
 50 gtngtnytn cnytnacntg ymgngnccn carwsnggnc cnggncngc nmgnccngtn 1440
 ytnytnytn aygcngcnga ywsngargcn carmgngny tngtnngngc nytnngngar 1500
 ytnytnmgng cngcnynng nggngngmgn gaygtnathg tngayytnng ggargngmgn 1560
 55 caygtnngcm gngtnngncc nytnccntgg ytntgggng cnmgnacnmg ngtnngcmgn 1620
 garcarggna cngtnytn nytnnggwsn ggngcngayy tnmngncngt nwsnggnccn 1680

gayccnmngng cngcncnnyt nytnngcnytn ytncaaygcng cncnmgncncc nytnnytn 1740
 ytnngentayt tywsnmngnyt ntgygcnaar ggngayathc cncncnccnyt nmngncnytn 1800
 5 ccnmgntaym gnytnytnmg ngayytncn mgnytnytnm gngcnytnnga ygcnmngncn 1860
 ttygengarg cnacnwsntg gggnmngnytn ggngcnmgnc armgnmgncnca rwsnmngnytn 1920
 garytntgyw snmgnytnnga rmngngargcn gcnmgnytnng cngayytngg n 1971
 10

Rodent, e.g., mouse, embodiment (see SEQ ID NO: 19 and 20). Predicted signal sequence indicated, but may vary by a few positions and depending upon cell type.

15 cagctccggg ccaggccctg ctgccctctt gcagacagga aagacatggg ctctgcgccc 60
 tgatcctaca gaagctc atg ggg agc ccc aga ctg gca gcc ttg ctc ctg 110
 Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu
 -20 -15
 20 tct ctc ccg cta ctg ctc atc ggc ctc gct gtg tct gct cgg gtt gcc 158
 Ser Leu Pro Leu Leu Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala
 -10 -5 -1 1
 25 tgc ccc tgc ctg cgg agt tgg acc agc cac tgt ctc ctg gcc tac cgt 206
 Cys Pro Cys Leu Arg Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg
 5 10 15 20
 30 gtg gat aaa cgt ttt gct ggc ctt cag tgg ggc tgg ttc cct ctc ttg 254
 Val Asp Lys Arg Phe Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu
 25 30 35
 35 gtg agg aaa tct aaa agt cct cct aaa ttt gaa gac tat tgg agg cac 302
 Val Arg Lys Ser Lys Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His
 40 45 50
 40 agg aca cca gca tcc ttc cag agg aag ctg cta ggc agc cct tcc ctg 350
 Arg Thr Pro Ala Ser Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu
 55 60 65
 45 tct gag gaa agc cat cga att tcc atc ccc tcc tca gcc atc tcc cac 398
 Ser Glu Glu Ser His Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His
 70 75 80
 50 aga ggc caa cgc acc aaa agg gcc cag cct tca gct gca gaa gga aga 446
 Arg Gly Gln Arg Thr Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg
 85 90 95 100
 55 gaa cat ctc cct gaa gca ggg tca caa aag tgt gga gga cct gaa ttc 494
 Glu His Leu Pro Glu Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe
 105 110 115
 tcc ttt gat ttg ctg ccc gag gtg cag gct gtt cgg gtg act att cct 542
 Ser Phe Asp Leu Leu Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro
 120 125 130

	gca ggc ccc aag gca cgt gtg cgc ctt tgt tat cag tgg gca ctg gaa	590
	Ala Gly Pro Lys Ala Arg Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu	
	135 140 145	
5	tgt gaa gac ttg agt agc cct ttt gat acc cag aaa att gtg tct gga	638
	Cys Glu Asp Leu Ser Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly	
	150 155 160	
10	ggg cac act gta gac ctg cct tat gaa ttc ctt ctg ccc tgc atg tgc	686
	Gly His Thr Val Asp Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys	
	165 170 175 180	
15	ata gag gcc tcc tac ctg caa gag gac act gtg agg cgc aaa agt gtc	734
	Ile Glu Ala Ser Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Ser Val	
	185 190 195	
20	cct tcc aga gct ggc ctg aag ctt atg gct cag act tct ggc agt caa	782
	Pro Ser Arg Ala Gly Leu Lys Leu Met Ala Gln Thr Ser Gly Ser Gln	
	200 205 210	
25	tac gct tca ctg act aca gcc agc ac	808
	Tyr Ala Ser Leu Thr Thr Ala Ser	
	215 220	
30	Reverse translation of rodent, e.g., mouse, DCRS9 (SEQ ID NO: 21):	
	atgggnwsnc cnmgnytnge ngcnytnytn ytnwsnytn cnytnytny nathggnytn	60
35	gcngtnwsng cnmgngtnge ntgyccntgy ytnmgnwsnt ggacnwsnca ytggytnytn	120
	gcntaymgng tngayaarmg nttygcnggn ytncartggg gntggttycc nytnytnngtn	180
40	mgnaarwsna arwsnccncc naarttygar gaytaytggm gncaymgnac nccngcnwsn	240
	ttycarmgna arytnytnng nwsnccnwsn ytnwsngarg arwsncaymg nathwsnath	300
	ccnwsnwsng cnathwsnca ymgnggncar mgnacnaarm gngcncarcc nwsngcngcn	360
45	garggnmgng arcayytncc ngargcnggn wsncaraart gyggnggncc ngarttywsn	420
	ttygayytny tnccngargt ncargcngtn mgngtnacna thccngcngg nccnaargcn	480
50	mgngtnmgny tntgytayca rtgggcnyn gartgygarg ayytnwsnws nccnttygay	540
	acncaraara thgtnwsngg nggncayacn gtngayytn cntaygartt yytnytnccn	600
	tgyatgtgya thgargcnws ntayytn car gargayacng tnmgnmgnaa rwsngtnccn	660
55	wsnmgngcng gnytnaaryt natggcncar acnwsnggnw sncartaygc nwsnytnacn	720
	acngcnwsn	729

Table 5: Nucleotide and polypeptide sequences of DNAX Cytokine Receptor Subunit like embodiments (DCRS10). Primate, e.g., human, embodiment (see SEQ ID NO: 22 and 23).

5	ttttgagcag aggcttccta ggctccgtag aaatttgcac acagcttcca cttcctgctt	60
	cagagcctgt tcttctactt acctggggccc ggagaagggtg gagggagacg agaagccgcc	120
	gagagccgac taccctccgg gccagtcctg tctgtccgtg gtggatctaa gaaactaga	179
10	atg aac cga agc att cct gtg gag gtt gat gaa tca gaa cca tac cca	227
	Met Asn Arg Ser Ile Pro Val Glu Val Asp Glu Ser Glu Pro Tyr Pro	
	1 5 10 15	
15	agt cag ttg ctg aaa cca atc cca gaa tat tcc ccg gaa gag gaa tca	275
	Ser Gln Leu Leu Lys Pro Ile Pro Glu Tyr Ser Pro Glu Glu Glu Ser	
	20 25 30	
20	gaa cca cct gct cca aat ata agg aac atg gca ccc aac agc ttg tct	323
	Glu Pro Pro Ala Pro Asn Ile Arg Asn Met Ala Pro Asn Ser Leu Ser	
	35 40 45	
25	gca ccc aca atg ctt cac aat tcc tcc gga gac ttt tct caa gct cac	371
	Ala Pro Thr Met Leu His Asn Ser Ser Gly Asp Phe Ser Gln Ala His	
	50 55 60	
30	tca acc ctg aaa ctt gca aat cac cag cgg cct gta tcc cgg cag gtc	419
	Ser Thr Leu Lys Leu Ala Asn His Gln Arg Pro Val Ser Arg Gln Val	
	65 70 75 80	
	acc tgc ctg cgc act caa gtt ctg gag gac agt gaa gac agt ttc tgc	467
	Thr Cys Leu Arg Thr Gln Val Leu Glu Asp Ser Glu Asp Ser Phe Cys	
	85 90 95	
35	agg aga cac cca ggc ctg ggc aaa gct ttc cct tct ggg tgc tct gca	515
	Arg Arg His Pro Gly Leu Gly Lys Ala Phe Pro Ser Gly Cys Ser Ala	
	100 105 110	
40	gtc agc gag cct gcg tct gag tct gtg gtt gga gcc ctc cct gca gag	563
	Val Ser Glu Pro Ala Ser Glu Ser Val Val Gly Ala Leu Pro Ala Glu	
	115 120 125	
45	cat cag ttt tca ttt atg gaa aaa cgt aat caa tgg ctg gta tct cag	611
	His Gln Phe Ser Phe Met Glu Lys Arg Asn Gln Trp Leu Val Ser Gln	
	130 135 140	
50	ctt tca gcg gct tct cct gac act ggc cat gac tca gac aaa tca gac	659
	Leu Ser Ala Ala Ser Pro Asp Thr Gly His Asp Ser Asp Lys Ser Asp	
	145 150 155 160	
	caa agt tta cct aat gcc tca gca gac tcc ttg ggc ggt agc cag gag	707
	Gln Ser Leu Pro Asn Ala Ser Ala Asp Ser Leu Gly Gly Ser Gln Glu	
	165 170 175	
55	atg gtg caa cgg ccc cag cct cac agg aac cga gca ggc ctg gat ctg	755
	Met Val Gln Arg Pro Gln Pro His Arg Asn Arg Ala Gly Leu Asp Leu	
	180 185 190	

	cca acc ata gac acg gga tat gat tcc cag ccc cag gat gtc ctg ggc	803
	Pro Thr Ile Asp Thr Gly Tyr Asp Ser Gln Pro Gln Asp Val Leu Gly	
	195 200 205	
5	atc agg cag ctg gaa agg ccc ctg ccc ctc acc tcc gtg tgt tac ccc	851
	Ile Arg Gln Leu Glu Arg Pro Leu Pro Leu Thr Ser Val Cys Tyr Pro	
	210 215 220	
10	cag gac ctc ccc aga cct ctc agg tcc agg gag ttc cct cag ttt gaa	899
	Gln Asp Leu Pro Arg Pro Leu Arg Ser Arg Glu Phe Pro Gln Phe Glu	
	225 230 235 240	
15	cct cag agg tat cca gca tgt gca cag atg ctg cct ccc aat ctt tcc	947
	Pro Gln Arg Tyr Pro Ala Cys Ala Gln Met Leu Pro Pro Asn Leu Ser	
	245 250 255	
20	cca cat gct cca tgg aac tat cat tac cat tgt cct gga agt ccc gat	995
	Pro His Ala Pro Trp Asn Tyr His Tyr His Cys Pro Gly Ser Pro Asp	
	260 265 270	
	cac cag gtg cca tat ggc cat gac tac cct cga gca gcc tac cag caa	1043
	His Gln Val Pro Tyr Gly His Asp Tyr Pro Arg Ala Ala Tyr Gln Gln	
	275 280 285	
25	gtg atc cag ccg gct ctg cct ggg cag ccc ctg cct gga gcc agt gtg	1091
	Val Ile Gln Pro Ala Leu Pro Gly Gln Pro Leu Pro Gly Ala Ser Val	
	290 295 300	
30	aga ggc ctg cac cct gtg cag aag gtt atc ctg aat tat ccc agc ccc	1139
	Arg Gly Leu His Pro Val Gln Lys Val Ile Leu Asn Tyr Pro Ser Pro	
	305 310 315 320	
35	tgg gac caa gaa gag agg ccc gca cag aga gac tgc tcc ttt ccg ggg	1187
	Trp Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Cys Ser Phe Pro Gly	
	325 330 335	
40	ctt cca agg cac cag gac cag cca cat cac cag cca cct aat aga gct	1235
	Leu Pro Arg His Gln Asp Gln Pro His His Gln Pro Pro Asn Arg Ala	
	340 345 350	
	ggt gct cct ggg gag tcc ttg gag tgc cct gca gag ctg aga cca cag	1283
	Gly Ala Pro Gly Glu Ser Leu Glu Cys Pro Ala Glu Leu Arg Pro Gln	
	355 360 365	
45	gtt ccc cag cct ccg tcc cca gct gct gtg cct aga ccc cct agc aac	1331
	Val Pro Gln Pro Pro Ser Pro Ala Ala Val Pro Arg Pro Pro Ser Asn	
	370 375 380	
50	cct cca gcc aga gga act cta aaa aca agc aat ttg cca gaa gaa ttg	1379
	Pro Pro Ala Arg Gly Thr Leu Lys Thr Ser Asn Leu Pro Glu Glu Leu	
	385 390 395 400	
55	cgg aaa gtc ttt atc act tat tcg atg gac aca gct atg gag gtg gtg	1427
	Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val Val	
	405 410 415	
	aaa ttc gtg aac ttt ttg ttg gta aat ggc ttc caa act gca att gac	1475
	Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile Asp	
	420 425 430	

ata ttt gag gat aga atc cga ggc att gat atc att aaa tgg atg gag 1523
 Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met Glu
 435 440 445
 5 cgc tac ctt agg gat aag acc gtg atg ata atc gta gca atc agc ccc 1571
 Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser Pro
 450 455 460
 10 aaa tac aaa cag gac gtg gaa ggc gct gag tcg cag ctg gac gag gat 1619
 Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu Asp
 465 470 475 480
 15 gag cat ggc tta cat act aag tac att cat cga atg atg cag att gag 1667
 Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile Glu
 485 490 495
 20 ttc ata aaa caa gga agc atg aat ttc aga ttc atc cct gtg ctc ttc 1715
 Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe
 500 505 510
 25 cca aat gct aag aag gag cat gtg ccc acc tgg ctt cag aac act cat 1763
 Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His
 515 520 525
 gtc tac agc tgg ccc aag aat aaa aaa aac atc ctg ctg cgg ctg ctg 1811
 Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu
 530 535 540
 30 aga gag gaa gag tat gtg gct cct cca cgg ggg cct ctg ccc acc ctt 1859
 Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu
 545 550 555 560
 35 cag gtg gtt ccc ttg tgacaccgtt catccccaga tcaactgaggc caggccatgt 1914
 Gln Val Val Pro Leu
 565
 ttggggcctt gttctgacag cattctggct gaggttggtc ggtagcactc ctggctgggtt 1974
 40 tttttctgtt cctccccgag agggcctctg gccccagga aacctgttgt gcagagctct 2034
 tccccggaga cctccacaca ccctggcttt gaagtggagt ctgtgactgc tctgcattct 2094
 ctgctttttaa aaaaaccatt gcaggtgcca gtgtcccata tgttcctcct gacagtttga 2154
 45 tgtgtccatt ctgggcctct cagtgtcttag caagtagata atgtaaggga tgtggcagca 2214
 aatggaaatg actacaaaca ctctcctatc aatcacttca ggctactttt atgagtttagc 2274
 50 cagatgcttg tgtatcctca gaccaaactg attcatgtac aaataataaaa atgttttactc 2334
 ttttgtaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2377

MNRSIPVEVDESEYPYPSQLLKPIPEYSPEEESEPPAPNIRNMAPNSLSAPTMLHNSSGDFSQAHSTLKLANH
 QRPVSRQVTCLRTQVLEDSFDCRRHPGLGKAFPSGCSAVSEPASESVVGALPAEHQFSFMEKRNQWLVSQ
 LSAASPDGTGHDSDKSDQSLPNASADSLGGSQEMVQRPQPHRNRAGLDLPTIDTGYDSQPQDVLGIRQLERPL
 5 PLTSVCYPQDLRPLRSREFPQFEPQRYPACAQMLPPNLSPHAPWNYHYHCPGSPDHQVPYGHDPRAAYQQ
 VIQPALPGQPLPGASVRGLHPVQKVILNYPSPWDQEERPAQRDCSFPGLPRHQDQPHHQPPNRAGAPGESLE
 CPAELRPQVPQPPSPAAPRPPSNPPARGTLKTSNLPEELRKVFITYSMDTAMEVVKFVNFLLVNGFQTAID
 IFEDRIRGIDI IKWMERYLRDKTVMIIVAISP KYQDVEGAESQLDEDEHGLHTKYIHRMMQIEFIKQGS MN
 10 FRFIPVLF PNAKKEHVPTWLQNTHVYSWPKNKNILLRLLREEEYVAPPRGPLPTLQVVPL

Reverse translation of primate, e.g., human, DCRS10 (SEQ ID NO: 24):

15 atgaaymgw snathccngt ngargtngay garwsngarc cntayccnws ncarytnytn 60
 aarccnathc cngartayws nccngargar garwsngarc cncngcnc naayathmgn 120
 aayatggcnc cnaaywsnyt nwsngcncn acnatgytnc ayaaywsnws ngngaytty 180
 20 wsnccargcnc aywsnacnyt naarytngcn aaycaycarm gncngtnws nmgnccargtn 240
 acntgyytnm gnacncargt nytngargay wsngargayw snattytgymg nmgnccayccn 300
 ggnytnngna argcnttycc nwsnggntgy wsngcngtnw sngarccngc nwsngarwsn 360
 25 gtngtnngng cnytnccngc ngarcaycar ttywsnttya tggaraarmg naaycartgg 420
 ytnngtnwsnc arytnwsngc ngcnwsnccn gayacnggnc aygaywsnga yaarwsngay 480
 30 carwsnytn cnaaygcnw ngcngaywsn ytngngngnw sncargarat ggtnccarmgn 540
 ccncarccnc aymgnaaymg ngcnggnytn gayytnccna cnathgayac nggntaygay 600
 wsnccarccnc argaygtnyt nggnathmgn carytngarm gncnytncc nytnacnwsn 660
 35 gtntgytayc cncargayyt nccnmgnccn ytnmgnwsnm gngarttycc ncarttygar 720
 ccncarmgnt ayccngcntg ygcncaratg ytnccncna ayytnwsncc ncaygcncn 780
 40 tggaaaytayc aytaycaytg yccnggnwsn ccngaycayc argtnccnta yggncaygay 840
 tayccnmngng cngentayca rcargtnath carccngcny tnccnggna rccnytnccn 900
 ggngcnwsng tnmnggnytn ncayccngtn caraargtna thytnaayta yccnwsnccn 960
 45 tgggaycarg argarmgncc ngcncarmgn gaytgywsnt tyccnggnytn nccnmgnccay 1020
 cargaycarc ncaycayca rccncnaay mgngcnggng cncnggnga rwsnytngar 1080
 50 tgyccngcng arytnmgnc ncargtnccn carccncnw snccngcngc ngtnccnmgn 1140
 ccncnwsna ayccncngc nmnggnacn ytnaaracnw snaaytncc ngargarytn 1200
 mgnaargtn tyathacnta ywsnatggay acngcnatgg argtnngtnaa rtytgtnaay 1260
 55 tyytnytn tnaaygntt ycaracngcn athgayatht tygargaymg nathmnggng 1320
 athgayatha thaartggat ggarmgntay ytnmnggaya aracngtnat gathathgtn 1380

gcathwsnc cnaartayaa rcargaygtn garggngcng arwsncaryt ngaygargay 1440
 garcayggny tncayacnaa rtayathcay mgatgatgc arathgartt yathaarcay 1500
 5 ggnwsnatga ayttymgntt yathccngtn ytnttyccna aygcnaaraa rgarcaygtn 1560
 ccnacntggy tncaraayac ncaygtnay wsntggccna araayaaraa raayathytn 1620
 ytnmgnytny tnmngngarga rgartaygtn gcncncncnm gnggncnytn nccnacnytn 1680
 10 cargtngtnc cnytn 1695

Rodent, e.g., mouse, embodiment (see SEQ ID NO: 25 and 26).

15 cag gac ctc cct ggg cct ctg agg tcc agg gaa ttg cca cct cag ttt 48
 Gln Asp Leu Pro Gly Pro Leu Arg Ser Arg Glu Leu Pro Pro Gln Phe
 1 5 10 15

20 gaa ctt gag agg tat cca atg aac gcc cag ctg ctg ccg ccc cat cct 96
 Glu Leu Glu Arg Tyr Pro Met Asn Ala Gln Leu Leu Pro Pro His Pro
 20 25 30

25 tcc cca cag gcc cca tgg aac tgt cag tac tac tgc ccc gga ggg ccc 144
 Ser Pro Gln Ala Pro Trp Asn Cys Gln Tyr Tyr Cys Pro Gly Gly Pro
 35 40 45

30 tac cac cac cag gtg cca cac ggc cat ggc tac cct cca gca gca gcc 192
 Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala
 50 55 60

35 tac cag caa gta ctc cag cct gct ctg cct ggg cag gtc ctt cct ggg 240
 Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly
 65 70 75 80

40 gca agg gca aga ggc cca cgc cct gtg cag aag gtc atc ctg aat gac 288
 Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp
 85 90 95

45 tcc agc ccc caa gac caa gaa gag aga cct gca cag aga gac ttc tct 336
 Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser
 100 105 110

50 ttc ccg agg ctc ccg agg gac cag ctc tac cgc cca cca tct aat gga 384
 Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly
 115 120 125

55 gtg gaa gcc cct gag gag tcc ttg gac ctt cct gca gag ctg aga cca 432
 Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro
 130 135 140

cat ggt ccc cag gct cca tcc cta gct gcc gtg cct aga ccc cct agc 480
 His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser
 145 150 155 160

aac ccc tta gcc cga gga act cta aga acc agc aat ttg cca gaa gaa 528
 Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu
 165 170 175

	tta cgg aaa gtc ttt atc act tat tct atg gac aca gcc atg gag gtg	576
	Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val	
	180 185 190	
5	gtg aaa ttt gtg aac ttt ctg ttg gtg aac ggc ttc caa act gcg att	624
	Val Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile	
	195 200 205	
10	gac ata ttt gag gat aga atc cgg ggt att gat atc att aaa tgg atg	672
	Asp Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met	
	210 215 220	
15	gag cgc tat ctt cga gat aag aca gtg atg ata atc gta gca atc agc	720
	Glu Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser	
	225 230 235 240	
20	ccc aaa tac aaa cag gat gtg gaa ggc gct gag tcg cag ctg gac gag	768
	Pro Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu	
	245 250 255	
	gac gag cat ggc tta cat act aag tac att cat cgg atg atg cag att	816
	Asp Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile	
	260 265 270	
25	gag ttc ata agt cag gga agc atg aac ttc aga ttc atc cct gtg ctc	864
	Glu Phe Ile Ser Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu	
	275 280 285	
30	ttc oca aat gcc aag aag gag cat gtg ccg acc tgg ctt cag aac act	912
	Phe Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr	
	290 295 300	
35	cat gtt tac agc tgg ccc aag aat aag aaa aac atc ctg ctg cgg ctg	960
	His Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu	
	305 310 315 320	
40	ctc agg gag gaa gag tat gtg gct cct ccc cga ggc cct ctg ccc acc	1008
	Leu Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr	
	325 330 335	
	ctt cag gtg gta ccc ttg tgacgatggc cactccagct cagtgccagc	1056
	Leu Gln Val Val Pro Leu	
	340	
45	ctgtttctcac agcattcttc tagcggagct ggctggtggc acccaggccc tggaacacct	1116
	cttctacaga gtccctctgtc tcctgagtct gagttgtcct cgctgggctt ccagagcttc	1176
50	agtgcctgga tgctgcaggc gacagaaaca aacatctatg accacaaaaa ctctcatcac	1236
	ttcagctact tttatgagtc ggtcagatgc tctgtgtcct tagaccagtc taaatcatgc	1296
	tcaaataata aaatgattat tctttgt	1323
55	QDLPGPLRSRELPPQFELERYPMNAQLLPPHPSPQAPWNCQYYCPGGPYHHQVPHGHGYPPAAAYQQVLQPA LPGQVLPGARARGPRPVQKVILNDSSPDQEERPAQRDFSFPRLPRDQLYRPPSNGVEAPEESLDLPAELRP HGPQAPSLAAVPRPPSNPLARGTLRTSNLPEELRKVFITYSMDTAMEVVKFVNFLVNGFQTAIDIFEDRIR GIDIWKWMERYLRDKTVMIIVAISPKYKQDVEGAESQLDEDEHGLHTKYIHRMMQIEFISQGSMMNFRFIPVL FPNAKKEHVPTWLQNTHVYSWPKNKKNILLRLLREEEYVAPPRGPLPTLQVVPL.	

Reverse translation of rodent, e.g., mouse, DCRS6 (SEQ ID NO: 27):

5 cargayytnc cnggncnnyt nmgnwsnmgn garytnccnc cncarttyga rytngarmgn 60
 tayccnatga aygcncaryt nytncnccn cayccnwsnc cncargcncc ntggaaytgy 120
 cartaytayt gyccngggngg nccntaycay caycargtnc cncayggnc yggntayccn 180
 10 ccngcngcng cntaycarca rgtnytncar ccngcnytn cnggncargt nytncnggn 240
 gcnmgngcnm gnggncnmg nccngtnar aargtnathy tnaaygayws nwsnccncar 300
 15 gaycargarg armgncncgc ncarmgngay ttywsnttyc cnmgnytncc nmnggaycar 360
 ytnntaymgnc cncnwsnaa yggngtngar gcnccngarg arwsnytna yytnccngcn 420
 garytnmgnc cncayggnc ncargcnccn wsnytnngcng cngtnccnmg nccnccnwsn 480
 20 aayccnytn cnmnggnac nytnmgnaen wsnaayytnc cngargaryt nmgnaargtn 540
 ttyathacnt aywsnatgga yacngcnatg gargtngtna arttygtnaa yttyytnytn 600
 25 gtnaayggnt tycaracngc nathgayath ttygargaym gnathmgngg nathgayath 660
 athaartgga tggarmgnta yytnmgngay aaracngtna tgathathgt ngcnathwsn 720
 ccnaartaya arcargaygt ngarggngcn garwsncary tngaygarga ygarcaaygg 780
 30 ytncaayacna artayathca ymgntatgat carathgart tyathwsnca rggngwsnatg 840
 aayttymgnt tyathccngt nytnttyccn aaygcnaara argarcaygt nccnacntgg 900
 35 ytncaraaya cncaygtnta ywsntggccn aaraayaara araayathyt nytnmgnytn 960
 ytnmgngarg argartaygt ngcnccnccn mgnggncny tnccnacny ncartngtn 1020
 ccnytn 1026
 40

45 Table 6: Alignment of the cytoplasmic portions of various cytokine receptor subunits. The IL-17R_Hu (SEQ ID NO: 28) is GenBank AAB99730.1(U58917), gi|7657230; the IL-17R_Mu (SEQ ID NO: 29) is GenBank AAC52357.1(U31993), gi|6680411; the IL-17R_Ce (SEQ ID NO: 30) is GenBank AAA811100.1(U39997), gi|1353171; and the DCRS6_Ce (SEQ ID NO: 31) is EMBCAA90543.1(Z50177), gi|7503597. Of particular interest are motifs or features corresponding, in primate DCRS8 to: R/K at 339/340; D/E at 348/349; alpha helical regions from H353-Q365, C370-S381, E389-H396, K410-D414, and D485-H495; beta sheet regions correspond to F400-V404 and F458-Y462; E at 431; E/D at 442/443; Y/F at 458; D/E at 468-470; Y/F at 481; and Q/R/F at 523.

50

	DCRS7_Mu	RTALLHSADG-AGYERLVGALASALSQMP---LRVAVDLWSRRE-LSAHGALAWFHHQR
	DCRS7_Hu	RAALLLYSADD-SGFERLVGALASALCQLP---LRVAVDLWSRRE-LSAQGPVAFWFAQR
	IL-17R_Hu	RKVWIIYSADH-PLYVDVVLKFAQFLITACG--TEVALDLLEEQA-ISEAGVMTWVGRQK
5	IL-17R_Mu	RKVWIVYSADH-PLYVEVVLKFAQFLITACG--TEVALDLLEEQV-ISEVGVMTWVSRQK
	DCRS10	RKVFITYSMD----TAMEVVKFVNFLLVNG---FQTAIDIFEDR--IRGIDI IKWMERYL
	DCRS10_Mu	RKVFITYSMD----TAMEVVKFVNFLLVNG---FQTAIDIFEDR--IRGIDI IKWMERYL
	DCRS9_Hu	RPVLLLHAADS-EAQRRLVGALAE LLRAALGGGRDVIVDLWEGRH-VARVGPLPWLWAAR
	DCRS8_Hu	PKVFLCYSSKDGQNHMNVQC FAYFLQDFCG--CEVALDLWEDFS-LCREGQREWVIQKI
10	IL-17R_Ce	VKVMIVYADDN-DLHTDCVKKLVENLRNCAS--CDPVFDLEKLI--TAEIVPSRWLV DQI
	DCRS6_Hu	IKVLVVYPSEI--CFHHTICYFTEFLQNHCR--SEVILEKWQKKK-IAEMGPVQWLATQK
	DCRS6_Ce	FKVMLVCPEVS-GRDEDFMMRIADALKKSN---NKVVCDRWFE DSKNAEENMLHWVYEQT
		. : . : : * : *
15	DCRS7_Mu	RRILQEGGVVILLFSPA AVAQCC---QWLQLQTVEP---GP---HDA LAAWLSCVLPDFL
	DCRS7_Hu	RQTLQEGGVVLLFSPGAVALCS---EWLQDGVSGPGAHP---HDAFRASLSCVLPDFL
	IL-17R_Hu	QEMVESNSKIIIVLC SRGTRAKWQALLGRGAP-VRLRCDHGKPV-GDLFTAAMNMILPDFK
	IL-17R_Mu	QEMVESNSKIIILCSRG TQAKWKAILGWAEPVQLRCDHWKPA-GDLFTAAMNMILPDFK
	DCRS10	R---DKTVMIIVAI SPKYKQDVE----GAESQLDED-EHGL---HTKYIHRM-MQIEFIK
20	DCRS10_Mu	R---DKTVMIIVAI SPKYKQDVE----GAESQLDED-EHGL---HTKYIHRM-MQIEFIS
	DCRS9_Hu	TRVAREQGTVLLLWSGADLRPVS-----GPD P-RAAP-----LLA----LLHAAP
	DCRS8_Hu	H----ESQFIIIVCSKGMKYFVD---KKNYKHKGGRGSGK---GELFLVAVSAIAEKL R
	IL-17R_Ce	S----SLKKFIIIVSDCAEKILD---TEASETHQLVQARP--FADLFGPAMEMIIRDAT
	DCRS6_Hu	K----AADKVVFLLSNDVNSVCD---GTCGKSEGPSSENS---QDLFPLAFNLFCSDLR
25	DCRS6_Ce	K----IAEKIIVFHSAYYHPRCG---IYDVINNFFPCTDPR-----LAHIALT---PEAQ
		... *
	DCRS7_Mu	QGRATGR-----YVG VYFDGLLHPDSVPSPFRVAPLFSLP-SQLPAFLDALQ--GGCSTS
	DCRS7_Hu	QGRAPGS-----YVGACFDRLLHPDAVPALFRTVPVFTLP-SQLPDLFGALQ--QPRAPR
30	IL-17R_Hu	RPACFGT-----YVVCYFSEVSCDGDVPDLFGAAPRYPLM-DRFEEVYFRIQ--DLEMFO
	IL-17R_Mu	RPACFGT-----YVVCYFSGICSERDVPDLFNITSRYPLM-DRFEEVYFRIQ--DLEMFE
	DCRS10	QGSMNFR-----FIPVLF PNAK-KEHVPTWLQNTHVYSWP-KNKKNILLRLL-REEEYVA
	DCRS10_Mu	QGSMNFR-----FIPVLF PNAK-KEHVPTWLQNTHVYSWP-KNKKNILLRLL-REEEYVA
	DCRS9_Hu	RPL-----LLLAYFSRLCAKGDIPPLRALPRYRL- RDLPRLLRALD--ARPFAE
35	DCRS8_Hu	QAKQSSSAALSKFIAVYFDYSC-EGDVPGILD LSTKYRLM-DNLPQLCSHLHSRDHGLQE
	IL-17R_Ce	HNFPEAR---KKYAVVRFNYS P---HVPPNLAILNLPTFIPEQFAQLTAFLHN-VEHTER
	DCRS6_Hu	SQIHLHK-----YVVVYFREID-TKDDYNALSVC PKYHLM-KDATAFCAELL--HVKQQ
	DCRS6_Ce	RSVPKEV-----EYVLP RDQKLL--EDAFDITIADPLVIDIPIEDVAIPENVP--IH HESC
40		
	DCRS7_Mu	AGRPAD RVER-----VT-----QALRSALDSCTS-----
	DCRS7_Hu	SGRLQERAEQ-----VS-----RALQPALDSYFHPP-----
	IL-17R_Hu	PGRMHRVGELSGDNYLRS---PGGRQLRAALDRFRDWQVRCPDW
	IL-17R_Mu	PGRMHVREL TGDNYLQS---PSGRQLKEAVLRFQEWQTQCPDW
45	DCRS10	P----PRGPL-----PTLQVVPL-----
	DCRS10_Mu	P----PRGPL-----PTLQVVPL-----
	DCRS9_Hu	ATSWGRLGAR-----QRRQSRLELCSR-----
	DCRS8_Hu	PGQHTRQGSR-----RNYFRSKSGRS LYVAICNMHQFIDEEDW
	IL-17R_Ce	ANVTQNISEA-----Q-----IHEWNL CASRMMSFFVRNPW
50	DCRS6_Hu	VS---AGKR-----SQACHDGCCSL-----
	DCRS6_Ce	DSIDSRNNSK-----THSTD SGVSSLSS-----NS--

Table 6 shows comparison of the available sequences of primate, rodent, and various other receptors. Various conserved residues are aligned and indicated. The structurally homologous cytoplasmic domains most likely signal through pathways like IL-17, e.g., through NFkB. Similar to IL-1 signalling, it is likely that these receptors are involved in innate immunity and/or development.

As used herein, the term DCRS shall be used to describe a protein comprising amino acid sequences shown in Tables 1-5, respectively. In many cases, a substantial fragment thereof will be functionally or structurally equivalent, including, e.g., an extracellular or intracellular domain. The invention also includes a protein variation of the respective DCRS allele whose sequence is provided, e.g., a mutein or soluble extracellular construct. Typically, such agonists or antagonists will exhibit less than about 10% sequence differences, and thus will often have between 1 and 11 substitutions, e.g., 2-, 3-, 5-, 7-fold, and others. It also encompasses allelic and other variants, e.g., natural polymorphic, of the protein described. Typically, it will bind to its corresponding biological ligand, perhaps in a dimerized state with an alpha receptor subunit, with high affinity, e.g., at least about 100 nM, usually better than about 30 nM, preferably better than about 10 nM, and more preferably at better than about 3 nM. The term shall also be used herein to refer to related naturally occurring forms, e.g., alleles, polymorphic variants, and metabolic variants of the mammalian protein. Preferred forms of the receptor complexes will bind the appropriate ligand with an affinity and selectivity appropriate for a ligand-receptor interaction.

This invention also encompasses combinations of proteins or peptides having substantial amino acid sequence identity with an amino acid sequence in Tables 1-5. It will include sequence variants with relatively few residue substitutions, e.g., preferably less than about 3-5.

A substantial polypeptide "fragment", or "segment", is a stretch of amino acid residues of at least about 8 amino acids, generally at least 10 amino acids, more generally at least 12 amino acids, often at least 14 amino acids, more often at least 16 amino acids, typically at least 18 amino acids, more typically at least 20 amino acids, usually at least 22 amino acids, more usually at least 24 amino acids, preferably at least 26 amino acids, more preferably at least 28 amino acids, and, in particularly preferred embodiments, at least about 30 or more amino acids. This includes, e.g., 40, 50, 60, 70, 85, 100, 115, 130, 150, and other lengths. Sequences of segments of different proteins can be compared to one another over appropriate length stretches, typically between conserved motifs. In many situations, fragments may exhibit functional properties of the intact subunits, e.g., the extracellular domain of the transmembrane receptor may retain the ligand binding features, and may be used to prepare a soluble receptor-like complex.

Amino acid sequence homology, or sequence identity, is determined by optimizing residue matches. In some comparisons, gaps may be introduced, as required. See, e.g., Needleham, et al., (1970) J. Mol. Biol. 48:443-453; Sankoff, et al., (1983) chapter one in Time Warps, String Edits, and Macromolecules: The Theory and Practice of Sequence Comparison, Addison-Wesley, Reading, MA; and software packages from IntelliGenetics, Mountain View, CA; and the University of Wisconsin Genetics Computer Group (GCG), Madison, WI; each of which is incorporated herein by reference. This changes when considering conservative substitutions as matches. Conservative substitutions typically include substitutions within the following groups: glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. Homologous amino acid sequences are intended to include natural allelic and interspecies variations in the cytokine sequence. Typical homologous proteins or peptides will have from 50-100% homology (if gaps can be introduced), to 60-100% homology (if conservative substitutions are included) with an amino acid sequence segment of, e.g., Table 3 or 4. Homology measures will be at least about 70%, generally at least 76%, more generally at least 81%, often at least 85%, more often at least 88%, typically at least 90%, more typically at least 92%, usually at least 94%, more usually at least 95%, preferably at least 96%, and more preferably at least 97%, and in particularly preferred embodiments, at least 98% or more. The degree of homology will vary with the length of the compared segments. Homologous proteins or peptides, such as the allelic variants, will share most biological activities with the embodiments described in Tables 1-5.

As used herein, the term "biological activity" is used to describe, without limitation, effects on inflammatory responses, innate immunity, and/or morphogenic development by cytokine-like ligands. For example, these receptors should mediate phosphatase or phosphorylase activities, which activities are easily measured by standard procedures. See, e.g., Hardie, et al. (eds. 1995) The Protein Kinase FactBook vols. I and II, Academic Press, San Diego, CA; Hanks, et al. (1991) Meth. Enzymol. 200:38-62; Hunter, et al. (1992) Cell 70:375-388; Lewin (1990) Cell 61:743-752; Pines, et al. (1991) Cold Spring Harbor Symp. Quant. Biol. 56:449-463; and Parker, et al. (1993) Nature 363:736-738. The receptors, or portions thereof, may be useful as phosphate labeling enzymes to label general or specific substrates. The subunits may also be functional immunogens to elicit recognizing antibodies, or antigens capable of binding antibodies.

The terms ligand, agonist, antagonist, and analog of, e.g., a DCRS8 or DCRS9, include molecules that modulate the characteristic cellular responses to cytokine ligand proteins, as well as molecules possessing the more standard structural binding competition features of ligand-receptor interactions, e.g., where the receptor is a natural

receptor or an antibody. The cellular responses likely are typically mediated through receptor tyrosine kinase pathways.

Also, a ligand is a molecule which serves either as a natural ligand to which said receptor, or an analog thereof, binds, or a molecule which is a functional analog of the natural ligand. The functional analog may be a ligand with structural modifications, or may be a wholly unrelated molecule which has a molecular shape which interacts with the appropriate ligand binding determinants. The ligands may serve as agonists or antagonists, see, e.g., Goodman, et al. (eds. 1990) Goodman & Gilman's: The Pharmacological Bases of Therapeutics, Pergamon Press, New York.

Rational drug design may also be based upon structural studies of the molecular shapes of a receptor or antibody and other effectors or ligands. See, e.g., Herz, et al. (1997) J. Recept. Signal Transduct. Res. 17:671-776; and Chaiken, et al. (1996) Trends Biotechnol. 14:369-375. Effectors may be other proteins which mediate other functions in response to ligand binding, or other proteins which normally interact with the receptor. One means for determining which sites interact with specific other proteins is a physical structure determination, e.g., x-ray crystallography or 2 dimensional NMR techniques. These will provide guidance as to which amino acid residues form molecular contact regions. For a detailed description of protein structural determination, see, e.g., Blundell and Johnson (1976) Protein Crystallography, Academic Press, New York, which is hereby incorporated herein by reference.

II. Activities

The cytokine receptor-like proteins will have a number of different biological activities, e.g., modulating cell proliferation, or in phosphate metabolism, being added to or removed from specific substrates, typically proteins. Such will generally result in modulation of an inflammatory function, other innate immunity response, or a morphological effect. The subunit will probably have a specific low affinity binding to the ligand.

The DCRS8 and DCRS9 have characteristic motifs of receptors signaling through the JAK pathway. See, e.g., Ihle, et al. (1997) Stem Cells 15(suppl. 1):105-111; Silvennoinen, et al. (1997) APMIS 105:497-509; Levy (1997) Cytokine Growth Factor Review 8:81-90; Winston and Hunter (1996) Current Biol. 6:668-671; Barrett (1996) Baillieres Clin. Gastroenterol. 10:1-15; and Briscoe, et al. (1996) Philos. Trans. R. Soc. Lond. B. Biol. Sci. 351:167-171.

The biological activities of the cytokine receptor subunits will be related to addition or removal of phosphate moieties to substrates, typically in a specific manner, but occasionally in a non specific manner. Substrates may be identified, or conditions for

enzymatic activity may be assayed by standard methods, e.g., as described in Hardie, et al. (eds. 1995) The Protein Kinase FactBook vols. I and II, Academic Press, San Diego, CA; Hanks, et al. (1991) Meth. Enzymol. 200:38-62; Hunter, et al. (1992) Cell 70:375-388; Lewin (1990) Cell 61:743-752; Pines, et al. (1991) Cold Spring Harbor Symp. Quant. Biol. 56:449-463; and Parker, et al. (1993) Nature 363:736-738.

The receptor subunits may combine to form functional complexes, e.g., which may be useful for binding ligand or preparing antibodies. These will have substantial diagnostic uses, including detection or quantitation.

III. Nucleic Acids

This invention contemplates use of isolated nucleic acid or fragments, e.g., which encode these or closely related proteins, or fragments thereof, e.g., to encode a corresponding polypeptide, preferably one which is biologically active. In addition, this invention covers isolated or recombinant DNAs which encode combinations of such proteins or polypeptides having characteristic sequences, e.g., of the DCRSs. Typically, the nucleic acid is capable of hybridizing, under appropriate conditions, with a nucleic acid sequence segment shown in Tables 1-5, but preferably not with a corresponding segment of other receptors described in Table 6. Said biologically active protein or polypeptide can be a full length protein, or fragment, and will typically have a segment of amino acid sequence highly homologous, e.g., exhibiting significant stretches of identity, to one shown in Tables 1-5. Further, this invention covers the use of isolated or recombinant nucleic acid, or fragments thereof, which encode proteins having fragments which are equivalent to the DCRS8 or DCRS9 proteins. The isolated nucleic acids can have the respective regulatory sequences in the 5' and 3' flanks, e.g., promoters, enhancers, poly-A addition signals, and others from the natural gene. Combinations, as described, are also provided.

An "isolated" nucleic acid is a nucleic acid, e.g., an RNA, DNA, or a mixed polymer, which is substantially pure, e.g., separated from other components which naturally accompany a native sequence, such as ribosomes, polymerases, and flanking genomic sequences from the originating species. The term embraces a nucleic acid sequence which has been removed from its naturally occurring environment, and includes recombinant or cloned DNA isolates, which are thereby distinguishable from naturally occurring compositions, and chemically synthesized analogs or analogs biologically synthesized by heterologous systems. A substantially pure molecule includes isolated forms of the molecule, either completely or substantially pure.

An isolated nucleic acid will generally be a homogeneous composition of molecules, but will, in some embodiments, contain heterogeneity, preferably minor. This

heterogeneity is typically found at the polymer ends or portions not critical to a desired biological function or activity.

A "recombinant" nucleic acid is typically defined either by its method of production or its structure. In reference to its method of production, e.g., a product made by a process, the process is use of recombinant nucleic acid techniques, e.g., involving human intervention in the nucleotide sequence. Typically this intervention involves in vitro manipulation, although under certain circumstances it may involve more classical animal breeding techniques. Alternatively, it can be a nucleic acid made by generating a sequence comprising fusion of two fragments which are not naturally contiguous to each other, but is meant to exclude products of nature, e.g., naturally occurring mutants as found in their natural state. Thus, for example, products made by transforming cells with an unnaturally occurring vector is encompassed, as are nucleic acids comprising sequence derived using any synthetic oligonucleotide process. Such a process is often done to replace a codon with a redundant codon encoding the same or a conservative amino acid, while typically introducing or removing a restriction enzyme sequence recognition site. Alternatively, the process is performed to join together nucleic acid segments of desired functions to generate a single genetic entity comprising a desired combination of functions not found in the commonly available natural forms, e.g., encoding a fusion protein. Restriction enzyme recognition sites are often the target of such artificial manipulations, but other site specific targets, e.g., promoters, DNA replication sites, regulation sequences, control sequences, or other useful features may be incorporated by design. A similar concept is intended for a recombinant, e.g., fusion, polypeptide. This will include a dimeric repeat. Specifically included are synthetic nucleic acids which, by genetic code redundancy, encode equivalent polypeptides to fragments of DCRSs and fusions of sequences from various different related molecules, e.g., other cytokine receptor family members.

A "fragment" in a nucleic acid context is a contiguous segment of at least about 17 nucleotides, generally at least 21 nucleotides, more generally at least 25 nucleotides, ordinarily at least 30 nucleotides, more ordinarily at least 35 nucleotides, often at least 39 nucleotides, more often at least 45 nucleotides, typically at least 50 nucleotides, more typically at least 55 nucleotides, usually at least 60 nucleotides, more usually at least 66 nucleotides, preferably at least 72 nucleotides, more preferably at least 79 nucleotides, and in particularly preferred embodiments will be at least 85 or more nucleotides. Typically, fragments of different genetic sequences can be compared to one another over appropriate length stretches, particularly defined segments such as the domains described below.

A nucleic acid which codes for the DCRS8 or DCRS9 will be particularly useful to identify genes, mRNA, and cDNA species which code for itself or closely related proteins, as well as DNAs which code for polymorphic, allelic, or other genetic variants, e.g., from different individuals or related species. Preferred probes for such screens are those regions of the interleukin which are conserved between different polymorphic variants or which contain nucleotides which lack specificity, and will preferably be full length or nearly so. In other situations, polymorphic variant specific sequences will be more useful.

This invention further covers recombinant nucleic acid molecules and fragments having a nucleic acid sequence identical to or highly homologous to the isolated DNA set forth herein. In particular, the sequences will often be operably linked to DNA segments which control transcription, translation, and DNA replication. These additional segments typically assist in expression of the desired nucleic acid segment.

Homologous, or highly identical, nucleic acid sequences, when compared to one another, e.g., DCRS8 sequences, exhibit significant similarity. The standards for homology in nucleic acids are either measures for homology generally used in the art by sequence comparison or based upon hybridization conditions. Comparative hybridization conditions are described in greater detail below.

Substantial identity in the nucleic acid sequence comparison context means either that the segments, or their complementary strands, when compared, are identical when optimally aligned, with appropriate nucleotide insertions or deletions, in at least about 60% of the nucleotides, generally at least 66%, ordinarily at least 71%, often at least 76%, more often at least 80%, usually at least 84%, more usually at least 88%, typically at least 91%, more typically at least about 93%, preferably at least about 95%, more preferably at least about 96 to 98% or more, and in particular embodiments, as high at about 99% or more of the nucleotides, including, e.g., segments encoding structural domains such as the segments described below. Alternatively, substantial identity will exist when the segments will hybridize under selective hybridization conditions, to a strand or its complement, typically using a sequence derived from Tables 1-5. Typically, selective hybridization will occur when there is at least about 55% homology over a stretch of at least about 14 nucleotides, more typically at least about 65%, preferably at least about 75%, and more preferably at least about 90%. See, Kanehisa (1984) Nucl. Acids Res. 12:203-213, which is incorporated herein by reference. The length of homology comparison, as described, may be over longer stretches, and in certain embodiments will be over a stretch of at least about 17 nucleotides, generally at least about 20 nucleotides, ordinarily at least about 24 nucleotides, usually at least about 28 nucleotides, typically at least about 32 nucleotides, more typically at least about 40 nucleotides, preferably at least

about 50 nucleotides, and more preferably at least about 75 to 100 or more nucleotides. This includes, e.g., 125, 150, 175, 200, 225, 246, 273, and other lengths.

Stringent conditions, in referring to homology in the hybridization context, will be stringent combined conditions of salt, temperature, organic solvents, and other parameters typically controlled in hybridization reactions. Stringent temperature conditions will usually include temperatures in excess of about 30 C, more usually in excess of about 37 C, typically in excess of about 45 C, more typically in excess of about 55 C, preferably in excess of about 65 C, and more preferably in excess of about 70 C. Stringent salt conditions will ordinarily be less than about 500 mM, usually less than about 400 mM, more usually less than about 300 mM, typically less than about 200 mM, preferably less than about 100 mM, and more preferably less than about 80 mM, even down to less than about 20 mM. However, the combination of parameters is much more important than the measure of any single parameter. See, e.g., Wetmur and Davidson (1968) J. Mol. Biol. 31:349-370, which is hereby incorporated herein by reference.

The isolated DNA can be readily modified by nucleotide substitutions, nucleotide deletions, nucleotide insertions, and inversions of nucleotide stretches. These modifications result in novel DNA sequences which encode this protein or its derivatives. These modified sequences can be used to produce mutant proteins (muteins) or to enhance the expression of variant species. Enhanced expression may involve gene amplification, increased transcription, increased translation, and other mechanisms. Such mutant DCRS8-like derivatives include predetermined or site-specific mutations of the protein or its fragments, including silent mutations using genetic code degeneracy. "Mutant DCRS8" as used herein encompasses a polypeptide otherwise falling within the homology definition of the DCRS8 as set forth above, but having an amino acid sequence which differs from that of other cytokine receptor-like proteins as found in nature, whether by way of deletion, substitution, or insertion. In particular, "site specific mutant DCRS8" encompasses a protein having substantial sequence identity with a protein of Table 3, and typically shares most of the biological activities or effects of the forms disclosed herein.

Although site specific mutation sites are predetermined, mutants need not be site specific. Mammalian DCRS8 mutagenesis can be achieved by making amino acid insertions or deletions in the gene, coupled with expression. Substitutions, deletions, insertions, or many combinations may be generated to arrive at a final construct. Insertions include amino- or carboxy- terminal fusions. Random mutagenesis can be conducted at a target codon and the expressed mammalian DCRS mutants can then be screened for the desired activity, providing some aspect of a structure-activity relationship. Methods for making substitution mutations at predetermined sites in DNA

having a known sequence are well known in the art, e.g., by M13 primer mutagenesis. See also Sambrook, et al. (1989) and Ausubel, et al. (1987 and periodic Supplements).

The mutations in the DNA normally should not place coding sequences out of reading frames and preferably will not create complementary regions that could hybridize to produce secondary mRNA structure such as loops or hairpins.

The phosphoramidite method described by Beaucage and Carruthers (1981) Tetra. Letts. 22:1859-1862, will produce suitable synthetic DNA fragments. A double stranded fragment will often be obtained either by synthesizing the complementary strand and annealing the strand together under appropriate conditions or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

Polymerase chain reaction (PCR) techniques can often be applied in mutagenesis. Alternatively, mutagenesis primers are commonly used methods for generating defined mutations at predetermined sites. See, e.g., Innis, et al. (eds. 1990) PCR Protocols: A Guide to Methods and Applications Academic Press, San Diego, CA; and Dieffenbach and Dveksler (1995; eds.) PCR Primer: A Laboratory Manual Cold Spring Harbor Press, CSH, NY.

Certain embodiments of the invention are directed to combination compositions comprising the receptor or ligand sequences described. In other embodiments, functional portions of the sequences may be joined to encode fusion proteins. In other forms, variants of the described sequences may be substituted.

IV. Proteins, Peptides

As described above, the present invention encompasses primate DCRS6-10, e.g., whose sequences are disclosed in Tables 1-5, and described above. Allelic and other variants are also contemplated, including, e.g., fusion proteins combining portions of such sequences with others, including, e.g., epitope tags and functional domains.

The present invention also provides recombinant proteins, e.g., heterologous fusion proteins using segments from these primate or rodent proteins. A heterologous fusion protein is a fusion of proteins or segments which are naturally not normally fused in the same manner. Thus, the fusion product of, e.g., a DCRS8 with another cytokine receptor is a continuous protein molecule having sequences fused in a typical peptide linkage, typically made as a single translation product and exhibiting properties, e.g., sequence or antigenicity, derived from each source peptide. A similar concept applies to heterologous nucleic acid sequences. Combinations of various designated proteins into complexes are also provided.

In addition, new constructs may be made from combining similar functional or structural domains from other related proteins, e.g., cytokine receptors or Toll-like

receptors, including species variants. For example, ligand-binding or other segments may be "swapped" between different new fusion polypeptides or fragments. See, e.g., Cunningham, et al. (1989) Science 243:1330-1336; and O'Dowd, et al. (1988) J. Biol. Chem. 263:15985-15992, each of which is incorporated herein by reference. Thus, new chimeric polypeptides exhibiting new combinations of specificities will result from the functional linkage of receptor-binding specificities. For example, the ligand binding domains from other related receptor molecules may be added or substituted for other domains of this or related proteins. The resulting protein will often have hybrid function and properties. For example, a fusion protein may include a targeting domain which may serve to provide sequestering of the fusion protein to a particular subcellular organelle.

Candidate fusion partners and sequences can be selected from various sequence data bases, e.g., GenBank, c/o IntelliGenetics, Mountain View, CA; and BCG, University of Wisconsin Biotechnology Computing Group, Madison, WI, which are each incorporated herein by reference. In particular, combinations of polypeptide sequences provided in Tables 1-5 are particularly preferred. Variant forms of the proteins may be substituted in the described combinations.

The present invention particularly provides muteins which bind cytokine-like ligands, and/or which are affected in signal transduction. Structural alignment of human DCRSs with other members of the cytokine receptor family show conserved features/residues. See Table 6. Alignment of the human DCRS8 sequence with other members of the cytokine receptor family indicates various structural and functionally shared features. See also, Bazan, et al. (1996) Nature 379:591; Lodi, et al. (1994) Science 263:1762-1766; Sayle and Milner-White (1995) TIBS 20:374-376; and Gronenberg, et al. (1991) Protein Engineering 4:263-269.

Substitutions with either mouse sequences or human sequences are particularly preferred. Conversely, conservative substitutions away from the ligand binding interaction regions will probably preserve most signaling activities; and conservative substitutions away from the intracellular domains will probably preserve most ligand binding properties.

"Derivatives" of the primate DCRS8 include amino acid sequence mutants, glycosylation variants, metabolic derivatives and covalent or aggregative conjugates with other chemical moieties. Covalent derivatives can be prepared by linkage of functionalities to groups which are found in the DCRS8 amino acid side chains or at the N- or C- termini, e.g., by means which are well known in the art. These derivatives can include, without limitation, aliphatic esters or amides of the carboxyl terminus, or of residues containing carboxyl side chains, O-acyl derivatives of hydroxyl group-containing residues, and N-acyl derivatives of the amino terminal amino acid or amino-group

containing residues, e.g., lysine or arginine. Acyl groups are selected from the group of alkyl-moieties, including C3 to C18 normal alkyl, thereby forming alkanoyl aroyl species.

In particular, glycosylation alterations are included, e.g., made by modifying the glycosylation patterns of a polypeptide during its synthesis and processing, or in further processing steps. Particularly preferred means for accomplishing this are by exposing the polypeptide to glycosylating enzymes derived from cells which normally provide such processing, e.g., mammalian glycosylation enzymes. Deglycosylation enzymes are also contemplated. Also embraced are versions of the same primary amino acid sequence which have other minor modifications, including phosphorylated amino acid residues, e.g., phosphotyrosine, phosphoserine, or phosphothreonine.

A major group of derivatives are covalent conjugates of the receptors or fragments thereof with other proteins of polypeptides. These derivatives can be synthesized in recombinant culture such as N- or C-terminal fusions or by the use of agents known in the art for their usefulness in cross-linking proteins through reactive side groups. Preferred derivatization sites with cross-linking agents are at free amino groups, carbohydrate moieties, and cysteine residues.

Fusion polypeptides between the receptors and other homologous or heterologous proteins are also provided. Homologous polypeptides may be fusions between different receptors, resulting in, for instance, a hybrid protein exhibiting binding specificity for multiple different cytokine ligands, or a receptor which may have broadened or weakened specificity of substrate effect. Likewise, heterologous fusions may be constructed which would exhibit a combination of properties or activities of the derivative proteins. Typical examples are fusions of a reporter polypeptide, e.g., luciferase, with a segment or domain of a receptor, e.g., a ligand-binding segment, so that the presence or location of a desired ligand may be easily determined. See, e.g., Dull, et al., U.S. Patent No. 4,859,609, which is hereby incorporated herein by reference. Other gene fusion partners include glutathione-S-transferase (GST), bacterial β -galactosidase, trpE, Protein A, β -lactamase, alpha amylase, alcohol dehydrogenase, and yeast alpha mating factor. See, e.g., Godowski, et al. (1988) *Science* 241:812-816. Labeled proteins will often be substituted in the described combinations of proteins.

The phosphoramidite method described by Beaucage and Carruthers (1981) *Tetra. Letts.* 22:1859-1862, will produce suitable synthetic DNA fragments. A double stranded fragment will often be obtained either by synthesizing the complementary strand and annealing the strand together under appropriate conditions or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

Such polypeptides may also have amino acid residues which have been chemically modified by phosphorylation, sulfonation, biotinylation, or the addition or removal of

other moieties, particularly those which have molecular shapes similar to phosphate groups. In some embodiments, the modifications will be useful labeling reagents, or serve as purification targets, e.g., affinity ligands.

Fusion proteins will typically be made by either recombinant nucleic acid methods or by synthetic polypeptide methods. Techniques for nucleic acid manipulation and expression are described generally, for example, in Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual (2d ed.), Vols. 1-3, Cold Spring Harbor Laboratory, and Ausubel, et al. (eds. 1987 and periodic supplements) Current Protocols in Molecular Biology, Greene/Wiley, New York, which are each incorporated herein by reference. Techniques for synthesis of polypeptides are described, for example, in Merrifield (1963) J. Amer. Chem. Soc. 85:2149-2156; Merrifield (1986) Science 232: 341-347; and Atherton, et al. (1989) Solid Phase Peptide Synthesis: A Practical Approach, IRL Press, Oxford; each of which is incorporated herein by reference. See also Dawson, et al. (1994) Science 266:776-779 for methods to make larger polypeptides.

This invention also contemplates the use of derivatives of a DCRS8 other than variations in amino acid sequence or glycosylation. Such derivatives may involve covalent or aggregative association with chemical moieties. These derivatives generally fall into three classes: (1) salts, (2) side chain and terminal residue covalent modifications, and (3) adsorption complexes, for example with cell membranes. Such covalent or aggregative derivatives are useful as immunogens, as reagents in immunoassays, or in purification methods such as for affinity purification of a receptor or other binding molecule, e.g., an antibody. For example, a cytokine ligand can be immobilized by covalent bonding to a solid support such as cyanogen bromide-activated Sepharose, by methods which are well known in the art, or adsorbed onto polyolefin surfaces, with or without glutaraldehyde cross-linking, for use in the assay or purification of a cytokine receptor, antibodies, or other similar molecules. The ligand can also be labeled with a detectable group, for example radioiodinated by the chloramine T procedure, covalently bound to rare earth chelates, or conjugated to another fluorescent moiety for use in diagnostic assays.

A combination, e.g., including a DCRS8, of this invention can be used as an immunogen for the production of antisera or antibodies specific, e.g., capable of distinguishing between other cytokine receptor family members, for the combinations described. The complexes can be used to screen monoclonal antibodies or antigen-binding fragments prepared by immunization with various forms of impure preparations containing the protein. In particular, the term "antibodies" also encompasses antigen binding fragments of natural antibodies, e.g., Fab, Fab2, Fv, etc. The purified DCRS8 can also be used as a reagent to detect antibodies generated in response to the presence of

elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. Additionally, DCRS8 fragments may also serve as immunogens to produce the antibodies of the present invention, as described immediately below. For example, this invention contemplates antibodies having binding affinity to or being raised against the amino acid sequences shown in Tables 1-5, fragments thereof, or various homologous peptides. In particular, this invention contemplates antibodies having binding affinity to, or having been raised against, specific fragments which are predicted to be, or actually are, exposed at the exterior protein surface of the native DCRS8 or DCRS9. Complexes of combinations of proteins will also be useful, and antibody preparations thereto can be made.

The blocking of physiological response to the receptor ligands may result from the inhibition of binding of the ligand to the receptor, likely through competitive inhibition. Thus, in vitro assays of the present invention will often use antibodies or antigen binding segments of these antibodies, or fragments attached to solid phase substrates. These assays will also allow for the diagnostic determination of the effects of either ligand binding region mutations and modifications, or other mutations and modifications, e.g., which affect signaling or enzymatic function.

This invention also contemplates the use of competitive drug screening assays, e.g., where neutralizing antibodies to the receptor complexes or fragments compete with a test compound for binding to a ligand or other antibody. In this manner, the neutralizing antibodies or fragments can be used to detect the presence of a polypeptide which shares one or more binding sites to a receptor and can also be used to occupy binding sites on a receptor that might otherwise bind a ligand.

V. Making Nucleic Acids and Protein

DNA which encodes the protein or fragments thereof can be obtained by chemical synthesis, screening cDNA libraries, or by screening genomic libraries prepared from a wide variety of cell lines or tissue samples. Natural sequences can be isolated using standard methods and the sequences provided herein, e.g., in Tables 1-5. Other species counterparts can be identified by hybridization techniques, or by various PCR techniques, combined with or by searching in sequence databases, e.g., GenBank.

This DNA can be expressed in a wide variety of host cells for the synthesis of a full-length receptor or fragments which can in turn, for example, be used to generate polyclonal or monoclonal antibodies; for binding studies; for construction and expression of modified ligand binding or kinase/phosphatase domains; and for structure/function studies. Variants or fragments can be expressed in host cells that are transformed or transfected with appropriate expression vectors. These molecules can be substantially

free of protein or cellular contaminants, other than those derived from the recombinant host, and therefore are particularly useful in pharmaceutical compositions when combined with a pharmaceutically acceptable carrier and/or diluent. The protein, or portions thereof, may be expressed as fusions with other proteins. Combinations of the described
5 proteins, or nucleic acids encoding them, are particularly interesting.

Expression vectors are typically self-replicating DNA or RNA constructs containing the desired receptor gene or its fragments, usually operably linked to suitable genetic control elements that are recognized in a suitable host cell. These control elements are capable of effecting expression within a suitable host. The multiple genes
10 may be coordinately expressed, and may be on a polycistronic message. The specific type of control elements necessary to effect expression will depend upon the eventual host cell used. Generally, the genetic control elements can include a prokaryotic promoter system or a eukaryotic promoter expression control system, and typically include a transcriptional promoter, an optional operator to control the onset of transcription,
15 transcription enhancers to elevate the level of mRNA expression, a sequence that encodes a suitable ribosome binding site, and sequences that terminate transcription and translation. Expression vectors also usually contain an origin of replication that allows the vector to replicate independently of the host cell.

The vectors of this invention include those which contain DNA which encodes a
20 combination of proteins, as described, or a biologically active equivalent polypeptide. The DNA can be under the control of a viral promoter and can encode a selection marker. This invention further contemplates use of such expression vectors which are capable of expressing eukaryotic cDNAs coding for such proteins in a prokaryotic or eukaryotic host, where the vector is compatible with the host and where the eukaryotic cDNAs are
25 inserted into the vector such that growth of the host containing the vector expresses the cDNAs in question. Usually, expression vectors are designed for stable replication in their host cells or for amplification to greatly increase the total number of copies of the desirable gene per cell. It is not always necessary to require that an expression vector replicate in a host cell, e.g., it is possible to effect transient expression of the protein or its
30 fragments in various hosts using vectors that do not contain a replication origin that is recognized by the host cell. It is also possible to use vectors that cause integration of the protein encoding portions into the host DNA by recombination.

Vectors, as used herein, comprise plasmids, viruses, bacteriophage, integratable DNA fragments, and other vehicles which enable the integration of DNA fragments into
35 the genome of the host. Expression vectors are specialized vectors which contain genetic control elements that effect expression of operably linked genes. Plasmids are the most commonly used form of vector but all other forms of vectors which serve an equivalent

function and which are, or become, known in the art are suitable for use herein. See, e.g., Pouwels, et al. (1985 and Supplements) Cloning Vectors: A Laboratory Manual, Elsevier, N.Y., and Rodriguez, et al. (eds. 1988) Vectors: A Survey of Molecular Cloning Vectors and Their Uses, Butterworth, Boston, which are incorporated herein by reference.

5 Transformed cells are cells, preferably mammalian, that have been transformed or transfected with vectors constructed using recombinant DNA techniques. Transformed host cells usually express the desired proteins, but for purposes of cloning, amplifying, and manipulating its DNA, do not need to express the subject proteins. This invention further contemplates culturing transformed cells in a nutrient medium, thus permitting the
10 proteins to accumulate. The proteins can be recovered, either from the culture or, in certain instances, from the culture medium.

For purposes of this invention, nucleic sequences are operably linked when they are functionally related to each other. For example, DNA for a presequence or secretory leader is operably linked to a polypeptide if it is expressed as a preprotein or participates
15 in directing the polypeptide to the cell membrane or in secretion of the polypeptide. A promoter is operably linked to a coding sequence if it controls the transcription of the polypeptide; a ribosome binding site is operably linked to a coding sequence if it is positioned to permit translation. Usually, operably linked means contiguous and in reading frame, however, certain genetic elements such as repressor genes are not
20 contiguously linked but still bind to operator sequences that in turn control expression.

Suitable host cells include prokaryotes, lower eukaryotes, and higher eukaryotes. Prokaryotes include both gram negative and gram positive organisms, e.g., E. coli and B. subtilis. Lower eukaryotes include yeasts, e.g., S. cerevisiae and Pichia, and species of the genus Dictyostelium. Higher eukaryotes include established tissue culture cell lines
25 from animal cells, both of non-mammalian origin, e.g., insect cells, and birds, and of mammalian origin, e.g., human, primates, and rodents.

Prokaryotic host-vector systems include a wide variety of vectors for many different species. As used herein, E. coli and its vectors will be used generically to include equivalent vectors used in other prokaryotes. A representative vector for
30 amplifying DNA is pBR322 or many of its derivatives. Vectors that can be used to express the receptor or its fragments include, but are not limited to, such vectors as those containing the lac promoter (pUC-series); trp promoter (pBR322-trp); Ipp promoter (the pIN-series); lambda-pP or pR promoters (pOTS); or hybrid promoters such as ptac (pDR540). See Brosius, et al. (1988) "Expression Vectors Employing Lambda-, trp-, lac-,
35 and Ipp-derived Promoters", in Vectors: A Survey of Molecular Cloning Vectors and Their Uses, (eds. Rodriguez and Denhardt), Butterworth, Boston, Chapter 10, pp. 205-236, which is incorporated herein by reference.

Lower eukaryotes, e.g., yeasts and Dictyostelium, may be transformed with DCRS8 sequence containing vectors. For purposes of this invention, the most common lower eukaryotic host is the baker's yeast, Saccharomyces cerevisiae. It will be used to generically represent lower eukaryotes although a number of other strains and species are also available. Yeast vectors typically consist of a replication origin (unless of the integrating type), a selection gene, a promoter, DNA encoding the receptor or its fragments, and sequences for translation termination, polyadenylation, and transcription termination. Suitable expression vectors for yeast include such constitutive promoters as 3-phosphoglycerate kinase and various other glycolytic enzyme gene promoters or such inducible promoters as the alcohol dehydrogenase 2 promoter or metallothioneine promoter. Suitable vectors include derivatives of the following types: self-replicating low copy number (such as the YRp-series), self-replicating high copy number (such as the YEp-series); integrating types (such as the YIp-series), or mini-chromosomes (such as the YCp-series).

Higher eukaryotic tissue culture cells are normally the preferred host cells for expression of the functionally active interleukin or receptor proteins. In principle, many higher eukaryotic tissue culture cell lines are workable, e.g., insect baculovirus expression systems, whether from an invertebrate or vertebrate source. However, mammalian cells are preferred. Transformation or transfection and propagation of such cells has become a routine procedure. Examples of useful cell lines include HeLa cells, Chinese hamster ovary (CHO) cell lines, baby rat kidney (BRK) cell lines, insect cell lines, bird cell lines, and monkey (COS) cell lines. Expression vectors for such cell lines usually include an origin of replication, a promoter, a translation initiation site, RNA splice sites (if genomic DNA is used), a polyadenylation site, and a transcription termination site. These vectors also usually contain a selection gene or amplification gene. Suitable expression vectors may be plasmids, viruses, or retroviruses carrying promoters derived, e.g., from such sources as from adenovirus, SV40, parvoviruses, vaccinia virus, or cytomegalovirus. Representative examples of suitable expression vectors include pCDNA1; pCD, see Okayama, et al. (1985) Mol. Cell Biol. 5:1136-1142; pMC1neo PolyA, see Thomas, et al. (1987) Cell 51:503-512; and a baculovirus vector such as pAC 373 or pAC 610.

For secreted proteins and some membrane proteins, an open reading frame usually encodes a polypeptide that consists of a mature or secreted product covalently linked at its N-terminus to a signal peptide. The signal peptide is cleaved prior to secretion of the mature, or active, polypeptide. The cleavage site can be predicted with a high degree of accuracy from empirical rules, e.g., von-Heijne (1986) Nucleic Acids Research 14:4683-4690; and Nielsen, et al. (1997) Protein Eng. 10:1-12, and the precise amino acid composition of the signal peptide often does not appear to be critical to its function, e.g.,

Randall, et al. (1989) Science 243:1156-1159; and Kaiser, et al. (1987) Science 235:312-317. The mature proteins of the invention can be readily determined using standard methods.

It will often be desired to express these polypeptides in a system which provides a specific or defined glycosylation pattern. In this case, the usual pattern will be that provided naturally by the expression system. However, the pattern will be modifiable by exposing the polypeptide, e.g., an unglycosylated form, to appropriate glycosylating proteins introduced into a heterologous expression system. For example, the receptor gene may be co-transformed with one or more genes encoding mammalian or other glycosylating enzymes. Using this approach, certain mammalian glycosylation patterns will be achievable in prokaryote or other cells. Expression in prokaryote cells will typically lead to unglycosylated forms of protein.

The source of DCRS8 can be a eukaryotic or prokaryotic host expressing recombinant DCRS8, such as is described above. The source can also be a cell line, but other mammalian cell lines are also contemplated by this invention, with the preferred cell line being from the human species.

Now that the sequences are known, the primate DCRS8 or DCRS9, fragments, or derivatives thereof can be prepared by conventional processes for synthesizing peptides. These include processes such as are described in Stewart and Young (1984) Solid Phase Peptide Synthesis, Pierce Chemical Co., Rockford, IL; Bodanszky and Bodanszky (1984) The Practice of Peptide Synthesis, Springer-Verlag, New York; and Bodanszky (1984) The Principles of Peptide Synthesis, Springer-Verlag, New York; all of each which are incorporated herein by reference. For example, an azide process, an acid chloride process, an acid anhydride process, a mixed anhydride process, an active ester process (for example, p-nitrophenyl ester, N-hydroxysuccinimide ester, or cyanomethyl ester), a carbodiimidazole process, an oxidative-reductive process, or a dicyclohexylcarbodiimide (DCCD)/additive process can be used. Solid phase and solution phase syntheses are both applicable to the foregoing processes. Similar techniques can be used with partial DCRS8 or DCRS9 sequences.

The DCRS8 proteins, fragments, or derivatives are suitably prepared in accordance with the above processes as typically employed in peptide synthesis, generally either by a so-called stepwise process which comprises condensing an amino acid to the terminal amino acid, one by one in sequence, or by coupling peptide fragments to the terminal amino acid. Amino groups that are not being used in the coupling reaction typically must be protected to prevent coupling at an incorrect location.

If a solid phase synthesis is adopted, the C-terminal amino acid is bound to an insoluble carrier or support through its carboxyl group. The insoluble carrier is not

particularly limited as long as it has a binding capability to a reactive carboxyl group. Examples of such insoluble carriers include halomethyl resins, such as chloromethyl resin or bromomethyl resin, hydroxymethyl resins, phenol resins, tert-alkyloxycarbonylhydrazidated resins, and the like.

5 An amino group-protected amino acid is bound in sequence through condensation of its activated carboxyl group and the reactive amino group of the previously formed peptide or chain, to synthesize the peptide step by step. After synthesizing the complete sequence, the peptide is split off from the insoluble carrier to produce the peptide. This solid-phase approach is generally described by Merrifield, et al. (1963) in J. Am. Chem.
10 Soc. 85:2149-2156, which is incorporated herein by reference.

The prepared protein and fragments thereof can be isolated and purified from the reaction mixture by means of peptide separation, e.g., by extraction, precipitation, electrophoresis, various forms of chromatography, and the like. The receptors of this invention can be obtained in varying degrees of purity depending upon desired uses.

15 Purification can be accomplished by use of the protein purification techniques disclosed herein, see below, or by the use of the antibodies herein described in methods of immunoabsorbant affinity chromatography. This immunoabsorbant affinity chromatography is carried out by first linking the antibodies to a solid support and then contacting the linked antibodies with solubilized lysates of appropriate cells, lysates of
20 other cells expressing the receptor, or lysates or supernatants of cells producing the protein as a result of DNA techniques, see below.

Generally, the purified protein will be at least about 40% pure, ordinarily at least about 50% pure, usually at least about 60% pure, typically at least about 70% pure, more typically at least about 80% pure, preferable at least about 90% pure and more preferably
25 at least about 95% pure, and in particular embodiments, 97%-99% or more. Purity will usually be on a weight basis, but can also be on a molar basis. Different assays will be applied as appropriate. Individual proteins may be purified and thereafter combined.

VI. Antibodies

30 Antibodies can be raised to the various mammalian, e.g., primate DCRS8 or DCRS9 proteins and fragments thereof, both in naturally occurring native forms and in their recombinant forms, the difference being that antibodies to the active receptor are more likely to recognize epitopes which are only present in the native conformations. Denatured antigen detection can also be useful in, e.g., Western analysis. Anti-idiotypic
35 antibodies are also contemplated, which would be useful as agonists or antagonists of a natural receptor or an antibody.

Antibodies, including binding fragments and single chain versions, against predetermined fragments of the protein can be raised by immunization of animals with conjugates of the fragments with immunogenic proteins. Monoclonal antibodies are prepared from cells secreting the desired antibody. These antibodies can be screened for binding to normal or defective protein, or screened for agonistic or antagonistic activity. These monoclonal antibodies will usually bind with at least a K_D of about 1 mM, more usually at least about 300 μ M, typically at least about 100 μ M, more typically at least about 30 μ M, preferably at least about 10 μ M, and more preferably at least about 3 μ M or better.

The antibodies, including antigen binding fragments, of this invention can have significant diagnostic or therapeutic value. They can be potent antagonists that bind to the receptor and inhibit binding to ligand or inhibit the ability of the receptor to elicit a biological response, e.g., act on its substrate. They also can be useful as non-neutralizing antibodies and can be coupled to toxins or radionuclides to bind producing cells, or cells localized to the source of the interleukin. Further, these antibodies can be conjugated to drugs or other therapeutic agents, either directly or indirectly by means of a linker.

The antibodies of this invention can also be useful in diagnostic applications. As capture or non-neutralizing antibodies, they might bind to the receptor without inhibiting ligand or substrate binding. As neutralizing antibodies, they can be useful in competitive binding assays. They will also be useful in detecting or quantifying ligand. They may be used as reagents for Western blot analysis, or for immunoprecipitation or immunopurification of the respective protein. Likewise, nucleic acids and proteins may be immobilized to solid substrates for affinity purification or detection methods. The substrates may be, e.g., solid resin beads or sheets of plastic.

Protein fragments may be joined to other materials, particularly polypeptides, as fused or covalently joined polypeptides to be used as immunogens. Mammalian cytokine receptors and fragments may be fused or covalently linked to a variety of immunogens, such as keyhole limpet hemocyanin, bovine serum albumin, tetanus toxoid, etc. See (1969) Microbiology, Hoeber Medical Division, Harper and Row; Landsteiner (1962) Specificity of Serological Reactions, Dover Publications, New York; and Williams, et al. (1967) Methods in Immunology and Immunochemistry, Vol. 1, Academic Press, New York; each of which is incorporated herein by reference, for descriptions of methods of preparing polyclonal antisera. A typical method involves hyperimmunization of an animal with an antigen. The blood of the animal is then collected shortly after the repeated immunizations and the gamma globulin is isolated.

In some instances, it is desirable to prepare monoclonal antibodies from various mammalian hosts, such as mice, rodents, primates, humans, etc. Description of

techniques for preparing such monoclonal antibodies may be found in, e.g., Stites, et al. (eds.) Basic and Clinical Immunology (4th ed.), Lange Medical Publications, Los Altos, CA, and references cited therein; Harlow and Lane (1988) Antibodies: A Laboratory Manual, CSH Press; Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press, New York; and particularly in Kohler and Milstein (1975) Nature 256:495-497, which discusses one method of generating monoclonal antibodies. Each of these references is incorporated herein by reference. Summarized briefly, this method involves injecting an animal with an immunogen. The animal is then sacrificed and cells taken from its spleen, which are then fused with myeloma cells. The result is a hybrid cell or "hybridoma" that is capable of reproducing in vitro. The population of hybridomas is then screened to isolate individual clones, each of which secrete a single antibody species to the immunogen. In this manner, the individual antibody species obtained are the products of immortalized and cloned single B cells from the immune animal generated in response to a specific site recognized on the immunogenic substance.

Other suitable techniques involve in vitro exposure of lymphocytes to the antigenic polypeptides or alternatively to selection of libraries of antibodies in phage or similar vectors. See, Huse, et al. (1989) "Generation of a Large Combinatorial Library of the Immunoglobulin Repertoire in Phage Lambda," Science 246:1275-1281; and Ward, et al. (1989) Nature 341:544-546, each of which is incorporated herein by reference. The polypeptides and antibodies of the present invention may be used with or without modification, including chimeric or humanized antibodies. Frequently, the polypeptides and antibodies will be labeled by joining, either covalently or non-covalently, a substance which provides for a detectable signal. A wide variety of labels and conjugation techniques are known and are reported extensively in both the scientific and patent literature. Suitable labels include radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent moieties, chemiluminescent moieties, magnetic particles, and the like. Patents, teaching the use of such labels include U.S. Patent Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241. Also, recombinant or chimeric immunoglobulins may be produced, see Cabilly, U.S. Patent No. 4,816,567; or made in transgenic mice, see Mendez, et al. (1997) Nature Genetics 15:146-156; Abgenix; and Medarex. These references are incorporated herein by reference.

The antibodies of this invention can also be used for affinity chromatography in isolating the DCRS8 proteins or peptides. Columns can be prepared where the antibodies are linked to a solid support, e.g., particles, such as agarose, Sephadex, or the like, where a cell lysate may be passed through the column, the column washed, followed by increasing concentrations of a mild denaturant, whereby the purified protein will be

released. Alternatively, the protein may be used to purify antibody. Appropriate cross absorptions or depletions may be applied.

The antibodies may also be used to screen expression libraries for particular expression products. Usually the antibodies used in such a procedure will be labeled with a moiety allowing easy detection of presence of antigen by antibody binding.

Antibodies raised against a cytokine receptor will also be used to raise anti-idiotypic antibodies. These will be useful in detecting or diagnosing various immunological conditions related to expression of the protein or cells which express the protein. They also will be useful as agonists or antagonists of the ligand, which may be competitive inhibitors or substitutes for naturally occurring ligands.

A cytokine receptor protein that specifically binds to or that is specifically immunoreactive with an antibody generated against a defined immunogen, such as an immunogen consisting of the amino acid sequence of SEQ ID NO: 14, is typically determined in an immunoassay. The immunoassay typically uses a polyclonal antiserum which was raised, e.g., to a protein of SEQ ID NO: 14. This antiserum is selected to have low crossreactivity against other cytokine receptor family members, preferably from the same species, and any such crossreactivity is removed by immunoabsorption prior to use in the immunoassay.

In order to produce antisera for use in an immunoassay, the protein, e.g., of SEQ ID NO: 14, is isolated as described herein. For example, recombinant protein may be produced in a mammalian cell line. An appropriate host, e.g., an inbred strain of mice such as Balb/c, is immunized with the selected protein, typically using a standard adjuvant, such as Freund's adjuvant, and a standard mouse immunization protocol (see Harlow and Lane, supra). Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used as an immunogen. Polyclonal sera are collected and titered against the immunogen protein in an immunoassay, e.g., a solid phase immunoassay with the immunogen immobilized on a solid support. Polyclonal antisera with a titer of 10^4 or greater are selected and tested for their cross reactivity against other cytokine receptor family members using a competitive binding immunoassay such as the one described in Harlow and Lane, supra, at pages 570-573. Preferably at least two cytokine receptor family members are used in this determination. These cytokine receptor family members can be produced as recombinant proteins and isolated using standard molecular biology and protein chemistry techniques as described herein.

Immunoassays in the competitive binding format can be used for the crossreactivity determinations. For example, the protein of SEQ ID NO: 14 can be immobilized to a solid support. Proteins added to the assay compete with the binding of

the antisera to the immobilized antigen. The ability of the above proteins to compete with the binding of the antisera to the immobilized protein is compared to the other proteins. The percent crossreactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% crossreactivity with each of the proteins listed above are selected and pooled. The cross-reacting antibodies are then removed from the pooled antisera by immunoabsorption with the above-listed proteins.

The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein to the immunogen protein (e.g., the DCRS8 like protein of SEQ ID NO: 14). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is determined. If the amount of the second protein required is less than twice the amount of the protein of the selected protein or proteins that is required, then the second protein is said to specifically bind to an antibody generated to the immunogen.

It is understood that these cytokine receptor proteins are members of a family of homologous proteins that comprise at least 9 so far identified members, 6 mammalian and 3 worm embodiments. For a particular gene product, such as the DCRS8, the term refers not only to the amino acid sequences disclosed herein, but also to other proteins that are allelic, non-allelic, or species variants. It is also understood that the terms include nonnatural mutations introduced by deliberate mutation using conventional recombinant technology such as single site mutation, or by excising short sections of DNA encoding the respective proteins, or by substituting new amino acids, or adding new amino acids. Such minor alterations typically will substantially maintain the immunoidentity of the original molecule and/or its biological activity. Thus, these alterations include proteins that are specifically immunoreactive with a designated naturally occurring DCRS8 protein. The biological properties of the altered proteins can be determined by expressing the protein in an appropriate cell line and measuring the appropriate effect, e.g., upon transfected lymphocytes. Particular protein modifications considered minor would include conservative substitution of amino acids with similar chemical properties, as described above for the cytokine receptor family as a whole. By aligning a protein optimally with the protein of the cytokine receptors and by using the conventional immunoassays described herein to determine immunoidentity, one can determine the protein compositions of the invention.

VII. Kits and quantitation

Both naturally occurring and recombinant forms of the cytokine receptor like molecules of this invention are particularly useful in kits and assay methods. For

example, these methods would also be applied to screening for binding activity, e.g., ligands for these proteins. Several methods of automating assays have been developed in recent years so as to permit screening of tens of thousands of compounds per year. See, e.g., a BIOMEK automated workstation, Beckman Instruments, Palo Alto, California, and Fodor, et al. (1991) Science 251:767-773, which is incorporated herein by reference. The latter describes means for testing binding by a plurality of defined polymers synthesized on a solid substrate. The development of suitable assays to screen for a ligand or agonist/antagonist homologous proteins can be greatly facilitated by the availability of large amounts of purified, soluble cytokine receptors in an active state such as is provided by this invention.

Purified protein can be coated directly onto plates for use in the aforementioned ligand screening techniques. However, non-neutralizing antibodies to these proteins can be used as capture antibodies to immobilize the respective receptor on the solid phase, useful, e.g., in diagnostic uses.

This invention also contemplates use of receptor subunit, fragments thereof, peptides, and their fusion products in a variety of diagnostic kits and methods for detecting the presence of the protein or its ligand. Alternatively, or additionally, antibodies against the molecules may be incorporated into the kits and methods. Typically the kit will have a compartment containing, e.g., a DCRS8 peptide or gene segment or a reagent which recognizes one or the other. Typically, recognition reagents, in the case of peptide, would be a receptor or antibody, or in the case of a gene segment, would usually be a hybridization probe.

A preferred kit for determining the concentration of DCRS8 in a sample would typically comprise a labeled compound, e.g., ligand or antibody, having known binding affinity for DCRS8, a source of DCRS8 (naturally occurring or recombinant) as a positive control, and a means for separating the bound from free labeled compound, e.g., a solid phase for immobilizing the DCRS8 in the test sample. Compartments containing reagents, and instructions, will normally be provided. Appropriate nucleic acid or protein containing kits are also provided.

Antibodies, including antigen binding fragments, specific for mammalian DCRS8 or a peptide fragment, or receptor fragments are useful in diagnostic applications to detect the presence of elevated levels of ligand and/or its fragments. Diagnostic assays may be homogeneous (without a separation step between free reagent and antibody-antigen complex) or heterogeneous (with a separation step). Various commercial assays exist, such as radioimmunoassay (RIA), enzyme-linked immunosorbent assay (ELISA), enzyme immunoassay (EIA), enzyme-multiplied immunoassay technique (EMIT), substrate-labeled fluorescent immunoassay (SLFIA) and the like. For example, unlabeled

antibodies can be employed by using a second antibody which is labeled and which recognizes the antibody to a cytokine receptor or to a particular fragment thereof. These assays have also been extensively discussed in the literature. See, e.g., Harlow and Lane (1988) Antibodies: A Laboratory Manual, CSH, and Coligan (ed. 1991 and periodic supplements) Current Protocols In Immunology Greene/Wiley, New York.

Anti-idiotypic antibodies may have similar use to serve as agonists or antagonists of cytokine receptors. These should be useful as therapeutic reagents under appropriate circumstances.

Frequently, the reagents for diagnostic assays are supplied in kits, so as to optimize the sensitivity of the assay. For the subject invention, depending upon the nature of the assay, the protocol, and the label, either labeled or unlabeled antibody, or labeled ligand is provided. This is usually in conjunction with other additives, such as buffers, stabilizers, materials necessary for signal production such as substrates for enzymes, and the like. Preferably, the kit will also contain instructions for proper use and disposal of the contents after use. Typically the kit has compartments for each useful reagent, and will contain instructions for proper use and disposal of reagents. Desirably, the reagents are provided as a dry lyophilized powder, where the reagents may be reconstituted in an aqueous medium having appropriate concentrations for performing the assay.

The aforementioned constituents of the diagnostic assays may be used without modification or may be modified in a variety of ways. For example, labeling may be achieved by covalently or non-covalently joining a moiety which directly or indirectly provides a detectable signal. In many of these assays, a test compound, cytokine receptor, or antibodies thereto can be labeled either directly or indirectly. Possibilities for direct labeling include label groups: radiolabels such as ^{125}I , enzymes (U.S. Pat. No. 3,645,090) such as peroxidase and alkaline phosphatase, and fluorescent labels (U.S. Pat. No. 3,940,475) capable of monitoring the change in fluorescence intensity, wavelength shift, or fluorescence polarization. Both of the patents are incorporated herein by reference. Possibilities for indirect labeling include biotinylation of one constituent followed by binding to avidin coupled to one of the above label groups.

There are also numerous methods of separating the bound from the free ligand, or alternatively the bound from the free test compound. The cytokine receptor can be immobilized on various matrixes followed by washing. Suitable matrices include plastic such as an ELISA plate, filters, and beads. Methods of immobilizing the receptor to a matrix include, without limitation, direct adhesion to plastic, use of a capture antibody, chemical coupling, and biotin-avidin. The last step in this approach involves the precipitation of antibody/antigen complex by any of several methods including those

utilizing, e.g., an organic solvent such as polyethylene glycol or a salt such as ammonium sulfate. Other suitable separation techniques include, without limitation, the fluorescein antibody magnetizable particle method described in Rattle, et al. (1984) Clin. Chem. 30(9):1457-1461, and the double antibody magnetic particle separation as described in
5 U.S. Pat. No. 4,659,678, each of which is incorporated herein by reference.

The methods for linking protein or fragments to various labels have been extensively reported in the literature and do not require detailed discussion here. Many of the techniques involve the use of activated carboxyl groups either through the use of carbodiimide or active esters to form peptide bonds, the formation of thioethers by
10 reaction of a mercapto group with an activated halogen such as chloroacetyl, or an activated olefin such as maleimide, for linkage, or the like. Fusion proteins will also find use in these applications.

Another diagnostic aspect of this invention involves use of oligonucleotide or polynucleotide sequences taken from the sequence of an cytokine receptor. These
15 sequences can be used as probes for detecting levels of the respective cytokine receptor in patients suspected of having an immunological disorder. The preparation of both RNA and DNA nucleotide sequences, the labeling of the sequences, and the preferred size of the sequences has received ample description and discussion in the literature. Normally an oligonucleotide probe should have at least about 14 nucleotides, usually at least about
20 18 nucleotides, and the polynucleotide probes may be up to several kilobases. Various labels may be employed, most commonly radionuclides, particularly ^{32}P . However, other techniques may also be employed, such as using biotin modified nucleotides for introduction into a polynucleotide. The biotin then serves as the site for binding to avidin or antibodies, which may be labeled with a wide variety of labels, such as radionuclides,
25 fluorescers, enzymes, or the like. Alternatively, antibodies may be employed which can recognize specific duplexes, including DNA duplexes, RNA duplexes, DNA-RNA hybrid duplexes, or DNA-protein duplexes. The antibodies in turn may be labeled and the assay carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected. The use of
30 probes to the novel RNA may be carried out in conventional techniques such as nucleic acid hybridization, plus and minus screening, recombinational probing, hybrid released translation (HRT), and hybrid arrested translation (HART). Antisense nucleic acids, which may be used to block protein expression, are also provided. See, e.g., Isis Pharmaceuticals, Sequitur, Inc., or Hybridon. This also includes amplification techniques
35 such as polymerase chain reaction (PCR).

Diagnostic kits which also test for the qualitative or quantitative presence of other markers are also contemplated. Diagnosis or prognosis may depend on the combination

of multiple indications used as markers. Thus, kits may test for combinations of markers. See, e.g., Viallet, et al. (1989) Progress in Growth Factor Res. 1:89-97.

VIII. Therapeutic Utility

5 This invention provides reagents with significant therapeutic value. See, e.g., Levitzki (1996) Curr. Opin. Cell Biol. 8:239-244. The cytokine receptors (naturally occurring or recombinant), fragments thereof, mutein receptors, and antibodies, along with compounds identified as having binding affinity to the receptors or antibodies, should be useful in the treatment of conditions exhibiting abnormal expression of the
10 receptors of their ligands. Such abnormality will typically be manifested by immunological disorders, e.g., innate immunity, or developmentally. Additionally, this invention should provide therapeutic value in various diseases or disorders associated with abnormal expression or abnormal triggering of response to the ligand. For example, the IL-1 ligands have been suggested to be involved in morphologic development, e.g.,
15 dorso-ventral polarity determination, and immune responses, particularly the primitive innate responses. See, e.g., Sun, et al. (1991) Eur. J. Biochem. 196:247-254; and Hultmark (1994) Nature 367:116-117.

Recombinant cytokine receptors, muteins, agonist or antagonist antibodies thereto, or antibodies can be purified and then administered to a patient. These reagents can be
20 combined for therapeutic use with additional active ingredients, e.g., in conventional pharmaceutically acceptable carriers or diluents, along with physiologically innocuous stabilizers and excipients. These combinations can be sterile, e.g., filtered, and placed into dosage forms as by lyophilization in dosage vials or storage in stabilized aqueous preparations. This invention also contemplates use of antibodies or binding fragments
25 thereof which are not complement binding.

Ligand screening using cytokine receptor or fragments thereof can be performed to identify molecules having binding affinity to the receptors. Subsequent biological assays can then be utilized to determine if a putative ligand can provide competitive binding, which can block intrinsic stimulating activity. Receptor fragments can be used
30 as a blocker or antagonist in that it blocks the activity of ligand. Likewise, a compound having intrinsic stimulating activity can activate the receptor and is thus an agonist in that it simulates the activity of ligand, e.g., inducing signaling. This invention further contemplates the therapeutic use of antibodies to cytokine receptors as antagonists.

The quantities of reagents necessary for effective therapy will depend upon many
35 different factors, including means of administration, target site, reagent physiological life, pharmacological life, physiological state of the patient, and other medicants administered. Thus, treatment dosages should be titrated to optimize safety and efficacy. Typically,

dosages used in vitro may provide useful guidance in the amounts useful for in situ administration of these reagents. Animal testing of effective doses for treatment of particular disorders will provide further predictive indication of human dosage. Various considerations are described, e.g., in Gilman, et al. (eds. 1990) Goodman and Gilman's: The Pharmacological Bases of Therapeutics, 8th Ed., Pergamon Press; and Remington's Pharmaceutical Sciences, 17th ed. (1990), Mack Publishing Co., Easton, Penn.; each of which is hereby incorporated herein by reference. Methods for administration are discussed therein and below, e.g., for oral, intravenous, intraperitoneal, or intramuscular administration, transdermal diffusion, and others. Pharmaceutically acceptable carriers will include water, saline, buffers, and other compounds described, e.g., in the Merck Index, Merck & Co., Rahway, New Jersey. Because of the likely high affinity binding, or turnover numbers, between a putative ligand and its receptors, low dosages of these reagents would be initially expected to be effective. And the signaling pathway suggests extremely low amounts of ligand may have effect. Thus, dosage ranges would ordinarily be expected to be in amounts lower than 1 mM concentrations, typically less than about 10 μ M concentrations, usually less than about 100 nM, preferably less than about 10 pM (picomolar), and most preferably less than about 1 fM (femtomolar), with an appropriate carrier. Slow release formulations, or slow release apparatus will often be utilized for continuous administration.

Cytokine receptors, fragments thereof, and antibodies or its fragments, antagonists, and agonists, may be administered directly to the host to be treated or, depending on the size of the compounds, it may be desirable to conjugate them to carrier proteins such as ovalbumin or serum albumin prior to their administration. Therapeutic formulations may be administered in many conventional dosage formulations. While it is possible for the active ingredient to be administered alone, it is preferable to present it as a pharmaceutical formulation. Formulations comprise at least one active ingredient, as defined above, together with one or more acceptable carriers thereof. Each carrier must be both pharmaceutically and physiologically acceptable in the sense of being compatible with the other ingredients and not injurious to the patient. Formulations include those suitable for oral, rectal, nasal, or parenteral (including subcutaneous, intramuscular, intravenous and intradermal) administration. The formulations may conveniently be presented in unit dosage form and may be prepared by methods well known in the art of pharmacy. See, e.g., Gilman, et al. (eds. 1990) Goodman and Gilman's: The Pharmacological Bases of Therapeutics, 8th Ed., Pergamon Press; and Remington's Pharmaceutical Sciences, 17th ed. (1990), Mack Publishing Co., Easton, Penn.; Avis, et al. (eds. 1993) Pharmaceutical Dosage Forms: Parenteral Medications Dekker, NY; Lieberman, et al. (eds. 1990) Pharmaceutical Dosage Forms: Tablets Dekker, NY; and

Lieberman, et al. (eds. 1990) Pharmaceutical Dosage Forms: Disperse Systems Dekker, NY. The therapy of this invention may be combined with or used in association with other therapeutic agents, particularly agonists or antagonists of other cytokine receptor family members.

5

IX. Screening

Drug screening using DCRS8 or fragments thereof can be performed to identify compounds having binding affinity to the receptor subunit, including isolation of associated components. Subsequent biological assays can then be utilized to determine if the compound has intrinsic stimulating activity and is therefore a blocker or antagonist in that it blocks the activity of the ligand. Likewise, a compound having intrinsic stimulating activity can activate the receptor and is thus an agonist in that it simulates the activity of a cytokine ligand. This invention further contemplates the therapeutic use of antibodies to the receptor as cytokine agonists or antagonists.

10

Similarly, complexes comprising multiple proteins may be used to screen for ligands or reagents capable of recognizing the complex. Most cytokine receptors comprise at least two subunits, which may be the same, or distinct. Alternatively, the transmembrane receptor may bind to a complex comprising a cytokine-like ligand associated with another soluble protein serving, e.g., as a second receptor subunit.

15

One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant DNA molecules expressing the DCRS8 in combination with another cytokine receptor subunit. Cells may be isolated which express a receptor in isolation from other functional receptors. Such cells, either in viable or fixed form, can be used for standard antibody/antigen or ligand/receptor binding assays. See also, Parce, et al. (1989) Science 246:243-247; and Owicki, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:4007-4011, which describe sensitive methods to detect cellular responses. Competitive assays are particularly useful, where the cells (source of putative ligand) are contacted and incubated with a labeled receptor or antibody having known binding affinity to the ligand, such as ^{125}I -antibody, and a test sample whose binding affinity to the binding composition is being measured. The bound and free labeled binding compositions are then separated to assess the degree of ligand binding. The amount of test compound bound is inversely proportional to the amount of labeled receptor binding to the known source. Many techniques can be used to separate bound from free ligand to assess the degree of ligand binding. This separation step could typically involve a procedure such as adhesion to filters followed by washing, adhesion to plastic followed by washing, or centrifugation of the cell membranes. Viable cells could also be used to screen for the effects of drugs on cytokine mediated functions, e.g., second messenger

20

25

30

35

levels, e.g., Ca^{++} ; cell proliferation; inositol phosphate pool changes; and others. Some detection methods allow for elimination of a separation step, e.g., a proximity sensitive detection system. Calcium sensitive dyes will be useful for detecting Ca^{++} levels, with a fluorimeter or a fluorescence cell sorting apparatus.

5

X. Ligands

The descriptions of the DCRS8 herein provides means to identify ligands, as described above. Such ligand should bind specifically to the respective receptor with reasonably high affinity. Various constructs are made available which allow either labeling of the receptor to detect its ligand. For example, directly labeling cytokine receptor, fusing onto it markers for secondary labeling, e.g., FLAG or other epitope tags, etc., will allow detection of receptor. This can be histological, as an affinity method for biochemical purification, or labeling or selection in an expression cloning approach. A two-hybrid selection system may also be applied making appropriate constructs with the available cytokine receptor sequences. See, e.g., Fields and Song (1989) Nature 340:245-246.

10

15

Most likely candidates will be structurally related to members of the IL-17 family. See, e.g., USSN 09/480,287.

The broad scope of this invention is best understood with reference to the following examples, which are not intended to limit the inventions to the specific embodiments.

20

EXAMPLES

I. General Methods

25

30

35

Some of the standard methods are described or referenced, e.g., in Maniatis, et al. (1982) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor Press; Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual, (2d ed.), vols. 1-3, CSH Press, NY; or Ausubel, et al. (1987 and Supplements) Current Protocols in Molecular Biology, Greene/Wiley, New York. Methods for protein purification include such methods as ammonium sulfate precipitation, column chromatography, electrophoresis, centrifugation, crystallization, and others. See, e.g., Ausubel, et al. (1987 and periodic supplements); Coligan, et al. (ed. 1996) and periodic supplements, Current Protocols In Protein Science Greene/Wiley, New York; Deutscher (1990) "Guide to Protein Purification" in Methods in Enzymology, vol. 182, and other volumes in this series; and manufacturer's literature on use of protein purification products, e.g., Pharmacia, Piscataway, N.J., or Bio-Rad, Richmond, CA. Combination

with recombinant techniques allow fusion to appropriate segments, e.g., to a FLAG sequence or an equivalent which can be fused via a protease-removable sequence. See, e.g., Hochuli (1990) "Purification of Recombinant Proteins with Metal Chelate Absorbent" in Setlow (ed.) Genetic Engineering, Principle and Methods 12:87-98, Plenum Press, N.Y.; and Crowe, et al. (1992) QIAexpress: The High Level Expression & Protein Purification System QUIAGEN, Inc., Chatsworth, CA.

Computer sequence analysis is performed, e.g., using available software programs, including those from the GCG (U. Wisconsin) and GenBank sources. Public sequence databases were also used, e.g., from GenBank and others.

Many techniques applicable to IL-10 receptors may be applied to the DCRSs, as described, e.g., in USSN 08/110,683 (IL-10 receptor), which is incorporated herein by reference.

II. Computational Analysis

Human sequences related to cytokine receptors were identified from genomic sequence database using, e.g., the BLAST server (Altschul, et al. (1994) Nature Genet. 6:119-129). Standard analysis programs may be used to evaluate structure, e.g., PHD (Rost and Sander (1994) Proteins 19:55-72) and DSC (King and Sternberg (1996) Protein Sci. 5:2298-2310). Standard comparison software includes, e.g., Altschul, et al. (1990) J. Mol. Biol. 215:403-10; Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chapman & Hall; Lander and Waterman (eds. 1995) Calculating the Secrets of Life: Applications of the Mathematical Sciences in Molecular Biology National Academy Press; and Speed and Waterman (eds. 1996) Genetic Mapping and DNA Sequencing (IMA Volumes in Mathematics and Its Applications, Vol 81) Springer Verlag. Each reference is incorporate herein by reference.

III. Cloning of full-length cDNAs; Chromosomal localization

PCR primers derived from the sequences are used to probe a human cDNA library. Sequences may be derived, e.g., from Tables 1-5, preferably those adjacent the ends of sequences. Full length cDNAs for primate, rodent, or other species DCRS8 are cloned, e.g., by DNA hybridization screening of λ gt10 phage. PCR reactions are conducted using T. aquaticus Taqplus DNA polymerase (Stratagene) under appropriate conditions. Extending partial length cDNA clones is typically routine.

Chromosome spreads are prepared. In situ hybridization is performed on chromosome preparations obtained from phytohemagglutinin-stimulated human lymphocytes cultured for 72 h. 5-bromodeoxyuridine was added for the final seven hours

of culture (60 µg/ml of medium), to ensure a posthybridization chromosomal banding of good quality.

A PCR fragment, amplified with the help of primers, is cloned into an appropriate vector. The vector is labeled by nick-translation with ^3H . The radiolabeled probe is
5 hybridized to metaphase spreads at final concentration of 200 ng/ml of hybridization solution as described, e.g., in Mattei, et al. (1985) Hum. Genet. 69:327-331.

After coating with nuclear track emulsion (KODAK NTB₂), slides are exposed. To avoid any slipping of silver grains during the banding procedure, chromosome spreads are first stained with buffered Giemsa solution and metaphase photographed. R-banding
10 is then performed by the fluorochrome-photolysis-Giemsa (FPG) method and metaphases rephotographed before analysis.

Similar appropriate methods are used for other species.

IV. Localization of mRNA

Human multiple tissue (Cat# 1, 2) and cancer cell line blots (Cat# 7757-1),
15 containing approximately 2 µg of poly(A)⁺ RNA per lane, are purchased from Clontech (Palo Alto, CA). Probes are radiolabeled with [α - ^{32}P] dATP, e.g., using the Amersham Rediprime random primer labeling kit (RPN1633). Prehybridization and hybridizations are performed, e.g., at 65° C in 0.5 M Na₂HPO₄, 7% SDS, 0.5 M EDTA (pH 8.0). High
20 stringency washes are conducted, e.g., at 65° C with two initial washes in 2 x SSC, 0.1% SDS for 40 min followed by a subsequent wash in 0.1 x SSC, 0.1% SDS for 20 min. Membranes are then exposed at -70° C to X-Ray film (Kodak) in the presence of intensifying screens. More detailed studies by cDNA library Southernblots are performed with selected appropriate human DCRS clones to examine their expression in
25 hemopoietic or other cell subsets.

Alternatively, two appropriate primers are selected from Tables 1-5. RT-PCR is used on an appropriate mRNA sample selected for the presence of message to produce a cDNA, e.g., a sample which expresses the gene.

Full length clones may be isolated by hybridization of cDNA libraries from
30 appropriate tissues pre-selected by PCR signal. Northern blots can be performed.

Message for genes encoding DCRS will be assayed by appropriate technology, e.g., PCR, immunoassay, hybridization, or otherwise. Tissue and organ cDNA preparations are available, e.g., from Clontech, Mountain View, CA. Identification of sources of natural expression are useful, as described. And the identification of functional
35 receptor subunit pairings will allow for prediction of what cells express the combination of receptor subunits which will result in a physiological responsiveness to each of the cytokine ligands.

For mouse counterpart distribution, e.g., Southern Analysis can be performed: DNA (5 µg) from a primary amplified cDNA library was digested with appropriate restriction enzymes to release the inserts, run on a 1% agarose gel and transferred to a nylon membrane (Schleicher and Schuell, Keene, NH).

5 Samples for mouse mRNA isolation may include: resting mouse fibroblastic L cell line (C200); Braf:ER (Braf fusion to estrogen receptor) transfected cells, control (C201); T cells, TH1 polarized (Mel14 bright, CD4+ cells from spleen, polarized for 7 days with IFN-γ and anti IL-4; T200); T cells, TH2 polarized (Mel14 bright, CD4+ cells from spleen, polarized for 7 days with IL-4 and anti-IFN-γ; T201); T cells, highly TH1
10 polarized (see Openshaw, et al. (1995) J. Exp. Med. 182:1357-1367; activated with anti-CD3 for 2, 6, 16 h pooled; T202); T cells, highly TH2 polarized (see Openshaw, et al. (1995) J. Exp. Med. 182:1357-1367; activated with anti-CD3 for 2, 6, 16 h pooled; T203); CD44- CD25+ pre T cells, sorted from thymus (T204); TH1 T cell clone D1.1, resting for 3 weeks after last stimulation with antigen (T205); TH1 T cell clone D1.1, 10
15 µg/ml ConA stimulated 15 h (T206); TH2 T cell clone CDC35, resting for 3 weeks after last stimulation with antigen (T207); TH2 T cell clone CDC35, 10 µg/ml ConA stimulated 15 h (T208); Mel14+ naive T cells from spleen, resting (T209); Mel14+ T cells, polarized to Th1 with IFN-γ/IL-12/anti-IL-4 for 6, 12, 24 h pooled (T210); Mel14+ T cells, polarized to Th2 with IL-4/anti-IFN-γ for 6, 13, 24 h pooled (T211); unstimulated
20 mature B cell leukemia cell line A20 (B200); unstimulated B cell line CH12 (B201); unstimulated large B cells from spleen (B202); B cells from total spleen, LPS activated (B203); metrizamide enriched dendritic cells from spleen, resting (D200); dendritic cells from bone marrow, resting (D201); monocyte cell line RAW 264.7 activated with LPS 4 h (M200); bone-marrow macrophages derived with GM and M-CSF (M201); macrophage
25 cell line J774, resting (M202); macrophage cell line J774 + LPS + anti-IL-10 at 0.5, 1, 3, 6, 12 h pooled (M203); macrophage cell line J774 + LPS + IL-10 at 0.5, 1, 3, 5, 12 h pooled (M204); aerosol challenged mouse lung tissue, Th2 primers, aerosol OVA challenge 7, 14, 23 h pooled (see Garlisi, et al. (1995) Clinical Immunology and Immunopathology 75:75-83; X206); Nippostrongylus-infected lung tissue (see Coffman,
30 et al. (1989) Science 245:308-310; X200); total adult lung, normal (O200); total lung, rag-1 (see Schwarz, et al. (1993) Immunodeficiency 4:249-252; O205); IL-10 K.O. spleen (see Kuhn, et al. (1991) Cell 75:263-274; X201); total adult spleen, normal (O201); total spleen, rag-1 (O207); IL-10 K.O. Peyer's patches (O202); total Peyer's patches, normal (O210); IL-10 K.O. mesenteric lymph nodes (X203); total mesenteric lymph nodes, normal (O211); IL-10 K.O. colon (X203); total colon, normal (O212); NOD mouse
35 pancreas (see Makino, et al. (1980) Jikken Dobutsu 29:1-13; X205); total thymus, rag-1 (O208); total kidney, rag-1 (O209); total heart, rag-1 (O202); total brain, rag-1 (O203);

total testes, rag-1 (O204); total liver, rag-1 (O206); rat normal joint tissue (O300); and rat arthritic joint tissue (X300).

Samples for human mRNA isolation may include, e.g.: peripheral blood mononuclear cells (monocytes, T cells, NK cells, granulocytes, B cells), resting (T100);
 5 peripheral blood mononuclear cells, activated with anti-CD3 for 2, 6, 12 h pooled (T101); T cell, TH0 clone Mot 72, resting (T102); T cell, TH0 clone Mot 72, activated with anti-CD28 and anti-CD3 for 3, 6, 12 h pooled (T103); T cell, TH0 clone Mot 72, anergic treated with specific peptide for 2, 7, 12 h pooled (T104); T cell, TH1 clone HY06, resting (T107); T cell, TH1 clone HY06, activated with anti-CD28 and anti-CD3 for 3, 6,
 10 12 h pooled (T108); T cell, TH1 clone HY06, anergic treated with specific peptide for 2, 6, 12 h pooled (T109); T cell, TH2 clone HY935, resting (T110); T cell, TH2 clone HY935, activated with anti-CD28 and anti-CD3 for 2, 7, 12 h pooled (T111); T cells CD4⁺CD45RO⁻ T cells polarized 27 days in anti-CD28, IL-4, and anti IFN- γ , TH2 polarized, activated with anti-CD3 and anti-CD28 4 h (T116); T cell tumor lines Jurkat
 15 and Hut78, resting (T117); T cell clones, pooled AD130.2, Tc783.12, Tc783.13, Tc783.58, Tc782.69, resting (T118); T cell random $\gamma\delta$ T cell clones, resting (T119); Splenocytes, resting (B100); Splenocytes, activated with anti-CD40 and IL-4 (B101); B cell EBV lines pooled WT49, RSB, JY, CVIR, 721.221, RM3, HSY, resting (B102); B cell line JY, activated with PMA and ionomycin for 1, 6 h pooled (B103); NK 20 clones
 20 pooled, resting (K100); NK 20 clones pooled, activated with PMA and ionomycin for 6 h (K101); NKL clone, derived from peripheral blood of LGL leukemia patient, IL-2 treated (K106); NK cytotoxic clone 640-A30-1, resting (K107); hematopoietic precursor line TF1, activated with PMA and ionomycin for 1, 6 h pooled (C100); U937 premonocytic line, resting (M100); U937 premonocytic line, activated with PMA and ionomycin for 1,
 25 6 h pooled (M101); elutriated monocytes, activated with LPS, IFN γ , anti-IL-10 for 1, 2, 6, 12, 24 h pooled (M102); elutriated monocytes, activated with LPS, IFN γ , IL-10 for 1, 2, 6, 12, 24 h pooled (M103); elutriated monocytes, activated with LPS, IFN γ , anti-IL-10 for 4, 16 h pooled (M106); elutriated monocytes, activated with LPS, IFN γ , IL-10 for 4, 16 h pooled (M107); elutriated monocytes, activated LPS for 1 h (M108); elutriated
 30 monocytes, activated LPS for 6 h (M109); DC 70% CD1a⁺, from CD34⁺ GM-CSF, TNF α 12 days, resting (D101); DC 70% CD1a⁺, from CD34⁺ GM-CSF, TNF α 12 days, activated with PMA and ionomycin for 1 hr (D102); DC 70% CD1a⁺, from CD34⁺ GM-CSF, TNF α 12 days, activated with PMA and ionomycin for 6 hr (D103); DC 95% CD1a⁺, from CD34⁺ GM-CSF, TNF α 12 days FACS sorted, activated with PMA and
 35 ionomycin for 1, 6 h pooled (D104); DC 95% CD14⁺, ex CD34⁺ GM-CSF, TNF α 12 days FACS sorted, activated with PMA and ionomycin 1, 6 hr pooled (D105); DC CD1a⁺ CD86⁺, from CD34⁺ GM-CSF, TNF α 12 days FACS sorted, activated with PMA and

ionomycin for 1, 6 h pooled (D106); DC from monocytes GM-CSF, IL-4 5 days, resting (D107); DC from monocytes GM-CSF, IL-4 5 days, resting (D108); DC from monocytes GM-CSF, IL-4 5 days, activated LPS 4, 16 h pooled (D109); DC from monocytes GM-CSF, IL-4 5 days, activated TNF α , monocyte supe for 4, 16 h pooled (D110); leiomyoma L11 benign tumor (X101); normal myometrium M5 (O115); malignant leiomyosarcoma GS1 (X103); lung fibroblast sarcoma line MRC5, activated with PMA and ionomycin for 1, 6 h pooled (C101); kidney epithelial carcinoma cell line CHA, activated with PMA and ionomycin for 1, 6 h pooled (C102); kidney fetal 28 wk male (O100); lung fetal 28 wk male (O101); liver fetal 28 wk male (O102); heart fetal 28 wk male (O103); brain fetal 28 wk male (O104); gallbladder fetal 28 wk male (O106); small intestine fetal 28 wk male (O107); adipose tissue fetal 28 wk male (O108); ovary fetal 25 wk female (O109); uterus fetal 25 wk female (O110); testes fetal 28 wk male (O111); spleen fetal 28 wk male (O112); adult placenta 28 wk (O113); and tonsil inflamed, from 12 year old (X100).

TaqMan quantitative PCR techniques have shown the DCRS6, in both mouse and human, to be expressed on T cells, including thymocytes and CD4⁺ naive and differentiated (hDCRS6 is also expressed on dendritic cells), in gastrointestinal tissue, including stomach, intestine, colon and associated lymphoid tissue, e.g., Peyer's patches and mesenteric lymph nodes, and upregulated in inflammatory models of bowel disease, e.g., IL-10 KO mice. The hDCRS7 was detected in both resting and activated dendritic cells, epithelial cells, and mucosal tissues, including GI and reproductive tracts. These data suggest that family members are expressed in mucosal tissues and immune system cell types, and/or in gastrointestinal, airway, and reproductive tract development.

As such, therapeutic indications include, e.g., short bowel syndrome, post chemo/radio-therapy or alcoholic recovery, combinations with ulcer treatments or arthritis medication, Th2 pregnancy skewing, stomach lining/tissue regeneration, loss of adsorptive surface conditions, etc. See, e.g., Yamada, et al. (eds. 1999) Textbook of Gastroenterology; Yamada, et al. (eds. 1999) Textbook and Atlas of Gastroenterology; Gore and Levine (2000) Textbook of Gastrointestinal Radiology; and (1987) Textbook of Pediatric Gastroenterology.

Similar samples may isolated in other species for evaluation.

Primers specific for IL-17RA were designed and used in Taqman quantative PCR against various human libraries. IL-17RA is highly expressed in innate immune myeloid cells including dendritic cells and monocytes. Expression is also detected in T-cell libraries. These data demonstrate the receptor is expressed in immune cell types and may be regulated by activation conditions.

**Table for IL-17RA
library description**

	CT for IL- 17RA_H
DC ex monocytes GM-CSF, IL-4, resting	16.97
U937 premonocytic line, activated	17.14
DC ex monocytes GM-CSF, IL-4, resting	17.53
DC 70% CD1a+, ex CD34+ GM-CSF, TNFa, resting	18.17
monocytes, LPS, gIFN, anti-IL-10	18.27
DC ex monocytes GM-CSF, IL-4, LPS activated 4+16 hr	18.51
DC ex monocytes GM-CSF, IL-4, monokine activated 4+16 hr	18.68
kidney epithelial carcinoma cell line CHA, activated	18.69
monocytes, LPS, 1 hr	18.72
monocytes, LPS, 6 hr	18.72
DC 70% CD1a+, ex CD34+ GM-CSF, TNFa, activated 1 hr	18.91
DC 70% CD1a+, ex CD34+ GM-CSF, TNFa, activated 6 hr	18.94
T cell, TH1 clone HY06, activated	18.99
lung fetal	19.15
T cell, TH1 clone HY06, resting	19.18
T cell, TH1 clone HY06, anergic	19.23
monocytes, LPS, gIFN, IL-10, 4+16 hr	19.3
spleen fetal	19.51
testes fetal	19.7
T cell, TH0 clone Mot 72, resting	19.71
T cell, TH0 clone Mot 72, resting	19.84
DC CD1a+ CD86+, ex CD34+ GM-CSF, TNFa, activated 1+6 hr	19.94
peripheral blood mononuclear cells, activated	20.01
hematopoietic precursor line TF1, activated	20.07
lung fibroblast sarcoma line MRC5, activated	20.18
Splenocytes, activated	20.21
T cell gd clones, resting	20.27
ovary fetal	20.45
T cells CD4+, TH2 polarized, activated	20.57
Splenocytes, resting	20.6
uterus fetal	20.62
DC 95% CD1a+, ex CD34+ GM-CSF, TNFa, activated 1+6 hr	20.94
epithelial cells, unstimulated	20.96
peripheral blood mononuclear cells, resting	20.97
adipose tissue fetal	21.13

B cell line JY, activated	21.28
monocytes, LPS, gIFN, IL-10	21.37
placenta 28 wk	21.38
NK 20 clones pooled, activated	21.55
pool of two normal human lung samples	21.63
normal human thyroid	21.65
epithelial cells, IL-1b activated	21.72
normal human skin	21.84
T cell, TH0 clone Mot 72, anergic	21.87
small intestine fetal	22.01
CD28- T cell clone in pME	22.08
T cell, TH2 clone HY935, activated	22.09
T cell clones, pooled, resting	22.29
Hashimoto's thyroiditis thyroid sample	22.3
NK 20 clones pooled, resting	22.4
B cell EBV lines, resting	22.45
T cell, TH2 clone HY935, resting	22.86
T cell, TH0 clone Mot 72, activated	23.3
monocytes, LPS, gIFN, anti-IL-10, 4+16 hr	23.39
T cell lines Jurkat and Hut78, resting	23.4
T cell, TH0 clone Mot 72, activated	23.56
<i>Pneumocystis carinii</i> pneumonia lung sample	24.05
U937 premonocytic line, resting	25.01
pool of rheumatoid arthritis samples, human	25.85
pool of three heavy smoker human lung samples	26.1
DC 95% CD14+, ex CD34+ GM-CSF, TNFa, activated 1+6 hr	32.69
kidney fetal	33.7
liver fetal	34.4
NK cytotoxic clone, resting	34.49
tonsil inflammed	35.02
normal w.t. monkey lung	35.45
gallbladder fetal	35.84
TR1 T cell clone	35.86
allergic lung sample	36.39
Psoriasis patient skin sample	36.44
normal human colon	37.34
brain fetal	37.35
<i>Ascaris</i> -challenged monkey lung, 4 hr.	37.75
<i>Ascaris</i> -challenged monkey lung, 24 hr.	40
heart fetal	40
normal w.t. monkey colon	40
ulcerative colitis human colon sample	40

Primers specific for DCRS6_H were designed and used in Taqman quantitative PCR against various human libraries. DCRS6_H is expressed in innate immune myeloid cells including dendritic cells and monocytes. Expression is also detected in T-cell libraries. These data demonstrate the receptor is expressed in immune cell types and may be regulated by activation conditions.

5

Table for DCRS6_H

library description	CT for DCRS6_H
T cell, TH0 clone Mot 72, resting	15.54
T cell, TH0 clone Mot 72, resting	15.7
DC ex monocytes GM-CSF, IL-4, resting	17.84
DC ex monocytes GM-CSF, IL-4, resting	18.19
DC ex monocytes GM-CSF, IL-4, LPS	18.3
activated 4+16 hr	
DC ex monocytes GM-CSF, IL-4, monokine	18.3
activated 4+16 hr	
T cell, TH1 clone HY06, resting	18.43
NK cytotoxic clone, resting	18.53
T cell clones, pooled, resting	18.8
T cell, TH1 clone HY06, activated	19.03
T cell, TH2 clone HY935, activated	19.1
TR1 T cell clone	19.12
T cells CD4+, TH2 polarized, activated	20.06
B cell EBV lines, resting	20.3
T cell, TH2 clone HY935, resting	20.48
kidney epithelial carcinoma cell line CHA, activated	21.07
T cell, TH1 clone HY06, anergic	21.14
normal human colon	21.29
NK 20 clones pooled, resting	21.49
T cell gd clones, resting	21.58
gallbladder fetal	22.21
kidney fetal	22.79
liver fetal	22.8
<i>Pneumocystic carinii</i> pneumonia lung sample	23.06
CD28- T cell clone in pME	23.18
T cell, TH0 clone Mot 72, anergic	23.2
ovary fetal	23.51
normal human thyroid	24.03
small intestine fetal	24.13
testes fetal	24.82
epithelial cells, IL-1b activated	26.08
pool of three heavy smoker human lung samples	26.49
placenta 28 wk	26.56
normal w.t. monkey lung	28.65
peripheral blood mononuclear cells,	33.39

activated	
<i>Ascaris</i> -challenged monkey lung, 4 hr.	36.59
spleen fetal	38.43
peripheral blood mononuclear cells, resting	40
T cell, TH0 clone Mot 72, activated	40
T cell lines Jurkat and Hut78, resting	40
Splenocytes, resting	40
Splenocytes, activated	40
B cell line JY, activated	40
NK 20 clones pooled, activated	40
hematopoietic precursor line TF1, activated	40
U937 premonocytic line, resting	40
U937 premonocytic line, activated	40
monocytes, LPS, gIFN, anti-IL-10	40
monocytes, LPS, gIFN, IL-10	40
monocytes, LPS, gIFN, anti-IL-10, 4+16 hr	40
monocytes, LPS, gIFN, IL-10, 4+16 hr	40
monocytes, LPS, 1 hr	40
monocytes, LPS, 6 hr	40
DC 70% CD1a+, ex CD34+ GM-CSF, TNFa, resting	40
DC 70% CD1a+, ex CD34+ GM-CSF, TNFa, activated 1 hr	40
DC 70% CD1a+, ex CD34+ GM-CSF, TNFa, activated 6 hr	40
DC 95% CD1a+, ex CD34+ GM-CSF, TNFa, activated 1+6 hr	40
DC 95% CD14+, ex CD34+ GM-CSF, TNFa, activated 1+6 hr	40
DC CD1a+ CD86+, ex CD34+ GM-CSF, TNFa, activated 1+6 hr	40
epithelial cells, unstimulated	40
lung fibroblast sarcoma line MRC5, activated	40
<i>Ascaris</i> -challenged monkey lung, 24 hr.	40
pool of two normal human lung samples	40
allergic lung sample	40
normal w.t. monkey colon	40
ulcerative colitis human colon sample	40
Hashimoto's thyroiditis thyroid sample	40
pool of rheumatoid arthritis samples, human	40
normal human skin	40
Psoriasis patient skin sample	40
tonsil inflamed	40
lung fetal	40
heart fetal	40
brain fetal	40
adipose tissue fetal	40
uterus fetal	40

T cell, TH0 clone Mot 72, activated 40

- 5 Primers specific for DCRS7_H were designed and used in Taqman quantative PCR against various human libraries. DCRS7_H is expressed in innate immune myeloid cells including dendritic cells and monocytes. Expression is also detected in fetal libraries. These data demonstrate the receptor is expressed in immune cell types and may be regulated by activation conditions.

library description	CT for DCRS7_H
fetal uterus	19.05
DC mix	19.34
fetal small intestine	19.46
fetal ovary	19.68
fetal testes	19.75
fetal lung	20.04
CHA	20.24
normal thyroid	20.32
DC/GM/IL-4	20.52
fetal spleen	20.86
normal lung	20.94
TF1	21
allergic lung #19	21.02
Psoriasis skin	21.07
fetal liver	21.15
MRC5	21.15
24 hr. Ascaris lung	21.17
hi dose IL-4 lung	21.23
CD1a+ 95%	21.32
Hashimotos thyroiditis	21.35
Crohns colon 4003197A	21.35
normal lung pool	21.36
70% DC resting	21.42
fetal kidney	21.58
adult placenta	21.68
lung 121897-1	21.8
Pneumocystis carinii lung	21.81
#20	
A549 unstim.	21.89
normal colon #22	21.94
18 hr. Ascaris lung	22.09
normal skin	22.1
Crohns colon 9609C144	22.13
fetal adipose tissue	22.35
D6	22.39

DC resting CD34-derived	22.45
DC TNF/TGFb act CD34-der.	22.54
fetal brain	22.9
DC CD40L activ. mono-deriv.	22.91
Crohns colon 403242A	22.91
ulcerative colitis colon #26	23
RA synovium pool	23.06
A549 activated	23.06
mono + IL-10	23.42
DC LPS	23.49
Mot 72 activated	23.66
CD1a+ CD86+	23.86
HY06 resting	23.87
U937 activated	23.97
inflammed tonsil	23.97
D1	24.06
M1	24.17
CD14+ 95%	24.21
lung 080698-2	24.28
4 hr. Ascaris lung	24.37
Jurkat activated pSPORT	24.42
DC resting mono-derived	24.48
HY06 activated	24.54
C+	24.64
Splenocytes resting	24.65
U937/CD004 resting	24.96
PBMC resting	25.8
Mot 72 resting	25.91
mono + anti-IL-10	26.14
NK pool	26.99
HY06 anti-peptide	27.34
mast cell pME	27.38
Tc gamma delta	28.14
TC1080 CD28- pMET7	31.05
PBMC activated	31.89
NK non cytotox.	32.3
RV-C30 TR1 pMET7	32.5
Bc	33.72
C-	33.8
Splenocytes activated	34.7
JY	35.05
NK cytotox.	36.44
NKL/IL-2	37.59
HY935 resting	37.6
NK pool activated	38.15
Mot 72 anti-peptide	38.87
fetal heart	40.92

B21 resting	42.05
Jurkat resting pSPORT	42.8
B21 activated	43.09
NKA6 pSPORT	44.85
HY935 activated	45
M6	45

5 Primers specific for DCRS9_H were designed and used in Taqman quantitative PCR against various human libraries. DCRS9_H is expressed T-cells, fetal lung, and resting monocytes. These data demonstrate the receptor is expressed in immune cell types and may be regulated by activation conditions.

Table for DCRS9_H
library description CT for
DCRS9_H

HY06 resting	22.35
fetal lung	22.63
HY06 anti-peptide	22.72
HY06 activated	22.96
U937/CD004 resting	24.16
fetal small intestine	24.94
JY	25.04
Mot 72 resting	25.12
Jurkat activated pSPORT	25.2
RV-C30 TR1 pMET7	26.51
fetal kidney	26.76
MRC5	27.2
Psoriasis skin	27.3
Tc gamma delta	27.37
Crohns colon	27.44
4003197A	
fetal spleen	27.72
normal lung	27.83
Hashimotos thyroiditis	28.03
B21 resting	28.32
TF1	28.39
NK cytotox.	28.44
TC1080 CD28- pMET7	28.61
Pneumocystis carinii lung #20	29.05
U937 activated	29.06
HY935 resting	29.09
CD1a+ 95%	29.13

B21 activated	29.2
Mot 72 activated	29.21
fetal testes	29.27
lung 080698-2	29.32
Jurkat resting	29.38
pSPORT	
CD14+ 95%	29.38
normal thyroid	29.53
Mot 72 anti-peptide	29.65
Splenocytes resting	29.85
Crohns colon	30.28
9609C144	
lung 121897-1	30.37
24 hr. Ascaris lung	30.59
hi dose IL-4 lung	30.8
CD1a+ CD86+	31.42
normal skin	31.73
fetal uterus	31.79
PBMC activated	31.82
inflammed tonsil	31.98
fetal brain	32.21
RA synovium pool	32.77
allergic lung #19	33.18
18 hr. Ascaris lung	33.42
adult placenta	33.43
normal lung pool	33.45
Crohns colon	33.52
403242A	
NK pool	33.72
HY935 activated	33.75
DC/GM/IL-4	34.28
DC resting mono-derived	34.57
fetal ovary	35.06
fetal adipose tissue	35.07
CHA	35.2
PBMC resting	35.95
Bc	36.19
A549 unstim.	36.4
fetal heart	36.87
ulcerative colitis colon #26	37.83
C-	38.32
4 hr. Ascaris lung	40.2
D6	40.62
C+	44.38

A549 activated	44.58
Splenocytes	45
activated	
NK pool activated	45
NKA6 pSPORT	45
NKL/IL-2	45
NK non cytotox.	45
mono + anti-IL-10	45
mono + IL-10	45
M1	45
M6	45
70% DC resting	45
D1	45
DC LPS	45
DC mix	45
fetal liver	45
mast cell pME	45
DC CD40L activ.	45
mono-deriv.	
DC resting CD34-	45
derived	
DC TNF/TGFb act	45
CD34-der.	
normal colon #22	45

V. Cloning of species counterparts

Various strategies are used to obtain species counterparts of the DCRSs, preferably from other primates or rodents. One method is by cross hybridization using closely related species DNA probes. It may be useful to go into evolutionarily similar species as intermediate steps. Another method is by using specific PCR primers based on the identification of blocks of similarity or difference between genes, e.g., areas of highly conserved or nonconserved polypeptide or nucleotide sequence. Sequence database searches may identify species counterparts.

VI. Production of mammalian protein

An appropriate, e.g., GST, fusion construct is engineered for expression, e.g., in *E. coli*. For example, a mouse IGIF pGex plasmid is constructed and transformed into *E. coli*. Freshly transformed cells are grown, e.g., in LB medium containing 50 µg/ml ampicillin and induced with IPTG (Sigma, St. Louis, MO). After overnight induction, the bacteria are harvested and the pellets containing the appropriate protein are isolated. The pellets are homogenized, e.g., in TE buffer (50 mM Tris-base pH 8.0, 10 mM EDTA and 2 mM pefabloc) in 2 liters. This material is passed through a microfluidizer (Microfluidics, Newton, MA) three times. The fluidized supernatant is spun down on a Sorvall GS-3 rotor for 1 h at 13,000 rpm. The resulting supernatant containing the cytokine receptor protein is filtered and passed over a glutathione-SEPHAROSE column equilibrated in 50 mM Tris-base pH 8.0. Fractions containing the DCRS8-GST fusion protein are pooled and cleaved, e.g., with thrombin (Enzyme Research Laboratories, Inc., South Bend, IN). The cleaved pool is then passed over a Q-SEPHAROSE column equilibrated in 50 mM Tris-base. Fractions containing DCRS8 are pooled and diluted in cold distilled H₂O, to lower the conductivity, and passed back over a fresh Q-Sepharose column, alone or in succession with an immunoaffinity antibody column. Fractions containing the DCRS8 protein are pooled, aliquoted, and stored in the -70° C freezer.

Comparison of the CD spectrum with cytokine receptor protein may suggest that the protein is correctly folded. See Hazuda, et al. (1969) *J. Biol. Chem.* 264:1689-1693.

VII. Preparation of specific antibodies

Inbred Balb/c mice are immunized intraperitoneally with recombinant forms of the protein, e.g., purified DCRS8 or stable transfected NIH-3T3 cells. Animals are boosted at appropriate time points with protein, with or without additional adjuvant, to further stimulate antibody production. Serum is collected, or hybridomas produced with harvested spleens.

Alternatively, Balb/c mice are immunized with cells transformed with the gene or fragments thereof, either endogenous or exogenous cells, or with isolated membranes enriched for expression of the antigen. Serum is collected at the appropriate time, typically after numerous further administrations. Various gene therapy techniques may be useful, e.g., in producing protein in situ, for generating an immune response. Serum or antibody preparations may be cross-absorbed or immunoselected to prepare substantially purified antibodies of defined specificity and high affinity.

Monoclonal antibodies may be made. For example, splenocytes are fused with an appropriate fusion partner and hybridomas are selected in growth medium by standard procedures. Hybridoma supernatants are screened for the presence of antibodies which bind to the DCRS8, e.g., by ELISA or other assay. Antibodies which specifically recognize specific DCRS8 embodiments may also be selected or prepared.

In another method, synthetic peptides or purified protein are presented to an immune system to generate monoclonal or polyclonal antibodies. See, e.g., Coligan (ed. 1991) Current Protocols in Immunology Wiley/Greene; and Harlow and Lane (1989) Antibodies: A Laboratory Manual Cold Spring Harbor Press. In appropriate situations, the binding reagent is either labeled as described above, e.g., fluorescence or otherwise, or immobilized to a substrate for panning methods. Nucleic acids may also be introduced into cells in an animal to produce the antigen, which serves to elicit an immune response. See, e.g., Wang, et al. (1993) Proc. Nat'l. Acad. Sci. 90:4156-4160; Barry, et al. (1994) BioTechniques 16:616-619; and Xiang, et al. (1995) Immunity 2: 129-135.

VIII. Production of fusion proteins

Various fusion constructs are made with DCRS8 or DCRS9. A portion of the appropriate gene is fused to an epitope tag, e.g., a FLAG tag, or to a two hybrid system construct. See, e.g., Fields and Song (1989) Nature 340:245-246.

The epitope tag may be used in an expression cloning procedure with detection with anti-FLAG antibodies to detect a binding partner, e.g., ligand for the respective cytokine receptor. The two hybrid system may also be used to isolate proteins which specifically bind to the receptor subunit.

IX. Structure activity relationship

Information on the criticality of particular residues is determined using standard procedures and analysis. Standard mutagenesis analysis is performed, e.g., by generating many different variants at determined positions, e.g., at the positions identified above, and evaluating biological activities of the variants. This may be performed to the extent of determining positions which modify activity, or to focus on specific positions to

determine the residues which can be substituted to either retain, block, or modulate biological activity.

Alternatively, analysis of natural variants can indicate what positions tolerate natural mutations. This may result from populational analysis of variation among individuals, or across strains or species. Samples from selected individuals are analyzed, e.g., by PCR analysis and sequencing. This allows evaluation of population polymorphisms.

X. Isolation of a ligand

A cytokine receptor can be used as a specific binding reagent to identify its binding partner, by taking advantage of its specificity of binding, much like an antibody would be used. The binding receptor may be a heterodimer of receptor subunits; or may involve, e.g., a complex of the DCRS8 with another cytokine receptor subunit. A binding reagent is either labeled as described above, e.g., fluorescence or otherwise, or immobilized to a substrate for panning methods.

The binding composition is used to screen an expression library made from a cell line which expresses a binding partner, i.e., ligand, preferably membrane associated. Standard staining techniques are used to detect or sort surface expressed ligand, or surface expressing transformed cells are screened by panning. Screening of intracellular expression is performed by various staining or immunofluorescence procedures. See also McMahan, et al. (1991) EMBO J. 10:2821-2832.

For example, on day 0, precoat 2-chamber permanox slides with 1 ml per chamber of fibronectin, 10 ng/ml in PBS, for 30 min at room temperature. Rinse once with PBS. Then plate COS cells at $2-3 \times 10^5$ cells per chamber in 1.5 ml of growth media. Incubate overnight at 37 C.

On day 1 for each sample, prepare 0.5 ml of a solution of 66 μ g/ml DEAE-dextran, 66 μ M chloroquine, and 4 μ g DNA in serum free DME. For each set, a positive control is prepared, e.g., of DCRS8-FLAG cDNA at 1 and 1/200 dilution, and a negative mock. Rinse cells with serum free DME. Add the DNA solution and incubate 5 hr at 37 C. Remove the medium and add 0.5 ml 10% DMSO in DME for 2.5 min. Remove and wash once with DME. Add 1.5 ml growth medium and incubate overnight.

On day 2, change the medium. On days 3 or 4, the cells are fixed and stained. Rinse the cells twice with Hank's Buffered Saline Solution (HBSS) and fix in 4% paraformaldehyde (PFA)/glucose for 5 min. Wash 3X with HBSS. The slides may be stored at -80 C after all liquid is removed. For each chamber, 0.5 ml incubations are performed as follows. Add HBSS/saponin (0.1%) with 32 μ l/ml of 1 M NaN_3 for 20 min. Cells are then washed with HBSS/saponin 1X. Add appropriate DCRS8 or

DCRS8/antibody complex to cells and incubate for 30 min. Wash cells twice with HBSS/saponin. If appropriate, add first antibody for 30 min. Add second antibody, e.g., Vector anti-mouse antibody, at 1/200 dilution, and incubate for 30 min. Prepare ELISA solution, e.g., Vector Elite ABC horseradish peroxidase solution, and preincubate for 30 min. Use, e.g., 1 drop of solution A (avidin) and 1 drop solution B (biotin) per 2.5 ml HBSS/saponin. Wash cells twice with HBSS/saponin. Add ABC HRP solution and incubate for 30 min. Wash cells twice with HBSS, second wash for 2 min, which closes cells. Then add Vector diaminobenzoic acid (DAB) for 5 to 10 min. Use 2 drops of buffer plus 4 drops DAB plus 2 drops of H₂O₂ per 5 ml of glass distilled water.

Carefully remove chamber and rinse slide in water. Air dry for a few minutes, then add 1 drop of Crystal Mount and a cover slip. Bake for 5 min at 85-90 C.

Evaluate positive staining of pools and progressively subclone to isolation of single genes responsible for the binding.

Alternatively, receptor reagents are used to affinity purify or sort out cells expressing a putative ligand. See, e.g., Sambrook, et al. or Ausubel, et al.

Another strategy is to screen for a membrane bound receptor by panning. The receptor cDNA is constructed as described above. Immobilization may be achieved by use of appropriate antibodies which recognize, e.g., a FLAG sequence of a DCRS8 fusion construct, or by use of antibodies raised against the first antibodies. Recursive cycles of selection and amplification lead to enrichment of appropriate clones and eventual isolation of receptor expressing clones.

Phage expression libraries can be screened by mammalian DCRS8. Appropriate label techniques, e.g., anti-FLAG antibodies, will allow specific labeling of appropriate clones.

We tested the ability of DCRS receptors to specifically bind IL-17 family cytokines. Recombinant FLAG-hIL-17 family cytokines were used in binding experiments on Baf/3 DCRS receptor transfected expressing recombinant IL-17R_H, DCRS6_H, DCRS7_H, DCRS8_H and DCRS9_H and analyzed by FACS. We can demonstrate specific binding of IL-17 family member IL-74 to DCRS6 expressing Baf/3 cells. In additional experiments we have shown IL-17 specific binding to IL-17R_H, DCRS7_H, DCRS8_H. Further experiments show IL-71 binding to DCRS8_Hu transfectants. These experiments demonstrate the sequence homology among IL-17 related cytokine receptors confers functional binding to IL-17 cytokines.

All citations herein are incorporated herein by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

Many modifications and variations of this invention can be made without departing from its spirit and scope, as will be apparent to those skilled in the art. The specific embodiments described herein are offered by way of example only, and the invention is to be limited by the terms of the appended claims, along with the full scope
5 of equivalents to which such claims are entitled; and the invention is not to be limited by the specific embodiments that have been presented herein by way of example.

WHAT IS CLAIMED IS:

1. A composition of matter selected from:

- a) a substantially pure or recombinant polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 14;
- b) a substantially pure or recombinant polypeptide comprising at least two distinct nonoverlapping segments of at least five amino acids identical to segments of SEQ ID NO: 14;
- c) a natural sequence DCRS8 comprising mature SEQ ID NO: 14;
- d) a fusion polypeptide comprising DCRS8 sequence;
- e) a substantially pure or recombinant polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids identical to segments of SEQ ID NO: 17 or 20;
- f) a substantially pure or recombinant polypeptide comprising at least two distinct nonoverlapping segments of at least five amino acids identical to segments of SEQ ID NO: 17 or 20;
- g) a natural sequence DCRS9 comprising mature SEQ ID NO: 17 or 20; or
- h) a fusion polypeptide comprising DCRS9 sequence.

2. The substantially pure or isolated antigenic polypeptide of Claim 1, wherein said distinct nonoverlapping segments of identity include:

- a) one of at least eight amino acids;
- b) one of at least four amino acids and a second of at least five amino acids;
- c) at least three segments of at least four, five, and six amino acids, or
- d) one of at least twelve amino acids.

3. The composition of matter of Claim 1, wherein said:

a) polypeptide:

- i) comprises a mature sequence of Table 3 or 4;
- ii) is an unglycosylated form of DCRS8 or DCRS9;
- iii) is from a primate, such as a human;
- iv) comprises at least seventeen amino acids of SEQ ID NO: 14 or 17;
- v) exhibits at least four nonoverlapping segments of at least seven amino acids of SEQ ID NO: 14 or 17;
- vi) is a natural allelic variant of DCRS8 or DCRS9;
- vii) has a length at least about 30 amino acids;

viii) exhibits at least two non-overlapping epitopes which are specific for a primate DCRS8 or DCRS9;

ix) is glycosylated;

x) has a molecular weight of at least 30 kD with natural glycosylation;

5 xi) is a synthetic polypeptide;

xii) is attached to a solid substrate;

xiii) is conjugated to another chemical moiety;

xiv) is a 5-fold or less substitution from natural sequence; or

xv) is a deletion or insertion variant from a natural sequence.

10

4. A composition comprising:

a) a substantially pure DCRS8 or DCRS9 and another cytokine receptor family member;

b) a sterile DCRS8 or DCRS9 polypeptide of Claim 1;

15 c) said DCRS8 or DCRS9 polypeptide of Claim 1 and a carrier, wherein said carrier is:

i) an aqueous compound, including water, saline, and/or buffer; and/or

ii) formulated for oral, rectal, nasal, topical, or parenteral administration.

20

5. The fusion polypeptide of Claim 1, comprising:

a) mature protein sequence of Table 3 or 4;

b) a detection or purification tag, including a FLAG, His6, or Ig sequence; or

c) sequence of another cytokine receptor protein.

25

6. A kit comprising a polypeptide of Claim 1, and:

a) a compartment comprising said protein or polypeptide; or

b) instructions for use or disposal of reagents in said kit.

30

7. A binding compound comprising an antigen binding site from an antibody, which specifically binds to a natural DCRS8 or DCRS9 polypeptide of Claim 1, wherein:

a) said binding compound is in a container;

b) said DCRS8 or DCRS9 polypeptide is from a human;

c) said binding compound is an Fv, Fab, or Fab2 fragment;

d) said binding compound is conjugated to another chemical moiety; or

35

e) said antibody:

i) is raised against a peptide sequence of a mature polypeptide of Table 3 or 4;

- ii) is raised against a mature DCRS8 or DCRS9;
- iii) is raised to a purified human DCRS8 or DCRS9;
- iv) is immunoselected;
- v) is a polyclonal antibody;
- vi) binds to a denatured DCRS8 or DCRS9;
- vii) exhibits a K_d to antigen of at least 30 μM;
- viii) is attached to a solid substrate, including a bead or plastic membrane;
- ix) is in a sterile composition; or
- x) is detectably labeled, including a radioactive or fluorescent label.

8. A kit comprising said binding compound of Claim 7, and:

- a) a compartment comprising said binding compound; or
- b) instructions for use or disposal of reagents in said kit.

9. A method of producing an antigen:antibody complex, comprising contacting under appropriate conditions a primate DCRS8 or DCRS9 polypeptide with an antibody of Claim 7, thereby allowing said complex to form.

10. The method of Claim 9, wherein:

- a) said complex is purified from other cytokine receptors;
- b) said complex is purified from other antibody;
- c) said contacting is with a sample comprising an interferon;
- d) said contacting allows quantitative detection of said antigen;
- e) said contacting is with a sample comprising said antibody; or
- f) said contacting allows quantitative detection of said antibody.

11. A composition comprising:

- a) a sterile binding compound of Claim 7, or
- b) said binding compound of Claim 7 and a carrier, wherein said carrier is:
 - i) an aqueous compound, including water, saline, and/or buffer; and/or
 - ii) formulated for oral, rectal, nasal, topical, or parenteral administration.

12. An isolated or recombinant nucleic acid encoding said polypeptide of Claim 1, wherein said:

- a) DCRS8 or DCRS9 is from a human; or
- b) said nucleic acid:
 - i) encodes an antigenic peptide sequence of Table 3 or 4;

- ii) encodes a plurality of antigenic peptide sequences of Table 3 or 4;
- iii) exhibits identity over at least thirteen nucleotides to a natural cDNA encoding said segment;
- iv) is an expression vector;
- 5 v) further comprises an origin of replication;
- vi) is from a natural source;
- vii) comprises a detectable label;
- viii) comprises synthetic nucleotide sequence;
- ix) is less than 6 kb, preferably less than 3 kb;
- 10 x) is from a primate;
- xi) comprises a natural full length coding sequence;
- xii) is a hybridization probe for a gene encoding said DCRS8 or DCRS9;
- or
- xiii) is a PCR primer, PCR product, or mutagenesis primer.

15

13. A cell or tissue comprising said recombinant nucleic acid of Claim 12.

14. The cell of Claim 13, wherein said cell is:

20

- a) a prokaryotic cell;
- b) a eukaryotic cell;
- c) a bacterial cell;
- d) a yeast cell;
- e) an insect cell;
- f) a mammalian cell;
- 25 g) a mouse cell;
- h) a primate cell; or
- i) a human cell.

25

15. A kit comprising said nucleic acid of Claim 12, and:

30

- a) a compartment comprising said nucleic acid;
- b) a compartment further comprising a primate DCRS8 or DCRS9 polypeptide;
- or
- c) instructions for use or disposal of reagents in said kit.

35

16. A nucleic acid which:

- a) hybridizes under wash conditions of 30 minutes at 30° C and less than 2M salt to the coding portion of SEQ ID NO: 13 or 16; or

- b) exhibits identity over a stretch of at least about 30 nucleotides to a primate DCRS8 or DCRS9.

17. The nucleic acid of Claim 16, wherein:

- 5 a) said wash conditions are at 45° C and/or 500 mM salt; or
b) said stretch is at least 55 nucleotides.

18. The nucleic acid of Claim 16, wherein:

- 10 a) said wash conditions are at 55° C and/or 150 mM salt; or
b) said stretch is at least 75 nucleotides.

19. A method of modulating physiology or development of a cell or tissue culture cells comprising contacting said cell with an agonist or antagonist of a mammalian DCRS8 or DCRS9.

15

20. The method of Claim 19, wherein said cell is transformed with a nucleic acid encoding said DCRS8 or DCRS9 and another cytokine receptor subunit.

DCRS7_Mu	RTALLHSADG-AGYERLVGALASALSQMP--LRVAVDLWSRRE-LSAHGALAWFHHQR
DCRS7_Hu	RAALLYSADD-SGFERLVGALASALCQLP--LRVAVDLWSRRE-LSAQGPVAFWHAQR
IL-17R_Hu	RKVWIIYSADH-PLYVDVVLKFAQFLLTAGC--TEVALDLLLEEQA-ISEAGVMTWVGRQK
IL-17R_Mu	RKVWIVVSADH-PLYVEVVLKFAQFLITAGC--TEVALDLLLEEQV-ISEVGVMTWVSRQK
DCRS10	RKVFITYSMD----TAMEVVVKFVNFLLVNG--FQTAIDIFEDR--IRGIDI IKWMERYL
DCRS10_Mu	RKVFITYSMD----TAMEVVVKFVNFLLVNG--FQTAIDIFEDR--IRGIDI IKWMERYL
DCRS9_Hu	RPVLLHAADS-EAQRRLVGALAEELLRAALGGRDVIVDLWEGRH-VARVGPLPWLWAAR
DCRS8_Hu	PKVFLCYSSKDGQNHMNVQCFAYFLQDFCG--CEVALDLWEDFS-LCREGQREWVIQKI
IL-17R_Ce	VKVMIVYADDN-DLHTDCVKKLVENLRNCAS--CDPVFDLEKLI--TAEIVPSRWLVDQI
DCRS6_Hu	IKVLVVYPSEI--CFHHTICYFTEFLQNHCR--SEVILEKWQKKK-IAEMGPVQWLATQK
DCRS6_Ce	EKVMLVCPEVS-GRDEDFMMRIADALKKSN--NKVVCDRWFEDSKNAEENMLHWVYEQT
	. : . : . : *

DCRS7_Mu	RRILQEGGVILLFSPAAVAQCQ--QWLQLQTVEP--GP--HDAIAAWLSCVLPDFL
DCRS7_Hu	RQTLQEGGVVLLFSPGAVALCS--EWLQDGVSGPGAHP--HDAFRASLSCVLPDFL
IL-17R_Hu	QEMVESNSKIIVLCSRGTAKWQALLGRGAP-VRLRCDHGKPV-GDLFTAAMNMILPDFK
IL-17R_Mu	QEMVESNSKIIILCSRGTQAKWKAILGWAEPVQLRCDHWKPA-GDLFTAAMNMILPDFK
DCRS10	R--DKTVMIIVAISPKYKQDVE--GAESQDDED-EHGL--HTKYIHRM-MQIEFIK
DCRS10_Mu	R--DKTVMIIVAISPKYKQDVE--GAESQDDED-EHGL--HTKYIHRM-MQIEFIS
DCRS9_Hu	TRVAREQGTVLLWSGADLRPVS--GPDP-RAAP-----LLA----LLHAAP
DCRS8_Hu	H----ESQFIIVVCSKGMKYFVD--KKNYKHKGGRGSGK--GELFLVAVSAIAEKLRL
IL-17R_Ce	S----SLKKFIIVVSDCAEKILD--TEASETHQLVQARP--FADLFGPAMEMIIRDAT
DCRS6_Hu	K----AADKVVFLLSNDVNSVCD--GTCGKSEGSPSENS--QDLFFPLAFNLFCSDLR
DCRS6_Ce	K----IAEKIIVFHSAYYHPRCG--IYDVINNFFPCTDPR-----LAHIALT---PEAQ
	... *

FIG. 1A

DCRS7_Mu	QGRATGR-----YVGVFDFGLLHPDSVPSPFRVAPLFSLP-SQLPAFLDALQ--GGCSTS
DCRS7_Hu	QGRAPGS-----YVGACFDRLLHPDAVPALFRTVPVFTLP-SQLPDDFLGALQ--QPRAPR
IL-17R_Hu	RPACFGT-----YVVCYFSEVSCDGDVPDLFGAAPRYPLM-DRFEEVYFRIQ--DLEMFO
IL-17R_Mu	RPACFGT-----YVVCYFSGICSERDVPDLFNITSRYPLM-DRFEEVYFRIQ--DLEMFE
DCRS10	QGS MNFR-----FIPVLF PNAK-KEHVPTWLQNTHVYSWP-KNKKNILLRLL-REEEYVA
DCRS10_Mu	QGS MNFR-----FIPVLF PNAK-KEHVPTWLQNTHVYSWP-KNKKNILLRLL-REEEYVA
DCRS9_Hu	RPL-----LLLAYFSRLCAKGDIPPLRALPRYRLI-RDLPRLLRALD--ARPFAE
DCRS8_Hu	QAKQSSAALS KFI AVYFDYSC-EGDVPGILDSTKYRIM-DNLPQLCSHLHSRDHGLQE
IL-17R_Ce	HNFPPEAR--KKYAVVRFNYS P--HVP PNLAILNLPTFIPEQFAQLTAF LHN-VEHTER
DCRS6_Hu	SQIHLHK-----YVVVYFREID-TKDDYNALSVCPKYHLM-KDATAFCAELL--HV KQO
DCRS6_Ce	RSVPKEV-----EYVLP RDQKLL--EDAFDITIADPLVIDIPIEDVAIPENVP--IH HESC
	. :
DCRS7_Mu	AGRPAD RVER-----VT-----QALRSALD SCTS-----
DCRS7_Hu	SGRLQERAEQ-----VS-----RALQPALDSYFHPP-----
IL-17R_Hu	PGRMHRVGELSGDNYLRS--PGGRQLRAALDRFRDWQVRCPDW
IL-17R_Mu	PGRMHHVREL TGDNYLQS--PSGRQLKEAVLRFQEWQTQCPDW
DCRS10	P-----PRGPL-----PTLQVVPL-----
DCRS10_Mu	P-----PRGPL-----PTLQVVPL-----
DCRS9_Hu	ATSWGRLGAR-----QRRQSRLELCSR-----
DCRS8_Hu	PGQHTROGSR-----RNYFRSKSGRSLYVAICNMHQFIDE EPDW
IL-17R_Ce	ANVTQNI SEA-----Q-----IHEWNLCASRMMMSFFVRNP NW
DCRS6_Hu	VS-----AGKR-----SQACHDGCCSL-----
DCRS6_Ce	DSIDSRNNSK-----THSTDSGVSSLSS-----NS--
	:

FIG. 1B

SEQUENCE SUBMISSION

SEQ ID NO: 1 is primate DCRS6 nucleotide sequence.
SEQ ID NO: 2 is primate DCRS6 polypeptide sequence.
SEQ ID NO: 3 is primate DCRS6 reverse translation.
SEQ ID NO: 4 is rodent DCRS6 nucleotide sequence.
SEQ ID NO: 5 is rodent DCRS6 polypeptide sequence.
SEQ ID NO: 6 is rodent DCRS6 reverse translation.
SEQ ID NO: 7 is primate DCRS7 nucleotide sequence.
SEQ ID NO: 8 is primate DCRS7 polypeptide sequence.
SEQ ID NO: 9 is primate DCRS7 reverse translation.
SEQ ID NO: 10 is rodent DCRS7 nucleotide sequence.
SEQ ID NO: 11 is rodent DCRS7 polypeptide sequence.
SEQ ID NO: 12 is rodent DCRS7 reverse translation.
SEQ ID NO: 13 is primate DCRS8 nucleotide sequence.
SEQ ID NO: 14 is primate DCRS8 polypeptide sequence.
SEQ ID NO: 15 is primate DCRS8 reverse translation.
SEQ ID NO: 16 is primate DCRS9 nucleotide sequence.
SEQ ID NO: 17 is primate DCRS9 polypeptide sequence.
SEQ ID NO: 18 is primate DCRS9 reverse translation.
SEQ ID NO: 19 is rodent DCRS9 nucleotide sequence.
SEQ ID NO: 20 is rodent DCRS9 polypeptide sequence.
SEQ ID NO: 21 is rodent DCRS9 reverse translation.
SEQ ID NO: 22 is primate DCRS10 nucleotide sequence.
SEQ ID NO: 23 is primate DCRS10 polypeptide sequence.
SEQ ID NO: 24 is primate DCRS10 reverse translation.
SEQ ID NO: 25 is rodent DCRS10 nucleotide sequence.
SEQ ID NO: 26 is rodent DCRS10 polypeptide sequence.
SEQ ID NO: 27 is rodent DCRS10 reverse translation.
SEQ ID NO: 28 is primate IL-17 receptor peptide sequence.
SEQ ID NO: 29 is rodent IL-17 receptor peptide sequence.
SEQ ID NO: 30 is worm IL-17 receptor peptide sequence.
SEQ ID NO: 31 is worm DCRS6 nucleotide sequence.

<110> Schering Corporation

<120> Mammalian Receptor Proteins; Related Reagents and
Methods

<130> DX01170K PCT

<140>

<141>

<150> US 60/206,862

<151> 2000-05-24

<160> 31

<170> PatentIn Ver. 2.0

<210> 1

<211> 1796

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism: primate; surmised
Homo sapiens

<220>

<221> CDS

<222> (4)..(1509)

<220>

<221> mat_peptide

<222> (46)..(1509)

<400> 1

gcg atg tcg ctc gtg ctg cta agc ctg gcc gcg ctg tgc agg agc gcc	48
Met Ser Leu Val Leu Leu Ser Leu Ala Leu Cys Arg Ser Ala	
-10 -5 -1 1	
gta ccc cga gag ccg acc gtt caa tgt ggc tct gaa act ggg cca tct	96
Val Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser	
5 10 15	
cca gag tgg atg cta caa cat gat cta atc ccg gga gac ttg agg gac	144
Pro Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp	
20 25 30	
ctc cga gta gaa cct gtt aca act agt gtt gca aca ggg gac tat tca	192
Leu Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser	
35 40 45	
att ttg atg aat gta agc tgg gta ctc cgg gca gat gcc agc atc cgc	240
Ile Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg	
50 55 60 65	
ttg ttg aag gcc acc aag att tgt gtg acg ggc aaa agc aac ttc cag	288
Leu Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln	
70 75 80	
tcc tac agc tgt gtg agg tgc aat tac aca gag gcc ttc cag act cag	336
Ser Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln	
85 90 95	
acc aga ccc tct ggt ggt aaa tgg aca ttt tcc tat atc ggc ttc cct	384
Thr Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro	
100 105 110	
gta gag ctg aac aca gtc tat ttc att ggg gcc cat aat att cct aat	432
Val Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn	
115 120 125	
gca aat atg aat gaa gat ggc cct tcc atg tct gtg aat ttc acc tca	480
Ala Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser	
130 135 140 145	
cca ggc tgc cta gac cac ata atg aaa tat aaa aaa aag tgt gtc aag	528
Pro Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys	
150 155 160	
gcc gga agc ctg tgg gat ccg aac atc act gct tgt aag aag aat gag	576
Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu	
165 170 175	
gag aca gta gaa gtg aac ttc aca acc act ccc ctg gga aac aga tac	624
Glu Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr	
180 185 190	

atg gct ctt atc caa cac agc act atc atc ggg ttt tct cag gtg ttt	672
Met Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe	
195 200 205	
gag cca cac cag aag aaa caa acg cga gct tca gtg gtg att cca gtg	720
Glu Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val	
210 215 220 225	
act ggg gat agt gaa ggt gct acg gtg cag ctg act cca tat ttt cct	768
Thr Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro	
230 235 240	
act tgt ggc agc gac tgc atc cga cat aaa gga aca gtt gtg ctc tgc	816
Thr Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys	
245 250 255	
cca caa aca ggc gtc cct ttc cct ctg gat aac aac aaa agc aag ccg	864
Pro Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro	
260 265 270	
gga ggc tgg ctg cct ctc ctc ctg ctg tct ctg ctg gtg gcc aca tgg	912
Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp	
275 280 285	
gtg ctg gtg gca ggg atc tat cta atg tgg agg cac gaa agg atc aag	960
Val Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys	
290 295 300 305	
aag act tcc ttt tct acc acc aca cta ctg ccc ccc att aag gtt ctt	1008
Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu	
310 315 320	
gtg gtt tac cca tct gaa ata tgt ttc cat cac aca att tgt tac ttc	1056
Val Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe	
325 330 335	
act gaa ttt ctt caa aac cat tgc aga agt gag gtc atc ctt gaa aag	1104
Thr Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys	
340 345 350	
tgg cag aaa aag aaa ata gca gag atg ggt cca gtg cag tgg ctt gcc	1152
Trp Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala	
355 360 365	
act caa aag aag gca gca gac aaa gtc gtc ttc ctt ctt tcc aat gac	1200
Thr Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp	
370 375 380 385	
gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag ggc agt ccc	1248
Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro	
390 395 400	
agt gag aac tct caa gac ctc ttc ccc ctt gcc ttt aac ctt ttc tgc	1296
Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys	
405 410 415	
agt gat cta aga agc cag att cat ctg cac aaa tac gtg gtg gtc tac	1344
Ser Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr	
420 425 430	

```

ttt aga gag att gat aca aaa gac gat tac aat gct ctc agt gtc tgc 1392
Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys
    435                440                445

ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt gca gaa ctt 1440
Pro Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu
    450                455                460                465

ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca caa gcc tgc 1488
Leu His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys
    470                475                480

cac gat ggc tgc tgc tcc ttg tagccaccc atgagaagca agagacctta 1539
His Asp Gly Cys Cys Ser Leu
    485

aaggcttcct atcccaccaa ttacagggaa aaaacgtgtg atgatcctga agcttactat 1599

gcagcctaca aacagcctta gtaattaaaa cattttatac caataaaaatt ttcaaataatt 1659

gctaactaat gtagcattaa ctaacgattg gaaactacat ttacaacttc aaagctgttt 1719

tatacataga aatcaattac agctttaatt gaaaactgta accattttga taatgcaaca 1779

ataaagcatc ttcagcc 1796

<210> 2
<211> 502
<212> PRT
<213> Unknown

<400> 2
Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
    -10                -5                -1    1

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
    5                10                15

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
    20                25                30

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
    35                40                45                50

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
    55                60                65

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
    70                75                80

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
    85                90                95

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
    100                105                110

Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
    115                120                125                130

```

Asn	Met	Asn	Glu	Asp	Gly	Pro	Ser	Met	Ser	Val	Asn	Phe	Thr	Ser	Pro	135	140	145
Gly	Cys	Leu	Asp	His	Ile	Met	Lys	Tyr	Lys	Lys	Lys	Cys	Val	Lys	Ala	150	155	160
Gly	Ser	Leu	Trp	Asp	Pro	Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Glu	165	170	175
Thr	Val	Glu	Val	Asn	Phe	Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	Met	180	185	190
Ala	Leu	Ile	Gln	His	Ser	Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	Glu	195	200	205
Pro	His	Gln	Lys	Lys	Gln	Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr	215	220	225
Gly	Asp	Ser	Glu	Gly	Ala	Thr	Val	Gln	Leu	Thr	Pro	Tyr	Phe	Pro	Thr	230	235	240
Cys	Gly	Ser	Asp	Cys	Ile	Arg	His	Lys	Gly	Thr	Val	Val	Leu	Cys	Pro	245	250	255
Gln	Thr	Gly	Val	Pro	Phe	Pro	Leu	Asp	Asn	Asn	Lys	Ser	Lys	Pro	Gly	260	265	270
Gly	Trp	Leu	Pro	Leu	Leu	Leu	Leu	Ser	Leu	Leu	Val	Ala	Thr	Trp	Val	275	280	285
Leu	Val	Ala	Gly	Ile	Tyr	Leu	Met	Trp	Arg	His	Glu	Arg	Ile	Lys	Lys	295	300	305
Thr	Ser	Phe	Ser	Thr	Thr	Thr	Leu	Leu	Pro	Pro	Ile	Lys	Val	Leu	Val	310	315	320
Val	Tyr	Pro	Ser	Glu	Ile	Cys	Phe	His	His	Thr	Ile	Cys	Tyr	Phe	Thr	325	330	335
Glu	Phe	Leu	Gln	Asn	His	Cys	Arg	Ser	Glu	Val	Ile	Leu	Glu	Lys	Trp	340	345	350
Gln	Lys	Lys	Lys	Ile	Ala	Glu	Met	Gly	Pro	Val	Gln	Trp	Leu	Ala	Thr	355	360	365
Gln	Lys	Lys	Ala	Ala	Asp	Lys	Val	Val	Phe	Leu	Leu	Ser	Asn	Asp	Val	375	380	385
Asn	Ser	Val	Cys	Asp	Gly	Thr	Cys	Gly	Lys	Ser	Glu	Gly	Ser	Pro	Ser	390	395	400
Glu	Asn	Ser	Gln	Asp	Leu	Phe	Pro	Leu	Ala	Phe	Asn	Leu	Phe	Cys	Ser	405	410	415
Asp	Leu	Arg	Ser	Gln	Ile	His	Leu	His	Lys	Tyr	Val	Val	Val	Tyr	Phe	420	425	430
Arg	Glu	Ile	Asp	Thr	Lys	Asp	Asp	Tyr	Asn	Ala	Leu	Ser	Val	Cys	Pro	435	440	445

Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
 455 460 465

His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His
 470 475 480

Asp Gly Cys Cys Ser Leu
 485

<210> 3

<211> 1506

<212> DNA

<213> reverse translation

<220>

<221> misc_feature

<222> (1)..(1506)

<223> n may be a, c, g, or t

<400> 3

atgwsnytnng tnytnytnws nytngcngcn ytntgymgnw sngcngtncc nmnggarccn 60
 acngtncart gyggwnwsnga racnggnccn wsncngart ggatgytnca rcaygayytn 120
 athccnggng ayytnmgnga yytnmgngtn garccngtna cnacnwsngt ngcnacnggn 180
 gaytaywsna thytnatgaa ygtnwsntgg gtnytnmgng cngaygcnws nathmgnytn 240
 ytnaargcna cnaarathtg ygtnacnggn aarwsnaayt tycarwsnta ywsntgygtn 300
 mgntgyaayt ayacngargc nttycaracn caracnmgnc cnwsngggng naartggacn 360
 ttywsntaya thggnttycc ngtngarytn aayacngtnt aytyathgg ngcnacayaay 420
 athccnaayg cnaayatgaa ygargayggn ccnwsnatgw sngtnaaytt yacnwsnccn 480
 ggntgyytnng aycayathat gaartayaar aaraartgyg tnaargcngg nwsnytnntgg 540
 gayccnaaya thacngcntg yaaraaraay gargaracng tngargtnaa yttyacnacn 600
 acnccnytnng gnaaymgnta yatggcnytn athcarcayw snacnathat hggnttywsn 660
 cargtnnttyg arccncayca raaraarcar acnmgngcnw sngtnngtnat hccngtnacn 720
 ggngaywsng arggngcnac ngtnrcarytn acnccntayt tyccnacntg yggwnsngay 780
 tgyathmgnc ayaarggnac ngtnngtnytn tgyccncara cnggngtncc nttyccnytn 840
 gayaayaaya arwsnaarcc nggnggntgg ytncnytny tnytnytnws nytnytnngtn 900
 gcnacntggg tnytngtngc nggnathtay ytnatgtggm gncaygarmg nathaaraar 960
 acnwsnttyw snacnacnac nytnytnccn ccnathaarg tnytngtngt ntayccnwsn 1020
 garathtgyt tycaycayac nathtgytay ttyacngart tyytncaraa ycaytgymgn 1080
 wsngargtna thytngaraa rtggcaraan aaraarathg cngaratggg nccngtnrcar 1140

tggytngcna cncaraaraa rgcngcngay aargtngtnt tyytnytnws naaygaygtn 1200
 aaywsngtnt gygayggnac ntgyggnaar wsngarggnw snccnwsnga raaywsncar 1260
 gayytnttyc cnytngcntt yaayytntty tgywsngayy tnmgnwsnca rathcayytn 1320
 cayaartayg tngtngtnta yttymngar athgayacna argaygayta yaaygcnytn 1380
 wsngtntgyc cnaartayca yytnatgaar gaygcnacng cnttytgygc ngarytnytn 1440
 caygtnaarc arcargtnws ngcnggnaar mgnwsncarg cntgycayga yggntgytgy 1500
 wsnytn 1506

<210> 4

<211> 637

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:rodent; surmised
Mus musculus .

<220>

<221> CDS

<222> (1)..(210)

<400> 4

gat ttc agc agc cag acg cat ctg cac aaa tac ctg gag gtc tat ctt	48
Asp Phe Ser Ser Gln Thr His Leu His Lys Tyr Leu Glu Val Tyr Leu	
1 5 10 15	
ggg gga gca gac ctc aaa ggc gac tat aat gcc ctg agt gtc tgc ccc	96
Gly Gly Ala Asp Leu Lys Gly Asp Tyr Asn Ala Leu Ser Val Cys Pro	
20 25 30	
caa tat cat ctc atg aag gac gcc aca gct ttc cac aca gaa ctt ctc	144
Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu	
35 40 45	
aag gct acg cag agc atg tca gtg aag aaa cgc tca caa gcc tgc cat	192
Lys Ala Thr Gln Ser Met Ser Val Lys Lys Arg Ser Gln Ala Cys His	
50 55 60	
gat agc tgt tca ccc ttg tagtccaccc gggggaatag agactctgaa	240
Asp Ser Cys Ser Pro Leu	
65 70	
gccttcctac tctcccttcc agtgacaaat gctgtgtgac gactctgaaa tgtgtgggag	300
aggctgtgtg gaggtagtgc tatgtacaaa cttgctttta aactggagtt tgcaaagtca	360
acctgagcat acacgcctga ggctagtcac ttggctggatt tatgaagaca acacagttac	420
agacaataat gagtgggacc tacatttggg atatacccaa agctgggtaa tgattatcac	480
tgagaaccac gcactctggc catgaggtaa tacggcactt ccctgtcagg ctgtctgtca	540
ggttgggtct gtcttgcact gcccatgctc tatgctgcac gtagaccgtt ttgtaacatt	600

ttaatctgtt aatgaataat ccgtttggga ggctctc

637

<210> 5
 <211> 70
 <212> PRT
 <213> Unknown

<400> 5
 Asp Phe Ser Ser Gln Thr His Leu His Lys Tyr Leu Glu Val Tyr Leu
 1 5 10 15
 Gly Gly Ala Asp Leu Lys Gly Asp Tyr Asn Ala Leu Ser Val Cys Pro
 20 25 30
 Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu
 35 40 45
 Lys Ala Thr Gln Ser Met Ser Val Lys Lys Arg Ser Gln Ala Cys His
 50 55 60
 Asp Ser Cys Ser Pro Leu
 65 70

<210> 6
 <211> 210
 <212> DNA
 <213> reverse translation

<220>
 <221> misc_feature
 <222> (1)..(210)
 <223> n may be a, c, g, or t

<400> 6
 gayttywsnw sncaracnca yytncayaar tayytnngarg tntayytnng nggngcngay 60
 ytnaarggng aytayaaygc nytnwsngtn tgyccncart aycayytnat gaargaygcn 120
 acngcnttyc ayacngaryt nytnaargcn acncarwsna tgwsngtnaa raarmgnwsn 180
 cargcntgyc aygaywsntg ywsnccnytn 210

<210> 7
 <211> 2308
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:primate; surmised
 Homo sapiens

<220>
 <221> CDS
 <222> (181)..(2289)

<220>

<221> mat_peptide
 <222> (241)..(2289)

<220>
 <221> misc_feature
 <222> (664)
 <223> Xaa translation depends on genetic code

<400> 7
 gagtcaggac tcccaggaca gagagtgcac aaactaccca gcacagcccc ctccgcccc 60
 tctggagggt gaagagggat tccagccct gccaccaca gacacgggct gactgggggtg 120
 tctgcccccc ttgggggcan ccacagggcc tcaggcctgg gtgccacctg gcactagaag 180
 atg cct gtg ccc tgg ttc ttg ctg tcc ttg gca ctg ggc cga agc cag 228
 Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser Gln
 -20 -15 -10 -5
 tgg atc ctt tct ctg gag agg ctt gtg ggg cct cag gac gct acc cac 276
 Trp Ile Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala Thr His
 -1 1 5 10
 tgc tct ccg ggc ctc tcc tgc cgc ctc tgg gac agt gac ata ctc tgc 324
 Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys
 15 20 25
 ctg cct ggg gac atc gtg cct gct ccg ggc ccc gtg ctg gcg cct acg 372
 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
 30 35 40
 cac ctg cag aca gag ctg gtg ctg agg tgc cag aag gag acc gac tgt 420
 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
 45 50 55 60
 gac ctc tgt ctg cgt gtg gct gtc cac ttg gcc gtg cat ggg cac tgg 468
 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
 65 70 75
 gaa gag cct gaa gat gag gaa aag ttt gga gga gca gct gac tta ggg 516
 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Leu Gly
 80 85 90
 gtg gag gag cct agg aat gcc tct ctc cag gcc caa gtc gtg ctc tcc 564
 Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
 95 100 105
 ttc cag gcc tac cct act gcc cgc tgc gtc ctg ctg gag gtg caa gtg 612
 Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val
 110 115 120
 cct gct gcc ctt gtg cag ttt ggt cag tct gtg ggc tct gtg gta tat 660
 Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
 125 130 135 140
 gac tgc ttc gag gct gcc cta ggg agt gag gta cga atc tgg tcc tat 708
 Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
 145 150 155
 act cag ccc agg tac gag aag gaa ctc aac cac aca cag cag ctg cct 756

Thr	Gln	Pro	Arg	Tyr	Glu	Lys	Glu	Leu	Asn	His	Thr	Gln	Gln	Leu	Pro	
			160					165					170			
gac	tgc	agg	ggg	ctc	gaa	gtc	tgg	aac	agc	atc	ccg	agc	tgc	tgg	gcc	804
Asp	Cys	Arg	Gly	Leu	Glu	Val	Trp	Asn	Ser	Ile	Pro	Ser	Cys	Trp	Ala	
		175					180					185				
ctg	ccc	tgg	ctc	aac	gtg	tca	gca	gat	ggg	gac	aac	gtg	cat	ctg	gtt	852
Leu	Pro	Trp	Leu	Asn	Val	Ser	Ala	Asp	Gly	Asp	Asn	Val	His	Leu	Val	
	190					195					200					
ctg	aat	gtc	tct	gag	gag	cag	cac	ttc	ggc	ctc	tcc	ctg	tac	tgg	aat	900
Leu	Asn	Val	Ser	Glu	Glu	Gln	His	Phe	Gly	Leu	Ser	Leu	Tyr	Trp	Asn	
205				210					215						220	
cag	gtc	cag	ggc	ccc	cca	aaa	ccc	cgg	tgg	cac	aaa	aac	ctg	act	gga	948
Gln	Val	Gln	Gly	Pro	Pro	Lys	Pro	Arg	Trp	His	Lys	Asn	Leu	Thr	Gly	
			225					230						235		
ccg	cag	atc	att	acc	ttg	aac	cac	aca	gac	ctg	gtt	ccc	tgc	ctc	tgt	996
Pro	Gln	Ile	Ile	Thr	Leu	Asn	His	Thr	Asp	Leu	Val	Pro	Cys	Leu	Cys	
			240					245					250			
att	cag	gtg	tgg	cct	ctg	gaa	cct	gac	tcc	gtt	agg	acg	aac	atc	tgc	1044
Ile	Gln	Val	Trp	Pro	Leu	Glu	Pro	Asp	Ser	Val	Arg	Thr	Asn	Ile	Cys	
		255					260					265				
ccc	ttc	agg	gag	gac	ccc	cgc	gca	cac	cag	aac	ctc	tgg	caa	gcc	gcc	1092
Pro	Phe	Arg	Glu	Asp	Pro	Arg	Ala	His	Gln	Asn	Leu	Trp	Gln	Ala	Ala	
	270					275					280					
cga	ctg	cga	ctg	ctg	acc	ctg	cag	agc	tgg	ctg	ctg	gac	gca	ccg	tgc	1140
Arg	Leu	Arg	Leu	Leu	Thr	Leu	Gln	Ser	Trp	Leu	Leu	Asp	Ala	Pro	Cys	
285				290					295						300	
tgc	ctg	ccc	gca	gaa	gcg	gca	ctg	tgc	tgg	cgg	gct	ccg	ggg	ggg	gac	1188
Ser	Leu	Pro	Ala	Glu	Ala	Ala	Leu	Cys	Trp	Arg	Ala	Pro	Gly	Gly	Asp	
			305					310					315			
ccc	tgc	cag	cca	ctg	gtc	cca	ccg	ctt	tcc	tgg	gag	aat	gtc	act	gtg	1236
Pro	Cys	Gln	Pro	Leu	Val	Pro	Pro	Leu	Ser	Trp	Glu	Asn	Val	Thr	Val	
			320					325					330			
gac	gtg	aac	agc	tgc	gag	aag	ctg	cag	ctg	cag	gag	tgc	ttg	tgg	gct	1284
Asp	Val	Asn	Ser	Ser	Glu	Lys	Leu	Gln	Leu	Gln	Glu	Cys	Leu	Trp	Ala	
		335					340					345				
gac	tcc	ctg	ggg	cct	ctc	aaa	gac	gat	gtg	cta	ctg	ttg	gag	aca	cga	1332
Asp	Ser	Leu	Gly	Pro	Leu	Lys	Asp	Asp	Val	Leu	Leu	Leu	Glu	Thr	Arg	
	350					355					360					
ggc	ccc	cag	gac	aac	aga	tcc	ctc	tgt	gcc	ttg	gaa	ccc	agt	ggc	tgt	1380
Gly	Pro	Gln	Asp	Asn	Arg	Ser	Leu	Cys	Ala	Leu	Glu	Pro	Ser	Gly	Cys	
365				370				375							380	
act	tca	cta	ccc	agc	aaa	gcc	tcc	acg	agg	gca	gct	cgc	ctt	gga	gag	1428
Thr	Ser	Leu	Pro	Ser	Lys	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	Gly	Glu	
			385					390					395			
tac	tta	cta	caa	gac	ctg	cag	tca	ggc	cag	tgt	ctg	cag	cta	tgg	gac	1476

Tyr	Leu	Leu	Gln	Asp	Leu	Gln	Ser	Gly	Gln	Cys	Leu	Gln	Leu	Trp	Asp	
			400					405					410			
gat	gac	ttg	gga	gcg	cta	tgg	gcc	tgc	ccc	atg	gac	aaa	tac	atc	cac	1524
Asp	Asp	Leu	Gly	Ala	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	Tyr	Ile	His	
		415					420					425				
aag	cgc	tgg	gcc	ctc	gtg	tgg	ctg	gcc	tgc	cta	ctc	ttt	gcc	gct	gcg	1572
Lys	Arg	Trp	Ala	Leu	Val	Trp	Leu	Ala	Cys	Leu		Phe	Ala	Ala	Ala	
	430					435					440					
ctt	tcc	ctc	atc	ctc	ctt	ctc	aaa	aag	gat	cac	gcg	aaa	ggg	tgg	ctg	1620
Leu	Ser	Leu	Ile	Leu	Leu	Leu	Lys	Lys	Asp	His	Ala	Lys	Gly	Trp	Leu	
445					450				455						460	
agg	ctc	ttg	aaa	cag	gac	gtc	cgc	tcg	ggg	gcg	gcc	gcc	agg	ggc	cgc	1668
Arg	Leu	Leu	Lys	Gln	Asp	Val	Arg	Ser	Gly	Ala	Ala	Ala	Arg	Gly	Arg	
			465					470					475			
gcg	gct	ctg	ctc	ctc	tac	tca	gcc	gat	gac	tcg	ggt	ttc	gag	cgc	ctg	1716
Ala	Ala	Leu	Leu	Leu	Tyr	Ser	Ala	Asp	Asp	Ser	Gly	Phe	Glu	Arg	Leu	
			480					485				490				
gtg	ggc	gcc	ctg	gcg	tcg	gcc	ctg	tgc	cag	ctg	ccg	ctg	cgc	gtg	gcc	1764
Val	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Cys	Gln	Leu	Pro	Leu	Arg	Val	Ala	
	495					500					505					
gta	gac	ctg	tgg	agc	cgt	cgt	gaa	ctg	agc	gcg	cag	ggg	ccc	gtg	gct	1812
Val	Asp	Leu	Trp	Ser	Arg	Arg	Glu	Leu	Ser	Ala	Gln	Gly	Pro	Val	Ala	
	510					515					520					
tgg	ttt	cac	gcg	cag	cgg	cgc	cag	acc	ctg	cag	gag	ggc	ggc	gtg	gtg	1860
Trp	Phe	His	Ala	Gln	Arg	Arg	Gln	Thr	Leu	Gln	Glu	Gly	Gly	Val	Val	
525					530				535						540	
gtc	ttg	ctc	ttc	tct	ccc	ggt	gcg	gtg	gcg	ctg	tgc	agc	gag	tgg	cta	1908
Val	Leu	Leu	Phe	Ser	Pro	Gly	Ala	Val	Ala	Leu	Cys	Ser	Glu	Trp	Leu	
			545					550					555			
cag	gat	ggg	gtg	tcc	ggg	ccc	ggg	gcg	cac	ggc	ccg	cac	gac	gcc	ttc	1956
Gln	Asp	Gly	Val	Ser	Gly	Pro	Gly	Ala	His	Gly	Pro	His	Asp	Ala	Phe	
		560					565					570				
cgc	gcc	tcg	ctc	agc	tgc	gtg	ctg	ccc	gac	ttc	ttg	cag	ggc	cgg	gcg	2004
Arg	Ala	Ser	Leu	Ser	Cys	Val	Leu	Pro	Asp	Phe	Leu	Gln	Gly	Arg	Ala	
		575				580						585				
ccc	ggc	agc	tac	gtg	ggg	gcc	tgc	ttc	gac	agg	ctg	ctc	cac	ccg	gac	2052
Pro	Gly	Ser	Tyr	Val	Gly	Ala	Cys	Phe	Asp	Arg	Leu	Leu	His	Pro	Asp	
	590					595					600					
gcc	gta	ccc	gcc	ctt	ttc	cgc	acc	gtg	ccc	gtc	ttc	aca	ctg	ccc	tcc	2100
Ala	Val	Pro	Ala	Leu	Phe	Arg	Thr	Val	Pro	Val	Phe	Thr	Leu	Pro	Ser	
605					610				615						620	
caa	ctg	cca	gac	ttc	ctg	ggg	gcc	ctg	cag	cag	cct	cgc	gcc	ccg	cgt	2148
Gln	Leu	Pro	Asp	Phe	Leu	Gly	Ala	Leu	Gln	Gln	Pro	Arg	Ala	Pro	Arg	
			625					630				635				
tcc	ggg	cgg	ctc	caa	gag	aga	gcg	gag	caa	gtg	tcc	cgg	gcc	ctt	cag	2196

Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln
 640 645 650
 cca gcc ctg gat agc tac ttc cat ccc ccg ggg acn tcc gcg ccg gga 2244
 Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Xaa Ser Ala Pro Gly
 655 660 665
 cgc ggg gtg gga cca ggg gcg gga cct ggg gcg ggg gac ggg act 2289
 Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly Thr
 670 675 680
 taaataaagg cagacgctg 2308

 <210> 8
 <211> 703
 <212> PRT
 <213> Unknown

 <400> 8
 Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser Gln
 -20 -15 -10 -5
 Trp Ile Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala Thr His
 -1 1 5 10
 Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys
 15 20 25
 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
 30 35 40
 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
 45 50 55 60
 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
 65 70 75
 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Leu Gly
 80 85 90
 Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
 95 100 105
 Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val
 110 115 120
 Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
 125 130 135 140
 Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
 145 150 155
 Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro
 160 165 170
 Asp Cys Arg Gly Leu Glu Val Trp Asn Ser Ile Pro Ser Cys Trp Ala
 175 180 185
 Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu Val

190	195	200
Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp Asn 205 210 215 220		
Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr Gly 225 230 235		
Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys 240 245 250		
Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile Cys 255 260 265		
Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala Ala 270 275 280		
Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro Cys 285 290 295 300		
Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly Asp 305 310 315		
Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr Val 320 325 330		
Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp Ala 335 340 345		
Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu Thr Arg 350 355 360		
Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly Cys 365 370 375 380		
Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu 385 390 395		
Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu Trp Asp 400 405 410		
Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His 415 420 425		
Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala 430 435 440		
Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Gly Trp Leu 445 450 455 460		
Arg Leu Leu Lys Gln Asp Val Arg Ser Gly Ala Ala Ala Arg Gly Arg 465 470 475		
Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly Phe Glu Arg Leu 480 485 490		
Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu Pro Leu Arg Val Ala 495 500 505		
Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln Gly Pro Val Ala		

510		515		520	
Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val Val					
525		530		535	540
Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu Cys Ser Glu Trp Leu					
	545		550		555
Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala Phe					
	560		565		570
Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala					
	575		580		585
Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp					
	590		595		600
Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe Thr Leu Pro Ser					
605		610		615	620
Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg					
	625		630		635
Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln					
	640		645		650
Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Xaa Ser Ala Pro Gly					
	655		660		665
Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly Thr					
	670		675		680

<210> 9
 <211> 2109
 <212> DNA
 <213> reverse translation

<220>
 <221> misc_feature
 <222> (1)..(2109)
 <223> n may be a, c, g, or t

<400> 9
 atgccngtnc cntgggttyt nytnwsnytn gcnytnngnm gnwsncartg gathytnwsn 60
 ytnfarmgny tngtnngncc ncargaygen acncaytgyw snccnggnyt nwsntgymgn 120
 ytntgggayw sngayathyt ntgyytncn ggngayathg tncngcncc nggncngtn 180
 ytnngcnccna cncayytnc racngarytn gtnytnmgnt gycaraarga racngaytgy 240
 gayytnatgyy tnmngntngc ngtncaaytn gcngtncaayg gncaytggga rgarcncgar 300
 gaygargara arttyggngg ngcngcngay ytngngntng argarcnmg naaygcwnsn 360
 ytnargcnc argtngtnt nwsnttycar gcntayccna cngcnmgntg ygtnytnytn 420
 gargtnarg tncngcngc nytngtncar ttyggncarw sngtnngnws ngtngtntay 480

gaytgyttyg argcngcny t nggnwsngar gtnmgnatht ggwsntayac ncarccnmgn 540
 taygaraarg arytnaayca yacncarcar ytncngayt gymgnggny t ngargtntgg 600
 aaywsnathc cnwsntgytg ggcnytnccn tgggytnaayg tnwsngcnga yggngayaay 660
 gtncayytng tnytnaaygt nwsngargar carcayttyg gnytnwsnyt ntaytggay 720
 cargtncarg gncncncnaa rccnmgttg cayaaraay tncnggnc ncarathath 780
 acnytnaayc ayacngayyt ngtnccntgy ytntgyathc argtntggcc nytngarccn 840
 gaywsngtnm gnacnaayat htgyccntty mgngargayc cnmgngcnca ycaraayyt 900
 tggcargcng cnmgnytnmg nytnytnacn ytncarwsnt ggytnytna ygcncntgy 960
 wsnytnccng cngargcngc nytnntgytg mgngcncng gngngaycc ntgycarccn 1020
 ytngtnccnc cnytnwsntg ggaraaygt acngtngayg tnaaywsnws ngaraarytn 1080
 carytncarg artgyytn t ggngaywsn ytnggncny tnaargayga ygtynytn 1140
 ytngaracnm gnggncnca rgayaaymgn wsnytnntgy cnytngarcc nwsnggntgy 1200
 acnwsnytn cnwsnaargc nwsnacnmgn gcngcnmgny tngngarta yytnytn car 1260
 gayytn carw snggncartg yytn carytn tgggaygayg ayytnggngc nytnntgggcn 1320
 tgyccnatgg ayaartayat hcayaarmgn tgggcn ytn tntggytngc ntgyytnytn 1380
 ttygcngcng cnytnwsnyt nathytnytn ytnaaraarg ayaygcnaa rggntggytn 1440
 mgytnytna arcargaygt nmgnwsnggn gcngcngcnm gnggmngnc ngcnytnytn 1500
 ytntaywsng cngaygayws nggnttygar mgytngtng gngcnytnge nwsngcnytn 1560
 tgy carytn cnytnmgnt ngcngtngay ytntggwsnm gnmngaryt nwsngcncar 1620
 gngcngtng cntggttyca ygcncarmgn mgncaracny tncargargg ngngtngtn 1680
 gtnytnytn tywsncngg ngcngtngcn ytntgywsng artggytnca rgayggngtn 1740
 wsnggncng gngcncaygg nccncaygay gcnttymng cnwsnytnws ntgyytnytn 1800
 ccngaytty tncarggnmg ngcncnggn wsntaygtng gngcntgytt ygaymgytn 1860
 ytncaycngc aygcngtncc ngcnytnnty mgncngtnc cngtnttyac nytnccnwsn 1920
 carytnccngc ayttyytngg ngcnytn car carccnmng cncnmgnws nggmngnytn 1980
 cargarmng cngarcargt nwsnmngcn ytncarccng cnytngayws ntayttyay 2040
 ccncnggna cnwsngcnc nggmngngn gtnggncng gngcnggnc ngngcnggn 2100
 gayggnacn 2109

<210> 10
 <211> 2314
 <212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:rodent; surmised
Mus musculus

<220>

<221> CDS

<222> (199)..(2292)

<220>

<221> mat_peptide

<222> (259)..(2292)

<400> 10

```

ccaaatcgaa agcacgggag ctgatactgg gcctggagtc caggctcact ggagtgggga 60

agcatggctg gagaggaatt ctagcccttg ctctctccca gggacacggg gctgattgtc 120

agcagggggcg aggggtctgc ccccccttgg gggggcagga cggggcctca ggcttgggtg 180

ctgtccggca cctggaag atg cct gtg tcc tgg ttc ctg ctg tcc ttg gca 231
          Met Pro Val Ser Trp Phe Leu Leu Ser Leu Ala
          -20                               -15               -10

ctg ggc cga aac cct gtg gtc gtc tct ctg gag aga ctg atg gag cct 279
Leu Gly Arg Asn Pro Val Val Val Ser Leu Glu Arg Leu Met Glu Pro
          -5                               -1    1               5

cag gac act gca cgc tgc tct cta ggc ctc tcc tgc cac ctc tgg gat 327
Gln Asp Thr Ala Arg Cys Ser Leu Gly Leu Ser Cys His Leu Trp Asp
          10                               15               20

ggg gac gtg ctc tgc ctg cct gga agc ctc cag tct gcc cca ggc cct 375
Gly Asp Val Leu Cys Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro
          25                               30               35

gtg cta gtg cct acc cgc ctg cag acg gag ctg gtg ctg agg tgt oca 423
Val Leu Val Pro Thr Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro
          40                               45               50               55

cag aag aca gat tgc gcc ctc tgt gtc cgt gtg gtg gtc cac ttg gcc 471
Gln Lys Thr Asp Cys Ala Leu Cys Val Arg Val Val Val His Leu Ala
          60                               65               70

gtg cat ggg cac tgg gca gag cct gaa gaa gct gga aag tct gat tca 519
Val His Gly His Trp Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser
          75                               80               85

gaa ctc cag gag tct agg aac gcc tct ctc cag gcc cag gtg gtg ctc 567
Glu Leu Gln Glu Ser Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu
          90                               95               100

tcc ttc cag gcc tac ccc atc gcc cgc tgt gcc ctg ctg gag gtc cag 615
Ser Phe Gln Ala Tyr Pro Ile Ala Arg Cys Ala Leu Leu Glu Val Gln
          105                               110               115

gtg ccc gct gac ctg gtg cag cct ggt cag tcc gtg ggt tct gcg gta 663
Val Pro Ala Asp Leu Val Gln Pro Gly Gln Ser Val Gly Ser Ala Val
          120                               125               130               135

```

ttt gac tgt ttc gag gct agt ctt ggg gct gag gta cag atc tgg tcc	711
Phe Asp Cys Phe Glu Ala Ser Leu Gly Ala Glu Val Gln Ile Trp Ser	
140 145 150	
tac acg aag ccc agg tac cag aaa gag ctc aac ctc aca cag cag ctg	759
Tyr Thr Lys Pro Arg Tyr Gln Lys Glu Leu Asn Leu Thr Gln Gln Leu	
155 160 165	
cct gac tgc agg ggt ctt gaa gtc cgg gac agc atc cag agc tgc tgg	807
Pro Asp Cys Arg Gly Leu Glu Val Arg Asp Ser Ile Gln Ser Cys Trp	
170 175 180	
gtc ctg ccc tgg ctc aat gtg tct aca gat ggt gac aat gtc ctt ctg	855
Val Leu Pro Trp Leu Asn Val Ser Thr Asp Gly Asp Asn Val Leu Leu	
185 190 195	
aca ctg gat gtc tct gag gag cag gac ttt agc ttc tta ctg tac ctg	903
Thr Leu Asp Val Ser Glu Glu Gln Asp Phe Ser Phe Leu Leu Tyr Leu	
200 205 210 215	
cgt cca gtc ccg gat gct ctc aaa tcc ttg tgg tac aaa aac ctg act	951
Arg Pro Val Pro Asp Ala Leu Lys Ser Leu Trp Tyr Lys Asn Leu Thr	
220 225 230	
gga cct cag aac att act tta aac cac aca gac ctg gtt ccc tgc ctc	999
Gly Pro Gln Asn Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu	
235 240 245	
tgc att cag gtg tgg tcg cta gag cca gac tct gag agg gtc gaa ttc	1047
Cys Ile Gln Val Trp Ser Leu Glu Pro Asp Ser Glu Arg Val Glu Phe	
250 255 260	
tgc ccc ttc ccg gaa gat ccc ggt gca cac agg aac ctc tgg cac ata	1095
Cys Pro Phe Arg Glu Asp Pro Gly Ala His Arg Asn Leu Trp His Ile	
265 270 275	
gcc agg ctg ccg gta ctg tcc cca ggg gta tgg cag cta gat gcg cct	1143
Ala Arg Leu Arg Val Leu Ser Pro Gly Val Trp Gln Leu Asp Ala Pro	
280 285 290 295	
tgc tgt ctg ccg ggc aag gta aca ctg tgc tgg cag gca cca gac cag	1191
Cys Cys Leu Pro Gly Lys Val Thr Leu Cys Trp Gln Ala Pro Asp Gln	
300 305 310	
agt ccc tgc cag cca ctt gtg cca cca gtg ccc cag aag aac gcc act	1239
Ser Pro Cys Gln Pro Leu Val Pro Pro Val Pro Gln Lys Asn Ala Thr	
315 320 325	
gtg aat gag cca caa gat ttc cag ttg gtg gca ggc cac ccc aac ctc	1287
Val Asn Glu Pro Gln Asp Phe Gln Leu Val Ala Gly His Pro Asn Leu	
330 335 340	
tgt gtc cag gtg agc acc tgg gag aag gtt cag ctg caa gcg tgc ttg	1335
Cys Val Gln Val Ser Thr Trp Glu Lys Val Gln Leu Gln Ala Cys Leu	
345 350 355	
tgg gct gac tcc ttg ggg ccc ttc aag gat gat atg ctg tta gtg gag	1383
Trp Ala Asp Ser Leu Gly Pro Phe Lys Asp Asp Met Leu Leu Val Glu	
360 365 370 375	

atg	aaa	acc	ggc	ctc	aac	aac	aca	tca	gtc	tgt	gcc	ttg	gaa	ccc	agt	1431
Met	Lys	Thr	Gly	Leu	Asn	Asn	Thr	Ser	Val	Cys	Ala	Leu	Glu	Pro	Ser	
				380					385					390		
ggc	tgt	aca	cca	ctg	ccc	agc	atg	gcc	tcc	acg	aga	gct	gct	cgc	ctg	1479
Gly	Cys	Thr	Pro	Leu	Pro	Ser	Met	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	
			395					400					405			
gga	gag	gag	ttg	ctg	caa	gac	ttc	cga	tca	cac	cag	tgt	atg	cag	ctg	1527
Gly	Glu	Glu	Leu	Leu	Gln	Asp	Phe	Arg	Ser	His	Gln	Cys	Met	Gln	Leu	
			410				415					420				
tgg	aac	gat	gac	aac	atg	gga	tcg	cta	tgg	gcc	tgc	ccc	atg	gac	aag	1575
Trp	Asn	Asp	Asp	Asn	Met	Gly	Ser	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	
	425					430					435					
tac	atc	cac	agg	cgc	tgg	gtc	cta	gta	tgg	ctg	gcc	tgc	cta	ctc	ttg	1623
Tyr	Ile	His	Arg	Arg	Trp	Val	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Leu	
440					445					450					455	
gct	gcg	gcg	ctt	ttc	ttc	ttc	ctc	ctt	cta	aaa	aag	gac	cgc	agg	aaa	1671
Ala	Ala	Ala	Leu	Phe	Phe	Phe	Leu	Leu	Leu	Lys	Lys	Asp	Arg	Arg	Lys	
				460					465					470		
gcg	gcc	cgt	ggc	tcc	cgc	acg	gcc	ttg	ctc	ctc	cac	tcc	gcc	gac	gga	1719
Ala	Ala	Arg	Gly	Ser	Arg	Thr	Ala	Leu	Leu	Leu	His	Ser	Ala	Asp	Gly	
			475					480					485			
gcg	ggc	tac	gag	cgc	ctg	gtg	gga	gca	ctg	gcg	tcc	gcg	ttg	agc	cag	1767
Ala	Gly	Tyr	Glu	Arg	Leu	Val	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Ser	Gln	
		490					495					500				
atg	cca	ctg	cgc	gtg	gcc	gtg	gac	ctg	tgg	agc	cgc	cgc	gag	ctg	agc	1815
Met	Pro	Leu	Arg	Val	Ala	Val	Asp	Leu	Trp	Ser	Arg	Arg	Glu	Leu	Ser	
	505					510					515					
gcg	cac	gga	gcc	cta	gcc	tgg	ttc	cac	cac	cag	cga	cgc	cgt	atc	ctg	1863
Ala	His	Gly	Ala	Leu	Ala	Trp	Phe	His	His	Gln	Arg	Arg	Arg	Ile	Leu	
520					525					530					535	
cag	gag	ggt	ggc	gtg	gta	atc	ctt	ctc	ttc	tcg	ccc	gcg	gcc	gtg	gcg	1911
Gln	Glu	Gly	Gly	Val	Val	Ile	Leu	Leu	Phe	Ser	Pro	Ala	Ala	Val	Ala	
				540					545					550		
cag	tgt	cag	cag	tgg	ctg	cag	ctc	cag	aca	gtg	gag	ccc	ggg	ccg	cat	1959
Gln	Cys	Gln	Gln	Trp	Leu	Gln	Leu	Gln	Thr	Val	Glu	Pro	Gly	Pro	His	
			555					560					565			
gac	gcc	ctc	gcc	gcc	tgg	ctc	agc	tgc	gtg	cta	ccc	gat	ttc	ctg	caa	2007
Asp	Ala	Leu	Ala	Ala	Trp	Leu	Ser	Cys	Val	Leu	Pro	Asp	Phe	Leu	Gln	
			570				575					580				
ggc	cgg	gcg	acc	ggc	cgc	tac	gtc	ggg	gtc	tac	ttc	gac	ggg	ctg	ctg	2055
Gly	Arg	Ala	Thr	Gly	Arg	Tyr	Val	Gly	Val	Tyr	Phe	Asp	Gly	Leu	Leu	
	585					590					595					
cac	cca	gac	tct	gtg	ccc	tcc	ccg	ttc	cgc	gtc	gcc	ccg	ctc	ttc	tcc	2103
His	Pro	Asp	Ser	Val	Pro	Ser	Pro	Phe	Arg	Val	Ala	Pro	Leu	Phe	Ser	
600					605					610					615	

```

ctg ccc tcg cag ctg ccg gct ttc ctg gat gca ctg cag gga ggc tgc 2151
Leu Pro Ser Gln Leu Pro Ala Phe Leu Asp Ala Leu Gln Gly Gly Cys
        620                625                630

tcc act tcc gcg ggg cga ccc gcg gac cgg gtg gaa cga gtg acc cag 2199
Ser Thr Ser Ala Gly Arg Pro Ala Asp Arg Val Glu Arg Val Thr Gln
        635                640                645

gcg ctg cgg tcc gcc ctg gac agc tgt act tct agc tcg gaa gcc cca 2247
Ala Leu Arg Ser Ala Leu Asp Ser Cys Thr Ser Ser Ser Glu Ala Pro
        650                655                660

ggc tgc tgc gag gaa tgg gac ctg gga ccc tgc act aca cta gaa 2292
Gly Cys Cys Glu Glu Trp Asp Leu Gly Pro Cys Thr Thr Leu Glu
        665                670                675

taaaagccga tacagtattc ct 2314

```

```

<210> 11
<211> 698
<212> PRT
<213> Unknown

```

```

<400> 11

```

```

Met Pro Val Ser Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Asn Pro
-20                -15                -10                -5

Val Val Val Ser Leu Glu Arg Leu Met Glu Pro Gln Asp Thr Ala Arg
        -1      1                5                10

Cys Ser Leu Gly Leu Ser Cys His Leu Trp Asp Gly Asp Val Leu Cys
        15                20                25

Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro Val Leu Val Pro Thr
        30                35                40

Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro Gln Lys Thr Asp Cys
        45                50                55                60

Ala Leu Cys Val Arg Val Val Val His Leu Ala Val His Gly His Trp
        65                70                75

Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser Glu Leu Gln Glu Ser
        80                85                90

Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser Phe Gln Ala Tyr
        95                100                105

Pro Ile Ala Arg Cys Ala Leu Leu Glu Val Gln Val Pro Ala Asp Leu
        110                115                120

Val Gln Pro Gly Gln Ser Val Gly Ser Ala Val Phe Asp Cys Phe Glu
        125                130                135                140

Ala Ser Leu Gly Ala Glu Val Gln Ile Trp Ser Tyr Thr Lys Pro Arg
        145                150                155

Tyr Gln Lys Glu Leu Asn Leu Thr Gln Gln Leu Pro Asp Cys Arg Gly

```

160					165					170					
Leu	Glu	Val	Arg	Asp	Ser	Ile	Gln	Ser	Cys	Trp	Val	Leu	Pro	Trp	Leu
		175					180					185			
Asn	Val	Ser	Thr	Asp	Gly	Asp	Asn	Val	Leu	Leu	Thr	Leu	Asp	Val	Ser
	190					195					200				
Glu	Glu	Gln	Asp	Phe	Ser	Phe	Leu	Leu	Tyr	Leu	Arg	Pro	Val	Pro	Asp
205					210					215					220
Ala	Leu	Lys	Ser	Leu	Trp	Tyr	Lys	Asn	Leu	Thr	Gly	Pro	Gln	Asn	Ile
				225					230					235	
Thr	Leu	Asn	His	Thr	Asp	Leu	Val	Pro	Cys	Leu	Cys	Ile	Gln	Val	Trp
			240					245					250		
Ser	Leu	Glu	Pro	Asp	Ser	Glu	Arg	Val	Glu	Phe	Cys	Pro	Phe	Arg	Glu
		255					260					265			
Asp	Pro	Gly	Ala	His	Arg	Asn	Leu	Trp	His	Ile	Ala	Arg	Leu	Arg	Val
	270					275					280				
Leu	Ser	Pro	Gly	Val	Trp	Gln	Leu	Asp	Ala	Pro	Cys	Cys	Leu	Pro	Gly
285					290					295					300
Lys	Val	Thr	Leu	Cys	Trp	Gln	Ala	Pro	Asp	Gln	Ser	Pro	Cys	Gln	Pro
				305					310					315	
Leu	Val	Pro	Pro	Val	Pro	Gln	Lys	Asn	Ala	Thr	Val	Asn	Glu	Pro	Gln
			320					325					330		
Asp	Phe	Gln	Leu	Val	Ala	Gly	His	Pro	Asn	Leu	Cys	Val	Gln	Val	Ser
		335					340					345			
Thr	Trp	Glu	Lys	Val	Gln	Leu	Gln	Ala	Cys	Leu	Trp	Ala	Asp	Ser	Leu
	350					355					360				
Gly	Pro	Phe	Lys	Asp	Asp	Met	Leu	Leu	Val	Glu	Met	Lys	Thr	Gly	Leu
365					370					375					380
Asn	Asn	Thr	Ser	Val	Cys	Ala	Leu	Glu	Pro	Ser	Gly	Cys	Thr	Pro	Leu
				385					390					395	
Pro	Ser	Met	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	Gly	Glu	Glu	Leu	Leu
			400					405					410		
Gln	Asp	Phe	Arg	Ser	His	Gln	Cys	Met	Gln	Leu	Trp	Asn	Asp	Asp	Asn
		415					420					425			
Met	Gly	Ser	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	Tyr	Ile	His	Arg	Arg
	430					435					440				
Trp	Val	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Ala	Ala	Leu	Phe
445					450					455					460
Phe	Phe	Leu	Leu	Leu	Lys	Lys	Asp	Arg	Arg	Lys	Ala	Ala	Arg	Gly	Ser
				465					470					475	
Arg	Thr	Ala	Leu	Leu	Leu	His	Ser	Ala	Asp	Gly	Ala	Gly	Tyr	Glu	Arg

480				485				490							
Leu	Val	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Ser	Gln	Met	Pro	Leu	Arg	Val
		495					500					505			
Ala	Val	Asp	Leu	Trp	Ser	Arg	Arg	Glu	Leu	Ser	Ala	His	Gly	Ala	Leu
		510				515					520				
Ala	Trp	Phe	His	His	Gln	Arg	Arg	Arg	Ile	Leu	Gln	Glu	Gly	Gly	Val
		525			530					535					540
Val	Ile	Leu	Leu	Phe	Ser	Pro	Ala	Ala	Val	Ala	Gln	Cys	Gln	Gln	Trp
			545						550					555	
Leu	Gln	Leu	Gln	Thr	Val	Glu	Pro	Gly	Pro	His	Asp	Ala	Leu	Ala	Ala
			560						565				570		
Trp	Leu	Ser	Cys	Val	Leu	Pro	Asp	Phe	Leu	Gln	Gly	Arg	Ala	Thr	Gly
		575					580					585			
Arg	Tyr	Val	Gly	Val	Tyr	Phe	Asp	Gly	Leu	Leu	His	Pro	Asp	Ser	Val
		590				595					600				
Pro	Ser	Pro	Phe	Arg	Val	Ala	Pro	Leu	Phe	Ser	Leu	Pro	Ser	Gln	Leu
					610					615					620
Pro	Ala	Phe	Leu	Asp	Ala	Leu	Gln	Gly	Gly	Cys	Ser	Thr	Ser	Ala	Gly
			625						630					635	
Arg	Pro	Ala	Asp	Arg	Val	Glu	Arg	Val	Thr	Gln	Ala	Leu	Arg	Ser	Ala
			640						645				650		
Leu	Asp	Ser	Cys	Thr	Ser	Ser	Ser	Glu	Ala	Pro	Gly	Cys	Cys	Glu	Glu
		655					660					665			
Trp	Asp	Leu	Gly	Pro	Cys	Thr	Thr	Leu	Glu						
		670				675									

<210> 12

<211> 2094

<212> DNA

<213> reverse translation

<220>

<221> misc_feature

<222> (1)..(2094)

<223> n may be a, c, g, or t

<400> 12

atgccngtnw sntgggttyt nytnwsnytn gcnytnngnm gnaayccngt ngtnngtnwsn 60

ytngarmgny tnatggarcc ncargayacn gcnmgntgyw snytnnggnyt nwsntgy cay 120

ytntggggyg gngaygtnyt ntgyytnccn ggnwsnytn arwsngcncc nggnccngtn 180

ytngtnccna cnmgnytnca racngarytn gtnytnmgnt gycncaraa racngaytgy 240

gcnytnatgyg tnmngntngt ngtncayytn gcngtncaayg gncaytgggc ngarccngar 300

gargcnggna arwsngayws ngarytnicar garwsnmgna aygcnwsnyt ncargcncar 360
 gtngtynytnw snttycargc ntayccnath gcnmgntgyg cnytnytnga rgtncargtn 420
 ccngcngayy tngtncarcc nggncarwsn gtnggnwsng cngtnttyga ytgyttygar 480
 gcnwsnytnng gngcngargt ncarathtgg wsntayacna arccnmgnta ycaraargar 540
 ytnaayytna cncarcaryt nccngaytgy mgnggnytnng argtnmgnga ywsnathcar 600
 wsntgytggg tnytnccntg gytnaaygt nwsnacngayg gngayaaygt nytnytnacn 660
 ytngaygt nwsngargar rgtayttywsn ttyytnytnt ayytnmgnc ngtnccngay 720
 gcnytnaarw snytnntggta yaaraayytn acnggnccnc araayathac nytnaaycay 780
 acngayytnng tnccntgyyt ntgyathcar gtntggwsny tngarccnga ywsngarmgn 840
 gtngarttyt gyccnttymg ngargayccn ggngcncaym gnaayytntg gcayathgcn 900
 mgnytnmgng tnytnwsncc ngngntntgg carytngayg cncntgytg yytnccnggn 960
 aargtnacny tntgytggca rgncncngay carwsnccnt gycarccnyt ngtnccnccn 1020
 gtncncara araaygcnc ngtnaaygar ccncargayt tycarytngt ngcnggncay 1080
 ccnaayytnt gygtncargt nwsnacntgg garaargtnc arytncargc ntgyytnntgg 1140
 gcngaywsny tnggnccntt yaargaygay atgytnytng tngaratgaa racnggnytn 1200
 aayaayacnw sngtntgygc nytngarccn wsnggntgya cncnytncc nwsnatggcn 1260
 wsnacnmng cngcnmgnyt ngngargar ytnytncarg ayttymgnws ncaycartgy 1320
 atgcarytn ggaaygayga yaayatgggn wsnytnntgg cntgyccnat ggayaartay 1380
 athcaymgm gntgggtnyt ngtnntgytn gcntgyytny tnytnngcngc ngcnytnntty 1440
 ttyttyytny tnytnaaraa rgaymgmgn aargcngcnm gnggnwsnmg nacngcnytn 1500
 ytnytnacayw sngcngaygg ngcnggntay garmgnytnng tnggngcnytn ngcnwsngcn 1560
 ytnwsncara tgccnytnmg ngtnngcngtn gayytnntggw snmgngmnga rytnwsngcn 1620
 cayggngcny tngcntggtt ycaycaycar mgnmgmngna thytncarga rggnggngtn 1680
 gtnathytny tnttywsncc ngcngcngtn gcncartgyc arcartggyt ncarytnicar 1740
 acngtnarc cnggnccnca ygaygcnyn gngcngtgyt tnwsntgygt nytnccngay 1800
 ttyytncarg gnmngcncac ngngmngntay gtngngntnt aytygaygg nytnytnacay 1860
 ccngaywsng tnccnwsncc nttymgngtn gcncnytnnt tywsnytncc nwsncarytn 1920
 ccngcnttyy tngaygcnyn ncarggnggn tgywsnacnw sngcnggnmg nccngcngay 1980
 mgngtnarm gngtnacnca rgcnymngn wsngcnytnng aywsntgyac nwsnwsnwsn 2040
 gargcncng gntgytgyga rgartgggay ytnngnccnt gyacnacnytn ngar 2094

<210> 13
 <211> 2786
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism: primate; surmised
 Homo sapiens

<220>
 <221> CDS
 <222> (70)..(2283)

<220>
 <221> mat_peptide
 <222> (118)..(2283)

<220>
 <221> misc_feature
 <222> (9)..(134)
 <223> Xaa translation (9, 18, 26, 109, 120, 134) depends
 on genetic code

<400> 13
 cccacgcntc cgggccagca gcgggcggcc ggggcgcaga gaacggcctg gctgggcgag 60
 cgacacggcc atg gcc ccg tgg ctg cag ctc tgc tcc gtc ttc ttt acg gtc 111
 Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val
 -15 -10 -5
 aac gcc tgc ctc aac ggc tcg cag ctg gct gtn gcc gct ggc ggg tcc 159
 Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Xaa Ala Ala Gly Gly Ser
 -1 1 5 10
 ggc cgc gcg cng ggc gcc gac acc tgt agc tgg ang gga gtg ggg cca 207
 Gly Arg Ala Xaa Gly Ala Asp Thr Cys Ser Trp Xaa Gly Val Gly Pro
 15 20 25 30
 gcc agc aga aac agt ggg ctg tac aac atc acc ttc aaa tat gac aat 255
 Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn
 35 40 45
 tgt acc acc tac ttg aat cca gtg ggg aag cat gtg att gct gac gcc 303
 Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala
 50 55 60
 cag aat atc acc atc agc cag tat gct tgc cat gac caa gtg gca gtc 351
 Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val
 65 70 75
 acc att ctt tgg tcc cca ggg gcc ctc ggc atc gaa ttc ctg aaa gga 399
 Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly
 80 85 90
 ttt cgg gta ata ctg gag gag ctg aag tcg gag gga aga cag ngc caa 447
 Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Xaa Gln
 95 100 105 110
 caa ctg att cta aag gat ccg aag cag ntc aac agt agc ttc aaa aga 495

Gln	Leu	Ile	Leu	Lys	Asp	Pro	Lys	Gln	Xaa	Asn	Ser	Ser	Phe	Lys	Arg	
				115					120					125		
act	gga	atg	gaa	tct	caa	cct	ttn	ctg	aat	atg	aaa	ttt	gaa	acg	gat	543
Thr	Gly	Met	Glu	Ser	Gln	Pro	Xaa	Leu	Asn	Met	Lys	Phe	Glu	Thr	Asp	
			130					135					140			
tat	ttc	gta	agg	ttg	tcc	ttt	tcc	ttc	att	aaa	aac	gaa	agc	aat	tac	591
Tyr	Phe	Val	Arg	Leu	Ser	Phe	Ser	Phe	Ile	Lys	Asn	Glu	Ser	Asn	Tyr	
		145					150					155				
cac	cct	ttc	ttc	ttt	aga	acc	cga	gcc	tgt	gac	ctg	ttg	tta	cag	ccg	639
His	Pro	Phe	Phe	Phe	Arg	Thr	Arg	Ala	Cys	Asp	Leu	Leu	Leu	Gln	Pro	
	160					165					170					
gac	aat	cta	gct	tgt	aaa	ccc	ttc	tgg	aag	cct	cgg	aac	ctg	aac	atc	687
Asp	Asn	Leu	Ala	Cys	Lys	Pro	Phe	Trp	Lys	Pro	Arg	Asn	Leu	Asn	Ile	
175					180					185					190	
agc	cag	cat	ggc	tcg	gac	atg	cag	gtg	tcc	ttc	gac	cac	gca	ccg	cac	735
Ser	Gln	His	Gly	Ser	Asp	Met	Gln	Val	Ser	Phe	Asp	His	Ala	Pro	His	
				195					200					205		
aac	ttc	ggc	ttc	cgt	ttc	ttc	tat	ctt	cac	tac	aag	ctc	aag	cac	gaa	783
Asn	Phe	Gly	Phe	Arg	Phe	Phe	Tyr	Leu	His	Tyr	Lys	Leu	Lys	His	Glu	
			210					215					220			
gga	cct	ttc	aag	cga	aag	acc	tgt	aag	cag	gag	caa	act	aca	gag	atg	831
Gly	Pro	Phe	Lys	Arg	Lys	Thr	Cys	Lys	Gln	Glu	Gln	Thr	Thr	Glu	Met	
		225				230						235				
acc	agc	tgc	ctc	ctt	caa	aat	gtt	tct	cca	ggg	gat	tat	ata	att	gag	879
Thr	Ser	Cys	Leu	Leu	Gln	Asn	Val	Ser	Pro	Gly	Asp	Tyr	Ile	Ile	Glu	
	240					245					250					
ctg	gtg	gat	gac	act	aac	aca	aca	aga	aaa	gtg	atg	cat	tat	gcc	tta	927
Leu	Val	Asp	Asp	Thr	Asn	Thr	Thr	Arg	Lys	Val	Met	His	Tyr	Ala	Leu	
255					260					265					270	
aag	cca	gtg	cac	tcc	ccg	tgg	gcc	ggg	ccc	atc	aga	gcc	gtg	gcc	atc	975
Lys	Pro	Val	His	Ser	Pro	Trp	Ala	Gly	Pro	Ile	Arg	Ala	Val	Ala	Ile	
				275					280					285		
aca	gtg	cca	ctg	gta	gtc	ata	tcg	gca	ttc	gcg	acg	ctc	ttc	act	gtg	1023
Thr	Val	Pro	Leu	Val	Val	Ile	Ser	Ala	Phe	Ala	Thr	Leu	Phe	Thr	Val	
			290					295					300			
atg	tgc	cgc	aag	aag	caa	caa	gaa	aat	ata	tat	tca	cat	tta	gat	gaa	1071
Met	Cys	Arg	Lys	Lys	Gln	Gln	Glu	Asn	Ile	Tyr	Ser	His	Leu	Asp	Glu	
		305					310					315				
gag	agc	tct	gag	tct	tcc	aca	tac	act	gca	gca	ctc	cca	aga	gag	agg	1119
Glu	Ser	Ser	Glu	Ser	Ser	Thr	Tyr	Thr	Ala	Ala	Leu	Pro	Arg	Glu	Arg	
		320				325					330					
ctc	cgg	ccg	cgg	ccg	aag	gtc	ttt	ctc	tgc	tat	tcc	agt	aaa	gat	ggc	1167
Leu	Arg	Pro	Arg	Pro	Lys	Val	Phe	Leu	Cys	Tyr	Ser	Ser	Lys	Asp	Gly	
335					340				345					350		
cag	aat	cac	atg	aat	gtc	gtc	cag	tgt	ttc	gcc	tac	ttc	ctc	cag	gac	1215

Gln	Asn	His	Met	Asn	Val	Val	Gln	Cys	Phe	Ala	Tyr	Phe	Leu	Gln	Asp		
				355					360					365			
ttc	tgt	ggc	tgt	gag	gtg	gct	ctg	gac	ctg	tgg	gaa	gac	ttc	agc	ctc	1263	
Phe	Cys	Gly	Cys	Glu	Val	Ala	Leu	Asp	Leu	Trp	Glu	Asp	Phe	Ser	Leu		
			370					375					380				
tgt	aga	gaa	ggg	cag	aga	gaa	tgg	gtc	atc	cag	aag	atc	cac	gag	tcc	1311	
Cys	Arg	Glu	Gly	Gln	Arg	Glu	Trp	Val	Ile	Gln	Lys	Ile	His	Glu	Ser		
		385					390					395					
cag	ttc	atc	att	gtg	gtt	tgt	tcc	aaa	ggg	atg	aag	tac	ttt	gtg	gac	1359	
Gln	Phe	Ile	Ile	Val	Val	Cys	Ser	Lys	Gly	Met	Lys	Tyr	Phe	Val	Asp		
	400					405					410						
aag	aag	aac	tac	aaa	cac	aaa	gga	ggg	ggc	cga	ggc	tcg	ggg	aaa	gga	1407	
Lys	Lys	Asn	Tyr	Lys	His	Lys	Gly	Gly	Gly	Arg	Gly	Ser	Gly	Lys	Gly		
415					420				425						430		
gag	ctc	ttc	ctg	gtg	gcg	gtg	tca	gcc	att	gcc	gaa	aag	ctc	cgc	cag	1455	
Glu	Leu	Phe	Leu	Val	Ala	Val	Ser	Ala	Ile	Ala	Glu	Lys	Leu	Arg	Gln		
				435				440						445			
gcc	aag	cag	agt	tcg	tcc	gcg	gcg	ctc	agc	aag	ttt	atc	gcc	gtc	tac	1503	
Ala	Lys	Gln	Ser	Ser	Ser	Ala	Ala	Leu	Ser	Lys	Phe	Ile	Ala	Val	Tyr		
			450					455					460				
ttt	gat	tat	tcc	tgc	gag	gga	gac	gtc	ccc	ggg	atc	cta	gac	ctg	agt	1551	
Phe	Asp	Tyr	Ser	Cys	Glu	Gly	Asp	Val	Pro	Gly	Ile	Leu	Asp	Leu	Ser		
		465					470					475					
acc	aag	tac	aga	ctc	atg	gac	aat	ctt	cct	cag	ctc	tgt	tcc	cac	ctg	1599	
Thr	Lys	Tyr	Arg	Leu	Met	Asp	Asn	Leu	Pro	Gln	Leu	Cys	Ser	His	Leu		
	480					485					490						
cac	tcc	cga	gac	cac	ggc	ctc	cag	gag	ccg	ggg	cag	cac	acg	cga	cag	1647	
His	Ser	Arg	Asp	His	Gly	Leu	Gln	Glu	Pro	Gly	Gln	His	Thr	Arg	Gln		
495					500					505					510		
ggc	agc	aga	agg	aac	tac	ttc	cgg	agc	aag	tca	ggc	cgg	tcc	cta	tac	1695	
Gly	Ser	Arg	Arg	Asn	Tyr	Phe	Arg	Ser	Lys	Ser	Gly	Arg	Ser	Leu	Tyr		
				515					520					525			
gtc	gcc	att	tgc	aac	atg	cac	cag	ttt	att	gac	gag	gag	ccc	gac	tgg	1743	
Val	Ala	Ile	Cys	Asn	Met	His	Gln	Phe	Ile	Asp	Glu	Glu	Pro	Asp	Trp		
			530					535					540				
ttc	gaa	aag	cag	ttc	gtt	ccc	ttc	cat	cct	cct	cca	ctg	cgc	tac	cgg	1791	
Phe	Glu	Lys	Gln	Phe	Val	Pro	Phe	His	Pro	Pro	Pro	Leu	Arg	Tyr	Arg		
		545					550					555					
gag	cca	gtc	ttg	gag	aaa	ttt	gat	tcg	ggc	ttg	gtt	tta	aat	gat	gtc	1839	
Glu	Pro	Val	Leu	Glu	Lys	Phe	Asp	Ser	Gly	Leu	Val	Leu	Asn	Asp	Val		
	560					565					570						
atg	tgc	aaa	cca	ggg	cct	gag	agt	gac	ttc	tgc	cta	aag	gta	gag	gcg	1887	
Met	Cys	Lys	Pro	Gly	Pro	Glu	Ser	Asp	Phe	Cys	Leu	Lys	Val	Glu	Ala		
575					580					585					590		
gct	gtt	ctt	ggg	gca	acc	gga	cca	gcc	gac	tcc	cag	cac	gag	agt	cag	1935	

Ala Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln
595 600 605

cat ggg ggc ctg gac caa gac ggg gag gcc cgg cct gcc ctt gac ggt 1983
His Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly
610 615 620

agc gcc gcc ctg caa ccc ctg ctg cac acg gtg aaa gcc ggc agc ccc 2031
Ser Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro
625 630 635

tcg gac atg ccg cgg gac tca ggc atc tat gac tcg tct gtg ccc tca 2079
Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser
640 645 650

tcc gag ctg tct ctg cca ctg atg gaa gga ctc tcg acg gac cag aca 2127
Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr
655 660 665 670

gaa acg tct tcc ctg acg gag agc gtg tcc tcc tct tca ggc ctg ggt 2175
Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly
675 680 685

gag gag gaa cct cct gcc ctt cct tcc aag ctc ctc tct tct ggg tca 2223
Glu Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser
690 695 700

tgc aaa gca gat ctt ggt tgc cgc agc tac act gat gaa ctc cac gcg 2271
Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala
705 710 715

gtc gcc cct ttg taacaaaacg aaagagtcta agcattgcc ctttagctgc 2323
Val Ala Pro Leu
720

tgctccctc tgattcccca gctcatctcc ctggttgcat ggcccacttg gagctgaggt 2383

ctcatacaag gatatttgga gtgaaatgct ggccagtact tgttctccct tgccccaacc 2443

ctttaccgga tatcttgaca aactctccaa ttttctaaaa tgatatggag ctctgaaagg 2503

catgtccata aggtctgaca acagcttgcc aaatttggtt agtccttgga tcagagcctg 2563

ttgtggggagg tagggaggaa atatgtaaag aaaaacagga agatacctgc actaatcatt 2623

cagacttcat tgagctctgc aaactttgcc tgtttgctat tggctacctt gatttgaaat 2683

gctttgtgaa aaaaggcact tttaacatca tagccacaga aatcaagtgc cagtctatct 2743

ggaatccatg ttgtattgca gataatgttc tcatttattt ttg 2786

<210> 14
<211> 738
<212> PRT
<213> Unknown

<400> 14
Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val Asn Ala
-15 -10 -5 -1

Cys	Leu	Asn	Gly	Ser	Gln	Leu	Ala	Xaa	Ala	Ala	Gly	Gly	Ser	Gly	Arg	1	5	10	15
Ala	Xaa	Gly	Ala	Asp	Thr	Cys	Ser	Trp	Xaa	Gly	Val	Gly	Pro	Ala	Ser	20	25	30	
Arg	Asn	Ser	Gly	Leu	Tyr	Asn	Ile	Thr	Phe	Lys	Tyr	Asp	Asn	Cys	Thr	35	40	45	
Thr	Tyr	Leu	Asn	Pro	Val	Gly	Lys	His	Val	Ile	Ala	Asp	Ala	Gln	Asn	50	55	60	
Ile	Thr	Ile	Ser	Gln	Tyr	Ala	Cys	His	Asp	Gln	Val	Ala	Val	Thr	Ile	65	70	75	80
Leu	Trp	Ser	Pro	Gly	Ala	Leu	Gly	Ile	Glu	Phe	Leu	Lys	Gly	Phe	Arg	85	90	95	
Val	Ile	Leu	Glu	Glu	Leu	Lys	Ser	Glu	Gly	Arg	Gln	Xaa	Gln	Gln	Leu	100	105	110	
Ile	Leu	Lys	Asp	Pro	Lys	Gln	Xaa	Asn	Ser	Ser	Phe	Lys	Arg	Thr	Gly	115	120	125	
Met	Glu	Ser	Gln	Pro	Xaa	Leu	Asn	Met	Lys	Phe	Glu	Thr	Asp	Tyr	Phe	130	135	140	
Val	Arg	Leu	Ser	Phe	Ser	Phe	Ile	Lys	Asn	Glu	Ser	Asn	Tyr	His	Pro	145	150	155	160
Phe	Phe	Phe	Arg	Thr	Arg	Ala	Cys	Asp	Leu	Leu	Leu	Gln	Pro	Asp	Asn	165	170	175	
Leu	Ala	Cys	Lys	Pro	Phe	Trp	Lys	Pro	Arg	Asn	Leu	Asn	Ile	Ser	Gln	180	185	190	
His	Gly	Ser	Asp	Met	Gln	Val	Ser	Phe	Asp	His	Ala	Pro	His	Asn	Phe	195	200	205	
Gly	Phe	Arg	Phe	Phe	Tyr	Leu	His	Tyr	Lys	Leu	Lys	His	Glu	Gly	Pro	210	215	220	
Phe	Lys	Arg	Lys	Thr	Cys	Lys	Gln	Glu	Gln	Thr	Thr	Glu	Met	Thr	Ser	225	230	235	240
Cys	Leu	Leu	Gln	Asn	Val	Ser	Pro	Gly	Asp	Tyr	Ile	Ile	Glu	Leu	Val	245	250	255	
Asp	Asp	Thr	Asn	Thr	Thr	Arg	Lys	Val	Met	His	Tyr	Ala	Leu	Lys	Pro	260	265	270	
Val	His	Ser	Pro	Trp	Ala	Gly	Pro	Ile	Arg	Ala	Val	Ala	Ile	Thr	Val	275	280	285	
Pro	Leu	Val	Val	Ile	Ser	Ala	Phe	Ala	Thr	Leu	Phe	Thr	Val	Met	Cys	290	295	300	
Arg	Lys	Lys	Gln	Gln	Glu	Asn	Ile	Tyr	Ser	His	Leu	Asp	Glu	Glu	Ser	305	310	315	320

Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg
 325 330 335
 Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn
 340 345 350
 His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys
 355 360 365
 Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg
 370 375 380
 Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe
 385 390 395 400
 Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys
 405 410 415
 Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu
 420 425 430
 Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys
 435 440 445
 Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp
 450 455 460
 Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys
 465 470 475 480
 Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His Ser
 485 490 495
 Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser
 500 505 510
 Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala
 515 520 525
 Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu
 530 535 540
 Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu Pro
 545 550 555 560
 Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met Cys
 565 570 575
 Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala Val
 580 585 590
 Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His Gly
 595 600 605
 Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser Ala
 610 615 620
 Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp
 625 630 635 640

Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu
645 650 655

Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr
660 665 670

Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu
675 680 685

Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys
690 695 700

Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val Ala
705 710 715 720

Pro Leu

<210> 15
<211> 2214
<212> DNA
<213> reverse translation

<220>
<221> misc_feature
<222> (1)..(2214)
<223> n may be a, c, g, or t

<400> 15
atggcncncnt ggytncaryt ntgywsngtn ttyttyacng tnaaygcntg yytnaayggn 60
wsncarytng cngtngcngc nggnggnwsn ggnmgngcnn nnggngcnga yacntgywsn 120
tggnnnggng tnggnccngc nwsnmgnaay wsnggnytn tnaayathac nttyaartay 180
gayaaytgga cnacntayyt naayccngtn ggnaarcayg tnathgcnga ygcncaraay 240
athacnathw sncartaygc ntgycaayg cargtngcng tnacnathyt ntggwsnccn 300
ggngcnytn gnatgarrt yytnaarggn ttmngngtna thytnngarga rytnaarwsn 360
garggngmnc arnnncarca rytnathytn aargayccna arcarnnnnaa ywsnwsntty 420
aarmgnacng gnatggarws ncarccnnnn ytnaayatga arttygarac ngaytaytty 480
gtngmnytnw snttywsntt yathaaraay garwsnaayt aycayccntt yttyttymgn 540
acnmngcncnt gygayytnyt nytnccarccn gayaayytn cngtgyaarcc nttytggaar 600
ccnmgnaayy tnaayathws ncarcayggn wsngayatgc argtnwsntt ygaycaygcn 660
ccncayaayt tyggnttymg nttyttytay ytncaytaya arytnaarca ygarggncn 720
ttyaarmgna aracntgyaa rcargarcar acnacngara tgacnwsntg yytnytnar 780
aaygtwnsnc cnggngayta yathathgar ytngtngayg ayacnaayac nacnmgnaar 840
gtnatgcayt aygcnynnaa rccngtncay wsncntggg cnggncnat hmgngcngtn 900

gcnathacng tncnnytngt ngtnathwsn gcnttygcna cnytnntyac ngtnatgtgy 960
 mgnaaraarc arcargaraa yathtaywsn cayytngayg argarwsnws ngarwsnwsn 1020
 acntayacng cngcnynce nmgngarmgn ytnmgncnm gncnaargt nttyytnngy 1080
 taywsnwsna argayggna raaycaytg aaygtngtnc artgyttygc ntayttyytn 1140
 cargayttyt gyggntgyga rgtngcnyn gnaytntggg argayttyws nytntgymgn 1200
 garggncarm gngartgggt nathcaraar athcaygarw sncarttyat hathgtngtn 1260
 tgywsnaarg gnatgaarta ytygtngay aaraaraayt ayaarcayaa rggngnggn 1320
 mgnggnwsng gnaargnga rytnttyytn gtngcngtnw sngcnathgc ngaraarytn 1380
 mgncargcna arcarwsnws nwsngcngcn ytnwsnaart tyathgcngt ntayttygay 1440
 taywsntgyg arggngaygt nccnggnath ytngayytnw snacnaarta ymgnytnatg 1500
 gayaayytn cncarytnng ywsncayytn caywsnmngn aycayggnyt ncargarccn 1560
 ggnarcaya cnmngncargg nwsnmgnmgn aaytaytym gnwsnaarws nggnmgnwsn 1620
 ytnnaygtng cnathtgyaa yatgcaycar ttyathgayg argarccnga ytggttygar 1680
 aarcarttyg tncnttyca yccncncn ytnmgntaym gngarccngt nytngaraar 1740
 ttygaywsng gnytnngtnyt naaygaygt atgtgyaarc cnggncnga rwsngaytty 1800
 tgyytnaarg tngargcngc ngtnytnngn gcnacnggnc cngcngayws ncarcaygar 1860
 wsncarcayg gnggnytna ycargaygn gargcnmgnc cngcnynnga yggngwsngcn 1920
 gcnytnarc cnytnynca yacngtnaar gcnggnwsnc cnwsngayat gccnmngay 1980
 wsnggnatht aygaywsnws ngtnccnwsn wsngarytnw snytnccnyt natggarggn 2040
 ytnwsnacng aycaracnga racnwsnwsn ytnacngarw sngtnwsnws nwsnwsnggn 2100
 ytnngngarg argarccncc ngcnynccn wsnaarytny tnwsnwsngg nwsntgyaar 2160
 gcngayytn gntgymgnws ntayacngay garytnayg cngtngcncc nytn 2214

<210> 16

<211> 2012

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>

<221> CDS

<222> (1) .. (1971)

<220>

<221> mat_peptide

<222> (70)..(1971)

<400> 16

atg ggg agc tcc aga ctg gca gcc ctg ctc ctg cct ctc ctc ctc ata	48
Met Gly Ser Ser Arg Leu Ala Ala Leu Leu Leu Pro Leu Leu Leu Ile	
-20 -15 -10	
gtc atc gac ctc tct gac tct gct ggg att ggc ttt cgc cac ctg ccc	96
Val Ile Asp Leu Ser Asp Ser Ala Gly Ile Gly Phe Arg His Leu Pro	
-5 -1 1 5	
cac tgg aac acc cgc tgt cct ctg gcc tcc cac acg gaa gtt ctg cct	144
His Trp Asn Thr Arg Cys Pro Leu Ala Ser His Thr Glu Val Leu Pro	
10 15 20 25	
ata tcc ctt gcc gca cct ggt ggg ccc tct tct cca caa agc ctt ggt	192
Ile Ser Leu Ala Ala Pro Gly Gly Pro Ser Ser Pro Gln Ser Leu Gly	
30 35 40	
gtg tgc gag tct ggc act gtt ccc gct gtt tgt gcc agc atc tgc tgt	240
Val Cys Glu Ser Gly Thr Val Pro Ala Val Cys Ala Ser Ile Cys Cys	
45 50 55	
cag gtg gct cag gtc ttc aac ggg gcc tct tcc acc tcc tgg tgc aga	288
Gln Val Ala Gln Val Phe Asn Gly Ala Ser Ser Thr Ser Trp Cys Arg	
60 65 70	
aat cca aaa agt ctt cca cat tca agt tct ata gga gac aca aga tgc	336
Asn Pro Lys Ser Leu Pro His Ser Ser Ser Ile Gly Asp Thr Arg Cys	
75 80 85	
cag cac ctg ctc aga gga agc tgc tgc ctc gtc gtc acc tgt ctg aga	384
Gln His Leu Leu Arg Gly Ser Cys Cys Leu Val Val Thr Cys Leu Arg	
90 95 100 105	
aga gcc atc aca ttt cca tcc cct ccc cag aca tct ccc aca agg gac	432
Arg Ala Ile Thr Phe Pro Ser Pro Pro Gln Thr Ser Pro Thr Arg Asp	
110 115 120	
ttc gct cta aaa gga ccc aac ctt cgg atc cag aga cat ggg aaa gtc	480
Phe Ala Leu Lys Gly Pro Asn Leu Arg Ile Gln Arg His Gly Lys Val	
125 130 135	
ttc cca gat tgg act cac aaa ggc atg gag gtg ggc act ggg tac aac	528
Phe Pro Asp Trp Thr His Lys Gly Met Glu Val Gly Thr Gly Tyr Asn	
140 145 150	
agg aga tgg gtt cag ctg agt ggt gga ccc gag ttc tcc ttt gat ttg	576
Arg Arg Trp Val Gln Leu Ser Gly Gly Pro Glu Phe Ser Phe Asp Leu	
155 160 165	
ctg cct gag gcc cgg gct att cgg gtg acc ata tct tca ggc cct gag	624
Leu Pro Glu Ala Arg Ala Ile Arg Val Thr Ile Ser Ser Gly Pro Glu	
170 175 180 185	
gtc agc gtg cgt ctt tgt cac cag tgg gca ctg gag tgt gaa gag ctg	672
Val Ser Val Arg Leu Cys His Gln Trp Ala Leu Glu Cys Glu Glu Leu	
190 195 200	

agc agt ccc tat gat gtc cag aaa att gtg tct ggg ggc cac act gta	720
Ser Ser Pro Tyr Asp Val Gln Lys Ile Val Ser Gly Gly His Thr Val	
205 210 215	
gag ctg cct tat gaa ttc ctt ctg ccc tgt ctg tgc ata gag gca tcc	768
Glu Leu Pro Tyr Glu Phe Leu Leu Pro Cys Leu Cys Ile Glu Ala Ser	
220 225 230	
tac ctg caa gag gac act gtg agg cgc aaa aaa tgt ccc ttc cag agc	816
Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser	
235 240 245	
tgg cca gaa gcc tat ggc tcg gac ttc tgg aag tca gtg cac ttc act	864
Trp Pro Glu Ala Tyr Gly Ser Asp Phe Trp Lys Ser Val His Phe Thr	
250 255 260 265	
gac tac agc cag cac act cag atg gtc atg gcc ctg aca ctc cgc tgc	912
Asp Tyr Ser Gln His Thr Gln Met Val Met Ala Leu Thr Leu Arg Cys	
270 275 280	
cca ctg aag ctg gaa gct gcc ctc tgc cag agg cac gac tgg cat acc	960
Pro Leu Lys Leu Glu Ala Ala Leu Cys Gln Arg His Asp Trp His Thr	
285 290 295	
ctt tgc aaa gac ctc ccg aat gcc acg gct cga gag tca gat ggg tgg	1008
Leu Cys Lys Asp Leu Pro Asn Ala Thr Ala Arg Glu Ser Asp Gly Trp	
300 305 310	
tat gtt ttg gag aag gtg gac ctg cac ccc cag ctc tgc ttc aag gta	1056
Tyr Val Leu Glu Lys Val Asp Leu His Pro Gln Leu Cys Phe Lys Val	
315 320 325	
caa cca tgg ttc tct ttt gga aac agc agc cat gtt gaa tgc ccc cac	1104
Gln Pro Trp Phe Ser Phe Gly Asn Ser Ser His Val Glu Cys Pro His	
330 335 340 345	
cag act ggg tct ctc aca tcc tgg aat gta agc atg gat acc caa gcc	1152
Gln Thr Gly Ser Leu Thr Ser Trp Asn Val Ser Met Asp Thr Gln Ala	
350 355 360	
cag cag ctg att ctt cac ttc tcc tca aga atg cat gcc acc ttc agt	1200
Gln Gln Leu Ile Leu His Phe Ser Ser Arg Met His Ala Thr Phe Ser	
365 370 375	
gct gcc tgg agc ctc cca ggc ttg ggg cag gac act ttg gtg ccc ccc	1248
Ala Ala Trp Ser Leu Pro Gly Leu Gly Gln Asp Thr Leu Val Pro Pro	
380 385 390	
gtg tac act gtc agc cag gtg tgg cgg tca gat gtc cag ttt gcc tgg	1296
Val Tyr Thr Val Ser Gln Val Trp Arg Ser Asp Val Gln Phe Ala Trp	
395 400 405	
aag cac ctc ttg tgt cca gat gtc tct tac aga cac ctg ggg ctc ttg	1344
Lys His Leu Leu Cys Pro Asp Val Ser Tyr Arg His Leu Gly Leu Leu	
410 415 420 425	
atc ctg gca ctg ctg gcc ctc ctc acc cta ctg ggt gtt gtt ctg gcc	1392
Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu Ala	
430 435 440	

ctc acc tgc cgg cgc cca cag tca ggc ccg ggc cca gcg cgg cca gtg 1440
 Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro Val
 445 450 455

ctc ctc ctg cac gcg gcg gac tcg gag gcg cag ccg cgc ctg gtg gga 1488
 Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly
 460 465 470

gcg ctg gct gaa ctg cta cgg gca gcg ctg ggc ggc ggg cgc gac gtg 1536
 Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp Val
 475 480 485

atc gtg gac ctg tgg gag ggg agg cac gtg gcg cgc gtg ggc ccg ctg 1584
 Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro Leu
 490 495 500 505

ccg tgg ctc tgg gcg gcg cgg acg cgc gta gcg ccg gag cag ggc act 1632
 Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly Thr
 510 515 520

gtg ctg ctg ctg tgg agc ggc gcc gac ctt cgc ccg gtc agc ggc ccc 1680
 Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly Pro
 525 530 535

gac ccc cgc gcc gcg ccc ctg ctc gcc ctg ctc cac gct gcc ccg cgc 1728
 Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro Arg
 540 545 550

ccg ctg ctg ctg ctc gct tac ttc agt cgc ctc tgc gcc aag ggc gac 1776
 Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp
 555 560 565

atc ccc ccg ccg ctg cgc gcc ctg ccg cgc tac cgc ctg ctg cgc gac 1824
 Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp
 570 575 580 585

ctg ccg cgt ctg ctg cgg gcg ctg gac gcg ccg cct ttc gca gag gcc 1872
 Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu Ala
 590 595 600

acc agc tgg ggc cgc ctt ggg gcg ccg cag cgc agg cag agc cgc cta 1920
 Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg Leu
 605 610 615

gag ctg tgc agc cgg ctc gaa cga gag gcc gcc cga ctt gca gac cta 1968
 Glu Leu Cys Ser Arg Leu Glu Arg Glu Ala Ala Arg Leu Ala Asp Leu
 620 625 630

ggt tgagcagagc tccaccgcag tcccgggtgt ctgcggccgc t 2012
 Gly

<210> 17

<211> 657

<212> PRT

<213> Unknown

<400> 17

Met Gly Ser Ser Arg Leu Ala Ala Leu Leu Leu Pro Leu Leu Leu Ile
 -20 -15 -10

Val	Ile	Asp	Leu	Ser	Asp	Ser	Ala	Gly	Ile	Gly	Phe	Arg	His	Leu	Pro	-5	-1	1	5
His	Trp	Asn	Thr	Arg	Cys	Pro	Leu	Ala	Ser	His	Thr	Glu	Val	Leu	Pro	10	15	20	25
Ile	Ser	Leu	Ala	Ala	Pro	Gly	Gly	Pro	Ser	Ser	Pro	Gln	Ser	Leu	Gly	30	35	40	
Val	Cys	Glu	Ser	Gly	Thr	Val	Pro	Ala	Val	Cys	Ala	Ser	Ile	Cys	Cys	45	50	55	
Gln	Val	Ala	Gln	Val	Phe	Asn	Gly	Ala	Ser	Ser	Thr	Ser	Trp	Cys	Arg	60	65	70	
Asn	Pro	Lys	Ser	Leu	Pro	His	Ser	Ser	Ser	Ile	Gly	Asp	Thr	Arg	Cys	75	80	85	
Gln	His	Leu	Leu	Arg	Gly	Ser	Cys	Cys	Leu	Val	Val	Thr	Cys	Leu	Arg	90	95	100	105
Arg	Ala	Ile	Thr	Phe	Pro	Ser	Pro	Pro	Gln	Thr	Ser	Pro	Thr	Arg	Asp	110	115	120	
Phe	Ala	Leu	Lys	Gly	Pro	Asn	Leu	Arg	Ile	Gln	Arg	His	Gly	Lys	Val	125	130	135	
Phe	Pro	Asp	Trp	Thr	His	Lys	Gly	Met	Glu	Val	Gly	Thr	Gly	Tyr	Asn	140	145	150	
Arg	Arg	Trp	Val	Gln	Leu	Ser	Gly	Gly	Pro	Glu	Phe	Ser	Phe	Asp	Leu	155	160	165	
Leu	Pro	Glu	Ala	Arg	Ala	Ile	Arg	Val	Thr	Ile	Ser	Ser	Gly	Pro	Glu	170	175	180	185
Val	Ser	Val	Arg	Leu	Cys	His	Gln	Trp	Ala	Leu	Glu	Cys	Glu	Glu	Leu	190	195	200	
Ser	Ser	Pro	Tyr	Asp	Val	Gln	Lys	Ile	Val	Ser	Gly	Gly	His	Thr	Val	205	210	215	
Glu	Leu	Pro	Tyr	Glu	Phe	Leu	Leu	Pro	Cys	Leu	Cys	Ile	Glu	Ala	Ser	220	225	230	
Tyr	Leu	Gln	Glu	Asp	Thr	Val	Arg	Arg	Lys	Lys	Cys	Pro	Phe	Gln	Ser	235	240	245	
Trp	Pro	Glu	Ala	Tyr	Gly	Ser	Asp	Phe	Trp	Lys	Ser	Val	His	Phe	Thr	250	255	260	265
Asp	Tyr	Ser	Gln	His	Thr	Gln	Met	Val	Met	Ala	Leu	Thr	Leu	Arg	Cys	270	275	280	
Pro	Leu	Lys	Leu	Glu	Ala	Ala	Leu	Cys	Gln	Arg	His	Asp	Trp	His	Thr	285	290	295	
Leu	Cys	Lys	Asp	Leu	Pro	Asn	Ala	Thr	Ala	Arg	Glu	Ser	Asp	Gly	Trp	300	305	310	

Tyr Val Leu Glu Lys Val Asp Leu His Pro Gln Leu Cys Phe Lys Val
 315 320 325
 Gln Pro Trp Phe Ser Phe Gly Asn Ser Ser His Val Glu Cys Pro His
 330 335 340 345
 Gln Thr Gly Ser Leu Thr Ser Trp Asn Val Ser Met Asp Thr Gln Ala
 350 355 360
 Gln Gln Leu Ile Leu His Phe Ser Ser Arg Met His Ala Thr Phe Ser
 365 370 375
 Ala Ala Trp Ser Leu Pro Gly Leu Gly Gln Asp Thr Leu Val Pro Pro
 380 385 390
 Val Tyr Thr Val Ser Gln Val Trp Arg Ser Asp Val Gln Phe Ala Trp
 395 400 405
 Lys His Leu Leu Cys Pro Asp Val Ser Tyr Arg His Leu Gly Leu Leu
 410 415 420 425
 Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu Ala
 430 435 440
 Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro Val
 445 450 455
 Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly
 460 465 470
 Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp Val
 475 480 485
 Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro Leu
 490 495 500 505
 Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly Thr
 510 515 520
 Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly Pro
 525 530 535
 Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro Arg
 540 545 550
 Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp
 555 560 565
 Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp
 570 575 580 585
 Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu Ala
 590 595 600
 Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg Leu
 605 610 615
 Glu Leu Cys Ser Arg Leu Glu Arg Glu Ala Ala Arg Leu Ala Asp Leu
 620 625 630

Gly

<210> 18
 <211> 1971
 <212> DNA
 <213> reverse translation

<220>
 <221> misc_feature
 <222> (1)..(1971)
 <223> n may be a, c, g, or t

<400> 18
 atgggnwsnw snmgnytnge ngcnytnytn ytnccnytny tnytnathgt nathgayytn 60
 wsngaywsng cnggnathgg nttymgncay ytnccncayt ggaayacnmg ntgyccnytn 120
 gcnwsncaya cngargtnyt nccnathwsn ytngcngcnc cnggnggncc nwsnwsnccn 180
 carwsnytn gngtntgyga rwsnggnacn gtncngcng tntgygcnws nathtgytgy 240
 cargtngcnc argtnttyaa yggngcnwsn wsnacnwsnt ggtgymgnaa yccnaarwsn 300
 ytnccncayw snwsnwsnat hggngayacn mgntgyarc ayytnytnmg nggnwsntgy 360
 tgyytngtng tnaentgyyt nmgnmgngcn athacnttyc cnwsnccncc ncaracnwsn 420
 ccnacnmng aytyygcnyt naarggnccn aaytnmgna thcarmgna yggnaargtn 480
 ttyccngayt ggacncayaa rggnatggar gtnggnacng gntayaaymg nmngtgggtn 540
 carytnwsng gnggnccnga rttywsntty gayytnytn cngargcnmg ngcnathmgn 600
 gtnacnathw snwsnggncc ngargtnwsn gtnmgnytn gycaycartg ggcnytn gar 660
 tgygargary tnwsnwsncc ntaygaygtn caraarathg tnwsnggngg ncayacngtn 720
 garytnccnt aygarttyyt nytnccntgy ytntgyathg argcnwsnta yytnccargar 780
 gayacngtnm gnmgnaaraa rtgyccntty carwsntggc cngargcnta yggnwsngay 840
 ttytggaarw sngtncaytt yacngaytay wsncarcaya cncaratggt natggcnytn 900
 acnytnmgnt gyccnytnaa rytngargcn gcnytnctgy armgncayga ytggcayacn 960
 ytntgyaarg ayytnccnaa ygcnacngcn mgngarwsng ayggntggta ygtnytn gar 1020
 aargtngayy tncayccnca rytntgytty aargtnarc cntgggtyws nttyggnaay 1080
 wsnwsncayg tngartgycc ncaycaracn ggnwsnytna cnwsntggaa ygtnwsnatg 1140
 gayacncarg cncarcaryt nathytnca ytywsnwsnm gnatgcaygc nacnttywsn 1200
 gcngcntggw snytnccngg nytnngncar gayacnytn tncnccngt ntayacngtn 1260
 wsncargtn ggmgnwsnga ygtncartty gcntggaarc ayytnytnctg yccngaygtn 1320

wsntaymgnc ayytnggnytn nytnathytn gcnytnytnng cnytnytnac nytnytnngn 1380
 gtngtnytnng cnytnacntg ymgngmgnccn carwsnggnc cnggncngc nmgnccngtn 1440
 ytnytnytnnc aygcngcnga ywsngargcn carmgngmny tngtnggngc nytnngcngar 1500
 ytnytnmgng cngcnytnng nggnggngmgn gaygtnathg tngayytnng ggarggngmgn 1560
 caygtngcnm gngtnggnc nytnccntgg ytntgggngc cnmgnacnmg ngtnngcnmgn 1620
 garcarggna cngtnytnyt nytnnggwsn ggngcngayy tnmgnccngt nwsnggngccn 1680
 gayccnmngng cngcncnytn nytnngcnytn ytncaygng cncncmgncc nytnytnytn 1740
 ytnngcntayt tywsnmgnytn ntgygcnaar ggngayathc cncncncnytn nmngngcnytn 1800
 ccnmngntaym gnytnytnmg ngayytnccn mnytnytnm gngcnytnnga ygcnmgnccn 1860
 ttygcngarg cnacnwsntg gggngmnytn ggngcnmgnc armgngmgnca rwsnmgnytn 1920
 garytnngyw snmgnytnnga rmngngargcn gcnmgnytnng cngayytnng n 1971

<210> 19
 <211> 808
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:rodent; surmised
 Mus musculus

<220>
 <221> CDS
 <222> (78)..(806)

<220>
 <221> mat_peptide
 <222> (147)..(806)

<400> 19
 cagctccggg ccagggccctg ctgccctctt gcagacagga aagacatggt ctctgcgccc 60
 tgatcctaca gaagctc atg ggg agc ccc aga ctg gca gcc ttg ctc ctg 110
 Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu
 -20 -15
 tct ctc ccg cta ctg ctc atc ggc ctc gct gtg tct gct cgg gtt gcc 158
 Ser Leu Pro Leu Leu Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala
 -10 -5 -1 1
 tgc ccc tgc ctg cgg agt tgg acc agc cac tgt ctc ctg gcc tac cgt 206
 Cys Pro Cys Leu Arg Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg
 5 10 15 20
 gtg gat aaa cgt ttt gct ggc ctt cag tgg ggc tgg ttc cct ctc ttg 254
 Val Asp Lys Arg Phe Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu
 25 30 35
 gtg agg aaa tct aaa agt cct cct aaa ttt gaa gac tat tgg agg cac 302

Val	Arg	Lys	Ser	Lys	Ser	Pro	Pro	Lys	Phe	Glu	Asp	Tyr	Trp	Arg	His		
			40					45					50				
agg	aca	cca	gca	tcc	ttc	cag	agg	aag	ctg	cta	ggc	agc	cct	tcc	ctg	350	
Arg	Thr	Pro	Ala	Ser	Phe	Gln	Arg	Lys	Leu	Leu	Gly	Ser	Pro	Ser	Leu		
		55					60					65					
tct	gag	gaa	agc	cat	cga	att	tcc	atc	ccc	tcc	tca	gcc	atc	tcc	cac	398	
Ser	Glu	Glu	Ser	His	Arg	Ile	Ser	Ile	Pro	Ser	Ser	Ala	Ile	Ser	His		
	70					75					80						
aga	ggc	caa	cgc	acc	aaa	agg	gcc	cag	cct	tca	gct	gca	gaa	gga	aga	446	
Arg	Gly	Gln	Arg	Thr	Lys	Arg	Ala	Gln	Pro	Ser	Ala	Ala	Glu	Gly	Arg		
	85				90				95						100		
gaa	cat	ctc	cct	gaa	gca	ggg	tca	caa	aag	tgt	gga	gga	cct	gaa	ttc	494	
Glu	His	Leu	Pro	Glu	Ala	Gly	Ser	Gln	Lys	Cys	Gly	Gly	Pro	Glu	Phe		
				105				110						115			
tcc	ttt	gat	ttg	ctg	ccc	gag	gtg	cag	gct	gtt	cgg	gtg	act	att	cct	542	
Ser	Phe	Asp	Leu	Leu	Pro	Glu	Val	Gln	Ala	Val	Arg	Val	Thr	Ile	Pro		
			120					125					130				
gca	ggc	ccc	aag	gca	cgt	gtg	cgc	ctt	tgt	tat	cag	tgg	gca	ctg	gaa	590	
Ala	Gly	Pro	Lys	Ala	Arg	Val	Arg	Leu	Cys	Tyr	Gln	Trp	Ala	Leu	Glu		
		135					140					145					
tgt	gaa	gac	ttg	agt	agc	cct	ttt	gat	acc	cag	aaa	att	gtg	tct	gga	638	
Cys	Glu	Asp	Leu	Ser	Ser	Pro	Phe	Asp	Thr	Gln	Lys	Ile	Val	Ser	Gly		
	150					155					160						
ggg	cac	act	gta	gac	ctg	cct	tat	gaa	ttc	ctt	ctg	ccc	tgc	atg	tgc	686	
Gly	His	Thr	Val	Asp	Leu	Pro	Tyr	Glu	Phe	Leu	Leu	Pro	Cys	Met	Cys		
	165				170					175					180		
ata	gag	gcc	tcc	tac	ctg	caa	gag	gac	act	gtg	agg	cgc	aaa	agt	gtc	734	
Ile	Glu	Ala	Ser	Tyr	Leu	Gln	Glu	Asp	Thr	Val	Arg	Arg	Lys	Ser	Val		
				185					190					195			
cct	tcc	aga	gct	ggc	ctg	aag	ctt	atg	gct	cag	act	tct	ggc	agt	caa	782	
Pro	Ser	Arg	Ala	Gly	Leu	Lys	Leu	Met	Ala	Gln	Thr	Ser	Gly	Ser	Gln		
			200				205						210				
tac	gct	tca	ctg	act	aca	gcc	agc	ac								808	
Tyr	Ala	Ser	Leu	Thr	Thr	Ala	Ser										
		215					220										
<210>	20																
<211>	243																
<212>	PRT																
<213>	Unknown																
<400>	20																
Met	Gly	Ser	Pro	Arg	Leu	Ala	Ala	Leu	Leu	Leu	Ser	Leu	Pro	Leu	Leu		
			-20					-15					-10				
Leu	Ile	Gly	Leu	Ala	Val	Ser	Ala	Arg	Val	Ala	Cys	Pro	Cys	Leu	Arg		
	-5					-1	1				5						

Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe
 10 15 20 25
 Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys
 30 35 40
 Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser
 45 50 55
 Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His
 60 65 70
 Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr
 75 80 85
 Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu
 90 95 100 105
 Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu
 110 115 120
 Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala
 125 130 135
 Arg Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser
 140 145 150
 Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp
 155 160 165
 Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys Ile Glu Ala Ser Tyr
 170 175 180 185
 Leu Gln Glu Asp Thr Val Arg Arg Lys Ser Val Pro Ser Arg Ala Gly
 190 195 200
 Leu Lys Leu Met Ala Gln Thr Ser Gly Ser Gln Tyr Ala Ser Leu Thr
 205 210 215
 Thr Ala Ser
 220

<210> 21

<211> 729

<212> DNA

<213> reverse translation

<220>

<221> misc_feature

<222> (1)..(729)

<223> n may be a, c, g, or t

<400> 21

atgggnwsnc cnmgnytngc ngcnytnytn ytnwsnytn cnytnytnytn nathggnytn 60

gcngtnwsng cnmgngtngc ntgyccntgy ytnmgwnsnt ggacnwsnca ytggytnytn 120

gcntaymgng tngayaarmg nttygcnggn ytncartggg gntgggttycc nytnytnytn 180

```

mgnaarwsna arwsnccncc naarttygar gaytaytggm gncaymgnac nccngcnwsn 240
ttypcarmgna arytnytngg nwsnccnwsn ytnwsngarg arwsncaymg nathwsnath 300
ccnwsnwsng cnathwsnca ymgnggncar mgnacnaarm gngcncarcc nwsngcngcn 360
garggnmgng arcayytnc ngargcnggn wsncaraart gyggnggncc ngarttywsn 420
ttypgayytny tncngargt ncargcngtn mgngtnacna thccngcngg nccnaargcn 480
mgngtnmgny tntgytayca rtgggcnytn gartgygarg ayytnwsnws nccnttygay 540
acncaraara thgtwnsngg nggncayacn gtngayytnc cntaygartt yytnytncn 600
tgyatgtgya thgargcnws ntayytncar gargayacng tnmgnmgnaa rwsngtnccn 660
wsnmgngcng gnytnaaryt natggcncar acnwsnggnw sncartaygc nwsnytnacn 720
acngcnwsn 729

```

<210> 22

<211> 2377

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>

<221> CDS

<222> (180)..(1874)

<400> 22

```

ttttgagcag aggttccta ggctccgtag aaatttgcat acagcttcca cttcctgctt 60
cagagcctgt tcttctactt acctgggccc ggagaagggtg gagggagacg agaagccgcc 120
gagagccgac taccctccgg gccagtcctg tctgtccgtg gtggatctaa gaaactaga 179
atg aac cga agc att cct gtg gag gtt gat gaa tca gaa cca tac cca 227
Met Asn Arg Ser Ile Pro Val Glu Val Asp Glu Ser Glu Pro Tyr Pro
  1             5             10             15
agt cag ttg ctg aaa cca atc cca gaa tat tcc ccg gaa gag gaa tca 275
Ser Gln Leu Leu Lys Pro Ile Pro Glu Tyr Ser Pro Glu Glu Glu Ser
          20             25             30
gaa cca cct gct cca aat ata agg aac atg gca ccc aac agc ttg tct 323
Glu Pro Pro Ala Pro Asn Ile Arg Asn Met Ala Pro Asn Ser Leu Ser
          35             40             45
gca ccc aca atg ctt cac aat tcc tcc gga gac ttt tct caa gct cac 371
Ala Pro Thr Met Leu His Asn Ser Ser Gly Asp Phe Ser Gln Ala His
          50             55             60
tca acc ctg aaa ctt gca aat cac cag cgg cct gta tcc cgg cag gtc 419
Ser Thr Leu Lys Leu Ala Asn His Gln Arg Pro Val Ser Arg Gln Val
          65             70             75             80

```

acc tgc ctg cgc act caa gtt ctg gag gac agt gaa gac agt ttc tgc	467
Thr Cys Leu Arg Thr Gln Val Leu Glu Asp Ser Glu Asp Ser Phe Cys	
85 90 95	
agg aga cac cca ggc ctg ggc aaa gct ttc cct tct ggg tgc tct gca	515
Arg Arg His Pro Gly Leu Gly Lys Ala Phe Pro Ser Gly Cys Ser Ala	
100 105 110	
gtc agc gag cct gcg tct gag tct gtg gtt gga gcc ctc cct gca gag	563
Val Ser Glu Pro Ala Ser Glu Ser Val Val Gly Ala Leu Pro Ala Glu	
115 120 125	
cat cag ttt tca ttt atg gaa aaa cgt aat caa tgg ctg gta tct cag	611
His Gln Phe Ser Phe Met Glu Lys Arg Asn Gln Trp Leu Val Ser Gln	
130 135 140	
ctt tca gcg gct tct cct gac act ggc cat gac tca gac aaa tca gac	659
Leu Ser Ala Ala Ser Pro Asp Thr Gly His Asp Ser Asp Lys Ser Asp	
145 150 155 160	
caa agt tta cct aat gcc tca gca gac tcc ttg ggc ggt agc cag gag	707
Gln Ser Leu Pro Asn Ala Ser Ala Asp Ser Leu Gly Gly Ser Gln Glu	
165 170 175	
atg gtg caa cgg ccc cag cct cac agg aac cga gca ggc ctg gat ctg	755
Met Val Gln Arg Pro Gln Pro His Arg Asn Arg Ala Gly Leu Asp Leu	
180 185 190	
cca acc ata gac acg gga tat gat tcc cag ccc cag gat gtc ctg ggc	803
Pro Thr Ile Asp Thr Gly Tyr Asp Ser Gln Pro Gln Asp Val Leu Gly	
195 200 205	
atc agg cag ctg gaa agg ccc ctg ccc ctc acc tcc gtg tgt tac ccc	851
Ile Arg Gln Leu Glu Arg Pro Leu Pro Leu Thr Ser Val Cys Tyr Pro	
210 215 220	
cag gac ctc ccc aga cct ctc agg tcc agg gag ttc cct cag ttt gaa	899
Gln Asp Leu Pro Arg Pro Leu Arg Ser Arg Glu Phe Pro Gln Phe Glu	
225 230 235 240	
cct cag agg tat cca gca tgt gca cag atg ctg cct ccc aat ctt tcc	947
Pro Gln Arg Tyr Pro Ala Cys Ala Gln Met Leu Pro Pro Asn Leu Ser	
245 250 255	
cca cat gct cca tgg aac tat cat tac cat tgt cct gga agt ccc gat	995
Pro His Ala Pro Trp Asn Tyr His Tyr His Cys Pro Gly Ser Pro Asp	
260 265 270	
cac cag gtg cca tat ggc cat gac tac cct cga gca gcc tac cag caa	1043
His Gln Val Pro Tyr Gly His Asp Tyr Pro Arg Ala Ala Tyr Gln Gln	
275 280 285	
gtg atc cag ccg gct ctg cct ggg cag ccc ctg cct gga gcc agt gtg	1091
Val Ile Gln Pro Ala Leu Pro Gly Gln Pro Leu Pro Gly Ala Ser Val	
290 295 300	
aga ggc ctg cac cct gtg cag aag gtt atc ctg aat tat ccc agc ccc	1139
Arg Gly Leu His Pro Val Gln Lys Val Ile Leu Asn Tyr Pro Ser Pro	
305 310 315 320	

tgg gac caa gaa gag agg ccc gca cag aga gac tgc tcc ttt ccg ggg	1187
Trp Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Cys Ser Phe Pro Gly	
325 330 335	
ctt cca agg cac cag gac cag cca cat cac cag cca cct aat aga gct	1235
Leu Pro Arg His Gln Asp Gln Pro His His Gln Pro Pro Asn Arg Ala	
340 345 350	
ggg gct cct ggg gag tcc ttg gag tgc cct gca gag ctg aga cca cag	1283
Gly Ala Pro Gly Glu Ser Leu Glu Cys Pro Ala Glu Leu Arg Pro Gln	
355 360 365	
gtt ccc cag cct ccg tcc cca gct gct gtg cct aga ccc cct agc aac	1331
Val Pro Gln Pro Pro Ser Pro Ala Ala Val Pro Arg Pro Pro Ser Asn	
370 375 380	
cct cca gcc aga gga act cta aaa aca agc aat ttg cca gaa gaa ttg	1379
Pro Pro Ala Arg Gly Thr Leu Lys Thr Ser Asn Leu Pro Glu Glu Leu	
385 390 395 400	
cgg aaa gtc ttt atc act tat tcg atg gac aca gct atg gag gtg gtg	1427
Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val Val	
405 410 415	
aaa ttc gtg aac ttt ttg ttg gta aat ggc ttc caa act gca att gac	1475
Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile Asp	
420 425 430	
ata ttt gag gat aga atc cga ggc att gat atc att aaa tgg atg gag	1523
Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met Glu	
435 440 445	
cgc tac ctt agg gat aag acc gtg atg ata atc gta gca atc agc ccc	1571
Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser Pro	
450 455 460	
aaa tac aaa cag gac gtg gaa ggc gct gag tgc cag ctg gac gag gat	1619
Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu Asp	
465 470 475 480	
gag cat ggc tta cat act aag tac att cat cga atg atg cag att gag	1667
Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile Glu	
485 490 495	
ttc ata aaa caa gga agc atg aat ttc aga ttc atc cct gtg ctc ttc	1715
Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe	
500 505 510	
cca aat gct aag aag gag cat gtg ccc acc tgg ctt cag aac act cat	1763
Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His	
515 520 525	
gtc tac agc tgg ccc aag aat aaa aaa aac atc ctg ctg cgg ctg ctg	1811
Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu	
530 535 540	
aga gag gaa gag tat gtg gct cct cca cgg ggg cct ctg ccc acc ctt	1859
Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu	
545 550 555 560	

cag gtg gtt ccc ttg tgacaccgtt catccccaga tcactgaggc caggccatgt 1914
 Gln Val Val Pro Leu
 565

ttggggcctt gttctgacag cattctggct gaggtctggc ggtagcactc ctggctgggtt 1974
 tttttctgtt cctccccgag agggcctctg gccccagga aacctgttgt gcagagctct 2034
 tccccggaga cctccacaca ccttggtttt gaagtggagt ctgtgactgc tctgcattct 2094
 ctgcttttaa aaaaaccatt gcaggtgcca gtgtcccata tgttcctcct gacagtttga 2154
 tgtgtccatt ctgggcctct cagtgccttag caagtagata atgtaagga tgtggcagca 2214
 aatggaaatg actacaaaca ctctcctatc aatcattca ggctactttt atgagtttagc 2274
 cagatgcttg tgtatcctca gaccaaactg attcatgtac aaataataaa atgtttactc 2334
 ttttgtaaaa aaaaaaaaaa aaaaaaaaaag aaaaaaaaaa aaa 2377

<210> 23
 <211> 565
 <212> PRT
 <213> Unknown

<400> 23
 Met Asn Arg Ser Ile Pro Val Glu Val Asp Glu Ser Glu Pro Tyr Pro
 1 5 10 15
 Ser Gln Leu Leu Lys Pro Ile Pro Glu Tyr Ser Pro Glu Glu Glu Ser
 20 25 30
 Glu Pro Pro Ala Pro Asn Ile Arg Asn Met Ala Pro Asn Ser Leu Ser
 35 40 45
 Ala Pro Thr Met Leu His Asn Ser Ser Gly Asp Phe Ser Gln Ala His
 50 55 60
 Ser Thr Leu Lys Leu Ala Asn His Gln Arg Pro Val Ser Arg Gln Val
 65 70 75 80
 Thr Cys Leu Arg Thr Gln Val Leu Glu Asp Ser Glu Asp Ser Phe Cys
 85 90 95
 Arg Arg His Pro Gly Leu Gly Lys Ala Phe Pro Ser Gly Cys Ser Ala
 100 105 110
 Val Ser Glu Pro Ala Ser Glu Ser Val Val Gly Ala Leu Pro Ala Glu
 115 120 125
 His Gln Phe Ser Phe Met Glu Lys Arg Asn Gln Trp Leu Val Ser Gln
 130 135 140
 Leu Ser Ala Ala Ser Pro Asp Thr Gly His Asp Ser Asp Lys Ser Asp
 145 150 155 160
 Gln Ser Leu Pro Asn Ala Ser Ala Asp Ser Leu Gly Gly Ser Gln Glu
 165 170 175

Met Val Gln Arg Pro Gln Pro His Arg Asn Arg Ala Gly Leu Asp Leu
 180 185 190
 Pro Thr Ile Asp Thr Gly Tyr Asp Ser Gln Pro Gln Asp Val Leu Gly
 195 200 205
 Ile Arg Gln Leu Glu Arg Pro Leu Pro Leu Thr Ser Val Cys Tyr Pro
 210 215 220
 Gln Asp Leu Pro Arg Pro Leu Arg Ser Arg Glu Phe Pro Gln Phe Glu
 225 230 235 240
 Pro Gln Arg Tyr Pro Ala Cys Ala Gln Met Leu Pro Pro Asn Leu Ser
 245 250 255
 Pro His Ala Pro Trp Asn Tyr His Tyr His Cys Pro Gly Ser Pro Asp
 260 265 270
 His Gln Val Pro Tyr Gly His Asp Tyr Pro Arg Ala Ala Tyr Gln Gln
 275 280 285
 Val Ile Gln Pro Ala Leu Pro Gly Gln Pro Leu Pro Gly Ala Ser Val
 290 295 300
 Arg Gly Leu His Pro Val Gln Lys Val Ile Leu Asn Tyr Pro Ser Pro
 305 310 315 320
 Trp Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Cys Ser Phe Pro Gly
 325 330 335
 Leu Pro Arg His Gln Asp Gln Pro His His Gln Pro Pro Asn Arg Ala
 340 345 350
 Gly Ala Pro Gly Glu Ser Leu Glu Cys Pro Ala Glu Leu Arg Pro Gln
 355 360 365
 Val Pro Gln Pro Pro Ser Pro Ala Ala Val Pro Arg Pro Pro Ser Asn
 370 375 380
 Pro Pro Ala Arg Gly Thr Leu Lys Thr Ser Asn Leu Pro Glu Glu Leu
 385 390 395 400
 Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val Val
 405 410 415
 Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile Asp
 420 425 430
 Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met Glu
 435 440 445
 Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser Pro
 450 455 460
 Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu Asp
 465 470 475 480
 Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile Glu
 485 490 495

Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe
 500 505 510
 Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His
 515 520 525
 Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu
 530 535 540
 Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu
 545 550 555 560
 Gln Val Val Pro Leu
 565

<210> 24
 <211> 1695
 <212> DNA
 <213> reverse translation

<220>
 <221> misc_feature
 <222> (1)..(1695)
 <223> n may be a, c, g, or t

<400> 24
 atgaaymgnw snathccngt ngargtngay garwsngarc cntayccnws ncarytnytn 60
 aarccnathc cngartayws nccngargar garwsngarc cncngcncnc naayathmgn 120
 aayatggcnc cnaaywsnyt nwsngcncnc acnatgytnc ayaaywsnws nggngaytty 180
 wsncargcnc aywsnacnyt naarytngcn aaycaycarm gncngtnws nmgnrcargtn 240
 acntgyytnm gnacncargt nytngargay wsngargayw snttytgymg nmgnrcayccn 300
 ggnytnnggna argcnttycc nwsnggntgy wsngcngtnw sngarccngc nwsngarwsn 360
 gtngtnnggng cnytnccngc ngarcaycar ttywsnttya tggaraarmg naaycartgg 420
 ytngtnwsnc arytnwsngc ngcnwsnccn gayacnggnc aygaywsnga yaarwsngay 480
 carwsnytn cnaaygcnc nwcngaywsn ytngngngnw sncargarat ggtncarmgn 540
 ccncarccnc aymgnaaymg ngcnggnytn gayytnccna cnathgayac nggntaygay 600
 wsncarccnc argaygtnyt nggnathmgn carytngarm gncnytncc nytnacnwsn 660
 gtntgytayc cncargayyt nccnmgnccn ytnmgnwsnm gngarttycc ncarttygar 720
 ccncarmgnt ayccngcntg ygencaratg ytncncncna ayytnwsncc ncaygcncnc 780
 tggaaytayc aytaycaytg yccnggnwsn ccngaycayc argtnccnta yggncaygay 840
 tayccnmgng cngcntayca rcargtnath carccngcny tncnggnca rccnytnccn 900
 ggngcnwsng tnmnggnytn ncayccngtn caraargtna thytnaayta yccnwsnccn 960

tgggaycarg argarmgncc ngcncarmgn gaytgywsnt tyccnggnyt nccnmgnca 1020
 cargaycarc cncaycayca rccnccnaay mgngcnggng cncnggnga rwsnytngar 1080
 tgyccngcng arytnmgnc ncartnccn carccnccnw snccngcngc ngtnccnmgn 1140
 ccnccnwsna ayccncngc nmngngnacn ytnaaracnw snaaytncc ngargarytn 1200
 mgnaargtnt tyathacnta ywsnatggay acngcnatgg argtngtnaa rttygtnaay 1260
 ttyytnytng tnaayggntt ycaracngcn athgayatht tygargaymg nathmgnggn 1320
 athgayatha thaartggat ggarmgntay ytnmgngaya aracngtnat gathathgtn 1380
 gcnathwsnc cnaartayaa rcargaygtn gargngcng arwsncaryt ngaygargay 1440
 garcayggny tncayacnaa rtayathcay mgnatgatgc arathgartt yathaarc 1500
 ggnwsnatga ayttymgntt yathccngtn ytnttyccna aygcnaaraa rgarcaygtn 1560
 ccnacntggy tncaraayac ncaygtntay wsntggccna araayaaraa raayathytn 1620
 ytnmgnytny tnmnggarga rgartaygtn gcncnccnm gnggncnyt nccnacnytn 1680
 cargtngtnc cnytn 1695

<210> 25

<211> 1323

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:rodent; surmised
Mus musculus

<220>

<221> CDS

<222> (1)..(1026)

<400> 25

cag gac ctc cct ggg cct ctg agg tcc agg gaa ttg cca cct cag ttt 48
 Gln Asp Leu Pro Gly Pro Leu Arg Ser Arg Glu Leu Pro Pro Gln Phe

1 5 10 15

gaa ctt gag agg tat cca atg aac gcc cag ctg ctg ccg ccc cat cct 96
 Glu Leu Glu Arg Tyr Pro Met Asn Ala Gln Leu Leu Pro Pro His Pro

20 25 30

tcc cca cag gcc cca tgg aac tgt cag tac tac tgc ccc gga ggg ccc 144
 Ser Pro Gln Ala Pro Trp Asn Cys Gln Tyr Tyr Cys Pro Gly Gly Pro

35 40 45

tac cac cac cag gtg cca cac ggc cat ggc tac cct cca gca gca gcc 192
 Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala

50 55 60

tac cag caa gta ctc cag cct gct ctg cct ggg cag gtc ctt cct ggg 240
 Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly

65 70 75 80

gca agg gca aga ggc cca cgc cct gtg cag aag gtc atc ctg aat gac	288
Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp	
85 90 95	
tcc agc ccc caa gac caa gaa gag aga cct gca cag aga gac ttc tct	336
Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser	
100 105 110	
ttc ccg agg ctc ccg agg gac cag ctc tac cgc cca cca tct aat gga	384
Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly	
115 120 125	
gtg gaa gcc cct gag gag tcc ttg gac ctt cct gca gag ctg aga cca	432
Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro	
130 135 140	
cat ggt ccc cag gct cca tcc cta gct gcc gtg cct aga ccc cct agc	480
His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser	
145 150 155 160	
aac ccc tta gcc cga gga act cta aga acc agc aat ttg cca gaa gaa	528
Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu	
165 170 175	
tta cgg aaa gtc ttt atc act tat tct atg gac aca gcc atg gag gtg	576
Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val	
180 185 190	
gtg aaa ttt gtg aac ttt ctg ttg gtg aac ggc ttc caa act gcg att	624
Val Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile	
195 200 205	
gac ata ttt gag gat aga atc cgg ggt att gat atc att aaa tgg atg	672
Asp Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met	
210 215 220	
gag cgc tat ctt cga gat aag aca gtg atg ata atc gta gca atc agc	720
Glu Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser	
225 230 235 240	
ccc aaa tac aaa cag gat gtg gaa ggc gct gag tcg cag ctg gac gag	768
Pro Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu	
245 250 255	
gac gag cat ggc tta cat act aag tac att cat cgg atg atg cag att	816
Asp Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile	
260 265 270	
gag ttc ata agt cag gga agc atg aac ttc aga ttc atc cct gtg ctc	864
Glu Phe Ile Ser Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu	
275 280 285	
ttc cca aat gcc aag aag gag cat gtg ccg acc tgg ctt cag aac act	912
Phe Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr	
290 295 300	
cat gtt tac agc tgg ccc aag aat aag aaa aac atc ctg ctg cgg ctg	960
His Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu	
305 310 315 320	

ctc agg gag gaa gag tat gtg gct cct ccc cga ggc cct ctg ccc acc 1008
 Leu Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr
 325 330 335

ctt cag gtg gta ccc ttg tgacgatggc cactccagct cagtgccagc 1056
 Leu Gln Val Val Pro Leu
 340

ctgtttctcac agcattcttc tagcggagct ggctgggtggc acccaggccc tggaacacct 1116

cttctacaga gtcctctgtc tcttgagtct gagttgtcct cgctgggctt ccagagcttc 1176

agtgcctgga tgctgcaggt gacagaaaca aacatctatg accacaaaaa ctctcatcac 1236

ttcagctact tttatgagtc ggtcagatgc tctgtgtcct tagaccagtc taaatcatgc 1296

tcaaataata aaatgattat tctttgt 1323

<210> 26

<211> 342

<212> PRT

<213> Unknown

<400> 26

Gln Asp Leu Pro Gly Pro Leu Arg Ser Arg Glu Leu Pro Pro Gln Phe
 1 5 10 15

Glu Leu Glu Arg Tyr Pro Met Asn Ala Gln Leu Leu Pro Pro His Pro
 20 25 30

Ser Pro Gln Ala Pro Trp Asn Cys Gln Tyr Tyr Cys Pro Gly Gly Pro
 35 40 45

Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala
 50 55 60

Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly
 65 70 75 80

Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp
 85 90 95

Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser
 100 105 110

Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly
 115 120 125

Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro
 130 135 140

His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser
 145 150 155 160

Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu
 165 170 175

Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val

180					185					190					
Val	Lys	Phe	Val	Asn	Phe	Leu	Leu	Val	Asn	Gly	Phe	Gln	Thr	Ala	Ile
	195						200					205			
Asp	Ile	Phe	Glu	Asp	Arg	Ile	Arg	Gly	Ile	Asp	Ile	Ile	Lys	Trp	Met
	210						215				220				
Glu	Arg	Tyr	Leu	Arg	Asp	Lys	Thr	Val	Met	Ile	Ile	Val	Ala	Ile	Ser
	225				230					235					240
Pro	Lys	Tyr	Lys	Gln	Asp	Val	Glu	Gly	Ala	Glu	Ser	Gln	Leu	Asp	Glu
				245					250					255	
Asp	Glu	His	Gly	Leu	His	Thr	Lys	Tyr	Ile	His	Arg	Met	Met	Gln	Ile
			260					265						270	
Glu	Phe	Ile	Ser	Gln	Gly	Ser	Met	Asn	Phe	Arg	Phe	Ile	Pro	Val	Leu
		275					280					285			
Phe	Pro	Asn	Ala	Lys	Lys	Glu	His	Val	Pro	Thr	Trp	Leu	Gln	Asn	Thr
	290					295					300				
His	Val	Tyr	Ser	Trp	Pro	Lys	Asn	Lys	Lys	Asn	Ile	Leu	Leu	Arg	Leu
	305					310				315					320
Leu	Arg	Glu	Glu	Glu	Tyr	Val	Ala	Pro	Pro	Arg	Gly	Pro	Leu	Pro	Thr
				325					330					335	
Leu	Gln	Val	Val	Pro	Leu										
			340												

<210> 27
 <211> 1026
 <212> DNA
 <213> reverse translation

<220>
 <221> misc_feature
 <222> (1)..(1026)
 <223> n amy be a, c, g, or t

<400> 27
 cargayytnc cnggnccnyt nmgnwsnmgn garytncnc cncarttyga rytngarmgn 60
 tayccnatga aygcncaryt nytncncncn cayccnwsnc cncargcncc ntggaaytgy 120
 cartaytayt gyccngnggg nccntaycay caycargtnc cncayggncay yggntayccn 180
 ccngcngcng cntaycarca rgtnytncar ccngcnytn cnggncargt nytncnggn 240
 gcnmgngcnm gnggnccnmg nccngtn car aargtnathy tnaaygayws nwsnccncar 300
 gaycargarg armgnccngc ncarmngay ttywsnttyc cnmgnytncc nmngaycar 360
 ytnaymgnc cncnwsnaa yggngtn gar gcncngarg arwsnytn ga yytnccngcn 420
 garytnmgnc cncayggnc nccargcnccn wsnytn gcn gngtnccnmg nccnccnwsn 480

aayccnytn g cnmgnggnac nytnmgnacn wsnaayytnc cngargaryt nmgnaaargtn 540
ttyathacnt aywsnatgga yacngcnatg gargtngtna arttygtnaa yttyytnytn 600
gtnaayggnt tycaracngc nathgayath ttygargaym gnathmgngg nathgayath 660
athaartgga tggarmgnta yytnmgngay aaracngtna tgathathgt ngcnathwsn 720
ccnaartaya arcargaygt ngarggngcn garwsncary tngaygarga ygarcaayggn 780
ytncayacna artayathca ymgngatgatg carathgart tyathwsnca rggngwsnatg 840
aayttymgnt tyathccngt nytnnttyccn aaygcnaara argarcaygt nccnacntgg 900
ytncaraaya cncaygtnta ywsntggccn aaraayaara araayathyt nytnmgnytn 960
ytmgngarg argartaygt ngcncncncn mgngngccny tncnacny ncartngtn 1020
ccnytn 1026

<210> 28
<211> 207
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<400> 28
Arg Lys Val Trp Ile Ile Tyr Ser Ala Asp His Pro Leu Tyr Val Asp
1 5 10 15
Val Val Leu Lys Phe Ala Gln Phe Leu Leu Thr Ala Cys Gly Thr Glu
20 25 30
Val Ala Leu Asp Leu Leu Glu Glu Gln Ala Ile Ser Glu Ala Gly Val
35 40 45
Met Thr Trp Val Gly Arg Gln Lys Gln Glu Met Val Glu Ser Asn Ser
50 55 60
Lys Ile Ile Val Leu Cys Ser Arg Gly Thr Arg Ala Lys Trp Gln Ala
65 70 75 80
Leu Leu Gly Arg Gly Ala Pro Val Arg Leu Arg Cys Asp His Gly Lys
85 90 95
Pro Val Gly Asp Leu Phe Thr Ala Ala Met Asn Met Ile Leu Pro Asp
100 105 110
Phe Lys Arg Pro Ala Cys Phe Gly Thr Tyr Val Val Cys Tyr Phe Ser
115 120 125
Glu Val Ser Cys Asp Gly Asp Val Pro Asp Leu Phe Gly Ala Ala Pro
130 135 140
Arg Tyr Pro Leu Met Asp Arg Phe Glu Glu Val Tyr Phe Arg Ile Gln
145 150 155 160

```
<210> 29
<211> 208
<212> PRT
<213> Unknown
```

```
<220>
<223> Description of Unknown Organism:rodent; surmised
      Mus musculus
```

<400> 29															
Arg 1	Lys	Val	Trp	Ile 5	Val	Tyr	Ser	Ala	Asp 10	His	Pro	Leu	Tyr	Val 15	Glu
Val	Val	Leu	Lys 20	Phe	Ala	Gln	Phe	Leu	Ile	Thr	Ala	Cys	Gly 30	Thr	Glu
Val	Ala	Leu 35	Asp	Leu	Leu	Glu	Glu 40	Gln	Val	Ile	Ser	Glu 45	Val	Gly	Val
Met	Thr 50	Trp	Val	Ser	Arg	Gln 55	Lys	Gln	Glu	Met	Val 60	Glu	Ser	Asn	Ser
Lys 65	Ile	Ile	Ile	Leu	Cys 70	Ser	Arg	Gly	Thr	Gln 75	Ala	Lys	Trp	Lys	Ala 80
Ile	Leu	Gly	Trp	Ala 85	Glu	Pro	Ala	Val	Gln 90	Leu	Arg	Cys	Asp	His 95	Trp
Lys	Pro	Ala	Gly 100	Asp	Leu	Phe	Thr	Ala 105	Ala	Met	Asn	Met	Ile 110	Leu	Pro
Asp	Phe 115	Lys	Arg	Pro	Ala	Cys	Phe 120	Gly	Thr	Tyr	Val	Val 125	Cys	Tyr	Phe
Ser 130	Gly	Ile	Cys	Ser	Glu	Arg 135	Asp	Val	Pro	Asp	Leu 140	Phe	Asn	Ile	Thr
Ser 145	Arg	Tyr	Pro	Leu	Met 150	Asp	Arg	Phe	Glu	Glu 155	Val	Tyr	Phe	Arg	Ile 160
Gln	Asp	Leu	Glu	Met 165	Phe	Glu	Pro	Gly	Arg 170	Met	His	His	Val	Arg 175	Glu
Leu	Thr	Gly	Asp 180	Asn	Tyr	Leu	Gln	Ser 185	Pro	Ser	Gly	Arg	Gln 190	Leu	Lys
Glu	Ala	Val	Leu	Arg	Phe	Gln	Glu	Trp	Gln	Thr	Gln	Cys 205	Pro	Asp	Trp

<210> 30
 <211> 190
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism:worm; surmised
 Caenorabditis elegans

<400> 30
 Val Lys Val Met Ile Val Tyr Ala Asp Asp Asn Asp Leu His Thr Asp
 1 5 10 15
 Cys Val Lys Lys Leu Val Glu Asn Leu Arg Asn Cys Ala Ser Cys Asp
 20 25 30
 Pro Val Phe Asp Leu Glu Lys Leu Ile Thr Ala Glu Ile Val Pro Ser
 35 40 45
 Arg Trp Leu Val Asp Gln Ile Ser Ser Leu Lys Lys Phe Ile Ile Val
 50 55 60
 Val Ser Asp Cys Ala Glu Lys Ile Leu Asp Thr Glu Ala Ser Glu Thr
 65 70 75 80
 His Gln Leu Val Gln Ala Arg Pro Phe Ala Asp Leu Phe Gly Pro Ala
 85 90 95
 Met Glu Met Ile Ile Arg Asp Ala Thr His Asn Phe Pro Glu Ala Arg
 100 105 110
 Lys Lys Tyr Ala Val Val Arg Phe Asn Tyr Ser Pro His Val Pro Pro
 115 120 125
 Asn Leu Ala Ile Leu Asn Leu Pro Thr Phe Ile Pro Glu Gln Phe Ala
 130 135 140
 Gln Leu Thr Ala Phe Leu His Asn Val Glu His Thr Glu Arg Ala Asn
 145 150 155 160
 Val Thr Gln Asn Ile Ser Glu Ala Gln Ile His Glu Trp Asn Leu Cys
 165 170 175
 Ala Ser Arg Met Met Ser Phe Phe Val Arg Asn Pro Asn Trp
 180 185 190

<210> 31
 <211> 178
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism:worm; surmised
 Caenorabditis elegans

<400> 31

Phe Lys Val Met Leu Val Cys Pro Glu Val Ser Gly Arg Asp Glu Asp
 1 5 10 15

Phe Met Met Arg Ile Ala Asp Ala Leu Lys Lys Ser Asn Asn Lys Val
 20 25 30

Val Cys Asp Arg Trp Phe Glu Asp Ser Lys Asn Ala Glu Glu Asn Met
 35 40 45

Leu His Trp Val Tyr Glu Gln Thr Lys Ile Ala Glu Lys Ile Ile Val
 50 55 60

Phe His Ser Ala Tyr Tyr His Pro Arg Cys Gly Ile Tyr Asp Val Ile
 65 70 75 80

Asn Asn Phe Phe Pro Cys Thr Asp Pro Arg Leu Ala His Ile Ala Leu
 85 90 95

Thr Pro Glu Ala Gln Arg Ser Val Pro Lys Glu Val Glu Tyr Val Leu
 100 105 110

Pro Arg Asp Gln Lys Leu Leu Glu Asp Ala Phe Asp Ile Thr Ile Ala
 115 120 125

Asp Pro Leu Val Ile Asp Ile Pro Ile Glu Asp Val Ala Ile Pro Glu
 130 135 140

Asn Val Pro Ile His His Glu Ser Cys Asp Ser Ile Asp Ser Arg Asn
 145 150 155 160

Asn Ser Lys Thr His Ser Thr Asp Ser Gly Val Ser Ser Leu Ser Ser
 165 170 175

Asn Ser