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(54) **Titre : PROCEDES DE TRAITEMENT DE LA DOULEUR ET DE L'INFLAMMATION DANS LES TISSUS NEURONAUX AU MOYEN D'ANTAGONISTES DE L'IL-31**
(54) **Title: METHODS OF TREATING PAIN AND INFLAMMATION IN NEURONAL TISSUE USING IL-31 ANTAGONISTS**

(57) **Abrégé/Abstract:**
Use of antagonists to IL-31 are used to treat inflammation and pain by inhibiting, preventing, reducing, minimizing, limiting or minimizing stimulation in neuronal tissues. Such antagonists include antibodies and fragments, derivative, or variants thereof. Symptoms such as pain, tingle, sensitization, tickle associated with neuropathies are ameliorated.

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(54) Title: METHODS OF TREATING PAIN AND INFLAMMATION IN NEURONAL TISSUE USING IL-31 ANTAGONISTS

(57) Abstract: Use of antagonists to IL-31 are used to treat inflammation and pain by inhibiting, preventing, reducing, minimizing, limiting or minimizing stimulation in neuronal tissues. Such antagonists include antibodies and fragments, derivative, or variants thereof. Symptoms such as pain, tingle, sensitization, tickle associated with neuropathies are ameliorated.

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METHODS OF TREATING PAIN AND INFLAMMATION IN NEURONAL TISSUE USING IL-31 ANTAGONISTS

BACKGROUND OF THE INVENTION

[1] The inflammatory process activates the nervous system causing inflammatory pain and a disruption in motor function. Stimulation of sensory nerves produces vasodialtion and plasma extravasation, leading to neurogenic inflammation and stimulation causing sensory irritation, hypersensitivity and pain.

[2] Neurogenic inflammation is caused by activation of nociceptive and thermal-sensitive endings in tissues and can be caused by innate conditions, such as autoimmune diseases, including allergy, by viral infection, as well as by injury. The neurogenic inflammation from these conditions can affect the somatosensory system, which consists of various sensory receptors responsible for sensations such as pressure, touch, temperature, pain, itch, tickle, tingle, and numbness. Activated nerves can perpetuate chronic inflammation by inducing secretion of cytokines, activating monocytes and chemotaxis.

[3] Proteins active in neurogenic inflammation can serve as targets for therapeutic approaches to diagnosis and treatment of diseases.

[4] An example of a drug used to treat pain is Neurontin (gabapentin), which is used to treat diabetic peripheral neuropathy as post-herpatic neuralgia. Thus, there is a need for additional medication to treat neuropathic pain.

DESCRIPTION OF THE INVENTION

[5] The following definitions are provided to facilitate understanding of the inventions described herein.

[6] The term "antibody" or "antibody peptide(s)" refers to an intact antibody, or a binding fragment thereof that competes with the intact antibody for specific binding and includes chimeric, humanized, fully human, and bispecific antibodies. In certain embodiments, binding fragments are produced by recombinant DNA techniques. In additional embodiments, binding fragments are produced by enzymatic or chemical cleavage of intact antibodies. Binding fragments include, but are not limited to, Fab, Fab', F(ab').sub.2, Fv, and single-chain antibodies.

[7] The term "isolated antibody" refers to an antibody that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes.

In embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and including more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

[8] A "variant" anti- IL-31 antibody, refers herein to a molecule which differs in amino acid sequence from a "parent" anti- IL-31 antibody amino acid sequence by virtue of addition, deletion and/or substitution of one or more amino acid residue(s) in the parent antibody sequence. In an embodiment, the variant comprises one or more amino acid substitution(s) in one or more hypervariable region(s) of the parent antibody. For example, the variant may comprise at least one, e.g. from about one to about ten, and from about two to about five, substitutions in one or more hypervariable regions of the parent antibody. Ordinarily, the variant will have an amino acid sequence having at least 75% amino acid sequence identity with the parent antibody heavy or light chain variable domain sequences, more preferably at least 80%, more preferably at least 85%, more preferably at least 90%, and most preferably at least 95%. Identity or homology with respect to this sequence is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the parent antibody residues, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. None of N-terminal, C-terminal, or internal extensions, deletions, or insertions into the antibody sequence shall be construed as affecting sequence identity or homology. The variant retains the ability to bind human IL-31 and preferably has properties which are superior to those of the parent antibody. For example, the variant may have a stronger binding affinity, enhanced ability to inhibit IL-31-induced stimulation of immune cells. To analyze such properties, one should compare a Fab form of the variant to a Fab form of the parent antibody or a full length form of the variant to a full length form of the parent antibody, for example, since it has been found that the format of the anti-IL-31 antibody impacts its activity in the biological activity assays disclosed herein. The variant antibody of particular interest herein is one which displays at least about 10 fold, preferably at least about 20 fold, and most preferably at least about 50 fold, enhancement in biological activity when compared to the parent antibody.

[9] The term "parent antibody" as used herein refers to an antibody which is encoded by an amino acid sequence used for the preparation of the variant. Preferably, the parent antibody has a human framework region and, if present, has human antibody constant region(s). For example, the parent antibody may be a humanized or human antibody.

[10] The term "agonist" refers to any compound including a protein, polypeptide, peptide, antibody, antibody fragment, large molecule, or small molecule (less than 10 kD), that increases the

activity, activation or function of another molecule. IL-31 agonists cause, for example: stimulation of NK cells, T cell subsets and B cell subsets and dendritic cells.

[11] The term "antagonist" refers to any compound including a protein, polypeptide, peptide, antibody, antibody fragment, large molecule, or small molecule (less than 10 kD), that decreases the activity, activation or function of another molecule. IL-31 antagonists cause: decreased immune function of NK cells, T cell subsets and B cell subsets and dendritic cells; bind IL-31 such that the interaction of IL-31 protein is blocked, inhibited, reduced, antagonized or neutralized.

[12] A "bivalent antibody" other than a "multispecific" or "multifunctional" antibody, in certain embodiments, is understood to comprise binding sites having identical antigenic specificity.

[13] A "bispecific" or "bifunctional" antibody is a hybrid antibody having two different heavy/light chain pairs and two different binding sites. Bispecific antibodies may be produced by a variety of methods including, but not limited to, fusion of hybridomas or linking of Fab' fragments. See, e.g., Songsivilai & Lachmann, Clin. Exp. Immunol. 79:315-321 (1990); Kostelny et al., J. Immunol. 148:1547-1553 (1992).

[14] The term “chimeric antibody” or “chimeric antibodies” refers to antibodies whose light and heavy chain genes have been constructed, typically by genetic engineering, from immunoglobulin variable and constant region genes belonging to different species. For example, the variable segments of the genes from a mouse monoclonal antibody may be joined to human constant segments, such as gamma 1 and gamma 3. A typical therapeutic chimeric antibody is thus a hybrid protein composed of the variable or antigen-binding domain from a mouse antibody and the constant domain from a human antibody, although other mammalian species may be used.

[15] The term “epitope” includes any protein determinant capable of specific binding to an immunoglobulin or T-cell receptor. Epitopic determinants usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains and usually have specific three dimensional structural characteristics, as well as specific charge characteristics. More specifically, the term "IL-31 epitope" as used herein refers to a portion of a IL-31 polypeptide having antigenic or immunogenic activity in an animal, preferably in a mammal, and most preferably in a mouse or a human. An epitope having immunogenic activity is a portion of a IL-31 polypeptide that elicits an antibody response in an animal. An epitope having antigenic activity is a portion of a IL-31 polypeptide to which an antibody immunospecifically binds as determined by any method well known in the art, for example, by immunoassays. Antigenic epitopes need not necessarily be immunogenic.

[16] The term "epitope tagged" when used herein refers to the anti-IL-31 antibody fused to an "epitope tag". The epitope tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the IL-31 antibody. The epitope tag preferably is sufficiently unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least 6 amino acid residues

and usually between about 8-50 amino acid residues (preferably between about 9-30 residues). Examples include the flu HA tag polypeptide and its antibody 12CA5 (Field et al. Mol. Cell. Biol. 8:2159-2165 (1988)); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto (Evan et al., Mol. Cell. Biol. 5(12):3610-3616(1985)); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky et al., Protein Engineering 3(6):547-553(1990)). In certain embodiments, the epitope tag is a "salvage receptor binding epitope". As used herein, the term "salvage receptor binding epitope" refers to an epitope of the Fc region of an IgG molecule (e.g., IgG_1, IgG_2, IgG_3, or IgG_4) that is responsible for increasing the in vivo serum half-life of the IgG molecule.

[17] The term "fragment" as used herein refers to a peptide or polypeptide comprising an amino acid sequence of at least 5 contiguous amino acid residues, at least 10 contiguous amino acid residues, at least 15 contiguous amino acid residues, at least 20 contiguous amino acid residues, at least 25 contiguous amino acid residues, at least 40 contiguous amino acid residues, at least 50 contiguous amino acid residues, at least 60 contiguous amino residues, at least 70 contiguous amino acid residues, at least contiguous 80 amino acid residues, at least contiguous 90 amino acid residues, at least contiguous 100 amino acid residues, at least contiguous 125 amino acid residues, at least 150 contiguous amino acid residues of the amino acid sequence of a IL-31 polypeptide or an antibody that immunospecifically binds to a IL-31 polypeptide.

[18] As used herein, the term "immunoglobulin" refers to a protein consisting of one or more polypeptides substantially encoded by immunoglobulin genes. One form of immunoglobulin constitutes the basic structural unit of an antibody. This form is a tetramer and consists of two identical pairs of immunoglobulin chains, each pair having one light and one heavy chain. In each pair, the light and heavy chain variable regions are together responsible for binding to an antigen, and the constant regions are responsible for the antibody effector functions.

[19] Full-length immunoglobulin "light chains" are encoded by a variable region gene at the NH2-terminus and a kappa or lambda constant region gene at the COOH--terminus. Full-length immunoglobulin "heavy chains", are similarly encoded by a variable region gene and one of the other aforementioned constant region genes (about 330 amino acids). Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, and define the antibody's isotype as IgG (including IgG1, IgG4), IgM, IgA, IgD and IgE, respectively. Within light and heavy chains, the variable and constant regions are joined by a "J" region of about 12 or more amino acids, with the heavy chain also including a "D" region of about 10 more amino acids. (See generally, Fundamental Immunology (Paul, W., ed., 2nd ed. Raven Press, N.Y., 1989), Ch. 7.

[20] An immunoglobulin light or heavy chain variable region consists of a "framework" region interrupted by three hypervariable regions. Thus, the term "hypervariable region" refers to the amino acid residues of an antibody which are responsible for antigen binding. The hypervariable region comprises amino acid residues from a "Complementarity Determining Region" or "CDR" (See,

Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991) and Chothia and Lesk, 1987, J. Mol. Biol. 196: 901-917). "Framework Region" or "FR" residues are those variable domain residues other than the hypervariable region residues as herein defined. The sequences of the framework regions of different light or heavy chains are relatively conserved within a species. Thus, a "human framework region" is a framework region that is substantially identical (about 85% or more, usually 90-95% or more) to the framework region of a naturally occurring human immunoglobulin. The framework region of an antibody, that is the combined framework regions of the constituent light and heavy chains, serves to position and align the CDR's. The CDR's are primarily responsible for binding to an epitope of an antigen.

[21] Accordingly, the term "humanized" immunoglobulin refers to an immunoglobulin comprising a human framework region and one or more CDR's from a non-human (usually a mouse or rat) immunoglobulin. The non-human immunoglobulin providing the CDR's is called the "donor" and the human immunoglobulin providing the framework is called the "acceptor". Constant regions need not be present, but if they are, they must be substantially identical to human immunoglobulin constant regions, i.e., at least about 85-90%, preferably about 95% or more identical. Hence, all parts of a humanized immunoglobulin, except possibly the CDR's, are substantially identical to corresponding parts of natural human immunoglobulin sequences. A "humanized antibody" is an antibody comprising a humanized light chain and a humanized heavy chain immunoglobulin. For example, a humanized antibody would not encompass a typical chimeric antibody as defined above, e.g., because the entire variable region of a chimeric antibody is non-human.

[22] As used herein, the term "human antibody" includes and antibody that has an amino acid sequence of a human immunoglobulin and includes antibodies isolated from human immunoglobulin libraries or from animals transgenic for one or more human immunoglobulin and that do not express endogenous immunoglobulins, as described, for example, by Kucherlapati et al. in U.S. Patent No. 5,939,598.

[23] The term "genetically altered antibodies" means antibodies wherein the amino acid sequence has been varied from that of a native antibody. Because of the relevance of recombinant DNA techniques in the generation of antibodies, one need not be confined to the sequences of amino acids found in natural antibodies; antibodies can be redesigned to obtain desired characteristics. The possible variations are many and range from the changing of just one or a few amino acids to the complete redesign of, for example, the variable or constant region. Changes in the constant region will, in general, be made in order to improve or alter characteristics, such as complement fixation, interaction with membranes and other effector functions. Changes in the variable region will be made in order to improve the antigen binding characteristics.

[24] In addition to antibodies, immunoglobulins may exist in a variety of other forms including, for example, single-chain or Fv, Fab, and $(Fab')_2$, as well as diabodies, linear antibodies, multivalent or multispecific hybrid antibodies (as described above and in detail in: Lanzavecchia et al., Eur. J. Immunol. 17, 105 (1987)) and in single chains (e.g., Huston et al., Proc. Natl. Acad. Sci. U.S.A., 85 5879-5883 (1988) and Bird et al., Science, 242:423-426 (1988).

(See, generally, Hood et al., "Immunology", Benjamin, N.Y., 2nd ed. (1984), and Hunkapiller and Hood, Nature, 323:15-16 (1986).

[25] As used herein, the terms "single-chain Fv," "single-chain antibodies," "Fv" or "scFv" refer to antibody fragments that comprises the variable regions from both the heavy and light chains, but lacks the constant regions, but within a single polypeptide chain. Generally, a single-chain antibody further comprises a polypeptide linker between the VH and VL domains which enables it to form the desired structure which would allow for antigen binding. Single chain antibodies are discussed in detail by Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenburg and Moore eds. Springer-Verlag, New York, pp. 269-315 (1994); see also International Patent Application Publication No. WO 88/01649 and U.S. Pat. Nos. 4,946,778 and 5,260,203.

In specific embodiments, single-chain antibodies can also be bi-specific and/or humanized.

[26] A "Fab fragment" is comprised of one light chain and the C_{H1} and variable regions of one heavy chain. The heavy chain of a Fab molecule cannot form a disulfide bond with another heavy chain molecule.

[27] A "Fab' fragment" contains one light chain and one heavy chain that contains more of the constant region, between the C_{H1} and C_{H2} domains, such that an interchain disulfide bond can be formed between two heavy chains to form a $F(ab')_2$ molecule.

[28] A "$F(ab')_2$ fragment" contains two light chains and two heavy chains containing a portion of the constant region between the C_{H1} and C_{H2} domains, such that an interchain disulfide bond is formed between two heavy chains.

[29] The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy chain variable domain (V_H) connected to a light chain variable domain (V_L) in the same polypeptide chain (V_H-V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993).

[30] The term "linear antibodies" refers to the antibodies described in Zapata et al. Protein Eng. 8(10):1057-1062 (1995). Briefly, these antibodies comprise a pair of tandem Fd segments (V_H-

C_{H1}-V_H-C_{H1}) which form a pair of antigen binding regions. Linear antibodies can be bispecific or monospecific.

[31] The term "immunologically functional immunoglobulin fragment" as used herein refers to a polypeptide fragment that contains at least the variable domains of the immunoglobulin heavy and light chains. An immunologically functional immunoglobulin fragment of the invention is capable of binding to a ligand, preventing binding of the ligand to its receptor, interrupting the biological response resulting from ligand binding to the receptor, or any combination thereof.

[32] The term "monoclonal antibody" refers to an antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced.

[33] The present invention is based in part upon the discovery that the subunits of the heterodimeric receptor which binds IL-31, e.g. IL-31Ra and OSMRb, are expressed on neural cells such as dorsal root ganglion cells. Thus the present invention encompasses the use of antagonists to IL-31 in inhibiting pain and inflammation and the symptoms of inflammatory bowel disease, Crohn's disease, pruritis, and neurogenic pain and sensitization. The present invention also encompases the use of IL-31 agonists in improving sensitization through stimulation of the dorsal root gangion cells.

[34] IL-31 is the HUGO name for a cytokine that has been previously described as Zcyto17rlig in a published U.S. patent application (See published U.S. patent application number 20030224487, U.S. Patent application serial number 10/352,554, filed January 21, 2003, now issued U.S. Patent Number 7,064,186; Sprecher, Cindy et al., 2003). The heterodimeric receptor for IL-31, comprises a heterodimer formed between IL-31Ra and OncostatinM receptor beta (OSMRb). IL-31Ra is the HUGO name for a protein called zcytor17 in commonly-owned U.S. published patent application number 20030215838, U.S. patent application serial number 10/351,157, filed January 21, 2003. The polynucleotide and polypeptide sequences for human IL-31 are shown in SEQ ID NOs: 1 and 2, respectively.The polynucleotide and polypeptide sequences for murine IL-31 are shown in SEQ ID NOs: 3 and 4, respectively. As used herein the term, IL-31 shall mean zcytor17lig as used in U.S. patent publication number 20030224487, as shown above. IL-31Ra has been previously described in commonly-owned U.S. patent application serial number 09/892,949 filed June 26, 2001.

[35] The amino acid sequence for the OSMR, and IL-31RA receptors indicated that the encoded receptors belonged to the Class I cytokine receptor subfamily that includes, but is not limited to, the receptors for IL-2, IL-4, IL-7, Lif, IL-12, IL-15, EPO, TPO, GM-CSF and G-CSF (for a review see, Cosman, "The Hematopoietin Receptor Superfamily" in Cytokine 5(2): 95-106, 1993). The zcytor17 receptor is fully described in commonly-owned PCT Patent Application No. US01/20484 (WIPO publication No. WO 02/00721).

[36] The present invention includes the use of anti-IL-31, including antagonists, antibodies, binding proteins, variants and fragments, having anti-IL-31 activity. The invention includes administering to a subject the anti-IL-31 molecule and contemplates both human and veterinary therapeutic uses. Illustrative veterinary subjects include mammalian subjects, such as farm animals and domestic animals.

[37] The native polynucleotide and polypeptide sequences for the "long" form of IL-31RA are shown in SEQ ID NOs:5 and 6, respectively. The native polynucleotide and polypeptide sequences for the "short" form of IL-31RA are shown in SEQ ID NOs:7 and 8, respectively. Additional truncated forms of IL-31RA polypeptide appear to be naturally expressed. Both forms encode soluble IL-31RA receptors. The "long" soluble IL-31RA polynucleotide and polypeptide sequences are shown in SEQ ID NOs:9 and 10, respectively. The "short" soluble IL-31RA polynucleotide and polypeptide sequences are shown in SEQ ID NOs:11 and 12, respectively. The native polynucleotide and polypeptide sequences for mouse IL-31RA are shown in SEQ ID NOs:13 and 14, respectively. The native polynucleotide and polypeptide sequences for human OSMRbeta are shown in SEQ ID NOs:15 and 16, respectively. See PCT applications WO 02/00721 and WO 04/003140.

[38] IL-31 antagonists include anti-IL31 molecules such as antibodies that bind IL-31, including, variants, fragments or derivatives thereof and that inhibit, limit, reduce, minimize, prevent, or neutralize the effect of IL-31 has on binding its cognate receptor.

[39] In situ expression analysis revealed that IL-31RA and OSMRbeta are expressed in the spinal cord and dorsal root ganglion cells in humans. See Example 1. Therefore, IL-31 molecules, their agonists, or antagonists play a role in the maintenance of neurons and neurogenic inflammation and stimulation. This indicates that IL-31 agonists, antagonists can be used to treat a variety of neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease, Parkinson's disease, peripheral neuropathies, and demyelinating diseases including multiple sclerosis. The tissue specificity of IL-31RA and OSMRb suggests that IL-31 may be a growth and/or maintenance factor in the spinal cord and brain which can be used to treat spinal cord, brain or peripheral nervous system injuries.

[40] Methods of measuring the ability of IL-31 to stimulate pain are known to one of skill in the art. For example, dorsal root gangion cells can be isolated and cultured. See Voilley, N. et al., J. Neurosci., 27(20):8026-8033, 2001. For example, dorsal root ganglion cells are prepared from Wistar adult male (5-7 weeks) and newborn rats by 0.1% collagenase dissociation and plating on collagen coated P35 dishes in DMEM plus 5% fetal calf serum. Similarly methods of isolating dorsal root ganglion cells are described by Steinhoff, M. et al. (See Steinhoff, M. et al., Nature Medicine, 6(2):151-157, 2000). Briefly, dorsal root ganglion cells are minced in cold Dulbeccos' modified Eagle's Medium (DMEM) and incubated in DMEM containing .05mg/ml trypsin, 1 mg/ml

collagenase, and .01 mg/ml DNAse I for 45-60 minutes at 37 degrees C. SBTI is added to neutralize trypsin and the suspension is centrifuged at about 1,000 g for 1 min. Neurons in the pellet are suspended in DMEM containg 10% fetal bovine serum, 5 ng/ml nerve growth factor, 2 mM glutamine, 1 mg/ml penicillin/streptomycin and DNAse I, and plated on glass coverslips coated with Matrigel. Neurons are cultured fro 3-5 days before use. Expression of IL-31Ra at the plasma membranes is verified by immunofluorescence using an antibody.

[41] To measure the effect of IL-31 on dorsal root ganglion stimulation, intracellular calcium ion concentration is measured in the cultured neurons as described by Steinhoff et al., supra. The neurons are incubated in Hank's balanced salt solution, 20 mM HEPES, pH 7.4 containing 5uM Fura-2/AM (Molecular Probes, Eugene, Oregon) for 1 h at 37 degrees C. Coverslips are washed, mounted in a chamber (1 ml volume) on a Zeiss 100 TV inveted microscope and observed using a Zeiss x40 Fluar objective. Fleuorescence is measured at 340 nm and 380 nm to allow determination of calcium. Cells are exposed to IL-31 with and without other sensitization agents , and inhibition in the presence of IL-31 antagonists is measured..

[42] To measure the ability of an IL-31antagonist on effect of IL-31 binding to its cognate heterodimeric receptor on dorsal root gangion, or neural cells in general, on pain several mediators of pain can be measured, such as for example, but not limited to, prostaglandins, substance P, CGRP, galanin, Neuropeptide Y, histamine, bradykinin, cannabinoids, and mediators of the arachinoid acid pathway.

[43] In addition to the above in vitro methods to measure the ability of antagonists to IL-31 pain-inducing effect of IL-31 on neural cells, several in vivo models are also useful. See, for example, Honore, P. et al., Neuroscience, 98(3):585-598, 2000. This article describes several models for inflammatory pain, neuropathic pain and cancer pain. For example, one model measures the effect of an antagonist to IL-31, such as a subcutaneous injection of IL-31, with and with out the antagonist molecule, into the plantar surface of the hindpaw of a mouse. The mouse is euthanized 3 days after injection peripheral edema is measured. The effect of the IL-31 antagonist molecule to inhibit, limit, minimize, reduce, prevent, or neutralize the edema is measured. Additonal in vivo models are spinal nerve ligation, sciatic nerve transaction, sarcoma-induced bone cancer, behavioral analysis, and effects of morophine.

[44] Another mouse model of pain is mechanical allodynia. See for example, Sweitzer, S.M. et al., J. Neuroimm., 125:82-93, 2002. Briefly, rats or mice are tested for mechanical allodynia with 2- and/or 12-g von Frey filaments. First the animals are acclimated to the procedure and baseline measurement are taken. The IL-31 is administered in varying amounts. Allodynia is characterized as an intense withdrawl of the paw to a normally non-noxious stimuli in response to IL-31 administration. Comparision is made with and without administration of the IL-31 antagonists molecule.

[45] A proinflammatory neuropeptide, Substance P (SP), is made the dorsal ganglia and then transported to the periphery by nociceptive nerves A and C (15). SP can induce itch by releasing histamine from the mast cell granules. In the skin, SP can also cause erythema, edema and neurogenic inflammation releasing histamine, IL -1, prostaglandins and lysosomal enzymes but is quickly degraded in the dermis (16). The prior oral administration of antihistamines inhibits the pruritus caused by SP. Capsaicin obtained from hot pepper applied locally depletes SP from cutaneous nerves, and so diminishes pruritus. As the receptor subunits for IL-31 are expressed in the dorsal root ganglion cells, administration of the IL-31 antagonist molecules can decrease the stimulation of these cells and may decrease Substance P that may be induced by IL-31 administration.

[46] The binding of IL-31 to its receptor, i.e., IL-31RA and OSMR beta, on dorsal root ganglion cells can stimulate the somatosensory system, which consists of various sensory receptors responsible for sensations such as pressure, touch, temperature, pain, itch, tickle, tingle, and numbness. The binding of IL-31 to its cognate receptor can result in neurogenic inflammation and stimulation, which may lead to release of additional factors that induce neurogenic stimulus. One group of factors that mediate pain is the prostaglandins, which also contribute to local inflammation. Thus, an IL-31 antagonist may have benefit in acute inflammatory pain commonly treated with NSAIDs, such as myalgia, headache, joint pains from acute injuries or chronic pain such as that caused by osteoarthritis. Such neurogenic stimulus can be the result of inflammation caused by, for example, autoimmune reactions, such as allergy, viral infection, such as varicella, and injury, such as burn or trauma. Thus, antagonists that interfere with signal transduction induced by the binding of the IL-31 ligand to its cognate receptor can be useful in reducing, limiting, preventing, or minimizing neurogenic inflammation and the stimulation of the somatosensory system. As such, antagonists of IL-31-induced signal transduction in dorsal root ganglion cells can be used to treat pain, itch, tingling, associated with autoimmune diseases, viral infection, and trauma. Moreover, since neurogenic inflammation can result in a hypersensitivity of the nerve after the initial insult, antagonists of IL-31 can be effective treatment of symptoms. For example, some shingles patients experience the sensory symptoms of pain and/or itch long after the viral infection has been cleared or minimized. The neuralgia that accompanies acute herpes zoster, and postherpetic neuralgia are likely due to inflammation of the dorsal root ganglia and trigeminal ganglia, where viral antigens attract T cells and other inflammatory cells. Long lasting pain may result from persistent inflammation of the dermatome following a robust antiviral response. Consequently, the level or stage of viral infection may not be representative of the sensory perception of the subject. Thus, the beneficial effect of antagonizing IL-31-induced signal transduction may extend beyond the immediate state of viral infection or trauma.

[47] Neuropathy and sensory deficiency involve pain and loss of sensitivity, and can be related to such diseases as, atopy, diabetes, multiple sclerosis, and hypertension, for example. As IL-

31RA and OSBRbeta are proteins that are expressed in the spinal cord and dorsal root ganglion cells, antagonists of IL-31 may be useful to treat pain and sensory deficiencies. For example, IL-31 antagonists can be delivered topically, subcutaneously, centrally, or systemically, to treat diabetic peripherlneuropathy, postherpatic peripheral neuropathy, as well as pain, in general, including pain as a symptom in burn patients.

[48] Burn injuries cause intense and prolonged pain that is intensified when the wound dressing is changed. Frequent dressing changes are necessary to prevent infection and aid healing. The amount of pain experienced by patients during wound care remains a worldwide problem for burn victims as well as a number of other patient populations. When patients are at rest pain associated with burn can be treated with opioids, which have some unwanted effects. However, during wound care such as daily bandage changes, wound cleaning, staple removals etc., opioids are not enough, with a majority of burn patients reporting severe to excruciating pain during wound care.

[49] Since both members of the heterodimer for IL-31, i.e., IL-31RA and OSMRbeta are expressed in dorsal root ganglion cells, an antagonist to IL-31, such as a neutralizing antibody is useful to prevent, minimimize, limit and/or treat pain, including pain associated with burn or neuropathy. In vivo models mimicking burn are well known to one skilled in the art.

[50] Persistent pain can provoke hyperplasia such that less than the original stimulus can cause increased pain, also called allodynia. As both the IL-31RA and OSMR beta subunits are expressed on dorsal root gangion cells, an antagonist to IL-31 induced signal transduction in neuronal cells bearing these subunits can help to mitigate symptoms of allodynia.

[51] Polypeptides of the present invention, such as IL-31, as well as agonists, fragments, variants and/or chimeras thereof, can also be used to increase sensitization in mammals. For example, IL-31 polypeptides of the present invention, including agonists, can be used to increase sensitization (pain, heat, or mechanical) when delivered locally or topically, systemically, or centrally and measured in any models or experiments known to one skilled in the art and/or described herein. Also, the polypeptides of the present invention can be administered to enhance the sensitivity of spinal and neuronal cells in order to improve the function of the surviving neurons to neurotransmitters and therefore might be effective in Parkinson's or Alzheimers disease, as well as paralysis.

[52] Similarly, where a patient has an increased sensitization to pain, antagonists to IL-31 can be used to decrease the sensation of pain in a patient with neuropathy. For example a patient with diabetic neuropathy and postherpatic neuropathy, have chronic, enhanced pain, the antagonist to IL-31 may be useful to limit, prevent or decrease the pain.

[53] As a receptor for a protein that is proinflammatory, the presence of IL-31RA and OSMRbeta in the spinal cord and dorsal root ganglion indicate that antagonists of IL-31can be used to reduce inflammation in these tissues. Thus, conditions such as meningitis may benefit from administration of the antagonists, including antibodies.

[54] Diseases which involve neurogenic inflammation and stimulation and can benefit from antagonizing IL-31 induced pain in neuronal tissues, including dorsal root ganglion cells include: chronic pain, migraines, arthritis, osteoarthritis, rheumatoid arthritis, polyneuropathy, diabetic peripheralneuropathy, pain subsequent to nerve severence (eg. post-surgical pain), inflammatory conditions that involve a neurogenic pain-producing component, such as inflammatory bowel disease, nephritis, certain metastic carcinomas, and inflammation of the blood vessels. These diseases can also be treated by an antagonist of IL-31 induced signal transduction. In addition, skin conditions, including radiation irritation and burns, chemical burns, multiple chemical sensitivity, prickly heat, rhinitis, thermal burns, sunburn, reddening of the skin and chemically induced lesions, and acute allergic reactions such as acute asthma attack and inflammation of the lung caused by chemical exposure, and hives as well as conjunctivitis and gum disease can be treated with IL-31 antagonists. Additionally, scapuloperoneal syndromes are heterogeneous neuromuscular disorders which are characterized by weakness in the distribution of shoulder girdle and peroneal muscles. Both neurogenic (scapuloperoneal spinal muscular atrophy, SPSMA) and myopathic (scapuloperoneal muscular dystrophy, SPMD) scapuloperoneal syndromes have been described. The chromosomal locus for SPMD has recently been assigned to chromosome 12q, which is the same locus as for IL-31. Thus, IL-31 antagonists can be used to treat these diseases.

[55] In the United States approximately 500,000 people suffer from inflammatory bowel disease, which can involve either or both the small and large bowel. Ulcerative colitis and Crohn's disease are the best-known forms of inflammatory bowel disease, and both are categorized as "idiopathic" inflammatory bowel disease because the etiology for them is unknown.

[56] Crohn's disease can involve any part of the gastrointenstinal tract, but most frequently involves the distal small bowel and colon. Inflammation can produce anything from a small ulcer over a lymphoid follicle to a deep fissuring ulcer to transmural scarring and chronic inflammation. Although the etiology is unknown, infectious and immunologic mechanisms have been proposed. Symptoms are variable and can include diarrhea, fever, and pain, as well as extra-intestinal manifestations of arthritis, uveitis, erythema nodosum, and ankylosing spondylitis.

[57] The traditional approach to treating inflammatory bowel disease is immunosuppression with azathioprine (see, for example, Rutgeerts, J. Gastroenterol. Hepatol. 17(Suppl.):S176-85 (2002)). More recently, the chimeric monoclonal anti-tumor necrosis factor antibody, infliximab, has been used to target specific pathogenic disease mechanisms, and allows thorough suppression of the disease process and healing of the bowel in the long term. However, this therapy is associated with problems of immunogenicity. The formation of antibodies to infliximab interferes with efficacy and is associated with infusion reactions.

[58] Irritable bowel syndrome (IBS) is a chronic functional gastrointestinal disorder. It is a heterogeneous condition characterized by a variety of bowel symptoms including abdominal pain

and bloating which are usually associated with altered bowel habit (Collins et al, 2001). It is estimated that between 12 and 20% of the U.S. population suffer from this condition. Differing criteria have been proposed for defining IBS, including the Manning criteria (Manning et al, 1978), the Rome criteria (Thompson et al, 1992), and most recently Rome II (Thompson et al., 1999). Research reports on IBS frequently classify patients with IBS into the two subtypes of constipation predominant (CON) and diarrhea predominant (DIA) and sometimes include a third subtype of alternating pattern (ALT).

[59] Anti-IL-31 molecules, antagonists, antibodies, binding proteins, variants and fragments, are useful in treating, detecting, and pain associated with Inflammatory Bowel Disease (IBD) and Irritable Bowel Syndrome (IBS).

[60] Inflammatory Bowel Disease (IBD) can affect the colon and/or rectum (Ulcerative colitis), or the small and large intestine (Crohn's Disease). The pathogenesis of these diseases is unclear, but they involve chronic inflammation of the affected tissues. Potential therapeutics include anti-IL-31 omolecules, including, anti-IL-31 antibodies, other binding proteins, variants, fragments, chimeras, and other IL-31 antagonists. These molecules could serve as a valuable therapeutic to reduce inflammation and pathological effects in IBD and related diseases.

[61] Ulcerative colitis (UC) is an inflammatory disease of the large intestine, commonly called the colon, characterized by inflammation and ulceration of the mucosa or innermost lining of the colon. This inflammation causes the colon to empty frequently, resulting in diarrhea. Symptoms include loosening of the stool and associated abdominal cramping, fever and weight loss. Although the exact cause of UC is unknown, recent research suggests that the body's natural defenses are operating against proteins in the body which the body thinks are foreign (an "autoimmune reaction"). Perhaps because they resemble bacterial proteins in the gut, these proteins may either instigate or stimulate the inflammatory process that begins to destroy the lining of the colon. As the lining of the colon is destroyed, ulcers form, releasing mucus, pus and blood. The disease usually begins in the rectal area and may eventually extend through the entire large bowel. Repeated episodes of inflammation lead to thickening of the wall of the intestine and rectum with scar tissue. Death of colon tissue or sepsis may occur with severe disease. The symptoms of ulcerative colitis vary in severity and their onset may be gradual or sudden. Attacks may be provoked by many factors, including respiratory infections or stress. Thus, the anti-IL-31 molecules of the present invention can be useful to treat and or detect UC.

[62] Although there is currently no cure for UC available, treatments are focused on suppressing the abnormal inflammatory process in the colon lining. Treatments including corticosteroids immunosuppressives (eg. azathioprine, mercaptopurine, and methotrexate) and aminosalicytates are available to treat the disease. However, the long-term use of immunosuppressives such as corticosteroids and azathioprine can result in serious side effects

including thinning of bones, cataracts, infection, and liver and bone marrow effects. In the patients in whom current therapies are not successful, surgery is an option. The surgery involves the removal of the entire colon and the rectum.

[63] There are several animal models that can partially mimic chronic ulcerative colitis. The most widely used model is the 2,4,6-trinitrobenesulfonic acid/ethanol (TNBS) induced colitis model, which induces chronic inflammation and ulceration in the colon. When TNBS is introduced into the colon of susceptible mice via intra-rectal instillation, it induces T-cell mediated immune response in the colonic mucosa, in this case leading to a massive mucosal inflammation characterized by the dense infiltration of T-cells and macrophages throughout the entire wall of the large bowel. Moreover, this histopathologic picture is accompanied by the clinical picture of progressive weight loss (wasting), bloody diarrhea, rectal prolapse, and large bowel wall thickening (Neurath et al. Intern. Rev. Immunol. 19:51-62, 2000).

[64] Another colitis model uses dextran sulfate sodium (DSS), which induces an acute colitis manifested by bloody diarrhea, weight loss, shortening of the colon and mucosal ulceration with neutrophil infiltration. DSS-induced colitis is characterized histologically by infiltration of inflammatory cells into the lamina propria, with lymphoid hyperplasia, focal crypt damage, and epithelial ulceration. These changes are thought to develop due to a toxic effect of DSS on the epithelium and by phagocytosis of lamina propria cells and production of TNF-alpha and IFN-gamma. DSS is regarded as a T cell-independent model because it is observed in T cell-deficient animals such as SCID mice.

[65] The administration of IL-31 antagonists or binding partners to these TNBS or DSS models can be used to measure the amelioration of symptoms and alter the course of gastrointestinal disease. IL-31 or may play a role in the inflammatory response and pain associated with colitis, and the neutralization of IL-31 activity by administrating antagonists is a potential therapeutic approach for IBD.

[66] Irritable Bowel Syndrome is one of the most common conditions in the gastrointestinal clinic. Yet, diagnosis and treatment for IBS remain limited. As the expression of IL-31 and IL-31RA1 have been correlated with upregulaiton of Crohn's disease (See Example 5). IL-31 antagonists, including anti-IL-31 antibodies, other binding proteins, variants, fragments, chimeras, and other IL-31 antagonists are useful in reducing symptoms and treatment of the disease.

[67] The administration of IL-31 antagonists or binding partners to a patient with IBD or IBS can be used to ameliorate symptoms and alter the course of gastrointestinal disease. IL-31 may play a role in the inflammatory response in colitis, and the neutralization of IL-31 activity by administrating antagonists is a potential therapeutic approach for IBD and/or IBS.

[68] For disorders related to IBS and IBD, clinical signs of improved function include, but are not limited to, reduction in pain, cramping and sensitivity, reduction in diarrhea and improved

stool consistency, reduced abdominal distension, and increased intestinal transit. Improvement can also be measured by a decrease in mean Crohn's Disease Activity Index (CDAI). See Best. W. et al., Gasttoenterology 70: 439-44, 1976. Additonally, improved function can be measured by a quality of life assessment as described by Irvine et al. (Irvine, E. et al., Gasttoenterology 106: 287-96, 1994.

[69] Animal models of irritable bowel syndrome are described by Mayer and Collins. Gastroenterol. 122:2032-2048 (2002). These models can be divided into those that are mediated primarily by CNS-directed mechanisms ("Stress Memory" models) and those with primary gut-directed etiologies ("Pain Memory" and "Immune Memory" models). In one model, animals are surgically prepared with electrodes implanted on the proximal colon and striated muscles, and catheters implanted in lateral ventricles of the brain. Rectal distension is performed by inflation of a balloon rectally inserted, and the pressure eliciting a characteristic visceromotor response is measured. A test compound, such as IL-31 antagonist and/or variants or antagonists, is administered via the appropriate route (p.o., i.p., s.c., i.v., or i.m.) and at the appropriate time (i.e. ~ 20 min, if i.p. or i.c.v.) prior to distention. Test compound is evaluated for its ability to affect colonic motility, abdominal contractions, and visceral pain.

[70] Additionally, disorders associated with inflammation of the intestine can be treated with the IL-31 antagonists such as fragments, agonists and antagonists thereof described herein. For example, Irritable Bowel Syndrome (IBS) is characterized by a very broad spectrum of symptoms (pain; bouts of diarrhea and/or constipation; abnormal gastrointestinal motility). It is difficult to pinpoint the etiology, and may have components related to stress, genetics, and/or inflammation. Simiarly, the anti-IL-31 molecules of the present invention, including antibodies and binding partners, can be used to treat Inflammatory Bowel Disease, (including colitis and Crohn's disease). IBD is more serious than IBS, and is characterized by diarrhea, pain, and malnutrition. Patients with IBD often have increased risk of gastrointestinal cancer.

[71] Gastrointestinal motor activity can be measured in a dog model as follows: Dogs are anesthetized and the abdominal cavity opened. Extraluminal force transducers (sensor to measure contraction) are sutured onto five (5) sites, i.e., the gastric antrum, 3 cm proximal to the pyloric ring, the duodenum, 5 cm distal to the pyloric ring, the jejunum, 70 cm distal to the pyloric ring, the ileum, 5 cm proximal to the ileum-colon junction, and the colon, 5 cm distal to the ileum-colon junction. The lead wires of these force transducers are taken out of the abdominal cavity and then brought out through a skin incision made between the scapulae, at which a connector is connected. After the operation, a jacket protector is placed on the dog to protect the connector. Measurement of the gastrointestinal motor activity is started two weeks after the operation. For ad libitum measurement, a telemeter (electrowave data transmitter) is connected with the connector to determine the contractive motility at each site of the gastrointestinal tract. The data is stored in a computer via a telemeter for analysis. A test compound, such as IL-31 antagonist is administered via the appropriate route (p.o.,

i.v., i.p., s.c., i.m.) at the appropriate time point to assess its ability to affect gastrointestinal motor activity. This can be performed in normal dogs or dogs in which gastroparesis/ileus has been induced. The above method is a modification of those in Yoshida. and Ito. J. Pharmacol. Experiment. Therap. 257, 781-787 (1991) and Furuta et al. Biol. Pharm. Bull. 25:103-1071 (2002).

[72] IL-31 may be a trigger for reactivation of latent viral infections, such as varicella infection. In primary varicella zoster virus (VZV) infection, the T cells most likely to be infected by varicella zoster virus are CD4 positive memory T cells expressing CLA and CCR4. These are skin-homing T cells, which may enhance cell-associated viremia and the transport of infectious virus to the skin and DRG. These cells are also the primary producers of IL-31. Thus, IL-31 in primary VZV infection may contribute to the itch/pain involved in the skin lesions. Reactivation of latent virus in DRG induces VZV-specific T cell responses, which contribute to the neurogenic inflammation. Skin-homing T cells are most easily infected with VZV, and *in vivo* transfer of virus from T cells to DRG has been observed. Postherpetic neuralgia is one of the major complications of herpes zoster caused by the reactivation of varicella-zoster virus and is characterized by severe pain. See Sato-Takeda, M. et al., Anesthesiology. 2006 104(5):1063-9. This reference also teaches a mouse model of postherpetic pain, which corresponds to postherpetic neuralgia. Briefly, BALB/c mice (MHC haplotype: H-2), C57BL/6 mice (MHC haplotype: H-2), and BALB/b mice, a congenic BALB/c strain with H-2, are transdermally inoculated on the hind paw with Herpes simplex virus type I. Unilaterally zosteriform skin lesion and pain-related responses (acute herpetic pain) are caused, and some mice show pain-related responses (postherpetic pain) after the cure of skin lesions. Herpes simplex virus type I antigen and CD3-positive cells are immunostained in the dorsal root ganglion in the acute phase. See also Argoff, C.E., et al., J Pain Symptom Manage. 2004 Oct;28(4):396-411. Thus, antagonists to IL-31may be useful to limit or prevent reactivation of viral infections with varicella.

[73] Mouse models for experimental allergic encephalomyelitis (EAE) has been used as a tool to investigate both the mechanisms of immune-mediated disease, and methods of potential therapeutic intervention. The model resembles human multiple sclerosis, and produces demyelination as a result of T-cell activation to neuroproteins such as myelin basic protein (MBP), or proteolipid protein (PLP). Inoculation with antigen leads to induction of CD4+, class II MHC-restricted T-cells (Th1). Changes in the protocol for EAE can produce acute, chronic-relapsing, or passive-transfer variants of the model (Weinberg et al., J. Immunol. 162:1818-26, 1999; Mijaba et al., Cell. Immunol. 186:94-102, 1999; and Glabinski, Meth. Enzym. 288:182-90, 1997). Administration of IL-31 antagonists or other soluble and fusion proteins may be useful to ameliorate symptoms and alter the course of disease.

[74] An antagonist to IL-31-induced signal transduction in dorsal root gangion cells can be useful to treat pruritus uraemicus; pruritis from hepatitis, hepatic failure, or cholestasis; from scabies

or athletes's foot; from pruritis associated with pregnancy; from pruritis in dualysis patients; and from pruritis from anaesthasia and psychological disorders as follows.

[75] Pruritus uraemicus or renal itch is an often intolerable symptom of chronic renal insufficiency (Blachley JD, Blankenship DM, Menter A et al. Uremic pruritus: skin divalent ion content and response to ultraviolet phototherapy. Am J Kidney Dis 1985; 5: 237-41.) being present in about 13 % of the cases; secondary skin lesions due to scratching can be seen. It is even more common in patients undergoing peritoneal dialysis or hemodialysis (Murphy M, Carmichael AJ. Renal itch. Clin Exp Dermatol 2000; 25: 103-6.); it can be localized or generalized. Itching is not present in acute renal failure. The treatment of renal pruritus is based on intensive and efficient dialysis to remove pruritogenic substances from the blood, and on the use of non-complement-activating membranes. One can also use UV therapy, emollient ointments, activated charcoal, cholestyramine (4 grams twice a day), phosphate binding agents. Sometimes parathyroidectomy is necessary.

[76] Pain antagonizes itch. See, for example, Ward, L. et al., Pain 64:129-138, 1996. As such a mediator of pain, such as an IL-31 antagonist can be used to treat pain associated with itch, thereby ameliorating not only the itch, or scratching behavior, but also the associated pain.

[77] Pruritus is a well-recognized manifestation among patients with liver diseases and intrahepatic or posthepatic cholestasis. Hepatic diseases leading to pruritus include primary biliary cirrhosis, B and C viral hepatitis, primary sclerosing cholangitis, carcinoma of bile ducts, alcoholic cirrhosis, autoimmune hepatitis and others. The pruritus is generalized and more intense on hands, feet and around tight-fitting clothes, while face, neck and genital area are rarely involved.

[78] Generalized pruritus is present in 1-8% of pregnant women. Pruritus gravidarum can be differentiated from pruritic dermatoses in pregnancy, such as pemphigoid gestationis (herpes gestationis), papular and pruritic dermatosis of pregnancy and others. Pruritus gravidarum manifests without any rash mostly in the third trimester of pregnancy, but it may also appear earlier, firstly on the abdomen and then becomes generalized. This symptom usually tends to be worse at night and disappears after delivery (within 1-4 weeks). Probably it is associated with intrahepatic cholestasis, as there is an increase of gamma GT and alkaline phosphatase, and sometimes also of direct bilirubin level in these patients. Pruritus is more frequent in multiple pregnancies and can recur in subsequent pregnancies or during the use of oral contraceptives. Additonally, pruritic urticarial papulas and plaques of pregnancy (PUPP), the most common dermatosis associated with pregnancy, does not respond to antihistamines and often persists beyond parturition.

[79] Some hematological disorders are known to be associated with pruritus. In polycythemia rubra vera with overproduction of all three hematopoietic cell lines, patients typically experience severe itch located on the trunk, but sparing the face, hands and feet, a few minutes after contact with warm water. Water-induced itching (aquagenic pruritus, or bath itch) can be present in

70% of the patients. The itch can last for about 15 minutes to one hour, and be so severe that the patients refuse to bathe. In the last decades pruritus has been described in patients with graft versus host reactions after bone marrow transplantation.

[80] Chronic delivery of IL-31 induces pruritis and alopecia in mice followed by the development of skin lesions resembling dermatitis suggesting that IL-31 may induce itching. See See Dillon S.R., et al., *Nat Immunol*: 5, 752 (2004). The involvement of IL-31 was tested in induction of the itch response by two methods as shown in Example 2: (i) capsaicin treatment of IL-31-treated mice and (ii) IL-31 treatment of Tac1 knockout mice, which have significantly reduced nociceptive pain responses because of lack of expression of neuropeptides. In addition, whether neutralization of IL-31 in IL-31 treated mice could prevent pruritis and alopecia was tested in Example 2.

[81] NC/Nga Mice spontaneously develop AD-like lesions that parallel human AD in many aspects, including clinical course and signs, histophathology and immunopathology when housed in non-specified pathogen –free (non-SPF) conditions at around 6-8 weeks of age. In contrast, NC/Nga mice kept under SPF conditions do not develop skin lesions. However, onset of spontaneous skin lesions and scratching behaviour can be synchronized in NC/Nga mice housed in a SPF facility by weekly intradermal injection of crude dust mite antigen. See Matsuoka H., et al., Allergy: 58, 139 (2003). Therefore, the development of AD in NC/Nga is a useful model for the evaluation of novel therapeutics for the treatment of AD.

[82] In addition to the NC/Nga model of spontaneous AD, epicutaneous sensitization of mice using OVA can also be used as a model to induce antigen-dependent epidermal and dermal thickening with a mononuclear infiltrate in skin of sensitized mice. This usually coincides with elevated serum levels of total and specific IgE, however no skin barrier dysfunction or pruritus normally occurs in this model. See Spergel J.M., et al., J Clin Invest, 101: 1614, (1998). This protocol can be modified in order to induce skin barrier disregulation and pruritis by sensitizing DO11.10 OVA TCR transgenic mice with OVA. Increasing the number of antigen-specific T cells that could recognize the sensitizing antigen may increase the level of inflammation in the skin to induce visible scratching behaviour and lichenification/scaling of the skin.

[83] Both the NC/Nga spontaneous AD model and the OVA epicutaneous DO11.10 model can be used to measure expression of IL-31 and IL-31RA in AD, as well as the ability of the antagonists described herein to inhibit, reduce, or neutralize the effects of IL-31. The antagonists described herein are useful to inhibit scratching associated with dermatitis and pruritic diseases including atopic dermatitis, prurigo nodularis, and eczema. In AD, the scratching behavior provoked by intensely itchy skin is believed to aggravate disease by breaking down skin barrier functions and activating keratinocytes, leading to chemokine production and increased inflammation. Many clinicians view AD as a self-propagating cycle, since lesions formed by frequent scratching are subject to infection and further antigen stimulation. The fact that patients with near total involvement

of body surface area may have unaffected skin in regions that are hard to scratch lends credence to this hypothesis. By preventing pruritis, administration of antagonists of IL-31 or its receptor can be effective in treating pruritic disease by decreasing IL-31-induced keratinocyte activation and neurological stimulation, thus breaking the link between inflammation and pruritis,. The reduction in pruritis could also decrease secretion of neurostimulatory factors and reduce the inflammation and excoriations associated with constant scratching, leading to an improvement in disease scores and/or a longer duration between disease flares. An inhibition, reduction, or prevention of scratching, alone, can be effective in treating pruritic diseases including, but not limited to, atopic dermatitis, prurigo nodularis, and eczema, since cessation of scratching will stop progression of dermatitis, the development of which is dependent on scratching.

[84] As used herein, the term "antibodies" includes polyclonal antibodies, affinity-purified polyclonal antibodies, monoclonal antibodies, and antigen-binding fragments, such as F(ab')2 and Fab proteolytic fragments. Genetically engineered intact antibodies or fragments, such as chimeric antibodies, Fv fragments, single chain antibodies and the like, as well as synthetic antigen-binding peptides and polypeptides, are also included. Non-human antibodies may be humanized by grafting non-human CDRs onto human framework and constant regions, or by incorporating the entire non-human variable domains (optionally “cloaking” them with a human-like surface by replacement of exposed residues, wherein the result is a “veneered” antibody). In some instances, humanized antibodies may retain non-human residues within the human variable region framework domains to enhance proper binding characteristics. Through humanizing antibodies, biological half-life may be increased, and the potential for adverse immune reactions upon administration to humans is reduced. Moreover, human antibodies can be produced in transgenic, non-human animals that have been engineered to contain human immunoglobulin genes as disclosed in WIPO Publication No. WO 98/24893. It is preferred that the endogenous immunoglobulin genes in these animals be inactivated or eliminated, such as by homologous recombination.

[85] Antibodies are considered to be specifically binding if: 1) they exhibit a threshold level of binding activity, and 2) they do not significantly cross-react with related polypeptide molecules. A threshold level of binding is determined if anti-IL-31 antibodies herein bind to a IL-31 polypeptide, peptide or epitope with an affinity at least 10-fold greater than the binding affinity to control (non-IL-31) polypeptide. It is preferred that the antibodies exhibit a binding affinity (Ka) of 106 M-1 or greater, preferably 107 M-1 or greater, more preferably 108 M-1 or greater, and most preferably 109 M-1 or greater. The binding affinity of an antibody can be readily determined by one of ordinary skill in the art, for example, by Scatchard analysis (Scatchard, G., Ann. NY Acad. Sci. 51: 660-672, 1949).

[86] Whether anti-IL-31 antibodies do not significantly cross-react with related polypeptide molecules is shown, for example, by the antibody detecting IL-31 polypeptide but not

known related polypeptides using a standard Western blot analysis (Ausubel et al., ibid.). Examples of known related polypeptides are those disclosed in the prior art, such as known orthologs, and paralogs, and similar known members of a protein family. Screening can also be done using non-human IL-31, and IL-31 mutant polypeptides. Moreover, antibodies can be "screened against" known related polypeptides, to isolate a population that specifically binds to the IL-31 polypeptides. For example, antibodies raised to IL-31 are adsorbed to related polypeptides adhered to insoluble matrix; antibodies specific to IL-31 will flow through the matrix under the proper buffer conditions. Screening allows isolation of polyclonal and monoclonal antibodies non-crossreactive to known closely related polypeptides (Antibodies: A Laboratory Manual, Harlow and Lane (eds.), Cold Spring Harbor Laboratory Press, 1988; Current Protocols in Immunology, Cooligan, et al. (eds.), National Institutes of Health, John Wiley and Sons, Inc., 1995). Screening and isolation of specific antibodies is well known in the art. See, Fundamental Immunology, Paul (eds.), Raven Press, 1993; Getzoff et al., Adv. in Immunol. 43: 1-98, 1988; Monoclonal Antibodies: Principles and Practice, Goding, J.W. (eds.), Academic Press Ltd., 1996; Benjamin et al., Ann. Rev. Immunol. 2: 67-101, 1984. Specifically binding anti-IL-31 antibodies can be detected by a number of methods in the art, and disclosed below.

[87] Preparation of monoclonal antibodies is well known to one skilled in the art. The purified mature recombinant human IL-31 polypeptide (amino acid residues 27 (Leu) to 167 (Thr) of SEQ ID NO:2) or the mouse ortholog, produced from expression systems can be used to generate monoclonal antibodies.

[88] The effect of administering the antagonists of IL-31 mediated signal transduction can be measured *in vivo* by a reduction, inhibition, prevention, minimization, neutralization of inflammation, of skin or dermal thickening, of recruitment of lymphocytes, and acanthosis, for example, and other symptoms or composites of symptoms, such as the Eczema Area and Severity Index (EASI), that are evident to one skilled in the art. Additional effects could include a change or decrease in the production of cytokines or chemokines by lesional skin, reduction in an atopy patch test score, and decrease in release of soluble factors such as cytokines, chemokines or neuropeptides, as measured by intradermal microdialysis or other methods. Assessments of degree of itch or pain can be measured using clinically approved instruments or tools such as the Visual Analogue Scale. Frequency of scratching can be monitored by limb movement meters, piezoelectric transducer devices attached to the fingernails, or time-lapse infrared photography or videography of nocturnal scratching in patients. Other methods for assessing a decrease in pain or itch are evident to one skilled in the art.

[89] Monoclonal antibodies purified from tissue culture media are characterized for their utility in an ELISA for the quantitative determination of recombinant and native human IL-31. The antibodies are selected and a quantitative assay is developed.

[90] Monoclonal antibodies purified from tissue culture media are characterized for their ability to block or reduce the receptor binding activity ("neutralization assay") of purified recombinant huIL-31 on neural cells expressing the IL-31Ra and OSMRb. A number of "neutralizing" monoclonal antibodies are identified in this manner. Hybridomas expressing the neutralizing monoclonal antibodies to human IL-31 described can then be deposited with the American Type Tissue Culture Collection (ATCC; Manassas VA) patent depository as original deposits under the Budapest Treaty.

[91] Five rat anti-mouse hybridomas were generated in a similar fashion and were given the following clone designations: clone 271.9.4.2.6, clone 271.26.6.6.1, clone 271.33.1.2.2, clone 271.33.3.2.1, and clone 271.39.4.6.5. The monoclonal antibodies produced by these clones were characterized in a number of ways including binning (i.e, determining if each antibody could inhibit the binding of any other binding), relative affinity, and neutralization. The monoclonal antibodies appear to fall into two separate bins with clone 271.33.3.2.1 binding to a separate epitope than the other four.

[92] Monoclonal antibodies in tissue culture media are characterized for their ability to block or reduce receptor binding when grown in the presence of the purified recombinant proteins human IL-31.

[93] Bidnding affinity of the monoclonal antibodies can be generated. Goat-anti-Rat IgG-Fc gamma specific Antibody (Jackson) is immobilized onto a CM5 Biacore chip. The assay is optimized to bind each mAb onto the anti-Rat capture surface and then a concentration series of IL-31 is injected across the mAb to see association (Ka) and dissociation (Kd). After each run, the surface is regenerated back to the anti-Rat Antibody with 2 injections of 20mM HCl. Data is generated for each and evaluation software (BIAevaluation software version 3.2, Pharmacia BIAcore, Uppsala, Sweden) is used to assess the kinetics of the anti-IL-31 antibody binding to the IL-31 protein

[94] Biochemical confirmation that the target molecule, IL-31, recognized by the putative anti-IL-31 mAbs is indeed IL-31 are performed by standard immunoprecipitation followed by SDS-PAGE analysis or western blotting procedures, both employing soluble membrane preparations from IL-31 transfected versus untransfected Baf3 cells. The mAbs are tested for their ability to specifically immunoprecipitate or western blot the soluble IL-31-muFc protein.

[95] Monoclonal antibodies to IL-31 are described in commonly-owned, U.S. Patent application 11/430,066, filed May 8, 2006, U.S. published patent application number 2006-0275296. These monoclonoal antibodies were purified from tissue culture media were characterized for their ability to block or inhibit the ability of IL-31 to bind to its receptor in a neutralization assay. Twenty "neutralizing" monoclonal antibodies were identified in this manner. The monoclonal antibodies produced by these clones were characterized in a number of ways including binning (i.e, determining if each antibody could inhibit the binding of any other binding), relative affinity, and neutralization.

The ten good neutralizing antibodies appear to be in the same bin, with the other monoclonal antibodies grouping into three separate bins. In addition, eight of the good neutralizing antibodies are IgG1 isotype and the other two are IgG2a isotype. Such monoclonal antibodies can be IgG1 or IgG4 so as to minimize complement binding and ADCC activity.

[96] Hybridomas expressing the neutralizing monoclonal antibodies to human IL-31 described above were deposited with the American Type Tissue Culture Collection (ATCC; Manassas VA) patent depository as original deposits under the Budapest Treaty and were given the following ATCC Accession No.s: ATCC Patent Deposit Designation PTA-6815, deposited on June 29, 2005; ATCC Patent Deposit Designation PTA-6816, deposited on June 29, 2005; ATCC Patent Deposit Designation PTA-6829, deposited on July 6, 2005; ATCC Patent Deposit Designation PTA-6830, deposited on July 6, 2005; ATCC Patent Deposit Designation PTA-6831, deposited on July 6, 2005; ATCC Patent Deposit Designation PTA-6871, deposited on July 19, 2005; ATCC Patent Deposit Designation PTA-6872, deposited on July 19, 2005; ATCC Patent Deposit Designation PTA-6875, deposited on July 19, 2005; and ATCC Patent Deposit Designation PTA-6873, deposited on July 19, 2005.

[97] A hybridoma expressing the neutralizing monoclonal antibodies to mouse IL-31 described herein was deposited with the American Type Tissue Culture Collection (ATCC; Manassas VA) patent depository as an original deposit under the Budapest Treaty and was given the following ATCC Accession No.: ATCC Patent Deposit Designation PTA-6874, , deposited on July 19, 2005. The monoclonal antibodies produced by these hybridoma clones can be cultured in a growth medium of 90% Iscove's Modified Dulbecco's medium with 2mM L-glutamine, 100 μg/mL penicillin, and 100 μg/mL streptomycin sulfate, and 10% Fetal Clone I Serum (Hyclone Laboratories). The clones can be propogated by starting cultures at 2 X 105 cells/mland maintaining between 1 X 105 and 5 X 105 cell/ml at 37 ºC and 5-6% CO. Cells can be adapted to serum free conditions upon subsequent transfers. Cells that are frozen are stored in 90% serum, 10% DMSO and stored in vapor phase of liquid nitrogen freezer.

[98] IL-31 antagonists generated by the methods described herein can be tested for neutralization, inhibition, reduction, antagonizaiton by a variety of methods. In addition neutralization can be tested by measuring a decrease in the production of pro-inflammatory chemokines such as TARC and MDC from keratinocyte cultures in the presence of ligand and the monoclonal antibody. Other biomarkers, such as MCP-1, MIP1a, TARC, MCP-1, MDC, IL-6, IL-8, I-309, SCYA19, MPIF-1, TECK, MIP-1b, SCYB13, GROa/MGSA, CTACK, SCCA1/Serpin B3, TSLP, and NT-4 may also be used. Neutralization can also be measured by the in vivo models described herein.

[99] The bioactive antagonists or antibody conjugates described herein can be delivered intravenously, intraarterially or intraductally, subcutaneously, topically, or may be introduced locally at the intended site of action.

[100] The antagonists of the present invention can be measured for their ability to bind the IL-31 ligand as determined by any of the in vivo models described herein, including but not limited to the NcNga model, the Ova epicutaneous model, the chronic hypersensitivity model, the chronic hapten model, the calcium flux model, the allodynia model.

[101] Additonal models to measure the inhibitory effects of the anti-IL-31 antibodies are known to one skilled in the art and described herein are described by Umeuchi, H. et al., European Journal of Pharmacology, 518: 133-139, 2005; and by Yoo, J. et al., J. Experimental Medicine, 202:541-549, 2005.

[102] Mouse models to measure neurogenic inflammation are known in the art. See, for example, Sweitzer, S.M., et al., J. Neuroimmunology 125: 82-93; 2002, and Honore, P., et al., Neuroscience, (98): 585-598, 2000. See also, Yonehara, N. and Yoshimura M., Pain, 2001 (92/1-2): pp. 259-265).

[103] Within aspects of the invention, the invention provides methods of treating inflammation in neuronal tissue of a mammal; methods of treating pain in a mammal; methods of antagonizing IL-31 induced signal transduction is dorsal root ganglion cells; methods for treating symptoms associated with burn; methods for treating symptoms associated with viral infection and for preventing reactivation of viral infection; and methods of treating pain associated with Inflammatory Bowel Disease. Within an embodiment, the Inflammatory Bowel Disease is Crohn's Disease.

[104] Within embodiments of these aspects, the invention provides, comprising admixing neuronal tissue with an IL-31 antagonist, wherein the inflammation, pain, dorsal root ganglion signal transduction, viral infection or reactivation, or burn tissue, or pain associated with Inflammatory Bowel Disease is reduced, limited, prevented, minimized or neutralized.

[105] Within other embodiments, the IL-31 antagonist binds a polypeptide comprising an amino acid sequence as shown in SEQ ID NO: 2 from residue 27 to residue 164. Within other embodiments, the antagonist is selected from: anti-idiotype antibodies; antibody fragments; chimeric antibodies; and humanized antibodies. Within another embodiment the antagonist an antibody. Within other embodiments the antibody is a monoclonal antibody. Within other embodiments the antibody specifically binds a polypeptide comprising the amino acid sequence of SEQ ID NO: 2 and wherein the polypeptide is capable of binding the monoclonal antibody produced by the hybridoma selected from the group consisting of: a) ATCC Patent Deposit Designation PTA-6815; b) ATCC Patent Deposit Designation PTA-6816; c) ATCC Patent Deposit Designation PTA-6829; d) ATCC Patent Deposit Designation PTA-6830; e) ATCC Patent Deposit Designation PTA-6831; f) ATCC Patent Deposit Designation PTA-6871; g) ATCC Patent Deposit Designation PTA-6872; h) ATCC

Patent Deposit Designation PTA-6875; and i) ATCC Patent Deposit Designation PTA-6873. Within another embodiment the monoclonal antibody is selected from a bin of antibodies wherein the hybridoma producing the antibody is selected from: a) ATCC Patent Deposit Designation PTA-6815; b) ATCC Patent Deposit Designation PTA-6829; c) ATCC Patent Deposit Designation PTA-6816; d) ATCC Patent Deposit Designation PTA-6871; and e) ATCC Patent Deposit Designation PTA-6830. Within another embodiment the monoclonal antibody is selected from a bin of antibodies wherein the hybridoma producing the antibody is selected from: a) ATCC Patent Deposit Designation PTA-6872; b) ATCC Patent Deposit Designation PTA-6873; c) ATCC Patent Deposit Designation PTA-6875; and d) ATCC Patent Deposit Designation PTA-6831.

[106] Within other embodiments the neuronal tissue comprises dorsal root ganglion or spinal cord tissues.

EXAMPLES

Example 1 In Situ Hybridization for IL-31RA, IL-31, and pOSMRb in Neuronal Tissues

[107] Five human brain tissue samples and a spinal cord sample all from the same individual, and a dorsal root ganglia (DRG) from a different patient were analyzed in this study.

[108] Probes used were probes to IL-31RA, IL-31, and OSMRbeta.

[109] Results are shown in Table 1:

Table 1

ISH analysis results:

Tissue/probe	IL-331RA	pOSMRb	IL-31
brain frontal lobe	-	-	-
brain hippocampus	-	-	-
brain parietal lobe	-	-	-
brain temporal lobe,	-	-	-
brain hypothalamus	-	+/ -	-
spinal cord	+	+	-
DRG	+	+	-

[110] Brain sections: There was no detectable amount of signal in all regions of the brain for all three probes. There was inconsistent staining of pOSMRb in a subset of neurons in the hypothalamus. The inconsistency may cause by very low level of pOSMRb expression that is around the level of detection.

[111] Spinal cord: There was positive staining in one region of the spinal cord. The information about the possible location or orientation of the spinal cord section was unavailable. The signal appears to be in the anterior (ventral) portion of the spinal cord. The opposite side/region (also

anterior) was negative. The positive signal appears to confine in a subset of larger neurons. Both IL-31RA and pOSMRb showed similar expression patterns in this area. IL-31 was negative.

[112] Dorsal Root Ganglion (DRG): A subset of unipolar neurons in the DRG was positive for both IL-31RA and pOSMRb. Small satellite cells were negative. IL-31 was negative in all cells including neurons.

[113] Thusm an IL-31 antagonist can be useful to ameliorate symptoms associated with neurogenic stimulation and neurogenic stimulation. As such the IL-31 antagonists, can be used to treat inflammation and pain associate with neural cell stimulation, such as dorsal root ganglion stimulation, and can be measured as a reduction, limitation, minimization, prevention, or neutralization of pain and inflammation.

Example 2 :IL-31 Involvement in Induction of the Itch Resonse

[114] A. Methods I (Capsaicin treatment of IL-31 treated mice)

[115] Ten week old BALB/c animals (CRL) were anaesthetized and injected with a long-lasting analgesic agent, bupranorphine hydrochloride, subcutaneously at 0.1 mg/kg before injection of 0.25 ml of 4 mg/ml solution of capsaicin in 10% ethanol + 10% Tween-80 in saline subcutaneously into scruff of neck. Animals were kept anaesthetized for at least 30 min following neurotoxin treatment. Forty-eight hours later, 14-day osmotic pumps were implanted subcutaneously for continuous delivery of 20 ug/day of IL-31 for 14 days. Mice were monitored daily for 6 days for alopecia and pruritis using the following criteria: 0 = no scratching, animal appears normal, 1 = thinning of coat in small areas, scratching noted, 2 = minor hair loss (small patches), scratching, 3 = moderate hair loss, scratching, and 4 = severe hair loss, excessive scratching.

[116] Results demonstrated that while non-capsaicin-treated mice showed a mean scratch/hairloss score of 2.625 following three days of IL-31 delivery, capsaicin-treated mice showed a significantly lower score of 1. Thus mice treated with capsaicin prior to IL-31 delivery showed both a delay in incidence of scratching and hairloss and a lower score in the intensity of scratching and hairloss over the six days of the experiment. These data suggest that IL-31 does induce some neuronal component that contributes to the alopecia and pruritis induced by IL-31. Therefore, neutralization of IL-31 may decrease the incidence and intensity of itch, and therefore dermatitis, in patients suffering from skin disorders that involve itch.

B. Methods II

[117] Mice that are homozygous null for the Tac1 gene express no detectible substance P or neurokinin A. These mice have significantly reduced nociceptive pain responses to moderate to intense stimuli and are therefore a useful tool for studying the contribution of tachykinin peptides to pain/itch processing and inflammatory disease states. Twelve week old, Tac1 knockout mice were implanted with 14-day osmotic pumps delivering 1ug/day of IL-31 protein and observed daily for

alopecia and pruritis using the following criteria: 0 = no scratching, animal appears normal, 1 = thinning of coat in small areas, scratching noted, 2 = minor hair loss (small patches), scratching, 3 = moderate hair loss, scratching, and 4 = severe hair loss, excessive scratching.

[118] Results of this study show that Tac1 deficient mice were less susceptible to IL-31 induced scratching/hairloss compared to wildtype control mice. While 100% (10/10) of wildtype mice had developed evidence of scratching and hairloss by day 6 of IL-31 treatment, only 33.3 % (2/6) Tac1 deficient mice were showing signs of scratching and hairloss at the same time-point. These data show that IL-31 induces a neuronal component that contributes to the scratch/hairloss phenotype in IL-31-treated mice and neutralization of IL-31 may decrease the incidence and intensity of scratching in the context of dermatitis.

C. Methods III (Administration of IL-31 neutralizing antibody)

[119] Normal female BALB/c mice (CRL) approximately 8 to 12 weeks old were implanted subcutaneously with 14-day osmotic pumps (Alzet, #2002) delivering 1ug/day mIL-31. Groups of mice received intraperitoneal (i.p.) injections of rat anti-mouse IL-31 monoclonal antibody 10mg/kg (200ug/mouse) twice weekly starting 1 week prior to IL-31 delivery. Control groups of mice received i.p. injections of vehicle (PBS/0.1%BSA) with the identical dosing schedules. Mice were scored daily for alopecia and pruritis using the following criteria: 0 = no scratching, animal appears normal, 1 = thinning of coat in small areas, scratching noted, 2 = minor hair loss (small patches), scratching, 3 = moderate hair loss, scratching, and 4 = severe hair loss, excessive scratching.

[120] In all experiments, mice treated with rat anti-mIL-31 mAb had a delay in onset of symptoms of approximately 5 to 7 days and a lower overall score for alopecia and pruritis. All groups of mAb treated mice (regardless of dose frequency or concentration) developed alopecia and pruritis similar to control mice by 13 day of the study. These data suggest that neutralization of IL-31 can delay the onset of the scratch/hairloss response induced by IL-31.

Example 3

IL-31RA/OSMRbeta receptor Luciferase assay

[121] The KZ134 plasmid was constructed with complementary oligonucleotides that contain STAT transcription factor binding elements from 4 genes, which includes a modified c-fos Sis inducible element (m67SIE, or hSIE) (Sadowski, H. et al., Science 261:1739-1744, 1993), the p21 SIE1 from the p21 WAF1 gene (Chin, Y. et al., Science 272:719-722, 1996), the mammary gland response element of the β-casein gene (Schmitt-Ney, M. et al., Mol. Cell. Biol. 11:3745-3755, 1991), and a STAT inducible element of the Fcg RI gene, (Seidel, H. et al., Proc. Natl. Acad. Sci. 92:3041-3045, 1995). These oligonucleotides contain Asp718-XhoI compatible ends and were ligated, using

standard methods, into a recipient firefly luciferase reporter vector with a c-fos promoter (Poulsen, L.K. et al., J. Biol. Chem. 273:6229-6232, 1998) digested with the same enzymes and containing a neomycin selectable marker. The KZ134 plasmid was used to stably transfect BaF3 cells, using standard transfection and selection methods, to make the BaF3/KZ134 cell line.

[122] A stable BaF3/KZ134 indicator cell line, expressing the full-length IL-31RA or IL-31RA/OSMRbeta receptor was constructed. Clones were diluted, plated and selected using standard techniques. Clones were screened by luciferase assay (see B, below) using the human IL-31 conditioned media or purified IL-31 protein as an inducer. Clones with the highest luciferase response (via STAT luciferase) and the lowest background were selected. Stable transfectant cell lines were selected. The cell lines were called BaF3/KZ134/IL-31RA or BaF3/KZ134/IL-31RA/OSMRbeta depending on the receptors transfected into the cell line.

[123] Similarly, BHK cell lines were also constructed using the method described herein, and were used in luciferase assays described herein. The cell lines were called BHK/KZ134/IL-31RA or BHK/KZ134/IL-31RA/OSMRbeta depending on the receptors transfected into the cell line.

[124] BaF3/KZ134/IL-31RA and BaF3/KZ134/IL-31RA/OSMRbeta cells were spun down and washed in mIL-3 free media. The cells were spun and washed 3 times to ensure removal of mIL-3. Cells were then counted in a hemacytometer. Cells were plated in a 96-well format at about 30,000 cells per well in a volume of 100 µl per well using the mIL-3 free media. The same procedure was used for untransfected BaF3/KZ134 cells for use as a control in the subsequent assay. BHK/KZ134/IL-31RA or BHK/KZ134/IL-31RA/OSMRbeta cells were plated in a 96-well format at 15,000 cells per well in 100 µl media. Parental BHK/KZ134 cells were used as a control.

[125] STAT activation of the BaF3/KZ134/ IL-31RA, BaF3/KZ134/ IL-31RA /OSMRbeta, BHK/KZ134/ IL-31RA, or BHK/KZ134/ IL-31RA /OSMRbeta cells is assessed using conditioned media or purified protein. One hundred microliters of the diluted conditioned media or protein is added to the BaF3/KZ134/ IL-31RA, BaF3/KZ134/IL-31RA/OSMRbeta, BHK/KZ134/IL-31RA, or BHK/KZ134/IL-31RA/OSMRbeta cells. The assay using the conditioned media is done in parallel on untransfected BaF3/KZ134 or BHK/KZ134 cells as a control. The total assay volume is 200 µl. The assay plates are incubated at 37°C, 5% CO_2 for 24 hours at which time the BaF3 cells are pelleted by centrifugation at 2000 rpm for 10 min., and the media is aspirated and 25 µl of lysis buffer (Promega) is added. For the BHK cell lines, the centrifugation step is not necessary as the cells are adherant. After 10 minutes at room temperature, the plates are measured for activation of the STAT reporter construct by reading them on a luminometer (Labsystems Luminoskan, model RS) which added 40 µl of luciferase assay substrate (Promega) at a five second integration.

Example 4

Luciferase Assay on Human Transformed Epithelial Cell Lines

via Transient Infection with an Adenoviral STAT/SRE Reporter Gene

[126] Inhibition, reduction, and/or neutralization of IL-31 activity can be measured by the luciferase assay. For example, human transformed cell lines can be seeded in 96-well flat-bottom plates at 10,000 cell/well in regular growth media as specified for each cell type. The following day, the cells are infected with an adenovirus reporter construct, KZ136, at a multiplicity of infection of 5000. The KZ136 reporter contains the STAT elements in addition to a serum response element. The total volume is 100 ul/well using DMEM supplemented with 2 mM L-glutamine (GibcoBRL), 1 mM Sodium Pyruvate (GibcoBRL) and 1x Insulin-Transferrin-Selenium supplement (GibcoBRL) (hereinafter referred to as serum-free media). Cells are cultured overnight.

[127] The following day, the media is removed and replaced with 100 µl of induction media. The induction media is human IL-31 diluted in serum-free media at 100ng/ml, 50 ng/ml, 25 ng/ml, 12.5 ng/ml, 6.25 ng/ml, 3.125 ng/ml and 1.56 ng/ml. A positive control of 20% FBS is used to validate the assay and to ensure the infection by adenovirus is successful. The cells are induced for 5 hours at which time the media is aspirated. The cells are then washed in 50 µl/well of PBS, and subsequently lysed in 30 µl/well of 1X cell lysis buffer (Promega). After a 10-minute incubation at room temperature, 25 µl/well of lysate is transferred to opaque white 96-well plates. The plates are then read on the Luminometer using 5-second integration with 40 µl/well injection of luciferase substrate (Promega).

Example 5

[128] IL-31 Analysis in Colon Tissues from Inflammatory Bowel Disease

[129] A) IL-31 Immunohistochemistry:

[130] A polyclonal antibody (rabbit anti-human IL-31 CEE, affinity purified to 1.0 mg/ml) was used to detect human IL-31 in gastrointestinal tissues from inflammatory bowel disease patients via an ABC-elite based detection system. Normal Rabbit Serum, Protein A purified to 1.66 mg/ml was used as a negative control using the same protocol and antibody concentrations.

[131] The protocol was as follows: ABC-HRP Elite (Vector Laboratories, PK-6100); Target Retrieval (ph 9) for 20' steam, 20' cooling to RT; Protein Block for 30'; Primary Ab (1:1,000-2,500) for 60'; Secondary Ab (Bi:ant-Rabbit) for 45'; ABC-HRP complex for 45'; and DAB substrate as recommended.

[132] In this study, a total of 19 individual GI tissues were analyzed with the rabbit anti-human IL-31 polyclonal antibody. In this group, there are five colon samples from normal tissue adjacent to IBD or cancer tissues. Nine samples were diagnosed with Crohn's disease and five with ulcerative colitis. Overall, it appears there are more cells positive in the Crohn's samples than the normal tissues adjacent to the IBD or cancer tissues or ulcerative colitits tissues. The predominate cells with signal in the Crohn's samples are located in the laminar propria and submucosa, with

infiltrating cells showing signal between the smooth muscle bundles. In granulomas, many larger cells in the nodule center are positive, however the cortex of these nodules, and Peyers patches appear negative. The epithelium of intestinal glands is occasionally positive. In ulcerative colitis samples, there are a small number of scattered cells in the submucosa and infiltrating cells between smooth muscle bundles are positive. The percentage of positive cells in ulcerative colitis samples is less than that of Crohn's, but similar, or slightly higher than that of "normal" samples. Cells in the laminar propria of ulcerative colitis are mostly negative. In summary, this study demonstrates that IL31 is upregulated in Crohn's GI samples. It appears that in this study, IL31 shows similar expression profiles in Ulcerative colitis samples and "Normal" controls.

[133] B) IL-31 In situ hybridization:

[134] A subset of the tissues was also analyzed using in situ hybridization (ISH). In ISH, IL-31 mRNA was observed in a few infiltrating cells in the submucosa and adipose tissues. Using IHC, we observed that IL31 protein stained positive in the previously mentioned cell population as well as in cells in the laminar propria and granuloma centers. The difference between these two assays could be explained by assay sensitivity.

[135] Example 6 IL-31Ra Analysis in Colon Tissues from Inflammatory Bowel Disease

[136] A) IL-31Ra Immunohistochemistry:

[137] A polyclonal antibody (rabbit anti-human IL-31RA (version 4) CEE, affinity purified to 1.33 mg/ml) was used to detect human IL-31RA in gastrointestinal tissues from inflammatory bowel disease patients via an ABC-elite based detection system. Normal Rabbit Serum, Protein A purified to 1.66 mg/ml was used as a negative control using the same protocol and antibody concentrations. The rabbit anti-human IL-31RA (version 4) antibody was used at 1:2000 (665ng/ml).

[138] The protocol was as follows: ABC-HRP Elite (Vector Laboratories, PK-6100); Target Retrieval (ph 9) for 20' steam, 20' cooling to RT; Protein Block for 30'; Primary Ab (1:2,000) for 60'; Secondary Ab for 45'; ABC-HRP complex for 45'; and DAB + Dako Cytomation for 10'.

[139] In this study, a total of 19 individual GI tissues were analyzed using the rabbit anti-human IL-31RA (version 4) CEE antibody. In this group, there are about five colon samples from normal tissue adjacent to IBD or cancer tissues. Nine samples were diagnosed with Crohn's disease and five with ulcerative colitis. Overall, it appears there are more cells positive in the Crohn's samples than normal tissue adjacent to IBD or cancer tissues or ulcerative colitis tissues. The positive cells in Crohn's are primarily located in the connective tissues of submucosa. Granulomas nodules are negative. Occasionally there is weak epithelium signal in the Crohn's samples. There was no detectable signal in the ulcerative colitis (UC) samples. A few cells in the submucosa were stained positive by IHC for the IL31RA protein.

[140] B) IL-31Ra In situ Hybridization:

[141] In a previous study five tissues were studied using ISH, three of which were Crohn's colons. In these Crohn's tissues, IL31RA mRNA was significantly upregulated compared to their normal counterparts, and the signal was localized to the cortex of granuloma nodules and many infiltrating cells in the connective tissues of submucosa and adipose tissue areas. Possible reasons for the discrepancy between IHC and in situ analysis includes transient mRNA expression, protein process time, IL31RA protein stability, and/or sensitivity differences between the two assays.

[142] Example 7 DSS-induced colitis studies in EμLck IL-31 transgenic mice

[143] EμLck IL-31 transgenic and non-transgenic littermate control mice were tested in a dextran sulfate sodium (DSS)-induced model of mucosal inflammation to look for potential differences in disease susceptibility and severity. Normal mice given 2-3% DSS in drinking water develop symptoms and pathology that mimic human inflammatory bowel disease (See, Strober, Fuss and Blumberg, Annu. Rev. Immunol. 2002). Mechanistically, DSS disrupts the mucosal epithelial barrier of the large intestine, which causes subsequent inflammation. As a result of this inflammation, DSS treated mice lose body weight and develop diarrhea. Mice are monitored for severity of colitis using a disease activity index (DAI), which is a cumulative score based on body weight, stool consistency and blood present in stool. DSS can be used to induce acute or chronic forms of colitis. Acute colitis is induced via delivery of DSS (2% or 3% in our studies) in drinking water from day 0 to day 7, while chronic colitis is induced via delivery of DSS in the drinking water for 5 days followed by a recovery phase of 7 to 12 days, before repeating the DSS treatment.

[144] Four studies in the EμLck IL-31 transgenic mice were performed. Regardless of whether the acute or chronic model of DSS was used, the EμLck IL-31 transgenic mice lost more body weight earlier when compared with littermate control mice. In fact, in 3 of 4 studies the IL-31 transgenic mice demonstrated significantly more weight loss compared to controls ($p < 0.001$, $p = 0.011$). Additionally, transgenic mice had significantly shorter colons compared to wildtype controls ($p<0.05$). The DAI score was significantly higher in IL-31 transgenic mice compared to non-transgenic controls in a chronic colitis study ($p < 0.001$).

[145] To determine if systemic delivery of IL-31 could influence the development of DSS-induced colitis in normal non-transgenic mice, we implanted animals with osmotic pumps delivering a daily dose of IL-31 or vehicle (PBS, 0.1% BSA) prior to DSS treatment. In one study, N3 generation, non-transgenic mice (B6C3F2 x C57BL/6) were implanted with pumps subcutaneously which delivered either 20 μg/day IL-31 or vehicle during the course of the DSS administration. There were no differences in weight loss, DAI score, or colon length between the IL-31 treated mice versus vehicle treated mice. A similar pump delivery study was also performed in normal C57BL/6 mice; mice were implanted with pumps that delivered 10 μg/day IL-31 or vehicle and given 2% DSS in the acute regime. Again, there were no differences between mice in any of the DSS-colitis parameters

whether implanted with IL-31 or vehicle-delivering pumps. Finally, a 2% DSS-acute colitis study was performed in IL-31RA deficient (IL-31RA-/-) mice. Again, there were no differences in body weight loss, DAI score or colon length between IL-31RA deficient mice and wildtype controls.

[146] In summary, IL-31 does not appear to directly effect mucosal inflammation induced by DSS since systemic delivery of IL-31 to normal mice in acute colitis studies had no effect on disease outcome. IL-31 transgenic animals may be more susceptible to DSS-induced colitis as a result of stress caused by the transgenic phenotype. However, EμLck IL-31 transgenic mice have increased numbers of activated CD4+ and CD8+ T cells in the peripheral lymph nodes (Dillon, et al, 2004) and the increased susceptibility to DSS-induced colitis observed in the EμLck IL-31 transgenic mice may be a consequence of the presence of these activated lymphocytes.

Example 8:

Effects of anti-IL31 Treatment by Sampling Dermal Interstitial Fluid with Microdialysis

[147] Microdialysis can be used with the molecules of the present invention to measure direct analysis of bioavailability and the distribution of antibodies in the skin. Microdialysis is use to collect and analyze the intercellular fluid. The antibody in the interstitial fluid can be determined using a species-specific anti-IgG cross-linked to a luminex bead. Further, an evaluation of free to IgG-bound IL31 is done using an anti-IL31 rather than anti-IgG as the secondary antibody. 2. Proinflammatory cytokines and chemokines produced by IL31 activation of keratinocytes and/or dorsal root ganglion is assayed. See British J. Dermatology 142(6); 1114-1120, (2000); J. Neurol. Neurosurg. Psychiatry 73; 299-302, (2002); Am J. Physiol Heart Circ. Physiol 286; 108-112, (2004); Neuroscience Letters 230; 117-120, (1997); and AAPS J. 7(3); E686-E692, (2005). See also Steinhoff, M., et al., J. Neuroscience, 23 (15): 6176-6180, 2003.

[148] Microdialysis probes are supplied by TSE Systems (Midland, Michigan). The probe is T-shaped and consists of a 3000 kDa membrane 0.3 mm OD by 4 mm L attached to a 15 mm stem. The inlet and outlet are connected to 0.12 mm ID peek tubing. The ex vivo analysis is performed using tubing lengths identical to that used for in vivo analysis. HMWCO probes are run with a push/pull pump system to minimize outward (into the interstitial) flow. However a push only (Harvard PHD 2000) is also used. Fluid loss due to Δp and $\Delta\Pi$ is determined at various flow rates. The efficiency (Ed) of the membrane is determined at various flow rates using known quantities of IgG in a mixing chamber to eliminate non-membrane (external) diffusion. The Ed of mouse IgG and mouse hemoglobin is determined and serve as in vivo controls. Quantitation is by goat anti-Rat-IgG coupled to Luminex beads and capture is reported with rabbit or donkey biotin-anti-rat IgG to reduce non-specific reactivity. Assays for mouse IgG and Hemoglobin is developed for controls in the in vivo studies. Bead coupling will be performed using a standard kit and protocol.

[149] Treatment of mice and rats with cytokines by osmotic pump, ID or through a microdialysis fiber is used. Antibody is injected by IV. The probe is UV sterilized. The microdialysis probe is inserted and blood an analytes are sampled. Quantification of IgG transport from circulation into the skin is measured using membrane parameters determined ex vivo, antibody permeability and the perfusion rate are estimated.

[150] The following steps are performed using one time point per animal pair and a sufficient number of time points to estimate circulating antibody levels and diffusion into the dermis/epidermis over time: i) a microdialysis membrane is inserted into the skin and a preliminary sample withdrawn at a rate determined by the ex vivo analysis. This control sample determines the baseline reactivity of the permeate fluid; 2) Rat anti-IL31 antibody is introduced by IV tail injection and at the predetermined time point an intraorbital blood sample is taken to determine circulating antibody levels; 3) a microdialysis sample of sufficient volume for analysis is taken at the protocol's pumping rate; 4) at the end of the analyte sampling another intraorbital sample is taken to determine anti-IL31 circulating levels.

[151] A multiplex analysis of Analyte and plasma is performed by Luminex and quantification determined for, 1.) anti-IL31 antibody, 2.) anti-mouse-IgG as a depletion/diffusion control, and 3.) anti-mouse Hemoglobin to control for microdialysis insertion trauma and blood vessel damage. Using the ex vivo determined membrane parameters and the measured influx rate of anti-IL31 into the analyte at a given circulating antibody concentration, an estimate of the skin diffusion rate is determined. The concentration of mouse IgG in the analyte is used to evaluate local depletion of proteins near the probe. A formula may need to be devised to compensate for local depletion in the diffusion analysis.

[152] From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

SEQUENCE LISTING IN ELECTRONIC FORM

This description contains a sequence listing in electronic form in ASCII text format (file no. 82587-90_ca_seqlist_v1_03July2008.txt).

A copy of the sequence listing in electronic form is available from the Canadian Intellectual Property Office.

The sequences in the sequence listing in electronic form are reproduced in the following Table.

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ctt cga ttc agg aca gtc aac agt acc agc tgg atg gaa gtc aac ttc 686
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Ser Leu Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr
    50                  55                  60
Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr
65                  70                  75                  80
Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys
                85                  90                  95
His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser
            100                 105                 110
Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
        115                 120                 125
Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
    130                 135                 140
Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
145                 150                 155                 160
Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp
                165                 170                 175
Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu
            180                 185                 190
Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
        195                 200                 205
Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln
    210                 215                 220
Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser
225                 230                 235                 240
Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
                245                 250                 255
Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu
            260                 265                 270
Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly
        275                 280                 285
Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro
    290                 295                 300
Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln
305                 310                 315                 320
Leu Glu Leu His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser
                325                 330                 335
Tyr Asn Ser Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala
            340                 345                 350
Ile Gln Glu Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val
        355                 360                 365
Ala Glu Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val
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370 375 380
Asn Thr Trp Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr
385 390 395 400
Thr Leu Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln
405 410 415
Gln Asp Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro
420 425 430
Met Leu His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala
435 440 445
Lys Glu Gly Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile
450 455 460
Gly Val Lys Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu
465 470 475 480
Arg Lys Gly Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly
485 490 495
Gly Lys Gly Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly
500 505 510
Leu Glu Ser Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala
515 520 525
Ser Thr Ser Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr
530 535 540
Leu Ser Phe Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly
545 550 555 560
Gly Gly Leu Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys
565 570 575
Lys Pro Asn Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro
580 585 590
Ala Glu Ser Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys
595 600 605
Leu Asn Leu Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile
610 615 620
Leu Lys Pro Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu
625 630 635 640
Val Val Asn Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala
645 650 655
Arg Thr Gly Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Tyr Val
660 665 670
Thr Cys Pro Phe Arg Pro Asp Cys Pro Leu Gly Lys Ser Phe Glu Glu
675 680 685
Leu Pro Val Ser Pro Glu Ile Pro Pro Arg Lys Ser Gln Tyr Leu Arg
690 695 700
Ser Arg Met Pro Glu Gly Thr Arg Pro Glu Ala Lys Glu Gln Leu Leu
705 710 715 720
Phe Ser Gly Gln Ser Leu Val Pro Asp His Leu Cys Glu Glu Gly Ala
725 730 735
Pro Asn Pro Tyr Leu Lys Asn Ser Val Thr Ala Arg Glu Phe Leu Val
740 745 750
Ser Glu Lys Leu Pro Glu His Thr Lys Gly Glu Val
755 760

<210> 7
<211> 2903
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (497)...(2485)

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ccacctcagc tgggaatgtg catcaggcaa ctcaagtttt tcaccacggc atgtgtctgt 120

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gaatgtccgc aaaacattag tttcactctt gtcgccaggt tggagtacaa tggcacgatc 180
ttggctcact gcaacctctg cctcccgggt tcaagcgatt ctcctgcctc agcctcccga 240
gtagctggga ttacagttaa caataatgca atccatttcc cagcataagt gggtaagtgc 300
cactttgact tgggctgggc ttaaaagcac aagaaaagct cgcagacaat cagagtggaa 360
acactcccac atcttagtgt ggataaatta aagtccagat tgttcttcct gtcctgactt 420
gtgctgtggg aggtggagtt gcctttgatg caaatccttt gagccagcag aacatctgtg 480
gaacatcccc tgatac atg aag ctc tct ccc cag cct tca tgt gtt aac ctg 532
                  Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu
                   1               5                  10

ggg atg atg tgg acc tgg gca ctg tgg atg ctc cct tca ctc tgc aaa   580
Gly Met Met Trp Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys
          15                  20                  25

ttc agc ctg gca gct ctg cca gct aag cct gag aac att tcc tgt gtc   628
Phe Ser Leu Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val
      30                  35                  40

tac tac tat agg aaa aat tta acc tgc act tgg agt cca gga aag gaa   676
Tyr Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu
  45                  50                  55                  60

acc agt tat acc cag tac aca gtt aag aga act tac gct ttt gga gaa   724
Thr Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu
                  65                  70                  75

aaa cat gat aat tgt aca acc aat agt tct aca agt gaa aat cgt gct   772
Lys His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala
              80                  85                  90

tcg tgc tct ttt ttc ctt cca aga ata acg atc cca gat aat tat acc   820
Ser Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr
          95                  100                 105

att gag gtg gaa gct gaa aat gga gat ggt gta att aaa tct cat atg   868
Ile Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met
      110                 115                 120

aca tac tgg aga tta gag aac ata gcg aaa act gaa cca cct aag att   916
Thr Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile
  125                 130                 135                 140

ttc cgt gtg aaa cca gtt ttg ggc atc aaa cga atg att caa att gaa   964
Phe Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu
                  145                 150                 155

tgg ata aag cct gag ttg gcg cct gtt tca tct gat tta aaa tac aca   1012
Trp Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr
              160                 165                 170

ctt cga ttc agg aca gtc aac agt acc agc tgg atg gaa gtc aac ttc   1060
Leu Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe
          175                 180                 185

gct aag aac cgt aag gat aaa aac caa acg tac aac ctc acg ggg ctg   1108
Ala Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu
      190                 195                 200

cag cct ttt aca gaa tat gtc ata gct ctg cga tgt gcg gtc aag gag   1156
Gln Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu
  205                 210                 215                 220

tca aag ttc tgg agt gac tgg agc caa gaa aaa atg gga atg act gag   1204
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Ser Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu
                225                 230                 235

gaa gaa gct cca tgt ggc ctg gaa ctg tgg aga gtc ctg aaa cca gct   1252
Glu Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala
            240                 245                 250

gag gcg gat gga aga agg cca gtg cgg ttg tta tgg aag aag gca aga   1300
Glu Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg
        255                 260                 265

gga gcc cca gtc cta gag aaa aca ctt ggc tac aac ata tgg tac tat   1348
Gly Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr
    270                 275                 280

cca gaa agc aac act aac ctc aca gaa aca atg aac act act aac cag   1396
Pro Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln
285                 290                 295                 300

cag ctt gaa ctg cat ctg gga ggc gag agc ttt tgg gtg tct atg att   1444
Gln Leu Glu Leu His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile
                305                 310                 315

tct tat aat tct ctt ggg aag tct cca gtg gcc acc ctg agg att cca   1492
Ser Tyr Asn Ser Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro
            320                 325                 330

gct att caa gaa aaa tca ttt cag tgc att gag gtc atg cag gcc tgc   1540
Ala Ile Gln Glu Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys
        335                 340                 345

gtt gct gag gac cag cta gtg gtg aag tgg caa agc tct gct cta gac   1588
Val Ala Glu Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp
    350                 355                 360

gtg aac act tgg atg att gaa tgg ttt ccg gat gtg gac tca gag ccc   1636
Val Asn Thr Trp Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro
365                 370                 375                 380

acc acc ctt tcc tgg gaa tct gtg tct cag gcc acg aac tgg acg atc   1684
Thr Thr Leu Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile
                385                 390                 395

cag caa gat aaa tta aaa cct ttc tgg tgc tat aac atc tct gtg tat   1732
Gln Gln Asp Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr
            400                 405                 410

cca atg ttg cat gac aaa gtt ggc gag cca tat tcc atc cag gct tat   1780
Pro Met Leu His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr
        415                 420                 425

gcc aaa gaa ggc gtt cca tca gaa ggt cct gag acc aag gtg gag aac   1828
Ala Lys Glu Gly Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn
    430                 435                 440

att ggc gtg aag acg gtc acg atc aca tgg aaa gag att ccc aag agt   1876
Ile Gly Val Lys Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser
445                 450                 455                 460

gag aga aag ggt atc atc tgc aac tac acc atc ttt tac caa gct gaa   1924
Glu Arg Lys Gly Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu
                465                 470                 475
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ggt gga aaa gga ttc tcc aag aca gtc aat tcc agc atc ttg cag tac   1972
Gly Gly Lys Gly Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr
            480                 485                 490

ggc ctg gag tcc ctg aaa cga aag acc tct tac att gtt cag gtc atg   2020
Gly Leu Glu Ser Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met
        495                 500                 505

gcc agc acc agt gct ggg gga acc aac ggg acc agc ata aat ttc aag   2068
Ala Ser Thr Ser Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys
    510                 515                 520

aca ttg tca ttc agt gtc ttt gag att atc ctc ata act tct ctg att   2116
Thr Leu Ser Phe Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile
525                 530                 535                 540

ggt gga ggc ctt ctt att ctc att atc ctg aca gtg gca tat ggt ctc   2164
Gly Gly Gly Leu Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu
                545                 550                 555

aaa aaa ccc aac aaa ttg act cat ctg tgt tgg ccc acc gtt ccc aac   2212
Lys Lys Pro Asn Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn
            560                 565                 570

cct gct gaa agt agt ata gcc aca tgg cat gga gat gat ttc aag gat   2260
Pro Ala Glu Ser Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp
        575                 580                 585

aag cta aac ctg aag gag tct gat gac tct gtg aac aca gaa gac agg   2308
Lys Leu Asn Leu Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg
    590                 595                 600

atc tta aaa cca tgt tcc acc ccc agt gac aag ttg gtg att gac aag   2356
Ile Leu Lys Pro Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys
605                 610                 615                 620

ttg gtg gtg aac ttt ggg aat gtt ctg caa gaa att ttc aca gat gaa   2404
Leu Val Val Asn Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu
                625                 630                 635

gcc aga acg ggt cag gaa aac aat tta gga ggg gaa aag aat ggg act   2452
Ala Arg Thr Gly Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr
            640                 645                 650

aga att ctg tct tcc tgc cca act tca ata taa gtgtggacta aaatgcgaga 2505
Arg Ile Leu Ser Ser Cys Pro Thr Ser Ile  *
        655                 660

aaggtgtcct gtggtctatg caaattagaa aggacatgca gagttttcca actaggaaga 2565
ctgaatctgt ggccccaaga gaaccatctc tgaagactgg gtatgtggtc ttttccacac 2625
atggaccacc tacggatgca atctgtaatg catgtgcatg agaagtctgt tattaagtag 2685
agtgtgaaaa catggttatg gtaataggaa cagcttttaa aatgcttttg tatttgggcc 2745
tttcatacaa aaaagccata ataccatttt catgtaatgc tatacttcta tactattttc 2805
atgtaatact atacttctat actattttca tgtaatacta tacttctata ctattttcat 2865
gtaatactat acttctatat taaagtttta cccactca                          2903

<210> 8
<211> 662
<212> PRT
<213> Homo sapiens

<400> 8
Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu Gly Met Met Trp
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1               5                  10                  15
Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala
            20                  25                  30
Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg
        35                  40                  45
Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr
    50                  55                  60
Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn
65                  70                  75                  80
Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe
                85                  90                  95
Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu
            100                 105                 110
Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg
        115                 120                 125
Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys
    130                 135                 140
Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro
145                 150                 155                 160
Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg
                165                 170                 175
Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg
            180                 185                 190
Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr
        195                 200                 205
Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp
    210                 215                 220
Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro
225                 230                 235                 240
Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly
                245                 250                 255
Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val
            260                 265                 270
Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn
        275                 280                 285
Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu
    290                 295                 300
His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser
305                 310                 315                 320
Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu
                325                 330                 335
Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp
            340                 345                 350
Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp
        355                 360                 365
Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser
    370                 375                 380
Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys
385                 390                 395                 400
Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His
                405                 410                 415
Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly
            420                 425                 430
Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys
        435                 440                 445
Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly
    450                 455                 460
Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly
465                 470                 475                 480
Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser
                485                 490                 495
Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Ser Thr Ser
            500                 505                 510
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Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe
        515                 520                 525
Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Gly Leu
    530                 535                 540
Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro Asn
545                 550                 555                 560
Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu Ser
                565                 570                 575
Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu
            580                 585                 590
Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro
        595                 600                 605
Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn
    610                 615                 620
Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly
625                 630                 635                 640
Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr Arg Ile Leu Ser
                645                 650                 655
Ser Cys Pro Thr Ser Ile
            660
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<210> 9
<211> 975
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(975)

<220>
<221> misc_feature
<222> (1)...(975)
<223> soluble IL-31RA "long" form

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Met Met Trp Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe
 1               5                  10                  15

agc ctg gca gct ctg cca gct aag cct gag aac att tcc tgt gtc tac   96
Ser Leu Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr
            20                  25                  30

tac tat agg aaa aat tta acc tgc act tgg agt cca gga aag gaa acc   144
Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr
        35                  40                  45

agt tat acc cag tac aca gtt aag aga act tac gct ttt gga gaa aaa   192
Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys
    50                  55                  60

cat gat aat tgt aca acc aat agt tct aca agt gaa aat cgt gct tcg   240
His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser
65                  70                  75                  80

tgc tct ttt ttc ctt cca aga ata acg atc cca gat aat tat acc att   288
Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
                85                  90                  95

gag gtg gaa gct gaa aat gga gat ggt gta att aaa tct cat atg aca   336
Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
```

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 100                 105                 110

tac tgg aga tta gag aac ata gcg aaa act gaa cca cct aag att ttc   384
Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
        115                 120                 125

cgt gtg aaa cca gtt ttg ggc atc aaa cga atg att caa att gaa tgg   432
Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp
    130                 135                 140

ata aag cct gag ttg gcg cct gtt tca tct gat tta aaa tac aca ctt   480
Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu
145                 150                 155                 160

cga ttc agg aca gtc aac agt acc agc tgg atg gaa gtc aac ttc gct   528
Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
                165                 170                 175

aag aac cgt aag gat aaa aac caa acg tac aac ctc acg ggg ctg cag   576
Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln
            180                 185                 190

cct ttt aca gaa tat gtc ata gct ctg cga tgt gcg gtc aag gag tca   624
Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser
        195                 200                 205

aag ttc tgg agt gac tgg agc caa gaa aaa atg gga atg act gag gaa   672
Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
    210                 215                 220

gaa gct cca tgt ggc ctg gaa ctg tgg aga gtc ctg aaa cca gct gag   720
Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu
225                 230                 235                 240

gcg gat gga aga agg cca gtg cgg ttg tta tgg aag aag gca aga gga   768
Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly
                245                 250                 255

gcc cca gtc cta gag aaa aca ctt ggc tac aac ata tgg tac tat cca   816
Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro
            260                 265                 270

gaa agc aac act aac ctc aca gaa aca atg aac act act aac cag cag   864
Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln
        275                 280                 285

ctt gaa ctg cat ctg gga ggc gag agc ttt tgg gtg tct atg att tct   912
Leu Glu Leu His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser
    290                 295                 300

tat aat tct ctt ggg aag tct cca gtg gcc acc ctg agg att cca gct   960
Tyr Asn Ser Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala
305                 310                 315                 320

att caa gaa aaa tag                                               975
Ile Gln Glu Lys  *
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<210> 10
<211> 324
<212> PRT
<213> Homo sapiens

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

<210> 11
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(720)

<220>
<221> misc_feature
<222> (1)...(720)
<223> soluble IL-31RA "short" form

<400> 11
atg atg tgg acc tgg gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc 48
Met Met Trp Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe
1 5 10 15

agc ctg gca gct ctg cca gct aag cct gag aac att tcc tgt gtc tac 96

```
Ser Leu Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr
                20                  25                  30

tac tat agg aaa aat tta acc tgc act tgg agt cca gga aag gaa acc   144
Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr
        35                  40                  45

agt tat acc cag tac aca gtt aag aga act tac gct ttt gga gaa aaa   192
Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys
    50                  55                  60

cat gat aat tgt aca acc aat agt tct aca agt gaa aat cgt gct tcg   240
His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser
65                  70                  75                  80

tgc tct ttt ttc ctt cca aga ata acg atc cca gat aat tat acc att   288
Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
                85                  90                  95

gag gtg gaa gct gaa aat gga gat ggt gta att aaa tct cat atg aca   336
Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
            100                 105                 110

tac tgg aga tta gag aac ata gcg aaa act gaa cca cct aag att ttc   384
Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
        115                 120                 125

cgt gtg aaa cca gtt ttg ggc atc aaa cga atg att caa att gaa tgg   432
Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp
    130                 135                 140

ata aag cct gag ttg gcg cct gtt tca tct gat tta aaa tac aca ctt   480
Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu
145                 150                 155                 160

cga ttc agg aca gtc aac agt acc agc tgg atg gaa gtc aac ttc gct   528
Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
                165                 170                 175

aag aac cgt aag gat aaa aac caa acg tac aac ctc acg ggg ctg cag   576
Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln
            180                 185                 190

cct ttt aca gaa tat gtc ata gct ctg cga tgt gcg gtc aag gag tca   624
Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser
        195                 200                 205

aag ttc tgg agt gac tgg agc caa gaa aaa atg gga atg act gag gaa   672
Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
    210                 215                 220

gaa ggc aag cta ctc cct gcg att ccc gtc ctg tct gct ctg gtg tag   720
Glu Gly Lys Leu Leu Pro Ala Ile Pro Val Leu Ser Ala Leu Val  *
225                 230                 235

<210> 12
<211> 239
<212> PRT
<213> Homo sapiens

<400> 12
Met Met Trp Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe
 1               5                  10                  15
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Ser Leu Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr
            20                  25                  30
Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr
        35                  40                  45
Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys
    50                  55                  60
His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser
65                  70                  75                  80
Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
                85                  90                  95
Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
            100                 105                 110
Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
        115                 120                 125
Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp
    130                 135                 140
Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu
145                 150                 155                 160
Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
                165                 170                 175
Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln
            180                 185                 190
Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser
        195                 200                 205
Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
    210                 215                 220
Glu Gly Lys Leu Leu Pro Ala Ile Pro Val Leu Ser Ala Leu Val
225                 230                 235
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<210> 13
<211> 1989
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(1989)

<400> 13

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atg ctg agc agc cag aag gga tcc tgc agc cag gaa cca ggg gca gcc   48
Met Leu Ser Ser Gln Lys Gly Ser Cys Ser Gln Glu Pro Gly Ala Ala
 1               5                  10                  15

cac gtc cag cct ctg ggt gtg aac gct gga ata atg tgg acc ttg gca   96
His Val Gln Pro Leu Gly Val Asn Ala Gly Ile Met Trp Thr Leu Ala
            20                  25                  30

ctg tgg gca ttc tct ttc ctc tgc aaa ttc agc ctg gca gtc ctg ccg   144
Leu Trp Ala Phe Ser Phe Leu Cys Lys Phe Ser Leu Ala Val Leu Pro
        35                  40                  45

act aag cca gag aac att tcc tgc gtc ttt tac ttc gac aga aat ctg   192
Thr Lys Pro Glu Asn Ile Ser Cys Val Phe Tyr Phe Asp Arg Asn Leu
    50                  55                  60

act tgc act tgg aga cca gag aag gaa acc aat gat acc agc tac att   240
Thr Cys Thr Trp Arg Pro Glu Lys Glu Thr Asn Asp Thr Ser Tyr Ile
65                  70                  75                  80

gtg act ttg act tac tcc tat gga aaa agc aat tat agt gac aat gct   288
Val Thr Leu Thr Tyr Ser Tyr Gly Lys Ser Asn Tyr Ser Asp Asn Ala
                85                  90                  95
```

```
aca gag gct tca tat tct ttt ccc cgt tcc tgt gca atg ccc cca gac   336
Thr Glu Ala Ser Tyr Ser Phe Pro Arg Ser Cys Ala Met Pro Pro Asp
            100                 105                 110

atc tgc agt gtt gaa gta caa gct caa aat gga gat ggt aaa gtt aaa   384
Ile Cys Ser Val Glu Val Gln Ala Gln Asn Gly Asp Gly Lys Val Lys
        115                 120                 125

tct gac atc aca tat tgg cat tta atc tcc ata gca aaa acc gaa cca   432
Ser Asp Ile Thr Tyr Trp His Leu Ile Ser Ile Ala Lys Thr Glu Pro
    130                 135                 140

cct ata att tta agt gtg aat cca att tgt aat aga atg ttc cag ata   480
Pro Ile Ile Leu Ser Val Asn Pro Ile Cys Asn Arg Met Phe Gln Ile
145                 150                 155                 160

caa tgg aaa ccg cgt gaa aag act cgt ggg ttt cct tta gta tgc atg   528
Gln Trp Lys Pro Arg Glu Lys Thr Arg Gly Phe Pro Leu Val Cys Met
                165                 170                 175

ctt cgg ttc aga act gtc aac agt agc cgc tgg acg gaa gtc aat ttt   576
Leu Arg Phe Arg Thr Val Asn Ser Ser Arg Trp Thr Glu Val Asn Phe
            180                 185                 190

gaa aac tgt aaa cag gtc tgc aac ctc aca gga ctt cag gct ttc aca   624
Glu Asn Cys Lys Gln Val Cys Asn Leu Thr Gly Leu Gln Ala Phe Thr
        195                 200                 205

gaa tat gtc ctg gct cta cga ttc agg ttc aat gac tca aga tat tgg   672
Glu Tyr Val Leu Ala Leu Arg Phe Arg Phe Asn Asp Ser Arg Tyr Trp
    210                 215                 220

agc aag tgg agc aaa gaa gaa acc aga gtg act atg gag gaa gtt cca   720
Ser Lys Trp Ser Lys Glu Glu Thr Arg Val Thr Met Glu Glu Val Pro
225                 230                 235                 240

cat gtc ctg gac ctg tgg aga att ctg gaa cca gca gac atg aac gga   768
His Val Leu Asp Leu Trp Arg Ile Leu Glu Pro Ala Asp Met Asn Gly
                245                 250                 255

gac agg aag gtg cga ttg ctg tgg aag aag gca aga gga gcc ccc gtc   816
Asp Arg Lys Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val
            260                 265                 270

ttg gag aaa aca ttt ggc tac cac ata cag tac ttt gca gag aac agc   864
Leu Glu Lys Thr Phe Gly Tyr His Ile Gln Tyr Phe Ala Glu Asn Ser
        275                 280                 285

act aac ctc aca gag ata aac aac atc acc acc cag cag tat gaa ctg   912
Thr Asn Leu Thr Glu Ile Asn Asn Ile Thr Thr Gln Gln Tyr Glu Leu
    290                 295                 300

ctt ctg atg agc cag gca cac tct gtg tcc gtg act tct ttt aat tct   960
Leu Leu Met Ser Gln Ala His Ser Val Ser Val Thr Ser Phe Asn Ser
305                 310                 315                 320

ctt ggc aag tcc caa gag acc atc ctg agg atc cca gat gtc cat gag  1008
Leu Gly Lys Ser Gln Glu Thr Ile Leu Arg Ile Pro Asp Val His Glu
                325                 330                 335

aag acc ttc cag tac att aag agc atg cag gcc tac ata gcc gag ccc  1056
Lys Thr Phe Gln Tyr Ile Lys Ser Met Gln Ala Tyr Ile Ala Glu Pro
            340                 345                 350
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ctg ttg gtg gtg aac tgg caa agc tcc att cct gcg gtg gac act tgg   1104
Leu Leu Val Val Asn Trp Gln Ser Ser Ile Pro Ala Val Asp Thr Trp
        355                 360                 365

ata gtg gag tgg ctc cca gaa gct gcc atg tcg aag ttc cct gcc ctt   1152
Ile Val Glu Trp Leu Pro Glu Ala Ala Met Ser Lys Phe Pro Ala Leu
    370                 375                 380

tcc tgg gaa tct gtg tct cag gtc acg aac tgg acc atc gag caa gat   1200
Ser Trp Glu Ser Val Ser Gln Val Thr Asn Trp Thr Ile Glu Gln Asp
385                 390                 395                 400

aaa cta aaa cct ttc aca tgc tat aat ata tca gtg tat cca gtg ttg   1248
Lys Leu Lys Pro Phe Thr Cys Tyr Asn Ile Ser Val Tyr Pro Val Leu
                405                 410                 415

gga cac cga gtt gga gag ccg tat tca atc caa gct tat gcc aaa gaa   1296
Gly His Arg Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu
            420                 425                 430

gga act cca tta aaa ggt cct gag acc agg gtg gag aac atc ggt ctg   1344
Gly Thr Pro Leu Lys Gly Pro Glu Thr Arg Val Glu Asn Ile Gly Leu
        435                 440                 445

agg aca gcc acg atc aca tgg aag gag att cct aag agt gct agg aat   1392
Arg Thr Ala Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Ala Arg Asn
    450                 455                 460

gga ttt atc aac aat tac act gta ttt tac caa gct gaa ggt gga aaa   1440
Gly Phe Ile Asn Asn Tyr Thr Val Phe Tyr Gln Ala Glu Gly Gly Lys
465                 470                 475                 480

gaa ctc tcc aag act gtt aac tct cat gcc ctg cag tgt gac ctg gag   1488
Glu Leu Ser Lys Thr Val Asn Ser His Ala Leu Gln Cys Asp Leu Glu
                485                 490                 495

tct ctg aca cga agg acc tct tat act gtt tgg gtc atg gcc agc acc   1536
Ser Leu Thr Arg Arg Thr Ser Tyr Thr Val Trp Val Met Ala Ser Thr
            500                 505                 510

aga gct gga ggt acc aac ggg gtg aga ata aac ttc aag aca ttg tca   1584
Arg Ala Gly Gly Thr Asn Gly Val Arg Ile Asn Phe Lys Thr Leu Ser
        515                 520                 525

atc agt gtg ttt gaa att gtc ctt cta aca tct cta gtt gga gga ggc   1632
Ile Ser Val Phe Glu Ile Val Leu Leu Thr Ser Leu Val Gly Gly Gly
    530                 535                 540

ctt ctt cta ctt agc atc aaa aca gtg act ttt ggc ctc aga aag cca   1680
Leu Leu Leu Leu Ser Ile Lys Thr Val Thr Phe Gly Leu Arg Lys Pro
545                 550                 555                 560

aac cgg ttg act ccc ctg tgt tgt cct gat gtt ccc aac cct gct gaa   1728
Asn Arg Leu Thr Pro Leu Cys Cys Pro Asp Val Pro Asn Pro Ala Glu
                565                 570                 575

agt agt tta gcc aca tgg ctc gga gat ggt ttc aag aag tca aat atg   1776
Ser Ser Leu Ala Thr Trp Leu Gly Asp Gly Phe Lys Lys Ser Asn Met
            580                 585                 590

aag gag act gga aac tct ggg aac aca gaa gac gtg gtc cta aaa cca   1824
Lys Glu Thr Gly Asn Ser Gly Asn Thr Glu Asp Val Val Leu Lys Pro
        595                 600                 605
```

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tgt ccc gtc ccc gcg gat ctc att gac aag ctg gta gtg aac ttt gag   1872
Cys Pro Val Pro Ala Asp Leu Ile Asp Lys Leu Val Val Asn Phe Glu
    610                 615                 620

aat ttt ctg gaa gta gtt ttg aca gag gaa gct gga aag ggt cag gcg   1920
Asn Phe Leu Glu Val Val Leu Thr Glu Glu Ala Gly Lys Gly Gln Ala
625                 630                 635                 640

agc att ttg gga gga gaa gcg aat gag tat atc tta tcc cag gaa cca   1968
Ser Ile Leu Gly Gly Glu Ala Asn Glu Tyr Ile Leu Ser Gln Glu Pro
                645                 650                 655

agc tgt cct ggc cat tgc tga                                      1989
Ser Cys Pro Gly His Cys  *
            660
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<210> 14
<211> 662
<212> PRT
<213> Mus musculus

<400> 14

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Met Leu Ser Ser Gln Lys Gly Ser Cys Ser Gln Glu Pro Gly Ala Ala
 1               5                  10                  15
His Val Gln Pro Leu Gly Val Asn Ala Gly Ile Met Trp Thr Leu Ala
            20                  25                  30
Leu Trp Ala Phe Ser Phe Leu Cys Lys Phe Ser Leu Ala Val Leu Pro
        35                  40                  45
Thr Lys Pro Glu Asn Ile Ser Cys Val Phe Tyr Phe Asp Arg Asn Leu
    50                  55                  60
Thr Cys Thr Trp Arg Pro Glu Lys Glu Thr Asn Asp Thr Ser Tyr Ile
65                  70                  75                  80
Val Thr Leu Thr Tyr Ser Tyr Gly Lys Ser Asn Tyr Ser Asp Asn Ala
                85                  90                  95
Thr Glu Ala Ser Tyr Ser Phe Pro Arg Ser Cys Ala Met Pro Pro Asp
            100                 105                 110
Ile Cys Ser Val Glu Val Gln Ala Gln Asn Gly Asp Gly Lys Val Lys
        115                 120                 125
Ser Asp Ile Thr Tyr Trp His Leu Ile Ser Ile Ala Lys Thr Glu Pro
    130                 135                 140
Pro Ile Ile Leu Ser Val Asn Pro Ile Cys Asn Arg Met Phe Gln Ile
145                 150                 155                 160
Gln Trp Lys Pro Arg Glu Lys Thr Arg Gly Phe Pro Leu Val Cys Met
                165                 170                 175
Leu Arg Phe Arg Thr Val Asn Ser Ser Arg Trp Thr Glu Val Asn Phe
            180                 185                 190
Glu Asn Cys Lys Gln Val Cys Asn Leu Thr Gly Leu Gln Ala Phe Thr
        195                 200                 205
Glu Tyr Val Leu Ala Leu Arg Phe Arg Phe Asn Asp Ser Arg Tyr Trp
    210                 215                 220
Ser Lys Trp Ser Lys Glu Glu Thr Arg Val Thr Met Glu Glu Val Pro
225                 230                 235                 240
His Val Leu Asp Leu Trp Arg Ile Leu Glu Pro Ala Asp Met Asn Gly
                245                 250                 255
Asp Arg Lys Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val
            260                 265                 270
Leu Glu Lys Thr Phe Gly Tyr His Ile Gln Tyr Phe Ala Glu Asn Ser
        275                 280                 285
Thr Asn Leu Thr Glu Ile Asn Asn Ile Thr Thr Gln Gln Tyr Glu Leu
    290                 295                 300
Leu Leu Met Ser Gln Ala His Ser Val Ser Val Thr Ser Phe Asn Ser
305                 310                 315                 320
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```
Leu Gly Lys Ser Gln Glu Thr Ile Leu Arg Ile Pro Asp Val His Glu
                325                 330                 335
Lys Thr Phe Gln Tyr Ile Lys Ser Met Gln Ala Tyr Ile Ala Glu Pro
            340                 345                 350
Leu Leu Val Val Asn Trp Gln Ser Ser Ile Pro Ala Val Asp Thr Trp
        355                 360                 365
Ile Val Glu Trp Leu Pro Glu Ala Ala Met Ser Lys Phe Pro Ala Leu
    370                 375                 380
Ser Trp Glu Ser Val Ser Gln Val Thr Asn Trp Thr Ile Glu Gln Asp
385                 390                 395                 400
Lys Leu Lys Pro Phe Thr Cys Tyr Asn Ile Ser Val Tyr Pro Val Leu
                405                 410                 415
Gly His Arg Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu
            420                 425                 430
Gly Thr Pro Leu Lys Gly Pro Glu Thr Arg Val Glu Asn Ile Gly Leu
        435                 440                 445
Arg Thr Ala Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Ala Arg Asn
    450                 455                 460
Gly Phe Ile Asn Asn Tyr Thr Val Phe Tyr Gln Ala Glu Gly Gly Lys
465                 470                 475                 480
Glu Leu Ser Lys Thr Val Asn Ser His Ala Leu Gln Cys Asp Leu Glu
                485                 490                 495
Ser Leu Thr Arg Arg Thr Ser Tyr Thr Val Trp Val Met Ala Ser Thr
            500                 505                 510
Arg Ala Gly Gly Thr Asn Gly Val Arg Ile Asn Phe Lys Thr Leu Ser
        515                 520                 525
Ile Ser Val Phe Glu Ile Val Leu Leu Thr Ser Leu Val Gly Gly Gly
    530                 535                 540
Leu Leu Leu Leu Ser Ile Lys Thr Val Thr Phe Gly Leu Arg Lys Pro
545                 550                 555                 560
Asn Arg Leu Thr Pro Leu Cys Cys Pro Asp Val Pro Asn Pro Ala Glu
                565                 570                 575
Ser Ser Leu Ala Thr Trp Leu Gly Asp Gly Phe Lys Lys Ser Asn Met
            580                 585                 590
Lys Glu Thr Gly Asn Ser Gly Asn Thr Glu Asp Val Val Leu Lys Pro
        595                 600                 605
Cys Pro Val Pro Ala Asp Leu Ile Asp Lys Leu Val Val Asn Phe Glu
    610                 615                 620
Asn Phe Leu Glu Val Val Leu Thr Glu Glu Ala Gly Lys Gly Gln Ala
625                 630                 635                 640
Ser Ile Leu Gly Gly Glu Ala Asn Glu Tyr Ile Leu Ser Gln Glu Pro
                645                 650                 655
Ser Cys Pro Gly His Cys
            660
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<210> 15
<211> 2940
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2940)

<400> 15

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atg gct cta ttt gca gtc ttt cag aca aca ttc ttc tta aca ttg ctg   48
Met Ala Leu Phe Ala Val Phe Gln Thr Thr Phe Phe Leu Thr Leu Leu
 1               5                  10                  15

tcc ttg agg act tac cag agt gaa gtc ttg gct gaa cgt tta cca ttg   96
Ser Leu Arg Thr Tyr Gln Ser Glu Val Leu Ala Glu Arg Leu Pro Leu
            20                  25                  30
```

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act cct gta tca ctt aaa gtt tcc acc aat tct acg cgt cag agt ttg   144
Thr Pro Val Ser Leu Lys Val Ser Thr Asn Ser Thr Arg Gln Ser Leu
         35                  40                  45

cac tta caa tgg act gtc cac aac ctt cct tat cat cag gaa ttg aaa   192
His Leu Gln Trp Thr Val His Asn Leu Pro Tyr His Gln Glu Leu Lys
     50                  55                  60

atg gta ttt cag atc cag atc agt agg att gaa aca tcc aat gtc atc   240
Met Val Phe Gln Ile Gln Ile Ser Arg Ile Glu Thr Ser Asn Val Ile
 65                  70                  75                  80

tgg gtg ggg aat tac agc acc act gtg aag tgg aac cag gtt ctg cat   288
Trp Val Gly Asn Tyr Ser Thr Thr Val Lys Trp Asn Gln Val Leu His
                 85                  90                  95

tgg agc tgg gaa tct gag ctc cct ttg gaa tgt gcc aca cac ttt gta   336
Trp Ser Trp Glu Ser Glu Leu Pro Leu Glu Cys Ala Thr His Phe Val
            100                 105                 110

aga ata aag agt ttg gtg gac gat gcc aag ttc cct gag cca aat ttc   384
Arg Ile Lys Ser Leu Val Asp Asp Ala Lys Phe Pro Glu Pro Asn Phe
        115                 120                 125

tgg agc aac tgg agt tcc tgg gag gaa gtc agt gta caa gat tct act   432
Trp Ser Asn Trp Ser Ser Trp Glu Glu Val Ser Val Gln Asp Ser Thr
    130                 135                 140

gga cag gat ata ttg ttc gtt ttc cct aaa gat aag ctg gtg gaa gaa   480
Gly Gln Asp Ile Leu Phe Val Phe Pro Lys Asp Lys Leu Val Glu Glu
145                 150                 155                 160

ggc acc aat gtt acc att tgt tac gtt tct agg aac att caa aat aat   528
Gly Thr Asn Val Thr Ile Cys Tyr Val Ser Arg Asn Ile Gln Asn Asn
                165                 170                 175

gta tcc tgt tat ttg gaa ggg aaa cag att cat gga gaa caa ctt gat   576
Val Ser Cys Tyr Leu Glu Gly Lys Gln Ile His Gly Glu Gln Leu Asp
            180                 185                 190

cca cat gta act gca ttc aac ttg aat agt gtg cct ttc att agg aat   624
Pro His Val Thr Ala Phe Asn Leu Asn Ser Val Pro Phe Ile Arg Asn
        195                 200                 205

aaa ggg aca aat atc tat tgt gag gca agt caa gga aat gtc agt gaa   672
Lys Gly Thr Asn Ile Tyr Cys Glu Ala Ser Gln Gly Asn Val Ser Glu
    210                 215                 220

ggc atg aaa ggc atc gtt ctt ttt gtc tca aaa gta ctt gag gag ccc   720
Gly Met Lys Gly Ile Val Leu Phe Val Ser Lys Val Leu Glu Glu Pro
225                 230                 235                 240

aag gac ttt tct tgt gaa acc gag gac ttc aag act ttg cac tgt act   768
Lys Asp Phe Ser Cys Glu Thr Glu Asp Phe Lys Thr Leu His Cys Thr
                245                 250                 255

tgg gat cct ggg acg gac act gcc ttg ggg tgg tct aaa caa cct tcc   816
Trp Asp Pro Gly Thr Asp Thr Ala Leu Gly Trp Ser Lys Gln Pro Ser
            260                 265                 270

caa agc tac act tta ttt gaa tca ttt tct ggg gaa aag aaa ctt tgt   864
Gln Ser Tyr Thr Leu Phe Glu Ser Phe Ser Gly Glu Lys Lys Leu Cys
        275                 280                 285
```

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aca cac aaa aac tgg tgt aat tgg caa ata act caa gac tca caa gaa   912
Thr His Lys Asn Trp Cys Asn Trp Gln Ile Thr Gln Asp Ser Gln Glu
    290                 295                 300

acc tat aac ttc aca ctc ata gct gaa aat tac tta agg aag aga agt   960
Thr Tyr Asn Phe Thr Leu Ile Ala Glu Asn Tyr Leu Arg Lys Arg Ser
305                 310                 315                 320

gtc aat atc ctt ttt aac ctg act cat cga gtt tat tta atg aat cct   1008
Val Asn Ile Leu Phe Asn Leu Thr His Arg Val Tyr Leu Met Asn Pro
                325                 330                 335

ttt agt gtc aac ttt gaa aat gta aat gcc aca aat gcc atc atg acc   1056
Phe Ser Val Asn Phe Glu Asn Val Asn Ala Thr Asn Ala Ile Met Thr
            340                 345                 350

tgg aag gtg cac tcc ata agg aat aat ttc aca tat ttg tgt cag att   1104
Trp Lys Val His Ser Ile Arg Asn Asn Phe Thr Tyr Leu Cys Gln Ile
        355                 360                 365

gaa ctc cat ggt gaa gga aaa atg atg caa tac aat gtt tcc atc aag   1152
Glu Leu His Gly Glu Gly Lys Met Met Gln Tyr Asn Val Ser Ile Lys
    370                 375                 380

gtg aac ggt gag tac ttc tta agt gaa ctg gaa cct gcc aca gag tac   1200
Val Asn Gly Glu Tyr Phe Leu Ser Glu Leu Glu Pro Ala Thr Glu Tyr
385                 390                 395                 400

atg gcg cga gta cgg tgt gct gat gcc agc cac ttc tgg aaa tgg agt   1248
Met Ala Arg Val Arg Cys Ala Asp Ala Ser His Phe Trp Lys Trp Ser
                405                 410                 415

gaa tgg agt ggt cag aac ttc acc aca ctt gaa gct gct ccc tca gag   1296
Glu Trp Ser Gly Gln Asn Phe Thr Thr Leu Glu Ala Ala Pro Ser Glu
            420                 425                 430

gcc cct gat gtc tgg aga att gtg agc ttg gag cca gga aat cat act   1344
Ala Pro Asp Val Trp Arg Ile Val Ser Leu Glu Pro Gly Asn His Thr
        435                 440                 445

gtg acc tta ttc tgg aag cca tta tca aaa ctg cat gcc aat gga aag   1392
Val Thr Leu Phe Trp Lys Pro Leu Ser Lys Leu His Ala Asn Gly Lys
    450                 455                 460

atc ctg ttc tat aat gta gtt gta gaa aac cta gac aaa cca tcc agt   1440
Ile Leu Phe Tyr Asn Val Val Val Glu Asn Leu Asp Lys Pro Ser Ser
465                 470                 475                 480

tca gag ctc cat tcc att cca gca cca gcc aac agc aca aaa cta atc   1488
Ser Glu Leu His Ser Ile Pro Ala Pro Ala Asn Ser Thr Lys Leu Ile
                485                 490                 495

ctt gac agg tgt tcc tac caa atc tgc gtc ata gcc aac aac agt gtg   1536
Leu Asp Arg Cys Ser Tyr Gln Ile Cys Val Ile Ala Asn Asn Ser Val
            500                 505                 510

ggt gct tct cct gct tct gta ata gtc atc tct gca gac ccc gaa aac   1584
Gly Ala Ser Pro Ala Ser Val Ile Val Ile Ser Ala Asp Pro Glu Asn
        515                 520                 525

aaa gag gtt gag gaa gaa aga att gca ggc aca gag ggt gga ttc tct   1632
Lys Glu Val Glu Glu Glu Arg Ile Ala Gly Thr Glu Gly Gly Phe Ser
    530                 535                 540
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ctg tct tgg aaa ccc caa cct gga gat gtt ata ggc tat gtt gtg gac   1680
Leu Ser Trp Lys Pro Gln Pro Gly Asp Val Ile Gly Tyr Val Val Asp
545                 550                 555                 560

tgg tgt gac cat acc cag gat gtg ctc ggt gat ttc cag tgg aag aat   1728
Trp Cys Asp His Thr Gln Asp Val Leu Gly Asp Phe Gln Trp Lys Asn
                565                 570                 575

gta ggt ccc aat acc aca agc aca gtc att agc aca gat gct ttt agg   1776
Val Gly Pro Asn Thr Thr Ser Thr Val Ile Ser Thr Asp Ala Phe Arg
            580                 585                 590

cca gga gtt cga tat gac ttc aga att tat ggg tta tct aca aaa agg   1824
Pro Gly Val Arg Tyr Asp Phe Arg Ile Tyr Gly Leu Ser Thr Lys Arg
        595                 600                 605

att gct tgt tta tta gag aaa aaa aca gga tac tct cag gaa ctt gct   1872
Ile Ala Cys Leu Leu Glu Lys Lys Thr Gly Tyr Ser Gln Glu Leu Ala
    610                 615                 620

cct tca gac aac cct cac gtg ctg gtg gat aca ttg aca tcc cac tcc   1920
Pro Ser Asp Asn Pro His Val Leu Val Asp Thr Leu Thr Ser His Ser
625                 630                 635                 640

ttc act ctg agt tgg aaa gat tac tct act gaa tct caa cct ggt ttt   1968
Phe Thr Leu Ser Trp Lys Asp Tyr Ser Thr Glu Ser Gln Pro Gly Phe
                645                 650                 655

ata caa ggg tac cat gtc tat ctg aaa tcc aag gcg agg cag tgc cac   2016
Ile Gln Gly Tyr His Val Tyr Leu Lys Ser Lys Ala Arg Gln Cys His
            660                 665                 670

cca cga ttt gaa aag gca gtt ctt tca gat ggt tca gaa tgt tgc aaa   2064
Pro Arg Phe Glu Lys Ala Val Leu Ser Asp Gly Ser Glu Cys Cys Lys
        675                 680                 685

tac aaa att gac aac ccg gaa gaa aag gca ttg att gtg gac aac cta   2112
Tyr Lys Ile Asp Asn Pro Glu Glu Lys Ala Leu Ile Val Asp Asn Leu
    690                 695                 700

aag cca gaa tcc ttc tat gag ttt ttc atc act cca ttc act agt gct   2160
Lys Pro Glu Ser Phe Tyr Glu Phe Phe Ile Thr Pro Phe Thr Ser Ala
705                 710                 715                 720

ggt gaa ggc ccc agt gct acg ttc acg aag gtc acg act ccg gat gaa   2208
Gly Glu Gly Pro Ser Ala Thr Phe Thr Lys Val Thr Thr Pro Asp Glu
                725                 730                 735

cac tcc tcg atg ctg att cat atc cta ctg ccc atg gtt ttc tgc gtc   2256
His Ser Ser Met Leu Ile His Ile Leu Leu Pro Met Val Phe Cys Val
            740                 745                 750

ttg ctc atc atg gtc atg tgc tac ttg aaa agt cag tgg atc aag gag   2304
Leu Leu Ile Met Val Met Cys Tyr Leu Lys Ser Gln Trp Ile Lys Glu
        755                 760                 765

acc tgt tat cct gac atc cct gac cct tac aag agc agc atc ctg tca   2352
Thr Cys Tyr Pro Asp Ile Pro Asp Pro Tyr Lys Ser Ser Ile Leu Ser
    770                 775                 780

tta ata aaa ttc aag gag aac cct cac cta ata ata atg aat gtc agt   2400
Leu Ile Lys Phe Lys Glu Asn Pro His Leu Ile Ile Met Asn Val Ser
785                 790                 795                 800
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gac tgt atc cca gat gct att gaa gtt gta agc aag cca gaa ggg aca   2448
Asp Cys Ile Pro Asp Ala Ile Glu Val Val Ser Lys Pro Glu Gly Thr
                805                 810                 815

aag ata cag ttc cta ggc act agg aag tca ctc aca gaa acc gag ttg   2496
Lys Ile Gln Phe Leu Gly Thr Arg Lys Ser Leu Thr Glu Thr Glu Leu
            820                 825                 830

act aag cct aac tac ctt tat ctc ctt cca aca gaa aag aat cac tct   2544
Thr Lys Pro Asn Tyr Leu Tyr Leu Leu Pro Thr Glu Lys Asn His Ser
        835                 840                 845

ggc cct ggc ccc tgc atc tgt ttt gag aac ttg acc tat aac cag gca   2592
Gly Pro Gly Pro Cys Ile Cys Phe Glu Asn Leu Thr Tyr Asn Gln Ala
    850                 855                 860

gct tct gac tct ggc tct tgt ggc cat gtt cca gta tcc cca aaa gcc   2640
Ala Ser Asp Ser Gly Ser Cys Gly His Val Pro Val Ser Pro Lys Ala
865                 870                 875                 880

cca agt atg ctg gga cta atg acc tca cct gaa aat gta cta aag gca   2688
Pro Ser Met Leu Gly Leu Met Thr Ser Pro Glu Asn Val Leu Lys Ala
                885                 890                 895

cta gaa aaa aac tac atg aac tcc ctg gga gaa atc cca gct gga gaa   2736
Leu Glu Lys Asn Tyr Met Asn Ser Leu Gly Glu Ile Pro Ala Gly Glu
            900                 905                 910

aca agt ttg aat tat gtg tcc cag ttg gct tca ccc atg ttt gga gac   2784
Thr Ser Leu Asn Tyr Val Ser Gln Leu Ala Ser Pro Met Phe Gly Asp
        915                 920                 925

aag gac agt ctc cca aca aac cca gta gag gca cca cac tgt tca gag   2832
Lys Asp Ser Leu Pro Thr Asn Pro Val Glu Ala Pro His Cys Ser Glu
    930                 935                 940

tat aaa atg caa atg gca gtc tcc ctg cgt ctt gcc ttg cct ccc ccg   2880
Tyr Lys Met Gln Met Ala Val Ser Leu Arg Leu Ala Leu Pro Pro Pro
945                 950                 955                 960

acc gag aat agc agc ctc tcc tca att acc ctt tta gat cca ggt gaa   2928
Thr Glu Asn Ser Ser Leu Ser Ser Ile Thr Leu Leu Asp Pro Gly Glu
                965                 970                 975

cac tac tgc taa                                                  2940
His Tyr Cys  *
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<210> 16
<211> 979
<212> PRT
<213> Homo sapiens

<400> 16

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Ser Leu Arg Thr Tyr Gln Ser Glu Val Leu Ala Glu Arg Leu Pro Leu
            20                  25                  30
Thr Pro Val Ser Leu Lys Val Ser Thr Asn Ser Thr Arg Gln Ser Leu
        35                  40                  45
His Leu Gln Trp Thr Val His Asn Leu Pro Tyr His Gln Glu Leu Lys
    50                  55                  60
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32aa

Met Val Phe Gln Ile Gln Ile Ser Arg Ile Glu Thr Ser Asn Val Ile
65 70 75 80
Trp Val Gly Asn Tyr Ser Thr Thr Val Lys Trp Asn Gln Val Leu His
85 90 95
Trp Ser Trp Glu Ser Glu Leu Pro Leu Glu Cys Ala Thr His Phe Val
100 105 110
Arg Ile Lys Ser Leu Val Asp Asp Ala Lys Phe Pro Glu Pro Asn Phe
115 120 125
Trp Ser Asn Trp Ser Ser Trp Glu Glu Val Ser Val Gln Asp Ser Thr
130 135 140
Gly Gln Asp Ile Leu Phe Val Phe Pro Lys Asp Lys Leu Val Glu Glu
145 150 155 160
Gly Thr Asn Val Thr Ile Cys Tyr Val Ser Arg Asn Ile Gln Asn Asn
165 170 175
Val Ser Cys Tyr Leu Glu Gly Lys Gln Ile His Gly Glu Gln Leu Asp
180 185 190
Pro His Val Thr Ala Phe Asn Leu Asn Ser Val Pro Phe Ile Arg Asn
195 200 205
Lys Gly Thr Asn Ile Tyr Cys Glu Ala Ser Gln Gly Asn Val Ser Glu
210 215 220
Gly Met Lys Gly Ile Val Leu Phe Val Ser Lys Val Leu Glu Glu Pro
225 230 235 240
Lys Asp Phe Ser Cys Glu Thr Glu Asp Phe Lys Thr Leu His Cys Thr
245 250 255
Trp Asp Pro Gly Thr Asp Thr Ala Leu Gly Trp Ser Lys Gln Pro Ser
260 265 270
Gln Ser Tyr Thr Leu Phe Glu Ser Phe Ser Gly Glu Lys Lys Leu Cys
275 280 285
Thr His Lys Asn Trp Cys Asn Trp Gln Ile Thr Gln Asp Ser Gln Glu
290 295 300
Thr Tyr Asn Phe Thr Leu Ile Ala Glu Asn Tyr Leu Arg Lys Arg Ser
305 310 315 320
Val Asn Ile Leu Phe Asn Leu Thr His Arg Val Tyr Leu Met Asn Pro
325 330 335
Phe Ser Val Asn Phe Glu Asn Val Asn Ala Thr Asn Ala Ile Met Thr
340 345 350
Trp Lys Val His Ser Ile Arg Asn Asn Phe Thr Tyr Leu Cys Gln Ile
355 360 365
Glu Leu His Gly Glu Gly Lys Met Met Gln Tyr Asn Val Ser Ile Lys
370 375 380
Val Asn Gly Glu Tyr Phe Leu Ser Glu Leu Glu Pro Ala Thr Glu Tyr
385 390 395 400
Met Ala Arg Val Arg Cys Ala Asp Ala Ser His Phe Trp Lys Trp Ser
405 410 415
Glu Trp Ser Gly Gln Asn Phe Thr Thr Leu Glu Ala Ala Pro Ser Glu
420 425 430
Ala Pro Asp Val Trp Arg Ile Val Ser Leu Glu Pro Gly Asn His Thr
435 440 445
Val Thr Leu Phe Trp Lys Pro Leu Ser Lys Leu His Ala Asn Gly Lys
450 455 460
Ile Leu Phe Tyr Asn Val Val Val Glu Asn Leu Asp Lys Pro Ser Ser
465 470 475 480
Ser Glu Leu His Ser Ile Pro Ala Pro Ala Asn Ser Thr Lys Leu Ile
485 490 495
Leu Asp Arg Cys Ser Tyr Gln Ile Cys Val Ile Ala Asn Asn Ser Val
500 505 510
Gly Ala Ser Pro Ala Ser Val Ile Val Ile Ser Ala Asp Pro Glu Asn
515 520 525
Lys Glu Val Glu Glu Glu Arg Ile Ala Gly Thr Glu Gly Gly Phe Ser
530 535 540
Leu Ser Trp Lys Pro Gln Pro Gly Asp Val Ile Gly Tyr Val Val Asp
545 550 555 560
Trp Cys Asp His Thr Gln Asp Val Leu Gly Asp Phe Gln Trp Lys Asn

Val Gly Pro Asn Thr Thr Ser Thr Val Ile Ser Thr Asp Ala Phe Arg
565 570 575
Pro Gly Val Arg Tyr Asp Phe Arg Ile Tyr Gly Leu Ser Thr Lys Arg
580 585 590
Ile Ala Cys Leu Leu Glu Lys Lys Thr Gly Tyr Ser Gln Glu Leu Ala
595 600 605
Pro Ser Asp Asn Pro His Val Leu Val Asp Thr Leu Thr Ser His Ser
610 615 620
Phe Thr Leu Ser Trp Lys Asp Tyr Ser Thr Glu Ser Gln Pro Gly Phe
625 630 635 640
Ile Gln Gly Tyr His Val Tyr Leu Lys Ser Lys Ala Arg Gln Cys His
645 650 655
Pro Arg Phe Glu Lys Ala Val Leu Ser Asp Gly Ser Glu Cys Cys Lys
660 665 670
Tyr Lys Ile Asp Asn Pro Glu Glu Lys Ala Leu Ile Val Asp Asn Leu
675 680 685
Lys Pro Glu Ser Phe Tyr Glu Phe Phe Ile Thr Pro Phe Thr Ser Ala
690 695 700
Gly Glu Gly Pro Ser Ala Thr Phe Thr Lys Val Thr Thr Pro Asp Glu
705 710 715 720
His Ser Ser Met Leu Ile His Ile Leu Leu Pro Met Val Phe Cys Val
725 730 735
Leu Leu Ile Met Val Met Cys Tyr Leu Lys Ser Gln Trp Ile Lys Glu
740 745 750
Thr Cys Tyr Pro Asp Ile Pro Asp Pro Tyr Lys Ser Ser Ile Leu Ser
755 760 765
Leu Ile Lys Phe Lys Glu Asn Pro His Leu Ile Ile Met Asn Val Ser
770 775 780
Asp Cys Ile Pro Asp Ala Ile Glu Val Val Ser Lys Pro Glu Gly Thr
785 790 795 800
Lys Ile Gln Phe Leu Gly Thr Arg Lys Ser Leu Thr Glu Thr Glu Leu
805 810 815
Thr Lys Pro Asn Tyr Leu Tyr Leu Leu Pro Thr Glu Lys Asn His Ser
820 825 830
Gly Pro Gly Pro Cys Ile Cys Phe Glu Asn Leu Thr Tyr Asn Gln Ala
835 840 845
Ala Ser Asp Ser Gly Ser Cys Gly His Val Pro Val Ser Pro Lys Ala
850 855 860
Pro Ser Met Leu Gly Leu Met Thr Ser Pro Glu Asn Val Leu Lys Ala
865 870 875 880
Leu Glu Lys Asn Tyr Met Asn Ser Leu Gly Glu Ile Pro Ala Gly Glu
885 890 895
Thr Ser Leu Asn Tyr Val Ser Gln Leu Ala Ser Pro Met Phe Gly Asp
900 905 910
Lys Asp Ser Leu Pro Thr Asn Pro Val Glu Ala Pro His Cys Ser Glu
915 920 925
Tyr Lys Met Gln Met Ala Val Ser Leu Arg Leu Ala Leu Pro Pro Pro
930 935 940
Thr Glu Asn Ser Ser Leu Ser Ser Ile Thr Leu Leu Asp Pro Gly Glu
945 950 955 960
His Tyr Cys
965 970 975

CLAIMS:

1. A use of a monoclonal antibody that specifically binds to an IL-31 polypeptide consisting of amino acid residues 27-164 of SEQ ID NO:2 for inhibiting IL-31-induced signal transduction in dorsal root ganglion cells; or for formulating a medicament for inhibiting IL-31-induced signal transduction in dorsal root ganglion cells.

2. The use according to claim 1, wherein the monoclonal antibody has a human Fc region.

3. The use according to claim 1 or 2, wherein the isotype of the monoclonal antibody is IgG.

4. The use according to any one of claims 1-3, wherein the isotype of the monoclonal antibody is IgG4.

5. A monoclonal antibody that specifically binds to an IL-31 polypeptide consisting of amino acid residues 27-164 of SEQ ID NO:2, for use in inhibiting IL-31-induced signal transduction in dorsal root ganglion cells; or for use in formulating a medicament for inhibiting IL-31-induced signal transduction in dorsal root ganglion cells.

6. The monoclonal antibody of claim 5, wherein the monoclonal antibody has a human Fc region.

7. The monoclonal antibody of claim 5 or 6, wherein the isotype of the monoclonal antibody is IgG.

8. The monoclonal antibody of any one of claims 5-7, wherein the isotype of the monoclonal antibody is IgG4.