



US008481021B2

(12) **United States Patent**
Sims et al.(10) **Patent No.:** **US 8,481,021 B2**
(45) **Date of Patent:** **Jul. 9, 2013**(54) **IL-1F5 POLYPEPTIDES**(75) Inventors: **John E Sims**, Seattle, WA (US); **Blair R Renshaw**, Renton, WA (US);
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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

(21) Appl. No.: **13/225,326**(22) Filed: **Sep. 2, 2011**(65) **Prior Publication Data**

US 2012/0020918 A1 Jan. 26, 2012

Related U.S. Application Data

(62) Division of application No. 11/900,235, filed on Sep. 10, 2007, now Pat. No. 8,034,771.

(60) Provisional application No. 60/843,311, filed on Sep. 8, 2006.

(51) **Int. Cl.****A61K 38/19** (2006.01)**A61K 38/16** (2006.01)**C07K 14/54** (2006.01)(52) **U.S. Cl.**USPC **424/85.2**; 514/12; 530/351(58) **Field of Classification Search**

None

See application file for complete search history.

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Primary Examiner — Ruixiang Li(74) *Attorney, Agent, or Firm* — Mary Kymne Hehman; Patricia Anne Perkin(57) **ABSTRACT**The present invention provides compositions and methods relating to IL-1R α 2 requiring proteins.**3 Claims, 2 Drawing Sheets**

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FIG. 1

Consensus	@XD	SEQ ID No
IL-1F5	~~~~~MVLSGALCFR <u>M</u> <u>K</u> <u>D</u> SALKVLYLHNN	44
IL-1F6	~~~~~MEKALKIDTPQQGS <u>I</u> <u>Q</u> <u>D</u> INHRVWVLQDQ	59
IL-1F8	~~~~~MNPQREAAPKSYA <u>I</u> <u>R</u> <u>D</u> SRQM VVLSGN	61
IL-1F9	MRGTPGDADGGGRAVYQSMCKPITGT <u>I</u> <u>N</u> <u>D</u> LNQQVWTLQGQ	63

FIG. 2

HuIL-1F5:

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESVVPNRWL
DASLSPVILGVQGSQCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTF
YRRDMGLTSSFESAAYPGWFLCTVPEADQPVRLTQLPENGGWNAIPITDFY
FQQCD (SEQ ID NO 1)

HuIL-1F6:

MEKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCR
HVETLEKDRGNPIYLGNGNLNCLMCAKVGDDQPTLQLKEKDIMDLYNQPE
PVKSFLFYHSQSGRNSTFESVAFPGWFIASVSEGGCPLIILTQELGKANTT
DFGLTMLF (SEQ ID NO 2)

HuIL-1F8:

MNPQREAAPKSYAIRDSRQMWWVLSGNSLIAAPLSRSIKPVTLHLIACRD
TEFSDKEKGNMVYLGIKGKDLCLFCAEIQGKPTLQLKEKNIMDLIVEKKA
QKPFLFFHNKEGSTSVFQSVSYPGWFIATSTTSGQPIFLTKERGITNNTN
FYLDSVE (SEQ ID NO 3)

HuIL-1F9:

MRGTPGDADGGGRAVYQSMCKPITGTINDLNQQVWTLQGQNLVAVPRS
DSVTPVTAVITCKYPEALEQGRGDPIYLGIONPEMCLYCEKVGEQPTLQ
LKEQKIMDLYGQPEPVKPFIFYRAKTGRTSTLESVAFPDWFIASSKRDQPII
LTSELGKSYNTAFELNIND (SEQ ID NO 4)

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IL-1F5 POLYPEPTIDES

This application claims the benefit of U.S. Non-provisional patent application Ser. No. 11/900,235, filed Sep. 10, 2007, which claims the benefit of U.S. Provisional Application No. 60/843,311, filed Sep. 8, 2006, both of which are hereby incorporated by reference in their entirety.

The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled A-1129.txt, created Oct. 12, 2011, which is 84 KB in size. The information in the electronic format of the Sequence Listing is incorporated herein by reference in its entirety.

Throughout this application various publications are referenced within parentheses or brackets. The disclosures of these publications in their entireties are hereby incorporated by reference in this application in order to more fully describe the state of the art to which this invention pertains.

FIELD OF THE INVENTION

This application provides nucleic acids, polypeptides, compositions, assays, and methods relating to variants of IL-1 Family members that signal through IL-1Rrp2.

BACKGROUND OF THE INVENTION

The IL-1 family includes several cytokines whose primary function is to mediate immune and inflammatory responses. The earliest members discovered were IL-1 alpha, IL-1 beta, IL-1 receptor antagonist (IL-1ra), and IL-18 (previously known as IGIF and sometimes IL-1 gamma). Following the discovery of additional proteins with homology to these IL-1 family members, a nomenclature system was adopted in which IL-1 alpha is referred to as IL-1F1, IL-1 beta as IL-1F2, IL-1ra as IL-1F3 and IL-18 as IL-1F4. Seven additional cytokines have been classified as IL-1 family members based on amino acid sequence similarity, identity of gene structure, and predicted or known three-dimensional structure (Sims, J. E. et al., *Trends Immunol* 22:537, 2001; Dunn, E., et al., *Trends Immunol* 22:533, 2001; Dunn, E. F., et al., *Biochemistry* 42:10938, 2003; Schmitz et al. *Immunity* 23:479-490, 2005).

IL-1 alpha, IL-1 beta and IL-1ra (IL-1F1-3, respectively) bind to receptors that are members of the immunoglobulin superfamily, the 80 kDa type I receptor (IL-1RI) and a 68 kDa type II receptor (IL-1RII), as well as a soluble proteolytic fragment of IL-1RII (sIL-1RII). Binding of IL-1 (alpha or beta) to the type I IL-1 receptor (IL-1R) results in recruitment of the IL-1R homolog, IL-1R accessory protein (IL-1RAcP or AcP), which does not directly bind the ligands but is required for signal transduction (Sims et al. *Trends Immunol* 22: 537, 2001); binding of IL-1ra does not. Signaling by IL-18 is very similar, although IL-18 utilizes a different receptor complex (Born, T. L., et al., *J Biol Chem* 273:29445, 1998). IL-1F5, F6, F8 and F9 make use of the IL-1R-related protein 2 (IL-1Rrp2), with F6, F8 and F9 agonizing this receptor pathway, and IL-1F5 antagonizing it (Debets, R., et al., *J Immunol* 167:1440, 2001; Towne et al. 2004 *J Biol Chem* 279(14): 13677).

Several members of the IL-1 family (IL-1 alpha, IL-1 beta, IL-18, IL-1F7 and IL-33) are synthesized as precursor molecules that are proteolytically cleaved, by caspase-1 in the case of IL-1 beta and IL-18, and by an unidentified protease or proteases for IL-33, IL-1 alpha and IL-1F7. IL-1ra is activated by signal peptidase cleavage of a short peptide from the n-terminus. However, little is known about what, if any, processing occurs with the remaining family members.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 provides an alignment of the N-terminal portions of wild type IL-1F5, F6, F8 and F9. There is a (Met or Ile)-Xaa-

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Asp sequence present in each of F5, F6, F8 and F9, marked by underlining of the Met/Ile and the Asp residues. There is a similar "aliphatic amino acid-X-Aspartate or other polar amino acid" motif present in all IL-1 family members, and this can be used to align IL-1 family sequences. The consensus motif is indicated by @XD where @ may be an aliphatic amino acid such as Met or Ile and X is any one amino acid D is Asp. In FIG. 1, the sequences are lined up using the Met/Ile-Xaa-Asp motif (Met 11 in F5, Ile15 in F6, Ile14 in F8, and Ile27 in F9 respectively), so that the natural N-termini (with initiating methionines) lie at different distances upstream of the aliphatic amino acid, @, of the motif.

FIG. 2 is the full length wild type amino acid sequences of IL-1F5, IL-1F6, IL-1F8 and IL-1F9.

SUMMARY OF THE INVENTION

In one aspect, the present invention provides an isolated IL-1F5 polypeptide that antagonizes signal transduction/activation through IL-1Rrp2, where the IL-1F5 polypeptide contains the sequence Met-Lys-Asp, which matches the consensus @XD depicted in FIG. 1, and wherein the polypeptide comprises nine amino acids on the N-terminal side of the above-referenced methionine. In one embodiment the IL-1F5 polypeptide is a human IL-1F5 polypeptide. In one embodiment, the IL-1F5 polypeptide of the invention comprises an amino acid sequence having a methionine at position ten of the amino acid sequence, position ten being relative to the N-terminal amino acid at position one of the amino acid sequence. In one embodiment, the IL-1F5 polypeptide of the invention comprises an amino acid sequence having a methionine at position ten of the amino acid sequence, position ten being relative to the N-terminal amino acid at position one of the amino acid sequence and an amino acid selected from the group consisting of valine and methionine at the N-terminal amino acid at position one. In one embodiment, the IL-1F5 polypeptide of the invention comprises an amino acid sequence having a methionine at position ten of the amino acid sequence, position ten being relative to the N-terminal amino acid at position one of the amino acid sequence and a leucine at position two of its amino acid sequence. In a particular embodiment the IL-1F5 polypeptide of the invention, comprises an amino acid sequence having a methionine at position ten of the amino acid sequence, position ten being relative to the N-terminal amino acid at position one of the amino acid sequence and an amino acid selected from the group consisting of valine and methionine at the N-terminal amino acid at position one and a leucine at position two.

In particular embodiments, the IL-1F5 polypeptide of the invention comprises at least 90%, at least 95%, at least 98% or at least 99% identity to SEQ ID NO 1 and a methionine at position ten of the amino acid sequence of the IL-1F5 polypeptide of the invention, position ten being relative to the N-terminal amino acid at position one. In some embodiments, the isolated IL-1F5 polypeptide of the invention antagonizes signal transduction/activation through IL-1Rrp2 more than the IL-1F5 polypeptide having the amino acid sequence of SEQ ID NO 1. In some embodiments, the isolated IL-1F5 polypeptide of the invention antagonizes signal transduction/activation through IL-1Rrp2 more than about 5 fold, 10 fold, 100 fold, 1,000 fold the level of antagonization of signal transduction/activation of the IL-1F5 polypeptide having the amino acid sequence of SEQ ID NO 1. The level of signal transduction/activation antagonization is measured according to the method described in Example 2A.

In a particular embodiment, the isolated IL-1F5 polypeptide of the invention has a methionine at position ten of its amino acid sequence relative to the N-terminal amino acid at position one and comprises an amino acid sequence selected from the group consisting of:

(SEQ ID NO 6)
VLSGALCFRMDKLSALKVLYLHNNQLLAGGLHAGKVIKGEEISVVPNRWLDASLSPVILG

VQGSQCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGW

FLCTVPEADQPVRLTQLPENGWGNAPITDFYFQQCD,

(SEQ ID NO 7)
MLSGALCFRMDKLSALKVLYLHNNQLLAGGLHAGKVIKGEEISVVPNRWLDASLSPVILG

VQGSQCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGW

FLCTVPEADQPVRLTQLPENGWGNAPITDFYFQQCDDYKDDDKHHH,

(SEQ ID NO 8)
MLSGALCFRMDKLSALKVLYLHNNQLLAGGLHAGKVIKGEEISVVPNRWLDASLSPVILG

VQGSQCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGW

FLCTVPEADQPVRLTQLPENGWGNAPITDFYFQQCD

and

(SEQ ID NO 9)
MLSGALCFRMDKLSALKVLYLHNNQLLAGGLHAGKVIKGEEISVVPNRWLDASLSPVILG

VQGSQCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGW

FLCTVPEADQPVRLTQLPENGWGNAPITDFYFQQCDDYKDDDKHHH.

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In another embodiment, a nucleic acid sequence encoding the isolated IL-1F5 polypeptide of the invention is provided. In another aspect of the invention, a recombinant vector that directs expression of a nucleic acid encoding an isolated IL-1F5 polypeptide of the invention is provided. In a particular embodiment, the vector of the invention comprises a nucleic acid sequence selected from the group consisting of:

In another aspect, a host cell transfected or transduced with a recombinant vector that directs expression of a nucleic acid encoding an IL-1F5 polypeptide of the invention is provided. In another aspect, a method of producing an isolated IL-1F5 polypeptide of the invention comprising culturing the host cell transfected or transduced with a recombinant vector that directs expression of an IL-1F5 polypeptide of the invention,

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(SEQ ID NO 69)
GTCTGAGTGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTAT

CTGCATAATAACCAAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTATTAAAGGT

GAAGAGATCAGCGTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCGTCATC

CTGGGTGTCCAGGTGGAAGCCAGTGCCTGTCATGTGGGGTGGGGCAGGAGCCGAC

TCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTGGTGCCAAGGAATCCAA

GAGCTTACCTTCTACCGGCGGGACATGGGGCTACCTCCAGCTTCGAGTCGGCTGC

CTACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCCTGTCAGACTCAC

CCAGCTTCCCAGAAATGGTGGCTGGAATGCCCCATCACAGACTTCTACTTCCAGCA

GTGTGACTAA

and

(SEQ ID NO 70)
ATGCTGAGTGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTAT

CTGCATAATAACCAAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTATTAAAGGT

GAAGAGATCAGCGTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCGTCATC

CTGGGTGTCCAGGTGGAAGCCAGTGCCTGTCATGTGGGGTGGGGCAGGAGCCGAC

TCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTGGTGCCAAGGAATCCAA

GAGCTTACCTTCTACCGGCGGGACATGGGGCTACCTCCAGCTTCGAGTCGGCTGC

CTACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCCTGTCAGACTCAC

CCAGCTTCCCAGAAATGGTGGCTGGAATGCCCCATCACAGACTTCTACTTCCAGCA

GTGTGACAGATCTGGCAGTTCGACTACAAGGACGACGACACAAGGGCAGTTC

ACCATCACCATCACCAGTAG.

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under conditions promoting expression and isolating the expressed IL-1F5 polypeptide is provided.

An antibody or a fragment thereof that specifically binds an IL-1F5 polypeptide and prevents IL-1F5 antagonism of signal transduction through IL-1Rrp2 is provided. In particular embodiments, an antibody that binds an IL-1F5 polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NO 6, SEQ ID NO 7, SEQ ID NO 8, and SEQ ID NO 9 is provided. In some embodiments, the IL-1F5 antibody of the invention, is a monoclonal antibody, particularly a chimeric antibody, a humanized antibody or a fully human antibody. The invention provides a composition, particularly a pharmaceutical composition, comprising the IL-1F5 antibody of the invention and a physiologically acceptable diluent, excipient or carrier. A method of stimulating the immune system of an immunosuppressed subject, comprising administering the anti-IL-1F5 antibody of the invention to an immunosuppressed subject in an amount sufficient to stimulate the patient's immune system is provided.

In another aspect, a composition, particularly a pharmaceutical composition, comprising an IL-1F5 polypeptide of the invention and a physiologically acceptable diluent, excipient or carrier is provided. In another embodiment, the invention provides a method of treating an inflammatory or autoimmune condition in a subject wherein the inflammatory or autoimmune condition is mediated by IL-1Rrp2, comprising administering to the subjecting an amount of the IL-1F5 polypeptide of the invention sufficient to reduce at least one symptom of the inflammatory or autoimmune condition in the subject. In one embodiment, the condition to be treated is an inflammatory condition of the skin, lungs or airways mediated by IL-1Rrp2. In a particular embodiment, the condition to be treated is selected from the group consisting of psoriasis, seborrheic dermatitis, atopic dermatitis, including chronic atopic dermatitis, allergic contact dermatitis, lichen simplex chronicus, pityriasis rubra pilaris, nummular dermatitis, asthma, allergic rhinitis, gastro-esophageal reflux disease, arthritic conditions including, rheumatoid arthritis, psoriatic arthritis, and osteoarthritis. In particular embodiments of the above methods, the subject is human.

In one aspect, the present invention provides an isolated IL-1F6 polypeptide that agonizes signal transduction/activation through IL-1Rrp2, where the IL-1F6 polypeptide contains the sequence Ile-Gln-Asp, which matches the consensus @XD described in FIG. 1, and wherein the polypeptide comprises nine amino acids on the N-terminal side of the above-referenced isoleucine. In one embodiment the IL-1F6

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polypeptide is a human IL-1F6 polypeptide. In one embodiment, the IL-1F6 polypeptide of the invention comprises an amino acid sequence having an isoleucine at position ten of its amino acid sequence, position ten being relative to the N-terminal amino acid at position one. In one embodiment, the IL-1F6 polypeptide of the invention comprises an amino acid sequence having an isoleucine at position ten of its amino acid sequence, position ten being relative to the N-terminal amino acid at position one and an amino acid selected from the group consisting of lysine and methionine at the N-terminal amino acid at position one. In one embodiment, the IL-1F6 polypeptide of the invention comprises an amino acid sequence having an isoleucine at position ten of its amino acid sequence, position ten being relative to the N-terminal amino acid at position one, and an isoleucine at position two of its amino acid sequence. In a particular embodiment the IL-1F6 polypeptide of the invention, comprises an amino acid sequence having a isoleucine at position ten of the amino acid sequence, position ten being relative to the N-terminal amino acid at position one, and an amino acid selected from the group consisting of lysine and methionine at the N-terminal amino acid at position and an isoleucine at position two.

In particular embodiments, the isolated IL-1F6 polypeptide comprises at least 90%, at least 95%, at least 97% or at least 98% identity to SEQ ID NO 2 or to SEQ ID NO 2 except that there is an arginine at amino acid position 12 rather than a glutamine and an isoleucine at position ten, position ten being relative to the N-terminal amino acid at position one of the IL-1F6 amino acid sequence of the invention. In some embodiments, the isolated IL-1F6 polypeptide of the invention agonizes signal transduction/activation through IL-1Rrp2 more than the IL-1F6 polypeptide having the N-terminal amino acid sequence of SEQ ID NO 2. In some embodiments, the isolated IL-1F6 polypeptide of the invention agonizes signal transduction/activation through IL-1Rrp2 more than about 5 fold, 10 fold, 100 fold, 200 fold, 1,000 fold, 2,000 fold, 10,000 fold, 50,000 fold the level of agonization of signal transduction/activation of the IL-1F6 polypeptide having the amino acid sequence of SEQ ID NO 2. The level of signal transduction/activation agonization is measured according to the method described in Example 2B.

In another aspect, the invention provides an isolated IL-1F6 polypeptide that agonizes signal transduction/activation through IL-1Rrp2, wherein the IL-1F6 polypeptide comprises an amino acid sequence having a isoleucine at position ten of its amino acid sequence, position ten being relative to the N-terminal amino acid at position one and an amino acid sequence selected from the group consisting of:

(SEQ ID NO 10)

KIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLG

LNLGLNLCMLCAKVGDPQTLQLKEKDIMDLNQPEPVKSFLFYHSQSGRNSTFESVAFPG

WFIAVSSEGGCPLILTQELGKANTTDFGLTMLF,

(SEQ ID NO 11)

KIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLG

LNLGLNLCMLCAKVGDPQTLQLKEKDIMDLNQPEPVKSFLFYHSQSGRNSTFESVAFPG

WFIAVSSEGGCPLILTQELGKANTTDFGLTMLFDYKDDDDKHHH,

(SEQ ID NO 12)

MIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYL

GLNLGLNLCMLCAKVGDPQTLQLKEKDIMDLNQPEPVKSFLFYHSQSGRNSTFESVAFPG

GWFIASSEGGCPLILTQELGKANTTDFGLTMLF,

-continued

(SEQ ID NO 13)

MIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYL

GLNGLNLCLMCAKVGDPQTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPP

WFIASSEGCGPLILTQELGKANTTDFGLTMLFDYKDDDDKHHH,

(SEQ ID NO 65)

KIDTPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLG

LNGLNLCLMCAKVGDPQTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPG

WFIASSEGCGPLILTQELGKANTTDFGLTMLF,

(SEQ ID NO 66)

KIDTPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLG

LNGLNLCLMCAKVGDPQTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPG

WFIASSEGCGPLILTQELGKANTTDFGLTMLFDYKDDDDKHHH,

(SEQ ID NO 67)

MIDTPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLG

LNGLNLCLMCAKVGDPQTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPG

WFIASSEGCGPLILTQELGKANTTDFGLTMLF

and

(SEQ ID NO 68)

MIDTPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLG

LNGLNLCLMCAKVGDPQTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPG

WFIASSEGCGPLILTQELGKANTTDFGLTMLFDYKDDDDKHHH.

In another embodiment, a nucleic acid sequence encoding the isolated IL-1F6 polypeptide of the invention is provided. In another aspect of the invention, a recombinant vector that directs expression of a nucleic acid encoding

an isolated IL-1F6 polypeptide of the invention is provided. In a particular embodiment, the vector of the invention comprises a nucleic acid sequence selected from the group consisting of:

(SEQ ID NO 71)

AAAATTGACACACCTCAGCGGGGAGCATTTCAGGATATCAATCATCGGGTGTGGGTT

CTTCAGGACCAGACGCTCATAGCAGTCCCAGGAAGGACCGTATGTCTCCAGTCACT

ATTGCCTTAATCTCATGCCGACATGTGGAGACCCCTTGAGAAAGACAGAGGGAACCCC

ATCTACCTGGGCCTGAATGGACTCAATCTCTGCCTGATGTGTGCTAAAGTCGGGGAC

CAGCCACACATGCAGCTGAAGGAAAAGGATATAATGGATTGTACAAACCAACCCGA

GCCTGTGAAGTCCTTTCTCTTCTACACAGCCAGAGTGGCAGGAACCTCCACCTTCGA

GTCTGTGGCTTTCCCTGGCTGGTTTCATCGCTGTGCTCTGAAGGAGGCTGTCTCTC

ATCCTTACCCAAGAACTGGGGAAAGCCAACACTACTGACTTTGGGTTAACTATGCTG

TTTTAA

and

(SEQ ID NO 72)

ATGATTGACACACCTCAGCGGGGAGCATTTCAGGATATCAATCATCGGGTGTGGGTT

CTTCAGGACCAGACGCTCATAGCAGTCCCAGGAAGGACCGTATGTCTCCAGTCACT

ATTGCCTTAATCTCATGCCGACATGTGGAGACCCCTTGAGAAAGACAGAGGGAACCCC

ATCTACCTGGGCCTGAATGGACTCAATCTCTGCCTGATGTGTGCTAAAGTCGGGGAC

CAGCCACACATGCAGCTGAAGGAAAAGGATATAATGGATTGTACAAACCAACCCGA

GCCTGTGAAGTCCTTTCTCTTCTACACAGCCAGAGTGGCAGGAACCTCCACCTTCGA

GTCTGTGGCTTTCCCTGGCTGGTTTCATCGCTGTGCTCTGAAGGAGGCTGTCTCTC

ATCCTTACCCAAGAACTGGGGAAAGCCAACACTACTGACTTTGGGTTAACTATGCTG

-continued

TTTAGATCTGGCAGTTCTGACTACAAGGACGACGACACAAGGGCAGTTCTCACCAT

CACCATCACCCTAG.

In another aspect, a host cell transfected or transduced with a recombinant vector that directs expression of a nucleic acid encoding an IL-1F6 polypeptide of the invention is provided. In another aspect, a method of producing an isolated IL-1F6 polypeptide of the invention comprising culturing the host cell transfected or transduced with a recombinant vector that directs expression of an IL-1F6 polypeptide of the invention, under conditions promoting expression and isolating the expressed IL-1F6 polypeptide is provided.

In another aspect, a composition, particularly a pharmaceutical composition, comprising an IL-1F6 polypeptide of the invention and a physiologically acceptable diluent, excipient or carrier is provided. A method of stimulating the immune system of an immunosuppressed subject, comprising administering the IL-1F6 polypeptide according to the invention to an immunosuppressed subject in an amount sufficient to stimulate the subject's immune system is provided.

An antibody that specifically binds IL-1F6, where IL-1F6 may be a full length IL-1F6 or a truncant of full length IL-1F6, and prevents proteolytic cleavage thereof, particularly proteolytic cleavage to a more active form where activity is relative to that of the full length IL-1F6, is provided. An antibody that binds an IL-1F6 polypeptide of the invention, and prevents signal transduction/activation through IL-1Rrp2 is also provided. In some embodiments, an antibody binding an IL-1F6 polypeptide selected from the group consisting of: SEQ ID NO 10, SEQ ID NO 11, SEQ ID NO 12, SEQ ID NO 13, SEQ ID NO 65, SEQ ID NO 66, SEQ ID NO 67 and SEQ ID NO 68 is provided. In some embodiments, the IL-1F6 antibody of the invention, is a monoclonal antibody, particularly a chimeric antibody, a humanized antibody or a fully human antibody. The invention provides a composition, particularly a pharmaceutical composition, comprising the IL-1F6 antibody of the invention and a physiologically acceptable diluent, excipient or carrier.

The invention also provides, a method of treating an inflammatory or autoimmune condition mediated by IL-1Rrp2, comprising administering the IL-1F6 antibody of the invention to a subject in an amount sufficient to ameliorate at least one symptom mediated by IL-1Rrp2 of the condition. In one embodiment, the condition to be treated is an inflammatory condition of the skin, lungs or airways mediated by IL-1Rrp2. In a particular embodiment, the condition to be treated is selected from the group consisting of psoriasis, seborrheic dermatitis, atopic dermatitis, including chronic atopic dermatitis, allergic contact dermatitis, lichen simplex chronicus, pityriasis rubra pilaris, nummular dermatitis, asthma, allergic rhinitis, gastro-esophageal reflux disease, arthritic conditions including, rheumatoid arthritis, psoriatic arthritis, and osteoarthritis. In particular embodiments, the subject to be treated in the above methods is a human.

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In one aspect, the present invention provides an isolated IL-1F8 polypeptide that agonizes signal transduction/activation through IL-1Rrp2, where the IL-1F8 polypeptide contains the sequence Ile-Arg-Asp, which matches the consensus @XD described in FIG. 1, and wherein the polypeptide comprises nine amino acids on the N-terminal side of the above-referenced isoleucine. In one embodiment the IL-1F8 polypeptide is a human IL-1F8 polypeptide. In one embodiment, the IL-1F8 polypeptide of the invention comprises an amino acid sequence having an isoleucine at position ten of its amino acid sequence, position ten being relative to the N-terminal amino acid at position one. In one embodiment, the IL-1F8 polypeptide of the invention comprises an amino acid sequence having an isoleucine at position ten of its amino acid sequence, position ten being relative to the N-terminal amino acid at position one and an amino acid selected from the group consisting of arginine and methionine at the N-terminal amino acid at position one. In one embodiment, the IL-1F8 polypeptide of the invention comprises an amino acid sequence having an isoleucine at position ten of its amino acid sequence, position ten being relative to the N-terminal amino acid at position one, and a glutamic acid at position two of its amino acid sequence. In a particular embodiment the IL-1F8 polypeptide of the invention, comprises an amino acid sequence having a isoleucine at position ten of the amino acid sequence, position ten being relative to the N-terminal amino acid at position one, and an amino acid selected from the group consisting of arginine and methionine at the N-terminal amino acid at position one and a glutamic acid at position two.

In particular embodiments, the isolated IL-1F8 polypeptide comprises at least 90%, at least 95%, or at least 98% identity to SEQ ID NO 3 and an isoleucine at position ten, position ten being relative to the N-terminal amino acid at position one of the IL-1F8 amino acid sequence of the invention. In some embodiments, the isolated IL-1F8 polypeptide of the invention agonizes signal transduction/activation through IL-1Rrp2 more than the IL-1F8 polypeptide having the amino acid sequence of SEQ ID NO 3. In some embodiments, the isolated IL-1F8 polypeptide of the invention agonizes signal transduction/activation through IL-1Rrp2 more than about 5 fold, 10 fold, 100 fold, 200 fold, 1,000 fold, 3,000 fold, 5,000 fold, 10,000 fold, 50,000 fold the level of agonization of signal transduction/activation of the IL-1F8 polypeptide having the amino acid sequence of SEQ ID NO 3. The level of signal transduction/activation agonization is measured according to the method described in Example 2B.

In another aspect, the invention provides an isolated IL-1F8 polypeptide that agonizes signal transduction/activation through IL-1Rrp2, wherein the IL-1F8 polypeptide comprises an amino acid sequence having a isoleucine at position ten of its amino acid sequence, position ten being relative to the N-terminal amino acid at position one and an amino acid sequence selected from the group consisting of:

(SEQ ID NO 14)

REAAPKSYAIRDSRQMVVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMVL

GIKGDLCFCAEIQ GKPTLQLKEKNIMDLVEKKAQKPFLLFFHNKEGSTSVFQSVSYPG

WFIATSTSGQPIFLTKEGINTNNTFYLDSE,

-continued

(SEQ ID NO 15)

REAAPKSYAIRDSRQMVWVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMYYL

GIKGDLCFLCAEIQGKPTLQLKEKNIMDLVVEKKAQKPFLFFHNKEGSTSVFQSVSYPG

WFIATSTTSGQPIFLTKERGITNNTNFYLDSEVDYKDDDDKHHH;

(SEQ ID NO 16)

MEAAPKSYAIRDSRQMVWVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMYY

LGIKGDLCFLCAEIQGKPTLQLKEKNIMDLVVEKKAQKPFLFFHNKEGSTSVFQSVSY

GWFIATSTTSGQPIFLTKERGITNNTNFYLDSE

and

(SEQ ID NO 17)

MEAAPKSYAIRDSRQMVWVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMYY

LGIKGDLCFLCAEIQGKPTLQLKEKNIMDLVVEKKAQKPFLFFHNKEGSTSVFQSVSY

GWFIATSTTSGQPIFLTKERGITNNTNFYLDSEVDYKDDDDKHHH.

In another embodiment, a nucleic acid sequence encoding the isolated IL-1F8 polypeptide of the invention is provided. In another aspect of the invention, a recombinant vector that directs expression of a nucleic acid encoding an isolated IL-1F8 polypeptide of the invention is provided. In a particular embodiment, the vector of the invention comprises a nucleic acid sequence selected from the group consisting of:

polypeptide of the invention comprising culturing the host cell transfected or transduced with a recombinant vector that directs expression of an IL-1F8 polypeptide of the invention, under conditions promoting expression and isolating the expressed IL-1F8 polypeptide is provided.

In another aspect, a composition, particularly a pharmaceutical composition, comprising an IL-1F8 polypeptide of the invention and a physiologically acceptable diluent,

(SEQ ID NO 73)

CGCGAGGCAGCACCCAAATCCTATGCTATTCGTGATTCTCGACAGATGGTGTGGGTC

CTGAGTGGAATTCCTTAATAGCAGCTCCTCTTAGCCGAGCATTAGCCTGTCACTC

TTCATTTAATAGCCTGTAGAGACACAGAATTCAGTGACAAGGAAAGGGTAATATG

GTTTACCTGGGAATCAAGGGAAGATCTCTGTCTCTTCTGTGCAGAAATTCAGGGC

AAGCCTACTTTGCAGCTTAAGGAAAAAATATCATGGACCTGTATGTGGAGAAGAA

AGCACAGAAGCCCTTTCTCTTTTCCACAATAAAGAAGGCTCCACTTCTGTCTTTCAG

TCAGTCTCTTACCCTGGCTGGTTCATAGCCACCTCCACCACATCAGGACAGCCCATCT

TTCTCACCAGGAGAGAGGCATAACTAATAACACTAATTCTACTTAGATTCTGTGG

AATAA

and

(SEQ ID NO 74)

ATGGAGGCAGCACCCAAATCCTATGCTATTCGTGATTCTCGACAGATGGTGTGGGTC

CTGAGTGGAATTCCTTAATAGCAGCTCCTCTTAGCCGAGCATTAGCCTGTCACTC

TTCATTTAATAGCCTGTAGAGACACAGAATTCAGTGACAAGGAAAGGGTAATATG

GTTTACCTGGGAATCAAGGGAAGATCTCTGTCTCTTCTGTGCAGAAATTCAGGGC

AAGCCTACTTTGCAGCTTAAGGAAAAAATATCATGGACCTGTATGTGGAGAAGAA

AGCACAGAAGCCCTTTCTCTTTTCCACAATAAAGAAGGCTCCACTTCTGTCTTTCAG

TCAGTCTCTTACCCTGGCTGGTTCATAGCCACCTCCACCACATCAGGACAGCCCATCT

TTCTCACCAGGAGAGAGGCATAACTAATAACACTAATTCTACTTAGATTCTGTGG

AAGGATCTGGCAGTTCTGACTACAAGGACGACGACACAAGGGCAGTTCTACCAT

CACCATCACCCTAG.

In another aspect, a host cell transfected or transduced with a recombinant vector that directs expression of a nucleic acid encoding an IL-1F8 polypeptide of the invention is provided. In another aspect, a method of producing an isolated IL-1F8

excipient or carrier is provided. A method of stimulating the immune system of an immunosuppressed subject, comprising administering the IL-1F8 polypeptide according of the invention to an immunosuppressed subject in an amount sufficient to

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stimulate the subject's immune system is provided. In particular embodiments of the above methods, the subject is a human.

An antibody that specifically binds IL-1F8, where IL-1F8 may be a full length IL-1F8 or a truncant of full length IL-1F8, and prevents proteolytic cleavage thereof, particularly proteolytic cleavage to a more active form where activity is relative to that of the full length IL-1F8, is provided. An antibody that binds an IL-1F8 polypeptide of the invention, and prevents signal transduction/activation through IL-1FRp2 is also provided. In some embodiments, an antibody binding an IL-1F8 polypeptide selected from the group consisting of: SEQ ID NO 14, SEQ ID NO 15, SEQ ID NO 16 and SEQ ID NO 17, is provided. In some embodiments, the IL-1F8 antibody of the invention, is a monoclonal antibody, particularly a chimeric antibody, a humanized antibody or a fully human antibody. The invention provides a composition, particularly a pharmaceutical composition, comprising the IL-1F8 antibody of the invention and a physiologically acceptable diluent, excipient or carrier.

The invention also provides, a method of treating an inflammatory or autoimmune condition mediated by IL-1Rrp2, comprising administering the IL-1F8 antibody of the invention to a subject in an amount sufficient to ameliorate at least one symptom mediated by IL-1Rrp2 of the condition. In one embodiment, the condition to be treated is an inflammatory condition of the skin, lungs or airways mediated by IL-1Rrp2. In a particular embodiment, the condition to be treated is selected from the group consisting of psoriasis, seborrheic dermatitis, atopic dermatitis, including chronic atopic dermatitis, allergic contact dermatitis, lichen simplex chronicus, pityriasis rubra pilaris, nummular dermatitis, asthma, allergic rhinitis, gastro-esophageal reflux disease, arthritic conditions including, rheumatoid arthritis, psoriatic arthritis, and osteoarthritis.

In one aspect, the present invention provides an isolated IL-1F9 polypeptide that agonizes signal transduction/activation through IL-1Rrp2, where the IL-1F9 polypeptide comprises the consensus sequence @XD described in FIG. 1, where the IL-1F9 polypeptide contains the sequence Ile-Asn-Asp, which matches the consensus @XD, and wherein the polypeptide comprises nine amino acids on the N-terminal side of the above-referenced isoleucine. In one embodiment the IL-1F9 polypeptide is a human IL-1F9 polypeptide. In one embodiment, the IL-1F9 polypeptide of the invention

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comprises an amino acid sequence having an isoleucine at position ten of its amino acid sequence, position ten being relative to the N-terminal amino acid at position one. In one embodiment, the IL-1F9 polypeptide of the invention comprises an amino acid sequence having an isoleucine at position ten of its amino acid sequence, position ten being relative to the N-terminal amino acid at position one and an amino acid selected from the group consisting of serine and methionine at the N-terminal amino acid at position one. In one embodiment, the IL-1F9 polypeptide of the invention comprises an amino acid sequence having an isoleucine at position ten of its amino acid sequence, position ten being relative to the N-terminal amino acid at position one, and a methionine at position two of its amino acid sequence. In a particular embodiment the IL-1F9 polypeptide of the invention, comprises an amino acid sequence having an isoleucine at position ten of the amino acid sequence, position ten being relative to the N-terminal amino acid at position one, and an amino acid selected from the group consisting of serine and methionine at the N-terminal amino acid at position and an glutamic acid at position two.

In particular embodiments, the isolated IL-1F9 polypeptide comprises at least 85% or at least 89% identity to SEQ ID NO 4 and an isoleucine at position ten, position ten being relative to the N-terminal amino acid at position one of the IL-1F9 amino acid sequence of the invention. In some embodiments, the isolated IL-1F9 polypeptide of the invention agonizes signal transduction/activation through IL-1Rrp2 more than the IL-1F9 polypeptide having the amino acid sequence of SEQ ID NO 4. In some embodiments, the isolated IL-1F9 polypeptide of the invention agonizes signal transduction/activation through IL-1Rrp2 more than about 5 fold, 10 fold, 50 fold, 100 fold, 600 fold, 1,000 fold, 3,000 fold, 5,000 fold, 10,000 fold or 50,000 fold the level of agonization of signal transduction/activation of the IL-1F9 polypeptide having the amino acid sequence of SEQ ID NO 4. The level of signal transduction/activation agonization is measured according to the method described in Example 2B.

In another aspect, the invention provides an isolated IL-1F9 polypeptide that agonizes signal transduction/activation through IL-1Rrp2, wherein the IL-1F9 polypeptide comprises an amino acid sequence having an isoleucine at position ten of its amino acid sequence, position ten being relative to the N-terminal amino acid at position one and an amino acid sequence selected from the group consisting of:

(SEQ ID NO 18)

SMCKPITGTINDLNQVWTLQGQNLVAVPRSDSVTPVTVAVITCKYPEALEQGRGDPIY
LGIQNPEMCLYCEKVGEQPTLQLKEQKIMDLYGQPEPVKPFIFYRAKTGRSTLESVAFF
DWFIIASSKRDQPIILTSELGKSYNTAFELNIND,

(SEQ ID NO 19)

SMCKPITGTINDLNQVWTLQGQNLVAVPRSDSVTPVTVAVITCKYPEALEQGRGDPIY
LGIQNPEMCLYCEKVGEQPTLQLKEQKIMDLYGQPEPVKPFIFYRAKTGRSTLESVAFF
DWFIIASSKRDQPIILTSELGKSYNTAFELNINDDYKDDDDKHHH,

(SEQ ID NO 20)

MMCKPITGTINDLNQVWTLQGQNLVAVPRSDSVTPVTVAVITCKYPEALEQGRGDPIY
LGIQNPEMCLYCEKVGEQPTLQLKEQKIMDLYGQPEPVKPFIFYRAKTGRSTLESVAFF
DWFIIASSKRDQPIILTSELGKSYNTAFELNIND
and

(SEQ ID NO 21)

MMCKPITGTINDLNQVWTLQGQNLVAVPRSDSVTPVTVAVITCKYPEALEQGRGDPIY

LGIQNPMECLYCEKVGEQPTLQLKEQKIMDLYGQPEPVKPFIFYRAKTGRSTSTLESVAFP

DWFIASSKRDPILITSELGKSYNTAFELNINDDYKDDDDKHHH.

In another embodiment, a nucleic acid sequence encoding the isolated IL-1F9 polypeptide of the invention is provided. In another aspect of the invention, a recombinant vector that directs expression of a nucleic acid encoding an isolated IL-1F9 polypeptide of the invention is provided. In a particular embodiment, the vector comprises a nucleic acid sequence selected from the group consisting of:

encoding an IL-1F9 polypeptide of the invention is provided. In another aspect, a method of producing an isolated IL-1F9 polypeptide of the invention comprising culturing the host cell transfected or transduced with a recombinant vector that directs expression of an IL-1F9 polypeptide of the invention, under conditions promoting expression and isolating the expressed IL-1F9 polypeptide is provided.

(SEQ ID NO 75)

TCAATGTGTAAACCTATTACTGGGACTATTAATGATTGAATCAGCAAGTGTGGACC
CTTCAGGGTCAGAACCTTGTGGCAGTTCACGAAGTGACAGTGTGACCCAGTCACT
GTTGCTGTTATCACATGCAAGTATCCAGAGGCTCTTGAGCAAGGCAGAGGGGATCCC
ATTTATTTGGGAATCCAGAATCCAGAAATGTGTTTGTATTGTGAGAAGGTTGGAGAA
CAGCCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTGTATGGCCAACCCGA
GCCCCGTGAAACCCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCTCCACCCTTGA
GTCTGTGGCCTTCCCGACTGGTTCATTGCCTCCTCCAAGAGAGACCAGCCCATCATT
CTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAATATAAATGAC
TAA,

(SEQ ID NO 76)

ATGTCAATGTGTAAACCTATTACTGGGACTATTAATGATTGAATCAGCAAGTGTGG
ACCCCTCAGGGTCAGAACCTTGTGGCAGTTCACGAAGTGACAGTGTGACCCAGTCACT
ACTGTTGCTGTTATCACATGCAAGTATCCAGAGGCTCTTGAGCAAGGCAGAGGGGAT
CCCATTTATTTGGGAATCCAGAATCCAGAAATGTGTTTGTATTGTGAGAAGGTTGGA
GAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTGTATGGCCAACC
CGAGCCCGTGAAACCCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCTCCACCCTT
GAGTCTGTGGCCTTCCCGACTGGTTCATTGCCTCCTCCAAGAGAGACCAGCCCATC
ATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAATATAAAT
GACAGATCTGGCAGTTCTGACTACAAGGACGACGACGACAAGGGCAGTTCTCACCA
TCACCATCACCCTAG
and

(SEQ ID NO 77)

ATGATGTGTAAACCTATTACTGGGACTATTAATGATTGAATCAGCAAGTGTGGACC
CTTCAGGGTCAGAACCTTGTGGCAGTTCACGAAGTGACAGTGTGACCCAGTCACT
GTTGCTGTTATCACATGCAAGTATCCAGAGGCTCTTGAGCAAGGCAGAGGGGATCCC
ATTTATTTGGGAATCCAGAATCCAGAAATGTGTTTGTATTGTGAGAAGGTTGGAGAA
CAGCCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTGTATGGCCAACCCGA
GCCCCGTGAAACCCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCTCCACCCTTGA
GTCTGTGGCCTTCCCGACTGGTTCATTGCCTCCTCCAAGAGAGACCAGCCCATCATT
CTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAATATAAATGAC
AGATCTGGCAGTTCTGACTACAAGGACGACGACGACAAGGGCAGTTCTCACCATCA
CCATCACCCTAG.

In another aspect, a host cell transfected or transduced with a recombinant vector that directs expression of a nucleic acid

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In another aspect, a composition, particularly a pharmaceutical composition, comprising an IL-1F9 polypeptide of

the invention and a physiologically acceptable diluent, excipient or carrier is provided. A method of stimulating the immune system of an immunosuppressed subject, comprising administering the IL-1F9 polypeptide according of the invention to an immunosuppressed subject in an amount sufficient to stimulate the subject's immune system is provided.

An antibody that specifically binds IL-1F9, where IL-1F9 may be a full length IL-1F9 or a truncant of full length IL-1F9, and prevents proteolytic cleavage thereof, particularly proteolytic cleavage to a more active form where activity is relative to that of the full length IL-1F9, is provided. An antibody that binds an IL-1F9 polypeptide of the invention, and prevents signal transduction/activation through IL-1Rrp2 is also provided. In some embodiments, an antibody binding an IL-1F9 polypeptide selected from the group consisting of: SEQ ID NO 18, SEQ ID NO 19, SEQ ID NO 20 and SEQ ID NO 21, is provided. In some embodiments, the IL-1F9 antibody of the invention, is a monoclonal antibody, particularly a chimeric antibody, a humanized antibody or a fully human antibody. The invention provides a composition, particularly a pharmaceutical composition, comprising the IL-1F9 antibody of the invention and a physiologically acceptable diluent, excipient or carrier.

The invention also provides, a method of treating an inflammatory or autoimmune condition mediated by IL-1Rrp2, comprising administering the IL-1F9 antibody of the invention to a subject in an amount sufficient to ameliorate at least one symptom mediated by IL-1Rrp2 of the condition. In one embodiment, the condition to be treated is an inflammatory condition of the skin, lungs or airways mediated by IL-1Rrp2. In a particular embodiment, the condition to be treated is selected from the group consisting of psoriasis, seborrheic dermatitis, atopic dermatitis, including chronic atopic dermatitis, allergic contact dermatitis, lichen simplex chronicus, pityriasis rubra pilaris, nummular dermatitis, asthma, allergic rhinitis, gastro-esophageal reflux disease, arthritic conditions including, rheumatoid arthritis, psoriatic arthritis, and osteoarthritis. In particular embodiments of the above methods, the subject is a human.

In another aspect, the invention provides a method of identifying a protease that cleaves an IL-1 family member comprising contacting a source of the protease with the IL-1 family member under conditions promoting proteolytic cleavage of the IL-1 family member, and determining if the IL-1 family member has been proteolytically cleaved. The invention further provides a method of identifying an inhibitor of a protease that cleaves an IL-1 family member comprising contacting the protease with the IL-1 family member in the presence, and absence, of a molecule that is a potential inhibitor, under conditions promoting proteolytic cleavage of the IL-1 family member, and determining if the IL-1 family member has been proteolytically cleaved, wherein if the IL-1 family member is not cleaved or is cleaved to a lesser degree in the presence of the molecule, the molecule is an inhibitor.

DETAILED DESCRIPTION

The present invention provides compositions, kits, and methods relating to members of the IL-1 family that require IL-1Rrp2 for signaling or inhibit signaling by competing with IL-1 family members that require IL-1Rrp2 for signaling (hereinafter "IL-1Rrp2 requiring polypeptides", for example, IL-1F5, F6, F8 and F9). Also provided are nucleic acids, and derivatives and fragments thereof, encoding such IL-1 family members. The invention further provides antigen binding proteins that bind to these IL-1 family members. The provided methods include, for example, methods of identifying

and/or isolating a protease that cleaves such an IL-1 family member, methods of making, identifying, or isolating molecules that modulate the interaction between an IL-1Rrp2-requiring IL-1 family member and a protease, methods of identifying other IL-1 family members that interact with IL-1 Rrp2 and methods of identifying other IL-1R family members that interact with IL-1F5, F6, F8 and/or F9.

The invention also provides IL-1 Rrp2 requiring polypeptides that have reproducibly high levels of biological activity as a result of the conformation of the amino terminal portion of the polypeptide. As shown in FIG. 1, there is a (Met or Ile)-Xaa-Asp sequence present in each of the IL-1 family members known to require IL-1Rrp2 for signaling (IL-1 F5, F6, F8 and F9), which is marked by underlining of the Met/Ile and the Asp residues. An IL-1Rrp2 requiring polypeptide having an N-terminus nine residues upstream of the Met/Ile is highly active, whereas an IL-1Rrp2 requiring polypeptide extending further upstream is poorly active. IL-1Rrp2 requiring polypeptides that have an N-terminus at eight or seven residues upstream of the Met/Ile are poorly active or inactive. Moreover, the exact amino acid present at N-terminus of the IL-1Rrp2 requiring polypeptides does not appear to be important. Several polypeptides were prepared, some of which had an N-terminal Met initially, which N-terminal Met was cleaved off by an intracellular methionyl aminopeptidase for some polypeptides; for others (those with bulky residues C-terminal to the Met) the aminopeptidase was not able to remove the methionine and for other polypeptides were prepared without an N-terminal Met as described in Example 1 below.

Polynucleotide and polypeptide sequences described herein are indicated using standard one- or three-letter abbreviations. Unless otherwise indicated, each polypeptide sequence has an amino terminus at the left and a carboxy terminus at the right; each single-stranded nucleic acid sequence, and the top strand of each double-stranded nucleic acid sequence, has a 5' terminus at the left and a 3' terminus at the right. A particular polypeptide or polynucleotide sequence also can be described by explaining how it differs from a reference sequence.

Unless otherwise defined herein, scientific and technical terms used in connection with the present invention shall have the meanings that are commonly understood by those of ordinary skill in the art. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. Generally, nomenclatures used in connection with, and techniques of, cell and tissue culture, molecular biology, immunology, microbiology, genetics and protein and nucleic acid chemistry and hybridization described herein are those well known and commonly used in the art. The methods and techniques of the present invention are generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification unless otherwise indicated. See, e.g., Sambrook et al. *Molecular Cloning: A Laboratory Manual*, 2d ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989) and Ausubel et al., *Current Protocols in Molecular Biology*, Greene Publishing Associates (1992), and Harlow and Lane *Antibodies: A Laboratory Manual* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1990), which are incorporated herein by reference. Enzymatic reactions and purification techniques are performed according to manufacturer's specifications, as commonly accomplished in the art or as described herein. The terminology used in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic

organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well known and commonly used in the art. Standard techniques can be used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients.

The following terms, unless otherwise indicated, shall be understood to have the following meanings:

The term "isolated molecule" (where the molecule is, for example, a polypeptide, a polynucleotide, or an antibody) is a molecule that by virtue of its origin or source of derivation (1) is not associated with naturally associated components that accompany it in its native state, (2) is substantially free of other molecules from the same species (3) is expressed by a cell from a different species, or (4) does not occur in nature. Thus, a molecule that is chemically synthesized, or synthesized in a cellular system different from the cell from which it naturally originates, will be "isolated" from its naturally associated components. A molecule also may be rendered substantially free of naturally associated components by isolation, using purification techniques well known in the art. Molecule purity or homogeneity may be assayed by a number of means well known in the art. For example, the purity of a polypeptide sample may be assayed using polyacrylamide gel electrophoresis and staining of the gel to visualize the polypeptide using techniques well known in the art. For certain purposes, higher resolution may be provided by using HPLC or other means well known in the art for purification.

The terms "IL-1Rrp2 inhibitor" and "IL-1Rrp2 antagonist" are used interchangeably. Each is a molecule that detectably inhibits at least one function of IL-1Rrp2. Conversely, an "IL-1Rrp2 agonist" is a molecule that detectably increases at least one function of IL-1Rrp2. The inhibition caused by an IL-1Rrp2 inhibitor need not be complete so long as it is detectable using an assay. Any assay of a function of IL-1Rrp2 can be used, examples of which are provided herein. Examples of functions of IL-1Rrp2 that can be inhibited by an IL-1Rrp2 inhibitor, or caused or increased by an IL-1Rrp2 agonist, include activation of NFkB signaling pathways; activation of MAP kinases (Erk, JNK, p38) and their signaling pathways; induction of cytokines; induction of chemokines; recruitment of neutrophils; enhancement of skin thickness (e.g., induction of acanthosis and/or hyperkeratosis resembling that found in psoriatic skin), downstream signaling, and so on. Examples of types of IL-1Rrp2 inhibitors and IL-1Rrp2 agonists include, but are not limited to, IL-1Rrp2 requiring polypeptides such as certain IL-1 family members (e.g., IL-1F6, F8 and F9, which are IL-1Rrp2 agonists, and IL-1F5, which is an IL-1Rrp2 antagonist), antibodies, antibody fragments, and antibody derivatives (for example, an antibody that binds an IL-1Rrp2 agonist and prevents proteolytic cleavage thereof).

The terms "peptide," "polypeptide" and "protein" each refers to a molecule comprising two or more amino acid residues joined to each other by peptide bonds. These terms encompass, e.g., native and artificial proteins, protein fragments and polypeptide analogs (such as muteins, variants, and fusion proteins) of a protein sequence as well as post-translationally, or otherwise covalently or non-covalently, modified proteins. A peptide, polypeptide, or protein may be monomeric or polymeric.

The term "polypeptide fragment" as used herein refers to a polypeptide that has an amino-terminal and/or carboxy-terminal deletion as compared to a corresponding full-length protein. Fragments can be, for example, at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 50, 70, 80, 90, 100, 150 or 200 amino acids in length. Fragments can also be, for example, at most 1,000, 750, 500, 250, 200, 175, 150, 125, 100, 90, 80, 70,

60, 50, 40, 30, 20, 15, 14, 13, 12, 11, or 10 amino acids in length. A fragment can further comprise, at either or both of its ends, one or more additional amino acids, for example, a sequence of amino acids from a different naturally-occurring protein (e.g., an Fc or leucine zipper domain) or an artificial amino acid sequence (e.g., an artificial linker sequence or a tag protein).

Polypeptides of the invention include polypeptides that have been modified in any way and for any reason, for example, to: (1) reduce susceptibility to proteolysis, (2) reduce susceptibility to oxidation, (3) alter binding affinity for forming protein complexes, (4) alter binding affinities, and (4) confer or modify other physicochemical or functional properties. Analogs include muteins of a polypeptide. For example, single or multiple amino acid substitutions (e.g., conservative amino acid substitutions) may be made in the naturally occurring sequence (e.g., in the portion of the polypeptide outside the domain(s) forming intermolecular contacts. A "conservative amino acid substitution" is one that does not substantially change the structural characteristics of the parent sequence (e.g., a replacement amino acid should not tend to break a helix that occurs in the parent sequence, or disrupt other types of secondary structure that characterize the parent sequence or are necessary for its functionality). Examples of art-recognized polypeptide secondary and tertiary structures are described in *Proteins, Structures and Molecular Principles* (Creighton, Ed., W. H. Freeman and Company, New York (1984)); *Introduction to Protein Structure* (C. Branden and J. Tooze, eds., Garland Publishing, New York, N.Y. (1991)); and Thornton et al. *Nature* 354:105 (1991), which are each incorporated herein by reference.

The present invention also provides non-peptide analogs of IL-1Rrp2-requiring polypeptides. Non-peptide analogs are commonly used in the pharmaceutical industry as drugs with properties analogous to those of the template peptide. These types of non-peptide compound are termed "peptide mimetics" or "peptidomimetics," see, for example, Fauchere, *J. Adv. Drug Res.* 15:29 (1986); Veber and Freidinger *TINS* p. 392 (1985); and Evans et al., *J. Med. Chem.* 30:1229 (1987), which are incorporated herein by reference. Peptide mimetics that are structurally similar to therapeutically useful peptides may be used to produce an equivalent therapeutic or prophylactic effect. Generally, peptidomimetics are structurally similar to a paradigm polypeptide (i.e., a polypeptide that has a desired biochemical property or pharmacological activity), such as a human antibody, but have one or more peptide linkages optionally replaced by a linkage selected from the group consisting of: $-\text{CH}_2\text{NH}-$, $-\text{CH}_2\text{S}-$, $-\text{CH}_2-\text{CH}_2-$, $-\text{CH}=\text{CH}(\text{cis and trans})-$, $-\text{COCH}_2-$, $-\text{CH}(\text{OH})\text{CH}_2-$, and $-\text{CH}_2\text{SO}-$, by methods well known in the art. Systematic substitution of one or more amino acids of a consensus sequence with a D-amino acid of the same type (e.g., D-lysine in place of L-lysine) may also be used to generate more stable peptides. In addition, constrained peptides comprising a consensus sequence or a substantially identical consensus sequence variation may be generated by methods known in the art (Rizo and Gierasch *Ann. Rev. Biochem.* 61:387 (1992), incorporated herein by reference), for example, by adding internal cysteine residues capable of forming intramolecular disulfide bridges which cyclize the peptide.

A "variant" of a polypeptide (e.g., an antibody) comprises an amino acid sequence wherein one or more amino acid residues are inserted into, deleted from and/or substituted into the amino acid sequence relative to another polypeptide sequence. Variants of the invention include fusion proteins.

A “derivative” of a polypeptide is a polypeptide (e.g., an antibody) that has been chemically modified, e.g., via conjugation to another chemical moiety (such as, for example, polyethylene glycol or albumin, e.g., human serum albumin), phosphorylation, and glycosylation. Unless otherwise indicated, the term “antibody” includes, in addition to antibodies comprising two full-length heavy chains and two full-length light chains, derivatives, variants, fragments, and muteins thereof, examples of which are described below.

An “antigen binding protein” is a protein comprising a portion that binds to an antigen and, optionally, a scaffold or framework portion that allows the antigen binding portion to adopt a conformation that promotes binding of the antigen binding protein to the antigen. Examples of antigen binding proteins include antibodies, antibody fragments (e.g., an antigen binding portion of an antibody), antibody derivatives, and antibody analogs. The antigen binding protein can comprise, for example, an alternative protein scaffold or artificial scaffold with one or more grafted complementarity determining regions (CDRs) or CDR derivatives. Such scaffolds include, but are not limited to, antibody-derived scaffolds comprising mutations introduced to, for example, stabilize the three-dimensional structure of the antigen binding protein as well as wholly synthetic scaffolds comprising, for example, a biocompatible polymer. See, for example, Korndorfer et al., 2003, *Proteins: Structure, Function, and Bioinformatics*, Volume 53, Issue 1:121-129; Roque et al., 2004, *Biotechnol. Prog.* 20:639-654. In addition, peptide antibody mimetics (“PAMs”) can be used, as well as scaffolds based on antibody mimetics utilizing fibronectin components as a scaffold.

An antigen binding protein can have, for example, the structure of a naturally occurring immunoglobulin. An “immunoglobulin” is a tetrameric molecule. In a naturally occurring immunoglobulin, each tetramer is composed of two identical pairs of polypeptide chains, each pair having one “light” (about 25 kDa) and one “heavy” chain (about 50-70 kDa). The amino-terminal portion of each chain includes a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The carboxy-terminal portion of each chain defines a constant region primarily responsible for effector function. Human light chains are classified as kappa and lambda light chains. Heavy chains are classified as mu, delta, gamma, alpha, or epsilon, and define the antibody’s isotype as IgM, IgD, IgG, IgA, 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* Ch. 7 (Paul, W., ed., 2nd ed. Raven Press, N.Y. (1989)) (incorporated by reference in its entirety for all purposes). The variable regions of each light/heavy chain pair form the antibody binding site such that an intact immunoglobulin has two binding sites.

Immunoglobulin chains exhibit the same general structure of relatively conserved framework regions (FR) joined by three hypervariable regions, also called complementarity determining regions or CDRs. From N-terminus to C-terminus, both light and heavy chains comprise the domains FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4. The assignment of amino acids to each domain is in accordance with the definitions of Kabat et al. in *Sequences of Proteins of Immunological Interest*, 5th Ed., US Dept. of Health and Human Services, PHS, NIH, NIH Publication no. 91-3242, 1991.

Antibodies can be obtained from sources such as serum or plasma that contain immunoglobulins having varied antigenic specificity. If such antibodies are subjected to affinity purification, they can be enriched for a particular antigenic

specificity. Such enriched preparations of antibodies often consist of less than about 10% antibody having specific binding activity for the particular antigen. The percentage of antigen-specific antibody can be increased by using multiple purification steps. Antibodies that are enriched by affinity purification using the antigen are often referred to as “monospecific.”

An “antibody” refers to an intact immunoglobulin or to an antigen binding portion thereof that competes with the intact antibody for specific binding, unless otherwise specified. Antigen binding portions may be produced by recombinant DNA techniques or by enzymatic or chemical cleavage of intact antibodies. Antigen binding portions include, inter alia, Fab, Fab', F(ab')₂, Fv, domain antibodies (dAbs), and CDR fragments, single-chain antibodies (scFv), chimeric antibodies, diabodies, triabodies, tetrabodies, and polypeptides that contain at least a portion of an immunoglobulin that is sufficient to confer specific antigen binding to the polypeptide.

Complementarity determining regions (CDRs) and framework regions (FR) of a given antibody may be identified using the system described by Kabat et al. in *Sequences of Proteins of Immunological Interest*, 5th Ed., US Dept. of Health and Human Services, PHS, NIH, NIH Publication no. 91-3242, 1991. One or more CDRs may be incorporated into a molecule either covalently or noncovalently to make it an antigen binding protein. An antigen binding protein may incorporate the CDR(s) as part of a larger polypeptide chain, may covalently link the CDR(s) to another polypeptide chain, or may incorporate the CDR(s) noncovalently. The CDRs permit the antigen binding protein to specifically bind to a particular antigen of interest.

An antigen binding protein may have one or more binding sites. If there is more than one binding site, the binding sites may be identical to one another or may be different. For example, a naturally occurring human immunoglobulin typically has two identical binding sites, while a “bispecific” or “bifunctional” antibody has two different binding sites.

The term “human antibody” includes all antibodies that have one or more variable and constant regions derived from human immunoglobulin sequences. In one embodiment, all of the variable and constant domains are derived from human immunoglobulin sequences (a fully human antibody). These antibodies may be prepared in a variety of ways, examples of which are described below, including through the immunization with an antigen of interest of a mouse that is genetically modified to express antibodies derived from human heavy and/or light chain-encoding genes.

A “humanized antibody” has a sequence that differs from the sequence of an antibody derived from a non-human species by one or more amino acid substitutions, deletions, and/or additions, such that the humanized antibody is less likely to induce an immune response, and/or induces a less severe immune response, as compared to the non-human species antibody, when it is administered to a human subject. In one embodiment, certain amino acids in the framework and constant domains of the heavy and/or light chains of the non-human species antibody are mutated to produce the humanized antibody. In another embodiment, the constant domain(s) from a human antibody are fused to the variable domain(s) of a non-human species. In another embodiment, one or more amino acid residues in one or more CDR sequences of a non-human antibody are changed to reduce the likely immunogenicity of the non-human antibody when it is administered to a human subject, wherein the changed amino acid residues either are not critical for immunospecific binding of the antibody to its antigen, or the changes to the amino acid sequence that are made are conservative changes, such

that the binding of the humanized antibody to the antigen is not significantly worse than the binding of the non-human antibody to the antigen. Examples of how to make humanized antibodies may be found in U.S. Pat. Nos. 6,054,297, 5,886,152 and 5,877,293.

The term "chimeric antibody" refers to an antibody that contains one or more regions from one antibody and one or more regions from one or more other antibodies. In one example of a chimeric antibody, a portion of the heavy and/or light chain is identical with, homologous to, or derived from an antibody from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is/are identical with, homologous to, or derived from an antibody (-ies) from another species or belonging to another antibody class or subclass. Also included are fragments of such antibodies that exhibit the desired biological activity (i.e., the ability to specifically bind an IL-1 family member). See, e.g., U.S. Pat. No. 4,816,567 and Morrison, 1985, Science 229:1202-07.

A "neutralizing antibody" or "an inhibitory antibody" is an antibody that inhibits the proteolytic activation of an IL-1 family member when an excess of the anti-IL-1 family member antibody reduces the amount of activation by at least about 20% using an assay such as those described herein in the Examples. In various embodiments, the antibody reduces the amount of amount of proteolytic activation of an IL-1 family member by at least 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99%, and 99.9%.

Fragments or analogs of antibodies can be readily prepared by those of ordinary skill in the art following the teachings of this specification and using techniques well-known in the art. Preferred amino- and carboxy-termini of fragments or analogs occur near boundaries of functional domains. Structural and functional domains can be identified by comparison of the nucleotide and/or amino acid sequence data to public or proprietary sequence databases. Computerized comparison methods can be used to identify sequence motifs or predicted protein conformation domains that occur in other proteins of known structure and/or function. Methods to identify protein sequences that fold into a known three-dimensional structure are known. See, e.g., Bowie et al., 1991, Science 253:164.

A "CDR grafted antibody" is an antibody comprising one or more CDRs derived from an antibody of a particular species or isotype and the framework of another antibody of the same or different species or isotype.

A "multi-specific antibody" is an antibody that recognizes more than one epitope on one or more antigens. A subclass of this type of antibody is a "bi-specific antibody" which recognizes two distinct epitopes on the same or different antigens.

An antigen binding protein "specifically binds" to an antigen (e.g., a human IL-1 family member) if it binds to the antigen with a dissociation constant of 1 nanomolar or less.

An "antigen binding domain," "antigen binding region," or "antigen binding site" is a portion of an antigen binding protein that contains amino acid residues (or other moieties) that interact with an antigen and contribute to the antigen binding protein's specificity and affinity for the antigen. For an antibody that specifically binds to its antigen, this will include at least part of at least one of its CDR domains.

An "epitope" is the portion of a molecule that is bound by an antigen binding protein (e.g., by an antibody). An epitope can comprise non-contiguous portions of the molecule (e.g., in a polypeptide, amino acid residues that are not contiguous in the polypeptide's primary sequence but that, in the context of the polypeptide's tertiary and quaternary structure, are near enough to each other to be bound by an antigen binding protein).

The "percent identity" of two polynucleotide or two polypeptide sequences is determined by comparing the sequences using the GAP computer program (a part of the GCG Wisconsin Package, version 10.3 (Accelrys, San Diego, Calif.)) using its default parameters.

The terms "polynucleotide," "oligonucleotide" and "nucleic acid" are used interchangeably throughout and include DNA molecules (e.g., cDNA or genomic DNA), RNA molecules (e.g., mRNA), analogs of the DNA or RNA generated using nucleotide analogs (e.g., peptide nucleic acids and non-naturally occurring nucleotide analogs), and hybrids thereof. The nucleic acid molecule can be single-stranded or double-stranded. In one embodiment, the nucleic acid molecules of the invention comprise a contiguous open reading frame encoding an antibody, or a fragment, derivative, mutein, or variant thereof, of the invention.

Two single-stranded polynucleotides are "the complement" of each other if their sequences can be aligned in an anti-parallel orientation such that every nucleotide in one polynucleotide is opposite its complementary nucleotide in the other polynucleotide, without the introduction of gaps, and without unpaired nucleotides at the 5' or the 3' end of either sequence. A polynucleotide is "complementary" to another polynucleotide if the two polynucleotides can hybridize to one another under moderately stringent conditions. Thus, a polynucleotide can be complementary to another polynucleotide without being its complement.

A "vector" is a nucleic acid that can be used to introduce another nucleic acid linked to it into a cell. One type of vector is a "plasmid," which refers to a linear or circular double stranded DNA molecule into which additional nucleic acid segments can be ligated. Another type of vector is a viral vector (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), wherein additional DNA segments can be introduced into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors comprising a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. An "expression vector" is a type of vector that can direct the expression of a chosen polynucleotide.

A nucleotide sequence is "operably linked" to a regulatory sequence if the regulatory sequence affects the expression (e.g., the level, timing, or location of expression) of the nucleotide sequence. A "regulatory sequence" is a nucleic acid that affects the expression (e.g., the level, timing, or location of expression) of a nucleic acid to which it is operably linked. The regulatory sequence can, for example, exert its effects directly on the regulated nucleic acid, or through the action of one or more other molecules (e.g., polypeptides that bind to the regulatory sequence and/or the nucleic acid). Examples of regulatory sequences include promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Further examples of regulatory sequences are described in, for example, Goeddel, 1990, Gene Expression Technology Methods in Enzymology 185, Academic Press, San Diego, Calif. and Baron et al., 1995, Nucleic Acids Res. 23:3605-06.

A "host cell" is a cell that can be used to express a nucleic acid, e.g., a nucleic acid of the invention. A host cell can be a prokaryote, for example, *E. coli*, or it can be a eukaryote, for example, a single-celled eukaryote (e.g., a yeast or other fungus), a plant cell (e.g., a tobacco or tomato plant cell), an animal cell (e.g., a human cell, a monkey cell, a hamster cell, a rat cell, a mouse cell, or an insect cell) or a hybridoma.

Examples of host cells include the COS-7 line of monkey kidney cells (ATCC CRL 1651) (see Gluzman et al., 1981, Cell 23:175), L cells, C127 cells, 3T3 cells (ATCC CCL 163), Chinese hamster ovary (CHO) cells or their derivatives such as Veggie CHO and related cell lines which grow in serum-free media (see Rasmussen et al., 1998, Cytotechnology 28:31) or CHO strain DX-B11, which is deficient in DHFR (see Urlaub et al., 1980, Proc. Natl. Acad. Sci. USA 77:4216-20), HeLa cells, BHK (ATCC CRL 10) cell lines, the CV1/EBNA cell line derived from the African green monkey kidney cell line CV1 (ATCC CCL 70) (see McMahan et al., 1991, EMBO J. 10:2821), human embryonic kidney cells such as 293, 293 EBNA or MSR 293, human epidermal A431 cells, human Colo205 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HL-60, U937, HaK or Jurkat cells. Typically, a host cell is a cultured cell that can be transformed or transfected with a polypeptide-encoding nucleic acid, which can then be expressed in the host cell. The phrase "recombinant host cell" can be used to denote a host cell that has been transformed or transfected with a nucleic acid to be expressed. A host cell also can be a cell that comprises the nucleic acid but does not express it at a desired level unless a regulatory sequence is introduced into the host cell such that it becomes operably linked with the nucleic acid. It is understood that the term host cell refers not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to, e.g., mutation or environmental influence, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

IL-1Rrp2 Requiring IL-1 Family Members

In one aspect, the present invention provides proteins (e.g., IL-1 family members, derivative, muteins and variants thereof) that require IL-1Rrp2 for signaling, e.g., human IL-1 F5, F6, F8 and F9. The IL-1 family members in accordance with the present invention include proteins that inhibit a biological activity of IL-1Rrp2, as well as proteins that stimulate a biological activity of IL-1Rrp2. Examples of such biological activities include activation of multiple kinase pathways, including ERK, p38MAPK, JNK, and IKK. In the skin, IL-1Rrp2 signaling can lead to an acanthotic, hyperkeratotic epidermis that resembles psoriatic skin, and in the lung it causes the recruitment of neutrophils.

Different IL-1 family members may utilize different domains of IL-1Rrp2 for signaling, or act by different mechanisms of action. Examples include but are not limited to proteins that cause signal transduction via IL-1Rrp2, and proteins that inhibit signal transduction. The site of action may be, for example, intracellular (e.g., by interfering with an intracellular signaling cascade) or extracellular. An antagonistic protein need not completely inhibit IL-1Rrp2 activity to find use in the present invention; rather, antagonistic proteins that reduce a particular activity of IL-1Rrp2 are contemplated for use as well. Discussions herein of particular mechanisms of action for antagonistic proteins in treating particular diseases are illustrative only, and the methods presented herein are not bound thereby.

Other derivatives of the IL-1 family members within the scope of this invention include covalent or aggregative conjugates of the proteins, or fragments thereof, with other proteins or polypeptides, such as by expression of recombinant fusion proteins comprising heterologous polypeptides fused to the N-terminus or C-terminus of an IL-1Rrp2 requiring protein. For example, the conjugated peptide may be a heterologous signal (or leader) polypeptide, e.g., the yeast alpha-

factor leader, or a peptide such as an epitope tag. IL-1Rrp2 requiring protein-containing fusion proteins can comprise peptides added to facilitate purification or identification of IL-1Rrp2 requiring polypeptides (e.g., poly-His). An IL-1Rrp2 requiring polypeptides also can be linked to the FLAG® peptide (DYKDDDDK; SEQ ID NO:5), described in Hopp et al., *Bio/Technology* 6:1204, 1988, and U.S. Pat. No. 5,011,912. The FLAG peptide is highly antigenic and provides an epitope reversibly bound by a specific monoclonal antibody (mAb), enabling rapid assay and facile purification of expressed recombinant protein. Reagents useful for preparing fusion proteins in which the FLAG peptide is fused to a given polypeptide are commercially available (Sigma, St. Louis, Mo.).

Additional, useful tag proteins include green fluorescent protein (GFP; Chalfie et al., *Science* 263:802, 1994), an N-terminal peptide that contains recognition sites for a monoclonal antibody, a specific endopeptidase, and a site-specific protein kinase (PKA; Blanas and Rutter, *Science* 256:1014, 1992), birA (Altman et al., *Science* 274:94, 1996) and glutathione S transferase (GST; Smith and Johnson, *Gene* 67:31, 1988).

Oligomers that contain one or more IL-1Rrp2 requiring proteins may be employed as agonists or antagonists. Oligomers may be in the form of covalently-linked or non-covalently-linked dimers, trimers, or higher oligomers. Oligomers comprising two or more IL-1Rrp2 requiring proteins are contemplated for use, with one example being a homodimer. Other oligomers include heterodimers, homotrimers, heterotrimers, homotetramers, heterotetramers, etc.

One embodiment is directed to oligomers comprising multiple IL-1Rrp2 requiring proteins joined via covalent or non-covalent interactions between peptide moieties fused to the IL-1Rrp2 requiring proteins. Such peptides may be peptide linkers (spacers), or peptides that have the property of promoting oligomerization. Leucine zippers and certain polypeptides derived from antibodies are among the peptides that can promote oligomerization of IL-1Rrp2 requiring proteins attached thereto, as described in more detail below.

In particular embodiments, the oligomers comprise from two to four IL-1Rrp2 requiring proteins. The IL-1Rrp2 requiring proteins of the oligomer may be in any form, such as any of the forms described above, e.g., variants or fragments. Preferably, the oligomers comprise IL-1Rrp2 requiring proteins that have activity (i.e., IL-1Rrp2 agonistic or antagonistic activity).

In one embodiment, an oligomer is prepared using polypeptides derived from immunoglobulins. Preparation of fusion proteins comprising certain heterologous polypeptides fused to various portions of antibody-derived polypeptides (including the Fc domain) has been described, e.g., by Ashkenazi et al., 1991, PNAS USA 88:10535; Byrn et al., 1990, Nature 344:677; and Hollenbaugh et al., 1992 "Construction of Immunoglobulin Fusion Proteins," in *Current Protocols in Immunology*, Suppl. 4, pages 10.19.1-10.19.11.

One embodiment of the present invention is directed to a dimer comprising two fusion proteins created by fusing an IL-1Rrp2 requiring polypeptides or fragment thereof to the Fc region of an antibody. The dimer can be made by, for example, inserting a gene fusion encoding the fusion protein into an appropriate expression vector, expressing the gene fusion in host cells transformed with the recombinant expression vector, and allowing the expressed fusion protein to assemble much like antibody molecules, whereupon inter-chain disulfide bonds form between the Fc moieties to yield the dimer.

The term "Fc polypeptide" as used herein includes native and mutein forms of polypeptides derived from the Fc region

of an antibody. Truncated forms of such polypeptides containing the hinge region that promotes dimerization also are included. Fusion proteins comprising Fc moieties (and oligomers formed therefrom) offer the advantage of facile purification by affinity chromatography over Protein A or Protein G columns.

One suitable Fc polypeptide, described in PCT application WO 93/10151 (hereby incorporated by reference), is a single chain polypeptide extending from the N-terminal hinge region to the native C-terminus of the Fc region of a human IgG1 antibody. Another useful Fc polypeptide is the Fc mutein described in U.S. Pat. No. 5,457,035 and in Baum et al., 1994, EMBO J. 13:3992-4001. The amino acid sequence of this mutein is identical to that of the native Fc sequence presented in WO 93/10151, except that amino acid 19 has been changed from Leu to Ala, amino acid 20 has been changed from Leu to Glu, and amino acid 22 has been changed from Gly to Ala. The mutein exhibits reduced affinity for Fc receptors.

In other embodiments, an IL-1Rrp2 requiring polypeptide or fragment thereof may be substituted for the variable portion of an antibody heavy and/or light chain.

Alternatively, the oligomer is a fusion protein comprising multiple IL-1Rrp2 requiring proteins, with or without peptide linkers (spacer peptides). Among the suitable peptide linkers are those described in U.S. Pat. Nos. 4,751,180 and 4,935,233.

Another method for preparing oligomeric IL-1Rrp2 requiring proteins involves use of a leucine zipper. Leucine zipper domains are peptides that promote oligomerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz et al., 1988, Science 240:1759), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble oligomeric proteins are described in PCT application WO 94/10308, and the leucine zipper derived from lung surfactant protein D (SPD) described in Hoppe et al., 1994, FEBS Letters 344:191, hereby incorporated by reference. The use of a modified leucine zipper that allows for stable trimerization of a heterologous protein fused thereto is described in Fanslow et al., 1994, Semin. Immunol. 6:267-78. In one approach, recombinant fusion proteins comprising an IL-1Rrp2 requiring protein, fragment or derivative fused to a leucine zipper peptide is expressed in suitable host cells, and the soluble oligomeric IL-1Rrp2 requiring polypeptides fragments or derivatives that form are recovered from the culture supernatant.

Antigen Binding Proteins

The present invention also provides antigen binding proteins that bind an IL-1Rrp2 requiring polypeptides (for example, an IL-1Rrp2 agonist or antagonist). Numerous types of antigen binding proteins and methods of making them are known in the art. In one aspect, the present invention provides antigen binding proteins that interfere with the proteolytic activation of an IL-1Rrp2 requiring polypeptides. Such antigen binding proteins can be made against an IL-1 family member such as IL-1F6, F8 or F9 (or F5), or a fragment, variant or derivative thereof, and screened in conventional assays for the ability to interfere with proteolytic activation of the IL-1Rrp2 requiring protein.

In another aspect, the present invention includes an antigen binding protein that demonstrates species selectivity, and an antigen binding protein that has one or more of the following characteristics: binds to both human and murine IL-1Rrp2 requiring protein, inhibits the proteolytic activation of human

IL-1Rrp2 requiring protein, inhibits the proteolytic activation of murine IL-1Rrp2 requiring protein, binds to or near the proteolytic cleavage site of IL-1Rrp2 requiring protein, causes relatively little down-regulation of cell-surface expressed IL-1Rrp2.

Fragments of antigen binding proteins are also included. Antigen-binding fragments of antigen binding proteins of the invention may be produced by conventional techniques. Examples of such fragments include, but are not limited to, Fab and F(ab')₂ fragments. Antibody fragments and derivatives produced by genetic engineering techniques also are contemplated.

Additional embodiments include chimeric antibodies, e.g., humanized versions of non-human (e.g., murine) monoclonal antibodies. Such humanized antibodies may be prepared by known techniques, and offer the advantage of reduced immunogenicity when the antibodies are administered to humans.

Also included are human or partially human antibodies prepared in non-human animals (for example, mice in which one or more endogenous immunoglobulin genes have been inactivated and replaced with human immunoglobulin). Antibodies produced in the animal incorporate human immunoglobulin polypeptide chains encoded by the human genetic material introduced into the animal.

In another aspect, the present invention provides monoclonal antibodies that bind to IL-1Rrp2 requiring protein(s). Monoclonal antibodies may be produced using any technique known in the art, e.g., by immortalizing spleen cells harvested from the transgenic animal after completion of the immunization schedule. The spleen cells can be immortalized using any technique known in the art, e.g., by fusing them with myeloma cells to produce hybridomas.

Monoclonal antibodies secreted by a hybridoma cell line can be purified using any technique known in the art. Hybridomas or mAbs may be further screened to identify mAbs with particular properties, such as the ability to block an IL-1Rrp2 induced activity. Examples of such screens are provided in the examples below.

Molecular evolution of the complementarity determining regions (CDRs) in the center of the antibody binding site also has been used to isolate antibodies with increased affinity, for example, antibodies having increased affinity for c-erbB-2, as described by Schier et al., 1996, J. Mol. Biol. 263:551. Accordingly, such techniques are useful in preparing antibodies to IL-1Rrp2 requiring proteins.

Antigen binding proteins may be prepared by any of a number of conventional techniques. For example, they may be purified from cells that naturally express them (e.g., an antibody can be purified from a hybridoma that produces it), or produced in recombinant expression systems, using any technique known in the art. See, for example, *Monoclonal Antibodies, Hybridomas: A New Dimension in Biological Analyses*, Kennet et al. (eds.), Plenum Press, New York (1980); and *Antibodies: A Laboratory Manual*, Harlow and Land (eds.), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (1988).

In one aspect, the present invention provides antigen-binding fragments of an anti-IL-1Rrp2 requiring polypeptides antibody of the invention. Such fragments can consist entirely of antibody-derived sequences or can comprise additional sequences. Examples of antigen-binding fragments include Fab, F(ab')₂, single chain antibodies, diabodies, triabodies, tetrabodies, and domain antibodies. Other examples are provided in Lunde et al., 2002, Biochem. Soc. Trans. 30:500-06.

In another aspect, the present invention provides an antigen binding protein that binds at or near the protease cleavage site of human IL-1 F6, F8 or F9, or IL-1 F5. Antigen binding

proteins that bind to the protease cleavage site can be made using any technique known in the art. For example, such antigen binding proteins can be isolated using the full-length an IL-1Rrp2 requiring protein, or a smaller fragment thereof comprising or consisting of the protease cleavage site (examples of which are provided herein). Antigen binding proteins so isolated can be screened to determine their binding specificity using any method known in the art (examples of which are provided herein). Such antigen binding proteins that function as IL-1Rrp2 antagonists may be employed in treating any IL-1Rrp2-induced condition, including but not limited to inflammatory conditions.

The present invention further provides multi-specific antigen binding proteins, for example, bispecific antigen binding protein, e.g., antigen binding protein that bind to two different epitopes of an IL-1Rrp2 requiring protein, or to an epitope of one IL-1Rrp2 requiring polypeptide and an epitope of another IL-1Rrp2 requiring protein, via two different antigen binding sites or regions. Numerous methods of preparing bispecific antibodies are known in the art.

Although human, partially human, or humanized antibodies will be suitable for many applications, particularly those involving administration of the antibody to a human subject, other types of antigen binding proteins will be suitable for certain applications. The non-human antibodies of the invention can be, for example, derived from any antibody-producing animal, such as mouse, rat, rabbit, goat, donkey, or non-human primate (such as monkey (e.g., cynomolgous or rhesus monkey) or ape (e.g., chimpanzee)). Non-human antibodies of the invention can be used, for example, in *in vitro* and cell-culture based applications, or any other application where an immune response to the antibody of the invention does not occur, is insignificant, can be prevented, is not a concern, or is desired

Peptibodies

An additional class of compounds useful in the practice of the methods of the present invention are compounds sometimes referred to as peptibodies. Such compounds are biologically active peptides having an increased *in vivo* half-life and reduced immunogenicity profile. This is accomplished by fusion of the peptide(s) with a vehicle, as described in U.S. Pat. No. 6,660,843 (the disclosure of which is incorporated by reference herein). Briefly, pharmacologically active compounds are prepared selecting at least one peptide that modulates the activity of a protein of interest, e.g., in this case selecting a peptide that antagonizes the activity of an IL-1Rrp2 requiring polypeptide (e.g., IL-1F6, F8, F9, or IL-1F5), as in a peptide that inhibits proteolytic cleavage of an IL-1Rrp2 agonist; and preparing a fusion protein of the selected peptide and multimerizing vehicle

One such vehicle is an Fc domain. The peptides screened as described above are expressed in a phage display library. The vehicle and the peptide may be linked through the N- or C-terminus of the peptide or the vehicle, as described further in U.S. Pat. No. 6,660,843. Derivatives of the above compounds are also encompassed by this invention.

Antagonistic molecules useful in the processes of this invention may be prepared by standard synthetic methods, recombinant DNA techniques, or any other methods of preparing peptides and fusion proteins. Compounds of this invention that encompass non-peptide portions may be synthesized by standard organic chemistry reactions, in addition to standard peptide chemistry reactions when applicable.

Peptibodies may be used to prepare derivative and other forms thereof, substantially as described for antibodies.

Nucleic Acids

In one aspect, the present invention provides isolated nucleic acid molecules. The nucleic acids comprise, for example, polynucleotides that encode all or part of an IL-1Rrp2 requiring polypeptide, for example, IL-1 F5, F6, F8 or F9, one or both chains of an antibody of the invention, or a fragment, derivative, mutein, or variant thereof, polynucleotides sufficient for use as hybridization probes, PCR primers or sequencing primers for identifying, analyzing, mutating or amplifying a polynucleotide encoding a polypeptide, antisense nucleic acids for inhibiting expression of a polynucleotide, and complementary sequences of the foregoing. The nucleic acids can be any length. They can be, for example, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 750, 1,000, 1,500, 3,000, 5,000 or more nucleotides in length, and/or can comprise one or more additional sequences, for example, regulatory sequences, and/or be part of a larger nucleic acid, for example, a vector. The nucleic acids can be single-stranded or double-stranded and can comprise RNA and/or DNA nucleotides, and artificial variants thereof (e.g., peptide nucleic acids).

Changes can be introduced by mutation into a nucleic acid, thereby leading to changes in the amino acid sequence of a polypeptide (e.g., an IL-1Rrp2 requiring polypeptides) that it encodes. Mutations can be introduced using any technique known in the art. In one embodiment, one or more particular amino acid residues are changed using, for example, a site-directed mutagenesis protocol. In another embodiment, one or more randomly selected residues is changed using, for example, a random mutagenesis protocol. However it is made, a mutant polypeptide can be expressed and screened for a desired property (e.g., binding to IL-1Rrp2 or blocking the proteolytic activation of an IL-1 family member such as IL-1 F5, F6, F8 or F9).

In another aspect, the present invention provides vectors comprising a nucleic acid encoding a polypeptide of the invention or a portion thereof. Examples of vectors include, but are not limited to, plasmids, viral vectors, non-episomal mammalian vectors and expression vectors, for example, recombinant expression vectors.

The recombinant expression vectors of the invention can comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell. The recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cells (e.g., SV40 early gene enhancer, Rous sarcoma virus promoter and cytomegalovirus promoter), those that direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences, see Voss et al., 1986, Trends Biochem. Sci. 11:287; Maniatis et al., 1987, Science 236:1237, incorporated by reference herein in their entireties), and those that direct inducible expression of a nucleotide sequence in response to particular treatment or condition (e.g., the metallothionin promoter in mammalian cells and the tet-responsive and/or streptomycin responsive promoter in both prokaryotic and eukaryotic systems (see *id.*)). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein.

In another aspect, the present invention provides host cells into which a recombinant expression vector of the invention has been introduced. A host cell can be any prokaryotic cell (for example, *E. coli*) or eukaryotic cell (for example, yeast, insect, or mammalian cells (e.g., CHO cells)). Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (e.g., for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (e.g., cells that have incorporated the selectable marker gene will survive, while the other cells die), among other methods.

Expression of Recombinant Proteins or Polypeptides

Any expression system known in the art can be used to make the recombinant polypeptides of the invention (i.e., recombinant IL-1Rrp2 polypeptides, recombinant antigen binding proteins, peptibodies and the like). In general, host cells are transformed with a recombinant expression vector that comprises DNA encoding a desired polypeptide. Among the host cells that may be employed are prokaryotes, yeast or higher eukaryotic cells. Prokaryotes include gram negative or gram positive organisms, for example *E. coli* or *bacilli*. Higher eukaryotic cells include insect cells and established cell lines of mammalian origin. Examples of suitable mammalian host cell lines include the COS-7 line of monkey kidney cells (ATCC CRL 1651) (Gluzman et al., 1981, Cell 23:175), L cells, 293 cells, C127 cells, 3T3 cells (ATCC CCL 163), Chinese hamster ovary (CHO) cells, HeLa cells, BHK (ATCC CRL 10) cell lines, and the CV1/EBNA cell line derived from the African green monkey kidney cell line CV1 (ATCC CCL 70) as described by McMahan et al., 1991, EMBO J. 10:2821. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are described by Pouwels et al. (*Cloning Vectors: A Laboratory Manual*, Elsevier, N.Y., 1985).

The transformed cells can be cultured under conditions that promote expression of the polypeptide, and the polypeptide recovered by conventional protein purification procedures. One such purification procedure includes the use of affinity chromatography, e.g., in the case of an antigen binding protein, over a matrix having all or a portion of the antigen (e.g., an IL-1Rrp2 requiring polypeptides or portion thereof) bound thereto, or in the case of an IL-1Rrp2 requiring protein, over a matrix having all or a portion of IL-1Rrp2, or an antigen binding protein that binds the IL-1Rrp2 requiring protein bound thereto. Polypeptides or proteins contemplated for use herein include substantially homogeneous recombinant mammalian IL-1Rrp2 requiring polypeptides, and/or antibodies thereto, substantially free of contaminating endogenous materials.

The proteins may be prepared, and screened for desired properties, by any of a number of known techniques. Certain of the techniques involve isolating a nucleic acid encoding a polypeptide chain (or portion thereof) of an IL-1Rrp2 requiring polypeptides of interest (e.g., IL-1F6, F8 or F (or IL-1F5), and manipulating the nucleic acid through recombinant DNA technology. Nucleic acids encoding antigen binding proteins that bind an IL-1Rrp2 requiring polypeptides can be similarly manipulated. The nucleic acid may be fused to another

nucleic acid of interest, or altered (e.g., by mutagenesis or other conventional techniques) to add, delete, or substitute one or more amino acid residues, for example.

Protease Isolation and Assay

The IL-1Rrp2 requiring proteins described herein will also be useful in identifying and/or isolating a protease or proteases that cleave the IL-1Rrp2 requiring proteins to yield the bioactive form thereof. Useful methods are described, for example, in the *Handbook Of Proteolytic Enzymes, Second Edition*, edited by A. Barrett, N. Rawlings and J. Woessner (Academic Press, 2004). In general, methods for identifying the protease(s) might include (a) testing known proteases for their ability to generate biologically active material; (b) screening cell supernatants, membranes, or lysates for their ability to generate biologically active material; and (c) using the full-length (uncleaved) IL-1Rrp2 requiring protein as an affinity reagent to purify the protease(s).

For example, known proteases can be tested for the ability to cleave an IL-1 Rrp2 requiring protein into bioactive form by contacting a known protease with the IL-1 Rrp2 requiring protein under conditions promoting protease activity, than determining what effect, if any, the protease had upon the biological activity of the IL-1Rrp2 requiring polypeptides (for example, activity as an agonist or an antagonist as described herein). Cells that express a protease (or proteases) that cleave IL-1Rrp2 requiring proteins, either intracellularly, as a soluble polypeptide or as a cell-surface associated protein, can be identified in a similar manner. It may further be possible to use an IL-1Rrp2 requiring protein to select a cell population enriched for protease expression by using a panning or cell sorting technique, many of which are known in the art. When a cellular source of the protease has been identified, the IL-1Rrp2 requiring protein(s) can be used in an effort to isolate the protease.

Specific screening methods are known in the art and along with integrated robotic systems and collections of chemical compounds/natural products are extensively incorporated in high throughput screening so that large numbers of test compounds can be tested for activity within a short amount of time. These methods include homogeneous assay formats such as fluorescence resonance energy transfer, fluorescence polarization, time-resolved fluorescence resonance energy transfer, scintillation proximity assays, reporter gene assays, fluorescence quenched enzyme substrate, chromogenic enzyme substrate and electrochemiluminescence.

One such assay is based on fluorescence resonance energy transfer (FRET; for example, HTRF®, Packard Instrument Company, Meriden, Conn.; LANCE™, PerkinElmer Life-Sciences, Wallac Oy., Turku, Finland) between two fluorescent labels, an energy donating long-lived chelate label and a short-lived organic acceptor. The energy transfer occurs when the two labels are brought in close proximity via the molecular interaction between an IL-1Rrp2 polypeptide and a protease that cleaves it.

Indications

In one aspect, the present invention provides methods of treating a subject. The method can, for example, have a generally salubrious effect on the subject, e.g., it can increase the subject's expected longevity. Alternatively, the method can, for example, treat, prevent, relieve, or ameliorate ("treat") a disease, disorder, condition, or illness ("a condition"). Among the conditions to be treated in accordance with the present invention are conditions characterized by inappropriate expression or activity of IL-1Rrp2 and/or agonists or antagonists thereof (e.g., IL-1F6, F8 and/or F9 for the former, IL-1F5 for the latter). In some such conditions, the expression or activity level of the receptor or agonist(s) thereof is too

high; in other cases the expression or activity level of an antagonist(s) thereof is too low. Treatment comprises administering an IL-1Rrp2 antagonist as described herein.

Conditions that fall within this category often exhibit an inflammatory skin phenotype with characteristics common to those seen in human psoriatic skin. Such characteristics include acanthosis, hyperkeratosis, dermal infiltrate, increased expression of keratin 6, increased expression of keratin 14, increased expression of ICAM-1 in dermis, basal keratinocytes and blood vessels, increased expression of macrophage marker BM8 in dermis and decreased expression in epidermis, and decreased expression of T cell marker CD3 in epidermis.

Specific medical conditions and diseases that are treatable or preventable with the IL-1Rrp2 antagonists of this invention include those associated with inflammatory skin diseases including, but not limited to psoriasis, seborrheic dermatitis, atopic dermatitis (including chronic atopic dermatitis or CAD), allergic contact dermatitis, lichen simplex chronicus, pityriasis rubra pilaris and nummular dermatitis.

Moreover, normal airway epithelium has relatively high expression of IL-1 family members F5, F6, F8 and F9, as well as the receptor IL-1Rrp2, and intranasal instillation of F8 or F9 leads to an influx of neutrophils into the lung. Accordingly IL-1Rrp2 antagonists may be indicated for inflammatory conditions of the airway, for example asthma and allergic rhinitis. IL-1F9 and IL-1Rrp2 are highly expressed in the esophagus, and the interaction between this cytokine/receptor pair may play a role in gastro-esophageal reflux disease (GERD), which may accordingly be ameliorated by IL-1Rrp2 antagonists.

IL-1 F8 and IL-1 Rrp2 are also expressed in synovial fibroblasts and chondrocytes, and are induced to higher levels in those cells by IL-1 and TNF. Moreover, these cells respond to exogenous IL-1 F8 by synthesizing IL-6, IL-8 and nitric oxide. Accordingly, the IL-1Rrp2 antagonists of the invention may have use in arthritic conditions mediated by the induced polypeptides (i.e., rheumatoid arthritis, psoriatic arthritis, other arthritic conditions in which TNF and/or IL-1 play a role, and osteoarthritis and related conditions in which nitric oxide plays a role).

The methods described herein can be treated with the IL-1 Rrp2 antagonists of this invention in combination with other cytokines, cytokine inhibitors and reagents (also referred to herein as immunomodulators). For example, IL-18 antagonists; including soluble IL-18 receptor, antibodies to IL-18 or the IL-18 receptor, IL-18 binding protein; TNF inhibitors, including ENBREL®; IL-1 inhibitors, including soluble forms of type II IL-1R, type II IL-1R, antibodies to IL-1, antibodies to type I IL-1R; and or other active agents that are effective in treating the disclosed medical conditions and diseases.

The compositions and/or methods of the present invention also can be used, for example, in cosmetic treatments, in veterinary treatments, to increase longevity, to treat reproductive defects, and to treat a variety of IL-1Rrp2 related disorders. In addition, in certain such conditions, the expression or activity level of IL-1Rrp2 agonists is too low, and the treatment comprises administering an IL-1Rrp2 agonist such as IL-1F6, F8 and/or F9; such treatments are also comprehended herein.

Therapeutic Methods and Administration of IL-1Rrp2 Antagonists

Certain methods provided herein comprise administering an IL-1 Rrp2 antagonist to a subject, thereby reducing an IL-1 family member-induced biological response that plays a role in a particular condition. In particular embodiments, methods

of the invention involve contacting endogenous IL-1Rrp2-expressing cells with an IL-1Rrp2 antagonist, e.g., via administration to a subject or in an ex vivo procedure.

The term "treatment" encompasses alleviation or prevention of at least one symptom or other aspect of a disorder, or reduction of disease severity, and the like. An IL-1 Rrp2 antagonist need not effect a complete cure, or eradicate every symptom or manifestation of a disease, to constitute a viable therapeutic agent. As is recognized in the pertinent field, drugs employed as therapeutic agents may reduce the severity of a given disease state, but need not abolish every manifestation of the disease to be regarded as useful therapeutic agents. Similarly, a prophylactically administered treatment need not be completely effective in preventing the onset of a condition in order to constitute a viable prophylactic agent. Simply reducing the impact of a disease (for example, by reducing the number or severity of its symptoms, or by increasing the effectiveness of another treatment, or by producing another beneficial effect), or reducing the likelihood that the disease will occur or worsen in a subject, is sufficient. One embodiment of the invention is directed to a method comprising administering to a patient an IL-1Rrp2 antagonist in an amount and for a time sufficient to induce a sustained improvement over baseline of an indicator that reflects the severity of the particular disorder.

As is understood in the pertinent field, pharmaceutical compositions comprising the molecules of the invention are administered to a subject in a manner appropriate to the indication. Pharmaceutical compositions may be administered by any suitable technique, including but not limited to parenterally, topically, or by inhalation. If injected, the pharmaceutical composition can be administered, for example, via intra-articular, intravenous, intramuscular, intrascleral, intraperitoneal or subcutaneous routes, by bolus injection, or continuous infusion. Localized administration, e.g. at a site of disease or injury is contemplated, as are transdermal delivery and sustained release from implants. Delivery by inhalation includes, for example, nasal or oral inhalation, use of a nebulizer, inhalation of the antagonist in aerosol form, and the like. Other alternatives include eyedrops; oral preparations including pills, syrups, lozenges or chewing gum; and topical preparations such as lotions, gels, sprays, and ointments.

Use of IL-1Rrp2 antagonist s thereto in ex vivo procedures also is contemplated. For example, a patient's blood or other bodily fluid may be contacted with an IL-1Rrp2 requiring polypeptides that binds an enzyme such as a protease ex vivo. The IL-1Rrp2 requiring polypeptides may be bound to a suitable insoluble matrix or solid support material.

Advantageously, IL-1Rrp2 antagonist are administered in the form of a composition comprising one or more additional components such as a physiologically acceptable carrier, excipient or diluent. Optionally, the composition additionally comprises one or more physiologically active agents, for example, a second inflammation- or immune-inhibiting substance, an anti-angiogenic substance, an analgesic substance, etc., non-exclusive examples of which are provided herein. In various particular embodiments, the composition comprises one, two, three, four, five, or six physiologically active agents in addition to an IL-1Rrp2 antagonist.

In one embodiment, the pharmaceutical composition comprise an IL-1Rrp2 antagonist of the invention together with one or more substances selected from the group consisting of a buffer, an antioxidant such as ascorbic acid, a low molecular weight polypeptide (such as those having fewer than 10 amino acids), a protein, an amino acid, a carbohydrate such as glucose, sucrose or dextrans, a chelating agent such as EDTA, glutathione, a stabilizer, and an excipient. Neutral buffered

saline or saline mixed with conspecific serum albumin are examples of appropriate diluents. In accordance with appropriate industry standards, preservatives such as benzyl alcohol may also be added. The composition may be formulated as a lyophilizate using appropriate excipient solutions (e.g., sucrose) as diluents. Suitable components are nontoxic to recipients at the dosages and concentrations employed. Further examples of components that may be employed in pharmaceutical formulations are presented in Remington's Pharmaceutical Sciences, 16th Ed. (1980) and 20th Ed. (2000), Mack Publishing Company, Easton, Pa.

Kits for use by medical practitioners include an IL-1Rrp2-inhibiting substance of the invention and a label or other instructions for use in treating any of the conditions discussed herein. In one embodiment, the kit includes a sterile preparation of one or more IL-1Rrp2 antagonist s thereto, which may be in the form of a composition as disclosed above, and may be in one or more vials.

Dosages and the frequency of administration may vary according to such factors as the route of administration, the particular IL-1Rrp2 antagonists employed, the nature and severity of the disease to be treated, whether the condition is acute or chronic, and the size and general condition of the subject. Appropriate dosages can be determined by procedures known in the pertinent art, e.g. in clinical trials that may involve dose escalation studies.

A IL-1Rrp2-inhibiting substance of the invention may be administered, for example, once or more than once, e.g., at regular intervals over a period of time. In particular embodiments, an IL-1Rrp2 antagonist is administered over a period of at least a month or more, e.g., for one, two, or three months or even indefinitely. For treating chronic conditions, long-term treatment is generally most effective. However, for treating acute conditions, administration for shorter periods, e.g. from one to six weeks, may be sufficient. In general, the IL-1Rrp2 antagonist is administered until the patient manifests a medically relevant degree of improvement over baseline for the chosen indicator or indicators.

Particular embodiments of the present invention involve administering an IL-1Rrp2 antagonist at a dosage of from about 1 ng of protein per kg of subject's weight per day ("1 ng/kg/day") to about 10 mg/kg/day, more preferably from about 500 ng/kg/day to about 5 mg/kg/day, and most preferably from about 5 micrograms/kg/day to about 2 mg/kg/day, to a subject. In additional embodiments, an IL-1Rrp2 antagonist is administered to adults one time per week, two times per week, or three or more times per week, to treat an IL-1Rrp2-mediated disease, condition or disorder, e.g., a medical disorder disclosed herein. If injected, the effective amount of IL-1Rrp2 antagonist per adult dose may range from 1-20 mg/m², and preferably is about 5-12 mg/m². Alternatively, a flat dose may be administered; the amount may range from 5-100 mg/dose. One range for a flat dose is about 20-30 mg per dose. In one embodiment of the invention, a flat dose of 25 mg/dose is repeatedly administered by injection. If a route of administration other than injection is used, the dose is appropriately adjusted in accordance with standard medical practices. One example of a therapeutic regimen involves injecting a dose of about 20-30 mg of IL-1Rrp2 antagonist to one to three times per week over a period of at least three weeks, though treatment for longer periods may be necessary to induce the desired degree of improvement. For pediatric subjects (age 4-17), one exemplary suitable regimen involves the

subcutaneous injection of 0.4 mg/kg, up to a maximum dose of 25 mg of IL-1Rrp2 antagonist administered two or three times per week.

Particular embodiments of the methods provided herein involve subcutaneous injection of from 0.5 mg to 10 mg, preferably from 3 to 5 mg, of an IL-1Rrp2 antagonist, once or twice per week. Another embodiment is directed to pulmonary administration (e.g., by nebulizer) of 3 or more mg of IL-1Rrp2 antagonist once a week.

Examples of therapeutic regimens provided herein comprise subcutaneous injection of an IL-1Rrp2 antagonist once a week, at a dose of 1.5 to 3 mg, to treat a condition in which IL-1Rrp2 signaling plays a role. Examples of such conditions are provided herein and include, for example, inflammatory conditions of the skin, including, but not limited to psoriasis, seborrheic dermatitis, atopic dermatitis (including chronic atopic dermatitis or CAD), allergic contact dermatitis, lichen simplex chronicus, pityriasis rubra pilaris and nummular dermatitis. Weekly administration of IL-1Rrp2 antagonist is continued until a desired result is achieved, e.g., the subject's symptoms subside. Treatment may resume as needed, or, alternatively, maintenance doses may be administered.

Other examples of therapeutic regimens provided herein comprise subcutaneous or intravenous administration of a dose of 1, 3, 5, 6, 7, 8, 9, 10, 11, 12, 15, or 20 milligrams of an IL-1Rrp2 inhibitor of the present invention per kilogram body mass of the subject (mg/kg). The dose can be administered once to the subject, or more than once at a certain interval, for example, once a day, three times a week, twice a week, once a week, three times a month, twice a month, once a month, once every two months, once every three months, once every six months, or once a year. The duration of the treatment, and any changes to the dose and/or frequency of treatment, can be altered or varied during the course of treatment in order to meet the particular needs of the subject.

In another embodiment, an IL-1Rrp2 antagonist is administered to the subject in an amount and for a time sufficient to induce an improvement, preferably a sustained improvement, in at least one indicator that reflects the severity of the disorder that is being treated. Various indicators that reflect the extent of the subject's illness, disease or condition may be assessed for determining whether the amount and time of the treatment is sufficient. Such indicators include, for example, clinically recognized indicators of disease severity, symptoms, or manifestations of the disorder in question. In one embodiment, an improvement is considered to be sustained if the subject exhibits the improvement on at least two occasions separated by two to four weeks. The degree of improvement generally is determined by a physician, who may make this determination based on signs, symptoms, biopsies, or other test results, and who may also employ questionnaires that are administered to the subject, such as quality-of-life questionnaires developed for a given disease.

Elevated levels of IL-1Rrp2, IL-1F6, IL-1F8 and/or IL-1F9 and/or activation of thereof, and/or decreased levels and/or activation of IL-1F5, are associated with a number of disorders, including, for example, inflammatory conditions of the skin, including, but not limited to psoriasis, seborrheic dermatitis, atopic dermatitis (including chronic atopic dermatitis or CAD), allergic contact dermatitis, lichen simplex chronicus, pityriasis rubra pilaris and nummular dermatitis. Other such conditions include inflammatory conditions of the airway, of the esophagus, and the joints.

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Subjects with a given disorder may be screened, to identify those individuals who have elevated IL-1Rrp2, IL-1F6, IL-1F8 and/or IL-1F9 activation (or decreased IL-1F5 activation), thereby identifying the subjects who may benefit most from treatment with an IL-1Rrp2 antagonist. Thus, treatment methods provided herein optionally comprise a first step of measuring a subject's IL-1Rrp2, IL-1F6, IL-1F8 and/or IL-1F9 (or IL-1F5) activation levels. An IL-1Rrp2 antagonist may be administered to a subject in whom IL-1Rrp2, IL-1F6, IL-1F8 and/or IL-1F9 activation is elevated above normal, and/or whose IL-1F5 activity is below normal.

A subject's levels of IL-1Rrp2, IL-1F6, IL-1F8, IL-1F9 and/or IL-1F5 activity may be monitored before, during and/or after treatment with an IL-1Rrp2 antagonist, to detect changes, if any, in IL-1Rrp2, IL-1F6, IL-1F8, IL-1F9 and/or IL-1F5 activity. For some disorders, the incidence of elevated IL-1Rrp2, IL-1F6, IL-1F8 and/or IL-1F9 activity, or decreased IL-1F5 activity, may vary according to such factors as the stage of the disease or the particular form of the disease. Known techniques may be employed for measuring IL-1Rrp2, IL-1F6, IL-1F8, IL-1F9 and/or IL-1F5 activity, e.g., in a subject's serum, blood or tissue samples. IL-1Rrp2, IL-1F6, IL-1F8, IL-1F9 and/or IL-1F5 activity may be measured using any suitable technique.

Particular embodiments of methods and compositions of the invention involve the use of an IL-1Rrp2 antagonist and one or more additional IL-1Rrp2 antagonists, for example, two or more IL-1Rrp2 requiring proteins of the invention, two or more antigen binding proteins of the invention, or combinations of IL-1Rrp2 requiring proteins and antigen binding proteins. In further embodiments, IL-1Rrp2 antagonists are administered alone or in combination with other agents useful for treating the condition with which the patient is afflicted. Examples of such agents include both proteinaceous and non-proteinaceous drugs. When multiple therapeutics are co-administered, dosages may be adjusted accordingly, as is recognized in the pertinent art. "Co-administration" and combination therapy are not limited to simultaneous administration, but also include treatment regimens in which an IL-1Rrp2 antagonist is administered at least once during a course of treatment that involves administering at least one other therapeutic agent to the patient.

Examples of other agents that may be co-administered with an IL-1 Rrp2 antagonist are other IL-1Rrp2 requiring proteins or antigen binding proteins, or therapeutic polypeptides that are chosen according to the particular condition to be treated. Alternatively, non-proteinaceous drugs that are useful in treating one of the particular conditions discussed above may be co-administered with IL-1Rrp2 antagonist.

Combination Therapy

In another aspect, the present invention provides a method of treating a subject with an IL-1Rrp2 antagonist, and one or more other treatments. In one embodiment, such a combination therapy achieves synergy or an additive effect by, for example, attacking multiple sites or molecular targets in a tumor. Types of combination therapies that can be used in connection with the present invention include inhibiting or activating (as appropriate) multiple nodes in a single disease-related pathway, multiple pathways in a target cell, and multiple cell types within a target tissue.

In another embodiment, a combination therapy method comprises administering to the subject two, three, four, five, six, or more of the agonists or antagonists described herein. In

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another embodiment, the method comprises administering to the subject two or more treatments that together inhibit or activate (directly or indirectly) IL-1Rrp2-mediated signal transduction. Examples of such methods include using combinations of two or more IL-1Rrp2 requiring proteins and/or antigen binding proteins, an IL-1Rrp2 requiring polypeptide or antigen binding protein and one or more other therapeutic moiety having anti-inflammatory properties (for example, non-steroidal anti-inflammatory agents, steroids, and/or immunomodulators), or an IL-1Rrp2 requiring polypeptide or antigen binding protein and one or more other treatments (e.g., surgery, ultrasound, or treatment effective to reduce inflammation). Furthermore, one or more IL-1Rrp2 antagonist can be used in combination with one or more molecules or other treatments, wherein the other molecule(s) and/or treatment(s) do not directly bind to or affect IL-1Rrp2, but which combination is effective for treating or preventing the condition being treated. In one embodiment, one or more of the molecule(s) and/or treatment(s) treats or prevents a condition that is caused by one or more of the other molecule(s) or treatment(s) in the course of therapy, e.g., nausea, fatigue, alopecia, cachexia, insomnia, etc. In every case where a combination of molecules and/or other treatments is used, the individual molecule(s) and/or treatment(s) can be administered in any order, over any length of time, which is effective, e.g., simultaneously, consecutively, or alternately. In one embodiment, the method of treatment comprises completing a first course of treatment with one molecule or other treatment before beginning a second course of treatment. The length of time between the end of the first course of treatment and beginning of the second course of treatment can be any length of time that allows the total course of therapy to be effective, e.g., seconds, minutes, hours, days, weeks, months, or even years.

In another embodiment, the method comprises administering one or more of the IL-1Rrp2 antagonists described herein and one or more other treatments (e.g., a therapeutic or palliative treatment). Where a method comprises administering more than one treatment to a subject, it is to be understood that the order, timing, number, concentration, and volume of the administrations is limited only by the medical requirements and limitations of the treatment, i.e., two treatments can be administered to the subject, e.g., simultaneously, consecutively, alternately, or according to any other regimen.

The specification is most thoroughly understood in light of the teachings of the references cited within the specification, which are hereby incorporated by reference. The following examples, both actual and prophetic, are provided for the purpose of illustrating specific embodiments or features of the instant invention and do not limit its scope.

EXAMPLE 1

Example 1A

Preparation of IL-1F6 Variants

This example describes the preparation of various N-terminal variants of IL-1F6. The various N-terminal deletion variants are shown in Table 1 below:

TABLE 1

Amino Acid Sequence of IL-1F6 Variants	
<p>N-Terminal amino acid sequence of IL-1F6 Variants SEQ(. . . indicates intervening amino acids of human IL-1F6 (SEQ ID NO 2; FLAG indicates the amino acid sequence DYKDDDDK; polyHis NO: indicates a chain of multiple histidines, typically about 6)</p>	
22 MEKALKIDTPQQGSIQDI . . . FGLTMLF-FLAG-polyHis	IL-1F6 Variant Polypeptides: (Hu indicates human; WT indicates full length wild type polypeptide, FpH indicates a FLAG poly His tag., the bold, italicized, upper case letter and number refers to the indicated amino acid and its position in SEQ ID NO 2 where the position is relative to the N-Terminal amino acid at position one of SEQ ID NO 2.) HuIL-1F6WT/FpH
23 MKIDTPQQGSIQDI . . . FGLTMLF-FLAG-polyHis	HuIL-1F6 K6 /FpH
24 MIDTPQQGSIQDI . . . FGLTMLF-FLAG-polyHis	HuIL-1F6 I7 /FpH
25 MDTPQQGSIQDI . . . FGLTMLF-FLAG-polyHis	HuIL-1F6 D8 /FpH
26 KIDTPQQGSIQDI . . . FGLTMLF	HuIL-1F6 K6

Note: The IL1-F6 polypeptide occurs in 2 isotypes. One isotype comprises a Q at amino acid 12, relative to the M a position one of the wild type IL-1F6 indicated in Table 1 as SEQ ID NO 22 and another that encodes R at position 12. Variants of both isotypes are provided by the compositions and methods of the invention.

The N-terminal variants that comprise a FLAG-polyHis C-terminal tag were prepared as described immediately below. N-terminal variants were amplified via PCR using as a template a cDNA clone encoding huIL-1F6 (AF201831). An N-terminal methionine was placed directly before the desired starting amino acid of each variant for proper translational initiation. FLAG® (Sigma-Aldrich, St. Louis, Mo.) and poly-His tags were added to the C-terminus for purification/detection. NdeI and XhoI sites were added to the 5' and 3' ends, respectively. The resulting amplicons were digested with NdeI and XhoI and subcloned into the *E. coli* expression vector, pAMG21 (ATCC # 98113). The resulting constructs were introduced into *E. coli* DH10B and expression was induced by the addition of [N-(3-oxo-hexanoyl)homoserine lactone]. The expressed polypeptides were then purified from bacterial lysates (soluble fraction) by affinity chromatography using Ni-NTA columns (Qiagen, Germantown, Md. Cat #30600) as per manufacturer's protocol, and tested for activity in a reporter assay substantially as described in Example 2. Results are shown in Table 5 below.

The N-terminal variant, HuIL-1F6K6, was prepared by PCR amplifying a template cDNA clone encoding huIL-1F6K6 variant. The primers used in PCR allowed the PCR products to be placed using the In-Fusion™ PCR cloning system (Clontech, Mountain View, Calif., cat# 631774), in accordance with manufacturer's protocol, into a pET-SUMO vector (Invitrogen, Carlsbad, Calif., cat K300-01). This procedure put a pH-SUMO tag 5' to the desired starting amino acid of the IL-1F6 variant in the vector resulting in the following nucleic acid sequence where the pH SUMO tag runs from the 5' end to the underlined nucleotide in bold which indicates the start of the nucleic acid sequence encoding HuIL-1F6K6:

(SEQ ID NO 78)
 ATGGGCAGCAGCCATCATCATCATCATCACGGCAGCGGCTGGTCCCGCG
 CGGCAGCGCTAGCATGTTCGACTCAGAAGTCAATCAAGAAGCTAAGCCAG
 30 AGGTCAAGCCAGAAGTCAAGCCTGAGACTCACATCAATTTAAGGTGTCC
 GATGGATCTTCAGAGATCTTCTCAAGATCAAAAAGACCACTCCTTTAAG
 AAGGTGATGGAAGCGTTCGCTAAAAGACAGGGTAAGGAAATGGACTCCT
 35 TAAGATTCTTGACGAGGTATTAGAATTAAGCTGATCAGACCCCTGAA
 GATTTGGACATGGAGGATAACGATATTATTAGGCTCACAGAGAACAGAT
 TGGTGGTAAATTGACACACCTCAGCGGGGAGCATTACAGGATATCAATC
 40 ATCGGGTGTGGTTCTTCAGGACCAGACGCTCATAGCAGTCCCAGGAAG
 GACCGTATGTCTCCAGTCACTATTGCCTTAATCTCATGCCGACATGTGGA
 GACCTTGAGAAAGACAGAGGGAACCCATCTACCTGGGCTGAATGGAC
 TCAATCTCTGCCTGATGTGTGCTAAAGTCGGGGACCAAGCCACATGCGAG
 45 CTGAAGGAAAAGGATATAATGGATTGTGACAAACCCGAGCCTGTGAA
 GTCCTTTCTCTTCTACACAGCCAGAGTGGCAGGAACCTCCACCTTCGAGT
 CTGTGGCTTTCCCTGGCTGGTTTCATCGCTGTGAGGAGGCTGT
 50 CCTCTCATCCTTACCAAGAACTGGGGAAAGCCAACTACTGACTTTGG
 GTTAACATATGCTGTTTAA.

The resulting construct was introduced into *E. coli* DH10B. Expression was carried out using Overnight Express™ Autoinduction System (Novagen, Darmstadt, Germany, cat# 71300-3) per manufacturer's protocol. The *E. Coli* cells were centrifuged and frozen.

Frozen *E. coli* cell pellets were thawed in TBS made in Roche Complete EDTA free protease inhibitor cocktail. After thawing, benzonase was added. Cells were lysed via passage through a Microfluidics microfluidizer 110L device (MFIC Corporation, Newton, Mass.) and resulting lysates clarified via centrifugation. Supernatants were sterile filtered and loaded onto 5 mL HisTrap (GE Biosciences, Piscataway, N.J.) Ni-sepharose columns equilibrated in Tris, NaCl, imidazole pH 7.4. Columns were washed with imidazole in TBS.

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Protein was eluted with a imidazole linear gradient. Eluted fractions were pooled and dialyzed into PBS using MWCO Slide-A-Lyzers (Pierce Biotechnology, Inc., Rockland, Ill.). LifeSensors SUMO Protease-1 was used to cleave the His-SUMO fusion partner from IL-1F6 variant. Cleavage reaction products were dialyzed into TBS containing EDTA, pH 7.4 using MWCO Slide-A-Lyzers. Dialyzed pools were then passed back over HisTrap Ni-Sepharose columns and flow-through fractions containing pure liberated IL-1F6 variant were retained, and tested for activity as described in Example 2B below. Results are shown in Table 7 below.

Example 1B

Preparation of IL-1F8 Variants

Variants of IL-1F8 comprising a FLAG-polyHis tag were prepared in a substantially similar manner as for IL-F6 FLAG-polyHis tag variants described in Example 1A above, using as a template a cDNA clone encoding huIL-1F8 (AF201833). Likewise, HuIL-1F8R5 (lacking a FLAG-polyHis tag), using as a template a cDNA clone encoding huIL-1F8 (AF201833), was prepared and purified in a substantially similar manner to HuIL-1F6K6 described in Example 1A above. The various N-terminal deletion variants are shown in Table 2 below:

TABLE 2

Amino Acid Sequence of IL-1F8 Variants	
<p>N-Terminal amino acid sequence of IL-1F8 Variants (. . . indicates intervening amino acids of human IL-1F8 (SEQ ID NO 3); () indicates that the enclosed amino acid is removed; FLAG indicates the SEQ ID amino acid sequence DYKDDDDK; polyHis indicates NO: a chain of multiple histidines, typically 6)</p>	<p>IL-1F8 Variant Polypeptide: (Hu indicates human; WT indicates full length wild type polypeptide, FpH indicates a FLAG poly His tag., he bold, italicized, upper case letter and number refers to the indicated amino acid and its position in SEQ ID NO 3 where the position is relative to the N-Terminal amino acid at position one of SEQ ID NO 3.)</p>
27 MNPQREAAPKSYAIR . . . FYLDSVE-FLAG-polyHis	HuIL-1F8WT/FpH
28 MQREAAPKSYAIR . . . FYLDSVE-FLAG-polyHis	HuIL-1F8 Q4 /FpH
29 MREAAPKSYAIR . . . FYLDSVE-FLAG-polyHis	HuIL-1F8 R5 /FpH
30 MEAAPKSYAIR . . . FYLDSVE-FLAG-polyHis	HuIL-1F8 E6 /FpH
31 (M)AAPKSYAIR . . . FYLDSVE-FLAG-polyHis	HuIL-1F8 A7 /FpH
32 REAAPKSYAIR . . . FYLDSVE	HuIL-1F8 R5

The FLAG-polyHis constructs were expressed in *E. coli*, and the expressed polypeptides purified from bacterial lysates (soluble fraction) by affinity chromatography using Ni-NTA columns (Qiagen Cat #30600) as per manufacturer's protocol. N-terminal sequencing indicated that, for one construct (HuIL-1F8A7/FpH), the N-terminal Met was removed (designated parenthetically in Table 2). Purified polypeptides were tested for activity in a reporter assay substantially as described in Example 2; results are shown in Table 5 below.

The pH-SUMO construct, encoding HuIL-1F8R5 was introduced into *E. coli* DH10B. Expression was carried out

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using Overnight Express™ Autoinduction System (Novagen, Darmstadt, Germany, cat# 71300-3) per manufacturer's protocol. The *E. coli* cells were centrifuged and frozen. Frozen *E. coli* cell pellets were thawed in TBS made in Roche Complete EDTA free protease inhibitor cocktail. After thawing, benzonase was added. Cells were lysed via passage through a Microfluidics microfluidizer 110L device (MFIC Corporation, Newton, Mass.) and resulting lysates clarified via centrifugation. Supernatants were sterile filtered and loaded onto 5 mL HisTrap (GE Biosciences, Piscataway, N.J.) Ni-sepharose columns equilibrated in Tris, NaCl, imidazole pH 7.4. Columns were washed with imidazole in TBS. Protein was eluted with a imidazole linear gradient. Eluted fractions were pooled and dialyzed into PBS using MWCO Slide-A-Lyzers (Pierce Biotechnology, Inc., Rockland, Ill.). LifeSensors SUMO Protease-1 was used to cleave the His-SUMO fusion partner from IL-1F6 variant. Cleavage reaction products were dialyzed into TBS containing EDTA, pH 7.4 using MWCO Slide-A-Lyzers. Dialyzed pools were then passed back over HisTrap Ni-Sepharose columns and flow-through fractions containing pure liberated IL-1F6 variant were retained, and tested for activity as described in Example 2B below. Results are shown in Table 7 below.

Example 1C

Preparation of IL-1F9 Variants

Variants of IL-1F9 comprising a C-terminal FLAG-polyHis tag were prepared in a substantially similar manner as described in Example 1A above, using as a template a cDNA clone encoding huIL-1F9 (AF200492). HuIL-1F9S18 (lacking a C-Terminal FLAG-polyHis tag), using as a template a cDNA clone encoding huIL-1F9 (AF200492), was prepared and purified in a substantially similar manner to HuIL-1F6K6

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described in Example 1A above except that an extra thymine base pair was removed using a site directed mutagenesis kit according to the manufacturer's instructions (Stratagene, LaJolla, Calif., cat# 200523). The resulting clone was cut with restriction enzymes Nde1 and Hind III and subcloned back into the pET-SUMO vector (Invitrogen, Carlsbad, Calif.). The various N-terminal deletion variants are shown in Table 3 below:

TABLE 3

Amino Acid Sequence of IL-1F9 Variants	
<p>N-Terminal amino acid sequence of IL-1F9 Variants</p> <p>(. . . indicates intervening amino acids of human IL-1F9 (SEQ ID NO 4); SEQ () indicate that the enclosed amino acid is removed; FLAG indicates the ID amino acid sequence DYKDDDDK; polyHis indicates a chain of multiple NO:histidines, typically 6.)</p>	
33 MRGTPGDADGGGRAVYQSMCKPITGT . . . FELNIND-FLAG-polyHis	IL-1F9 Variant Polypeptide: (Hu indicates human; WT indicates full length wild type polypeptide, FpH indicates a FLAG poly His tag., the bold, italicized, upper case letter and number refers to the indicated amino acid and its position in SEQ ID NO 4 where the position is relative to the N-Terminal amino acid at position one of SEQ ID NO 4.)
34 (M) SMCKPITGT . . . FELNIND-FLAG-polyHis	HuIL-1F9WT/FpH
35 MMCKPITGT . . . FELNIND-FLAG-polyHis	HuIL-1F9 S18 /FpH
36 (M) CKPITGT . . . FELNIND-FLAG-polyHis	HuIL-1F9 M19 /FpH
37 SMCKPITGT . . . FELNIND	HuIL-1F9 C20 /FpH
	HuIL-1F9 S18

The constructs were expressed in *E. coli*, and the expressed polypeptides purified from bacterial lysates (soluble fraction) as described previously. Similar to observations for HuIL-1F8, N-terminal sequencing indicated that, for one construct HuIL-1F9C20/FpH, the N-terminal Met was removed from the polypeptide. Purified polypeptides were also tested for activity in a reporter assay substantially as described in Example 2. Results are shown in Table 5 below.

The pH-SUMO construct, encoding HuIL-1F9S18 was introduced into *E. coli* DH10B. Expression was carried out using Overnight Express™ Autoinduction System (Novagen, Darmstadt, Germany, cat# 71300-3) per manufacturer's protocol. The *E. Coli* cells were centrifuged and frozen. Frozen *E. coli* cell pellets were thawed in TBS made in Roche Complete EDTA free protease inhibitor cocktail. After thawing, benzonase was added. Cells were lysed via passage through a Microfluidics microfluidizer 110L device (MFIC Corporation, Newton, Mass.) and resulting lysates clarified via centrifugation. Supernatants were sterile filtered and loaded onto 5 mL HisTrap (GE Biosciences, Piscataway, N.J.) Ni-sepharose columns equilibrated in Tris, NaCl, imidazole

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pH 7.4. Columns were washed with imidazole in TBS. Protein was eluted with a imidazole linear gradient. Eluted fractions were pooled and dialyzed into PBS using MWCO Slide-A-Lyzers (Pierce Biotechnology, Inc., Rockland, Ill.). LifeSensors SUMO Protease-1 was used to cleave the His-SUMO fusion partner from IL-1F6 variant. Cleavage reaction products were dialyzed into TBS containing EDTA, pH 7.4 using MWCO Slide-A-Lyzers. Dialyzed pools were then

passed back over HisTrap Ni-Sephadex columns and flow-through fractions containing pure liberated IL-1F6 variant were retained. and tested for activity as described in Example 2B below. Results are shown in Table 7 below.

Example 1D

Preparation of IL-1F5 Variants

Variants of IL-1F5 comprising a C-terminal FLAG-poly-His tag were prepared in a substantially similar manner as described in Example 1A above, using as a template a cDNA clone encoding huIL-1F5 (AF201830). HuIL-1F5V2, using as a template a cDNA clone encoding huIL-1F5 (AF201830), was prepared and purified in a substantially similar manner to HuIL-1F6K6 described in Example 1A. The various N-terminal deletion variants are shown in Table 4 below:

TABLE 4

Amino Acid Sequence of IL-1F5 Variants	
<p>N-Terminal amino acid sequence of IL-1F5 Variants (. . . indicates intervening amino acids of human IL-1F5 (SEQ ID NO 1); () indicated that the enclosed amino acid is removed; FLAG ID indicates the amino acid sequence DYKDDDDK; polyHis indicates a NO:chain of multiple histidines, typically 6.)</p>	<p>IL-1F5 Variant Polypeptide: (Hu indicates human; WT indicates full length wild type polypeptide, FpH indicates a FLAG poly His tag; the bold, italicized, upper case letter and number refers to the indicated amino acid and its position in SEQ ID NO 1, where the position is relative to the N-Terminal amino acid at position one of SEQ ID NO 1.)</p>
38 MVLSGALCFRMKDSA . . . FYFQQCD-FLAG-polyHis	HuIL-1F5 <i>M</i> 1/FpH
39 (M) VLSGALCFRMKDSA . . . FYFQQCD-FLAG-polyHis	HuIL-1F5 <i>V</i> 2/FpH
40 MLSGALCFRMKDSA . . . FYFQQCD-FLAG-polyHis	HuIL-1F5 <i>L</i> 3/FpH
41 (M) SGALCFRMKDSA . . . FYFQQCD-FLAG-polyHis	HuIL-1F5 <i>S</i> 4/FpH
42 (M) GALCFRMKDSA . . . FYFQQCD-FLAG-polyHis	HuIL-1F5 <i>G</i> 5/FpH
43 VLSGALCFRMKDSA . . . FYFQQCD	HuIL-1F5 <i>V</i> 2

HuIL-1F5M1/FpH was expressed in *E. coli* as a Glutathione-S-transferase (hereinafter “GST”) fusion. The GST domain was cleaved off by digestion with Factor Xa. HuIL-1F5V2/FpH was expressed in COS-1 cells. The remaining constructs were expressed as described above. A full-length form was also expressed in *E. coli*, and found to have the same N-terminal sequence as HuIL-1F5V2/FpH; this form was referred to as HuIL-1F5WT/FpH. The polypeptides were purified and tested for their ability to inhibit the activation of IL-1Rrp2 by IL-1F8 in a reporter assay substantially as described in Example 2. In this assay, each purified variant of IL-1F5 was added to IL-1Rrp2 transfected Jurkat cells at 5000, 500, or 50 ng/mL, and the cells were pre-incubated for 15 minutes. At that time, IL-1F8 (untagged, full-length—expressed in *E. coli*; HuIL-1F8WT/FpH) was added at a concentration of 150 ng/mL. The cells were then incubated with the F8/F5 mixtures for five hours at 37° C. Cell lysates were assayed for luciferase activity as previously reported (Towne et al. 2004 *J Biol Chem* 279(14):13677). Ratios of F5:F8 tested were 33.3:1, 3.3:1, and 0.33:1. Results are shown in Table 5 below.

The pH-SUMO construct, encoding HuIL-1FV2 was introduced into *E. coli* DH10B. Expression was carried out using Overnight Express™ Autoinduction System (Novagen, Darmstadt, Germany, cat# 71300-3) per manufacturer’s protocol. The *E. Coli* cells were centrifuged and frozen. Frozen *E. coli* cell pellets were thawed in TBS made in Roche Complete EDTA free protease inhibitor cocktail. After thawing, benzonase was added. Cells were lysed via passage through a Microfluidics microfluidizer 110L device (MFIC Corporation, Newton, Mass.) and resulting lysates clarified via centrifugation. Supernatants were sterile filtered and loaded onto 5 mL HisTrap (GE Biosciences, Piscataway, N.J.) Ni-sepharose columns equilibrated in Tris, NaCl, imidazole pH 7.4. Columns were washed

with imidazole in TBS. Protein was eluted with a imidazole linear gradient. Eluted fractions were pooled and dialyzed into PBS using MWCO Slide-A-Lyzers (Pierce Biotechnology, Inc., Rockland, Ill.). LifeSensors SUMO Protease-1 was used to cleave the His-SUMO fusion partner from IL-1F6 variant. Cleavage reaction products were dialyzed into TBS containing EDTA, pH 7.4 using MWCO Slide-A-Lyzers. Dialyzed pools were then passed back over HisTrap Ni-Sepharose columns and flow-through fractions containing pure liberated IL-1F6 variant were retained. and tested for activity as described in Example 2B below. Results are shown in Table 7 below.

EXAMPLE 2

Example 2A

Luciferase Assay of IL-1F Variants

This Example describes a reporter assay used to evaluate the activity of IL-1 family member variants, substantially as described in Towne et al., *J Biol Chem*. 279(14):13677 (2004) herein incorporated by reference in its entirety. Briefly, Jurkat E6.1 cells (7×10^5) are transiently transfected via FuGENE 6 (Roche Diagnostics, Basel, Switzerland) as per manufacturer’s protocol (i.e., cells are transfected with 200 ng reporter plasmid and 400 ng of either IL-1Rrp2-encoding or empty vector plasmids with a 1:3 DNA/FuGENE 6 ratio). Seventeen hours after transfection, cells are stimulated with the indicated cytokines or cytokine variants for five hours. Cells are lysed and luciferase activity is assessed using reporter lysis buffer (Promega) and Luciferase Assay Reagent (Promega). The results reported herein represent duplicate samples.

TABLE 5

HuIL-1F Variant	N-Terminal Sequence	SEQ ID NO:	Biological Activity*	Variant start Position**
HuIL-1F5 M1 /FpH	~~~~~MVL SGALCFR MD SALKVLYLHNN	44	none	-10
HuIL-1F5 V2 /FpH	~~~~~VL SGALCFR MD SALKVLYLHNN	45	>FL	-9
HuIL-1F5 L3 /FpH	~~~~~ML SGALCFR MD SALKVLYLHNN	46	>FL	-9
HuIL-1F5 S4 /FpH	~~~~~ SGALCFR MD SALKVLYLHNN	47	none	-7
HuIL-1F5 G5 /FpH	~~~~~ GALCFR MD SALKVLYLHNN	48	none	-6
HuIL-1F6 K6 /FpH	~~~~~MKIDTP QRGS Q DINHRVWLQDQ	49	=FL	-10
HuIL-1F6 I7 /FpH	~~~~~MIDTP QRGS Q DINHRVWLQDQ	50	>>FL	-9
HuIL-1F6 D8 /FpH	~~~~~MDTP QRGS Q DINHRVWLQDQ	51	=FL	-8
HuIL-1F8 Q4 /FpH	~~~~~MQREAA PKSYA R DSRQMVVLSGN	52	=FL	-11
HuIL-1F8 R5 /FpH	~~~~~MREAA PKSYA R DSRQMVVLSGN	53	=FL	-10
HuIL-1F8 E6 /FpH	~~~~~MEAA PKSYA R DSRQMVVLSGN	54	>>FL	-9
HuIL-1F8 A7 /FpH	~~~~~AA PKSYA R DSRQMVVLSGN	55	<FL	-7
HuIL-1F9 S18 /FpH	~~~~~SMCKPIT GT I NDLNQQVWTLQGQ	56	>>FL	-9
HuIL-1F9 M19 /FpH	~~~~~MMCKPIT GT I NDLNQQVWTLQGQ	57	>>FL	-9
HuIL-1F9 C20 /FpH	~~~~~CKPIT GT I NDLNQQVWTLQGQ	58	<FL	-7

*Biological activity is expressed relative to the activity of the relevant full-length polypeptide (FL).

**Indicates the position of the variant N-terminal amino acid relative to the Methionine or Isoleucine of the consensus sequence @XD. The aliphatic residue (met or ile) is indicated by enclosure in a box.

Analysis of these results indicated that all variants with enhanced activity relative to the relevant full length IL-1 family member have an N-terminal sequence that begins at position -9 relative to the aliphatic amino acid of the @XD consensus sequence (the aliphatic amino acid is shown as an '@' in the consensus sequence of FIG. 1

and enclosed in a box in the sequences of Table 5 above). There were sufficient data points available for some of the constructs to allow calculation of EC₅₀ values; for the remaining constructs, the data were insufficient for such calculations. The relevant constructs and their EC₅₀s are shown in Table 6 below.

TABLE 6

IL-1	Assayed Polypeptide:	EC ₅₀ (ng/ml)	Assayed Polypeptide:	EC ₅₀ (ng/ml)	Assayed Variants:	EC ₅₀ (ng/ml)
F6	HuF6WT (untagged):	>212	HuF6WT/FpH	>136	HuF6I7/FpH	2.8
F8	HuF8WT (untagged):	>193	HuF8WT/FpH	>258	HuF8I7/FpH	0.2
F9	HuF9WT (untagged):	>544	HuF9WT/FpH	>332	HuF9S718/FpH HuF9M19/FpH	1.0 1.1

These results demonstrated that the length of the N-terminus is important for biological activity of both agonistic and antagonistic IL-1 family members that signal via IL-1Rrp2.

Example 2B

IL-8 ELISA Assay of IL-1F Variants

A stable cell line expressing human IL-1Rrp2 off an inducible promoter was generated in Jurkat T-REx™ cells (Invitrogen). T-REx™ cell lines stably express the tetracycline repressor protein and, therefore, allow for inducible expression of the gene of interest (IL-1Rrp2) with doxycycline.

In order to access the activity of the IL-1F ligands IL-1Rrp2 expressing Jurkat T-REx™ cells were induced with doxycycline 24 hrs. prior to use. Cells were seeded at 200,000 cells/well in a 96-well round bottom tissue culture plate. The IL-1F ligands (full length (WT) untagged, full length (WT) tagged, truncated tagged or SUMO generated truncated untagged protein) were added to the wells as follows: full length IL-1F6, F8 and F9 were added at 50 µg/mL with an 8 point dilution series at 1:5 dilutions and truncated ligands were started at 2 µg/mL with 1:5 dilutions for 8 points. The cells were incubated with the ligands at 37° C., 5% CO2 for 24 hrs. Following incubation, cells were spun down and the supernatants were collected for analysis using QuantiGlo Human IL-8 ELISA Kit (R&D Systems) per the manufacture's instructions. The results for the tested polypeptides and variants are given as indicated in Table 7 below.

TABLE 7

IL-8 Elisa Assay Results		
SEQ ID Polypeptide	N-terminal polypeptide sequence A box frames the aliphatic amino acid which is indicated as @ of the consensus sequence: @XD where @ may be M or I, and X is one amino acid.	EC ₅₀ (µg/mL)
59 HuIL-1F6 WT	MEKALKIDTPQGS Q DINHRVWVLQDQ	12.94
50 HuIL-1F6 I7/FpH	~~~~~MIDTPQRGS Q DINHRVWVLQDQ	0.060
60 HuIL-1F6K6	~~~~~KIDTPQGS Q DINHRVWVLQDQ	0.000164
61 HuIL-1F8WT	MNPQREAAPKSYA R DSRQMVVWLSGN	10.47
54 HuIL-1F8 E6/FpH	~~~~~MEAAPKSYA R DSRQMVVWLSGN	0.002
62 HuIL-1F8R5	~~~~~REAAPKSYA R DSRQMVVWLSGN	0.000129
63 HuIL-1F9WT	MRGTPGDADGGGRAVYQSMCKPITGT T NDLNQQVWTLQGG	4.072
56 HuIL-1F9 S18/FpH	~~~~~SMCKPITGT T NDLNQQVWTLQGG	0.017
56 HuIL-1F9S18	~~~~~SMCKPITGT T NDLNQQVWTLQGG	0.001

These results demonstrated that the length of the N-terminus is important for biological activity of both agonistic and antagonistic IL-1 family members that signal via IL-1Rrp2 and that the particular N-terminal amino acid is not important. Further, these results demonstrate that polypeptides that do not comprise a C-terminal tag are more active than corresponding polypeptides comprising a C-terminal tag.

EXAMPLE 3

Preparation of Monoclonal Antibodies

IL-1 family member polypeptides may be employed as immunogens in generating monoclonal antibodies by conventional techniques, e.g., techniques described in U.S. Pat. No. 5,599,905, hereby incorporated by reference. It is recognized that polypeptides in various forms may be employed as immunogens, e.g., full length proteins, fragments thereof, fusion proteins thereof such as Fc fusions, cells expressing the recombinant protein on the cell surface, etc. Examples of useful peptides include those shown in FIG. 1.

To summarize an example of such a procedure, an N-terminal peptide of an IL-1Rrp2 requiring IL-1 family member, optionally having an additional C-terminal cysteine residue to facilitate conjugation, is conjugated to maleimide-activated keyhole limpet hemocyanin (KLH; obtainable for example from Pierce Biotechnology Inc., Rockford, Ill.) to yield an immunogen. For a first immunization, 100 micrograms of immunogen (containing 50 micrograms of peptide) is emulsified in complete Freund's adjuvant (CFA) at 1:1 ratio by volume and injected subcutaneously in a final volume of 200 microliters for each mouse.

Immunized animals are boosted three to four more times with additional immunogen to increase the antigen-specific response, at intervals of two to four weeks (although longer intervals may be employed. For example, a second injection of 50 micrograms of immunogen (containing 25 micrograms of peptide) mixed with incomplete Freund's adjuvant in a final volume of 200 µl is injected subcutaneously into each mouse about four weeks after the primary immunization. A

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third injection (20 micrograms of immunogen containing 10 micrograms of peptide mixed with an adjuvant such as Ribi adjuvant) may be given by subcutaneous and/or intraperitoneal route from about 10 to 30 days after the second injection. If desired, a fourth injection (20 micrograms of immunogen containing 10 micrograms of peptide mixed with incomplete Freund's adjuvant) may be given by subcutaneous and/or

65

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intraperitoneal route from about 14 to about 28 days after the third injection. A final injection is given, usually about five days prior to fusion, utilizing 50 micrograms of immunogen containing 25 micrograms of peptide in PBS, by intraperitoneal injection.

Serum samples may be periodically taken by retro-orbital bleeding or tail-tip excision for testing by peptide ELISA (enzyme-linked immunosorbent assay), or another suitable assay, to evaluate antibody titer. At the time of fusion, the animals are sacrificed, splenocytes harvested, and fused to the murine myeloma cell line SP2/O (ATCC CRL 1581). The resulting hybridoma cell lines are plated in multiple microtiter plates in a HAT selective medium (hypoxanthine, aminopterin, and thymidine) to facilitate proliferation of spleen cell-myeloma hybrid cells.

Hybridoma clones thus generated are screened for reactivity with the N-terminal portion of the relevant IL-1 family member. Initial screening of hybridoma supernatants may utilize a peptide ELISA, a whole cell ELISA and/or a cell-based assay suitable for high-throughput screening (fluorometric microvolume assay technology or FMAT, substantially as described by Fiscella, et al., Nature Biotechnology 21:302-307 (2003). Hybridomas that are positive in this screening method may be further cultured to provide larger amounts of antibody, which can then be purified as described below and screened by additional cell-based assay(s) (for example, a reporter assay, or another assay for biological activity of an IL-1 family member).

Selected hybridomas can be further cloned and tested to ensure stable production monoclonal antibody. Hybridomas can be cultured in vitro, or pass aged as ascites fluid in suitable host mammals. The resulting monoclonal antibodies may be purified by ammonium sulfate precipitation followed by gel exclusion chromatography, and/or affinity chromatography based on binding of antibody to Protein G, for example.

EXAMPLE 4

Purification of Hybridoma Antibodies for Screening

Hybridoma cells are cultured for a time and under conditions to yield a sample of about 35 ml of hybridoma superna-

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tant fluid. To each sample is added 12 ml of 4×-Protein A Binding Buffer (1.6 M citric acid, 100 mM tris, pH 9.15) and about 300 µl of a 67% slurry of MabSelect™ Media (GE Healthcare, Piscataway, N.J.). The resulting slurry is rotated gently over night at 4° C.

After overnight incubation, the samples are centrifuged to sediment the resin and the monoclonal antibodies bound thereto, for example at 2,000 RPM in a G3.8 centrifuge rotor (Beckman Coulter, Fullerton, Calif.) for 5 minutes at 4° C. with no brake. All but about 300 µl of the supernatant fluid is removed and the resin is resuspended to form a concentrated slurry.

The concentrated slurry is transferred to a microcentrifuge tube and sufficient 1×-Protein A Binding Buffer (400 mM citric acid, 25 mM tris, pH 8.9) is added to bring the total volume up to about 1 ml. The slurry is resuspended, then centrifuged at about 14,000 g for 5 seconds. The supernatant fluid is removed from the resulting pellet, which is washed a total of three times in a similar manner (i.e. by resuspending in about 1 ml of 1×-Protein A Binding Buffer, centrifuging, removing supernatant and resuspending in fresh buffer).

After three washes, the pellet is resuspended in 400 µl Elution Buffer (200 mM formic acid) and agitated for 10 min at room temperature, then centrifuged at 14,000 g for 5 seconds. The supernatant is carefully removed as eluate, and the pellet is eluted again in a manner similar to that described above for a total of three elution cycles. The eluates from the three elution cycles are combined, centrifuge at 14,000 g for 5 min room temperature and transferred to a fresh tube. The pH is adjusted to 7.8-8.2 by adding 2 M tris base (235 mM_p) and mixing quickly. The samples are again centrifuged at 14,000 g for 5 min at room temperature, and designated as pH Shift Soluble. A spectral scan of each sample (diluted by adding 20 µl of the sample to 700 µl water) is run from 250 to 350 nm, and protein concentration is verified by loading 0.5 µg each antibody-containing sample on a reducing 4-20% SDS-PAGE gel with an appropriate antibody standards.

Each reference cited herein is incorporated by reference in its entirety for all that it teaches and for all purposes.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 78

<210> SEQ ID NO 1

<211> LENGTH: 155

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 1

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

Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His
20 25 30

Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg
35 40 45

Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly
50 55 60

Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu
65 70 75 80

Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys

-continued

	85		90		95										
Ser	Phe	Thr	Phe	Tyr	Arg	Arg	Asp	Met	Gly	Leu	Thr	Ser	Ser	Phe	Glu
	100							105					110		
Ser	Ala	Ala	Tyr	Pro	Gly	Trp	Phe	Leu	Cys	Thr	Val	Pro	Glu	Ala	Asp
	115						120					125			
Gln	Pro	Val	Arg	Leu	Thr	Gln	Leu	Pro	Glu	Asn	Gly	Gly	Trp	Asn	Ala
	130					135					140				
Pro	Ile	Thr	Asp	Phe	Tyr	Phe	Gln	Gln	Cys	Asp					
145					150					155					

<210> SEQ ID NO 2
 <211> LENGTH: 158
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 2

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

<210> SEQ ID NO 3
 <211> LENGTH: 157
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

Met	Asn	Pro	Gln	Arg	Glu	Ala	Ala	Pro	Lys	Ser	Tyr	Ala	Ile	Arg	Asp
1				5					10					15	
Ser	Arg	Gln	Met	Val	Trp	Val	Leu	Ser	Gly	Asn	Ser	Leu	Ile	Ala	Ala
		20					25						30		
Pro	Leu	Ser	Arg	Ser	Ile	Lys	Pro	Val	Thr	Leu	His	Leu	Ile	Ala	Cys
		35				40						45			
Arg	Asp	Thr	Glu	Phe	Ser	Asp	Lys	Glu	Lys	Gly	Asn	Met	Val	Tyr	Leu
	50				55						60				
Gly	Ile	Lys	Gly	Lys	Asp	Leu	Cys	Leu	Phe	Cys	Ala	Glu	Ile	Gln	Gly
65				70					75					80	
Lys	Pro	Thr	Leu	Gln	Leu	Lys	Glu	Lys	Asn	Ile	Met	Asp	Leu	Tyr	Val
			85					90					95		
Glu	Lys	Lys	Ala	Gln	Lys	Pro	Phe	Leu	Phe	Phe	His	Asn	Lys	Glu	Gly
		100					105						110		

-continued

Ser Thr Ser Val Phe Gln Ser Val Ser Tyr Pro Gly Trp Phe Ile Ala
 115 120 125

Thr Ser Thr Thr Ser Gly Gln Pro Ile Phe Leu Thr Lys Glu Arg Gly
 130 135 140

Ile Thr Asn Asn Thr Asn Phe Tyr Leu Asp Ser Val Glu
 145 150 155

<210> SEQ ID NO 4
 <211> LENGTH: 169
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val Tyr
 1 5 10 15

Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln
 20 25 30

Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Ser
 35 40 45

Asp Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro
 50 55 60

Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln
 65 70 75 80

Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr
 85 90 95

Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu
 100 105 110

Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser
 115 120 125

Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys
 130 135 140

Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser Tyr Asn
 145 150 155 160

Thr Ala Phe Glu Leu Asn Ile Asn Asp
 165

<210> SEQ ID NO 5
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: FLAG peptide

<400> SEQUENCE: 5

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> SEQ ID NO 6
 <211> LENGTH: 154
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

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

Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His Ala
 20 25 30

Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg Trp
 35 40 45

-continued

Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly Ser
 50 55 60

Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu Glu
 65 70 75 80

Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys Ser
 85 90 95

Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu Ser
 100 105 110

Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp Gln
 115 120 125

Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala Pro
 130 135 140

Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
 145 150

<210> SEQ ID NO 7
 <211> LENGTH: 165
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (155)..(162)
 <223> OTHER INFORMATION: FLAG peptide tag
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (163)..(165)
 <223> OTHER INFORMATION: polyHis tag

<400> SEQUENCE: 7

Met Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala Leu Lys
 1 5 10 15

Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His Ala
 20 25 30

Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg Trp
 35 40 45

Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly Ser
 50 55 60

Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu Glu
 65 70 75 80

Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys Ser
 85 90 95

Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu Ser
 100 105 110

Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp Gln
 115 120 125

Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala Pro
 130 135 140

Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp Asp Tyr Lys Asp Asp Asp
 145 150 155 160

Asp Lys His His His
 165

<210> SEQ ID NO 8
 <211> LENGTH: 154
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

Met Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala Leu Lys

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

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<210> SEQ ID NO 9
<211> LENGTH: 165
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (155)..(162)
<223> OTHER INFORMATION: FLAG peptide tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (163)..(165)
<223> OTHER INFORMATION: polyHis tag

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<400> SEQUENCE: 9

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

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<210> SEQ ID NO 10

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<211> LENGTH: 153
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

Lys Ile Asp Thr Pro Gln Gln Gly Ser Ile Gln Asp Ile Asn His Arg
1           5           10           15

Val Trp Val Leu Gln Asp Gln Thr Leu Ile Ala Val Pro Arg Lys Asp
          20           25           30

Arg Met Ser Pro Val Thr Ile Ala Leu Ile Ser Cys Arg His Val Glu
          35           40           45

Thr Leu Glu Lys Asp Arg Gly Asn Pro Ile Tyr Leu Gly Leu Asn Gly
          50           55           60

Leu Asn Leu Cys Leu Met Cys Ala Lys Val Gly Asp Gln Pro Thr Leu
65           70           75           80

Gln Leu Lys Glu Lys Asp Ile Met Asp Leu Tyr Asn Gln Pro Glu Pro
          85           90           95

Val Lys Ser Phe Leu Phe Tyr His Ser Gln Ser Gly Arg Asn Ser Thr
          100          105          110

Phe Glu Ser Val Ala Phe Pro Gly Trp Phe Ile Ala Val Ser Ser Glu
          115          120          125

Gly Gly Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Lys Ala Asn Thr
          130          135          140

Thr Asp Phe Gly Leu Thr Met Leu Phe
145           150

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<210> SEQ ID NO 11
<211> LENGTH: 164
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (154)..(161)
<223> OTHER INFORMATION: FLAG peptide tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (162)..(164)
<223> OTHER INFORMATION: polyHis tag

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<400> SEQUENCE: 11

Lys Ile Asp Thr Pro Gln Gln Gly Ser Ile Gln Asp Ile Asn His Arg
1           5           10           15

Val Trp Val Leu Gln Asp Gln Thr Leu Ile Ala Val Pro Arg Lys Asp
          20           25           30

Arg Met Ser Pro Val Thr Ile Ala Leu Ile Ser Cys Arg His Val Glu
          35           40           45

Thr Leu Glu Lys Asp Arg Gly Asn Pro Ile Tyr Leu Gly Leu Asn Gly
          50           55           60

Leu Asn Leu Cys Leu Met Cys Ala Lys Val Gly Asp Gln Pro Thr Leu
65           70           75           80

Gln Leu Lys Glu Lys Asp Ile Met Asp Leu Tyr Asn Gln Pro Glu Pro
          85           90           95

Val Lys Ser Phe Leu Phe Tyr His Ser Gln Ser Gly Arg Asn Ser Thr
          100          105          110

Phe Glu Ser Val Ala Phe Pro Gly Trp Phe Ile Ala Val Ser Ser Glu
          115          120          125

Gly Gly Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Lys Ala Asn Thr
          130          135          140

Thr Asp Phe Gly Leu Thr Met Leu Phe Asp Tyr Lys Asp Asp Asp Asp

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-continued

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145          150          155          160

Lys His His His

<210> SEQ ID NO 12
<211> LENGTH: 153
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

Met Ile Asp Thr Pro Gln Gln Gly Ser Ile Gln Asp Ile Asn His Arg
1           5           10          15

Val Trp Val Leu Gln Asp Gln Thr Leu Ile Ala Val Pro Arg Lys Asp
          20          25          30

Arg Met Ser Pro Val Thr Ile Ala Leu Ile Ser Cys Arg His Val Glu
          35          40          45

Thr Leu Glu Lys Asp Arg Gly Asn Pro Ile Tyr Leu Gly Leu Asn Gly
          50          55          60

Leu Asn Leu Cys Leu Met Cys Ala Lys Val Gly Asp Gln Pro Thr Leu
65          70          75          80

Gln Leu Lys Glu Lys Asp Ile Met Asp Leu Tyr Asn Gln Pro Glu Pro
          85          90          95

Val Lys Ser Phe Leu Phe Tyr His Ser Gln Ser Gly Arg Asn Ser Thr
          100         105         110

Phe Glu Ser Val Ala Phe Pro Gly Trp Phe Ile Ala Val Ser Ser Glu
          115         120         125

Gly Gly Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Lys Ala Asn Thr
          130         135         140

Thr Asp Phe Gly Leu Thr Met Leu Phe
145          150

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<210> SEQ ID NO 13
<211> LENGTH: 164
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (154)..(161)
<223> OTHER INFORMATION: FLAG peptide tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (162)..(164)
<223> OTHER INFORMATION: polyHis tag

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<400> SEQUENCE: 13

Met Ile Asp Thr Pro Gln Gln Gly Ser Ile Gln Asp Ile Asn His Arg
1           5           10          15

Val Trp Val Leu Gln Asp Gln Thr Leu Ile Ala Val Pro Arg Lys Asp
          20          25          30

Arg Met Ser Pro Val Thr Ile Ala Leu Ile Ser Cys Arg His Val Glu
          35          40          45

Thr Leu Glu Lys Asp Arg Gly Asn Pro Ile Tyr Leu Gly Leu Asn Gly
          50          55          60

Leu Asn Leu Cys Leu Met Cys Ala Lys Val Gly Asp Gln Pro Thr Leu
65          70          75          80

Gln Leu Lys Glu Lys Asp Ile Met Asp Leu Tyr Asn Gln Pro Glu Pro
          85          90          95

Val Lys Ser Phe Leu Phe Tyr His Ser Gln Ser Gly Arg Asn Ser Thr
          100         105         110

Phe Glu Ser Val Ala Phe Pro Gly Trp Phe Ile Ala Val Ser Ser Glu

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-continued

115	120	125
Gly Gly Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Lys Ala Asn Thr		
130	135	140
Thr Asp Phe Gly Leu Thr Met Leu Phe Asp Tyr Lys Asp Asp Asp Asp		
145	150	155 160
Lys His His His		

<210> SEQ ID NO 14
 <211> LENGTH: 153
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 14

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

<210> SEQ ID NO 15
 <211> LENGTH: 164
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (154)..(161)
 <223> OTHER INFORMATION: FLAG peptide tag
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (162)..(164)
 <223> OTHER INFORMATION: polyHis tag

<400> SEQUENCE: 15

Arg Glu Ala Ala Pro Lys Ser Tyr Ala Ile Arg Asp Ser Arg Gln Met	
1 5 10 15	
Val Trp Val Leu Ser Gly Asn Ser Leu Ile Ala Ala Pro Leu Ser Arg	
20 25 30	
Ser Ile Lys Pro Val Thr Leu His Leu Ile Ala Cys Arg Asp Thr Glu	
35 40 45	
Phe Ser Asp Lys Glu Lys Gly Asn Met Val Tyr Leu Gly Ile Lys Gly	
50 55 60	
Lys Asp Leu Cys Leu Phe Cys Ala Glu Ile Gln Gly Lys Pro Thr Leu	
65 70 75 80	
Gln Leu Lys Glu Lys Asn Ile Met Asp Leu Tyr Val Glu Lys Lys Ala	

-continued

	85		90		95
Gln Lys Pro Phe Leu Phe Phe His Asn Lys Glu Gly Ser Thr Ser Val					
	100		105		110
Phe Gln Ser Val Ser Tyr Pro Gly Trp Phe Ile Ala Thr Ser Thr Thr					
	115		120		125
Ser Gly Gln Pro Ile Phe Leu Thr Lys Glu Arg Gly Ile Thr Asn Asn					
	130		135		140
Thr Asn Phe Tyr Leu Asp Ser Val Glu Asp Tyr Lys Asp Asp Asp Asp					
145	150		155		160

Lys His His His

<210> SEQ ID NO 16
 <211> LENGTH: 153
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16

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

<210> SEQ ID NO 17
 <211> LENGTH: 164
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (154)..(161)
 <223> OTHER INFORMATION: FLAG peptide tag
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (162)..(164)
 <223> OTHER INFORMATION: polyHis tag

<400> SEQUENCE: 17

Met Glu Ala Ala Pro Lys Ser Tyr Ala Ile Arg Asp Ser Arg Gln Met					
1	5		10		15
Val Trp Val Leu Ser Gly Asn Ser Leu Ile Ala Ala Pro Leu Ser Arg					
	20		25		30
Ser Ile Lys Pro Val Thr Leu His Leu Ile Ala Cys Arg Asp Thr Glu					
	35		40		45
Phe Ser Asp Lys Glu Lys Gly Asn Met Val Tyr Leu Gly Ile Lys Gly					

-continued

50	55	60
Lys Asp Leu Cys Leu Phe Cys Ala Glu Ile Gln Gly Lys Pro Thr Leu		
65	70	75
Gln Leu Lys Glu Lys Asn Ile Met Asp Leu Tyr Val Glu Lys Lys Ala		
	85	90
Gln Lys Pro Phe Leu Phe Phe His Asn Lys Glu Gly Ser Thr Ser Val		
	100	105
Phe Gln Ser Val Ser Tyr Pro Gly Trp Phe Ile Ala Thr Ser Thr Thr		
	115	120
Ser Gly Gln Pro Ile Phe Leu Thr Lys Glu Arg Gly Ile Thr Asn Asn		
	130	135
Thr Asn Phe Tyr Leu Asp Ser Val Glu Asp Tyr Lys Asp Asp Asp Asp		
	145	150
		155
		160

Lys His His His

<210> SEQ ID NO 18
 <211> LENGTH: 152
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 18

Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln Gln		
1	5	10
Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Ser Asp		
	20	25
Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro Glu		
	35	40
Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln Asn		
	50	55
Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr Leu		
	65	70
Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu Pro		
	85	90
Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser Thr		
	100	105
Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys Arg		
	115	120
Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser Tyr Asn Thr		
	130	135
		140
Ala Phe Glu Leu Asn Ile Asn Asp		
	145	150

<210> SEQ ID NO 19
 <211> LENGTH: 163
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (153)..(160)
 <223> OTHER INFORMATION: FLAG peptide tag
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (161)..(163)
 <223> OTHER INFORMATION: polyHis tag
 <400> SEQUENCE: 19

Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln Gln		
1	5	10
Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Ser Asp		

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

<210> SEQ ID NO 20
 <211> LENGTH: 152
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

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

<210> SEQ ID NO 21
 <211> LENGTH: 163
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (153)..(160)
 <223> OTHER INFORMATION: FLAG peptide tag
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (161)..(163)
 <223> OTHER INFORMATION: polyHis tag

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<400> SEQUENCE: 21

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

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<210> SEQ ID NO 22

<211> LENGTH: 172

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (159)..(166)

<223> OTHER INFORMATION: FLAG peptide tag

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (167)..(172)

<223> OTHER INFORMATION: polyHis tag

<400> SEQUENCE: 22

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

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-continued

Lys Asp Asp Asp Asp Lys His His His His His His
165 170

<210> SEQ ID NO 23
 <211> LENGTH: 168
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (155)..(162)
 <223> OTHER INFORMATION: FLAG peptide tag
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (163)..(168)
 <223> OTHER INFORMATION: polyHis tag

<400> SEQUENCE: 23

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

<210> SEQ ID NO 24
 <211> LENGTH: 167
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (154)..(161)
 <223> OTHER INFORMATION: FLAG peptide tag
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (162)..(167)
 <223> OTHER INFORMATION: polyHis tag

<400> SEQUENCE: 24

Met Ile Asp Thr Pro Gln Gln Gly Ser Ile Gln Asp Ile Asn His Arg
1 5 10 15
 Val Trp Val Leu Gln Asp Gln Thr Leu Ile Ala Val Pro Arg Lys Asp
20 25 30
 Arg Met Ser Pro Val Thr Ile Ala Leu Ile Ser Cys Arg His Val Glu
35 40 45
 Thr Leu Glu Lys Asp Arg Gly Asn Pro Ile Tyr Leu Gly Leu Asn Gly
50 55 60

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Leu Asn Leu Cys Leu Met Cys Ala Lys Val Gly Asp Gln Pro Thr Leu
65          70          75          80

Gln Leu Lys Glu Lys Asp Ile Met Asp Leu Tyr Asn Gln Pro Glu Pro
      85          90          95

Val Lys Ser Phe Leu Phe Tyr His Ser Gln Ser Gly Arg Asn Ser Thr
      100        105        110

Phe Glu Ser Val Ala Phe Pro Gly Trp Phe Ile Ala Val Ser Ser Glu
      115        120        125

Gly Gly Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Lys Ala Asn Thr
      130        135        140

Thr Asp Phe Gly Leu Thr Met Leu Phe Asp Tyr Lys Asp Asp Asp Asp
145          150          155          160

Lys His His His His His His
      165

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<210> SEQ ID NO 25
<211> LENGTH: 166
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (153)..(160)
<223> OTHER INFORMATION: FLAG peptide tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (161)..(166)
<223> OTHER INFORMATION: polyHis tag

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<400> SEQUENCE: 25

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Met Asp Thr Pro Gln Gln Gly Ser Ile Gln Asp Ile Asn His Arg Val
1          5          10          15

Trp Val Leu Gln Asp Gln Thr Leu Ile Ala Val Pro Arg Lys Asp Arg
      20          25          30

Met Ser Pro Val Thr Ile Ala Leu Ile Ser Cys Arg His Val Glu Thr
      35          40          45

Leu Glu Lys Asp Arg Gly Asn Pro Ile Tyr Leu Gly Leu Asn Gly Leu
      50          55          60

Asn Leu Cys Leu Met Cys Ala Lys Val Gly Asp Gln Pro Thr Leu Gln
65          70          75          80

Leu Lys Glu Lys Asp Ile Met Asp Leu Tyr Asn Gln Pro Glu Pro Val
      85          90          95

Lys Ser Phe Leu Phe Tyr His Ser Gln Ser Gly Arg Asn Ser Thr Phe
      100        105        110

Glu Ser Val Ala Phe Pro Gly Trp Phe Ile Ala Val Ser Ser Glu Gly
      115        120        125

Gly Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Lys Ala Asn Thr Thr
      130        135        140

Asp Phe Gly Leu Thr Met Leu Phe Asp Tyr Lys Asp Asp Asp Asp Lys
145          150          155          160

His His His His His His
      165

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<210> SEQ ID NO 26
<211> LENGTH: 153
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 26

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Lys Ile Asp Thr Pro Gln Gln Gly Ser Ile Gln Asp Ile Asn His Arg
1          5          10          15

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Val Trp Val Leu Gln Asp Gln Thr Leu Ile Ala Val Pro Arg Lys Asp
 20 25 30

Arg Met Ser Pro Val Thr Ile Ala Leu Ile Ser Cys Arg His Val Glu
 35 40 45

Thr Leu Glu Lys Asp Arg Gly Asn Pro Ile Tyr Leu Gly Leu Asn Gly
 50 55 60

Leu Asn Leu Cys Leu Met Cys Ala Lys Val Gly Asp Gln Pro Thr Leu
 65 70 75 80

Gln Leu Lys Glu Lys Asp Ile Met Asp Leu Tyr Asn Gln Pro Glu Pro
 85 90 95

Val Lys Ser Phe Leu Phe Tyr His Ser Gln Ser Gly Arg Asn Ser Thr
 100 105 110

Phe Glu Ser Val Ala Phe Pro Gly Trp Phe Ile Ala Val Ser Ser Glu
 115 120 125

Gly Gly Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Lys Ala Asn Thr
 130 135 140

Thr Asp Phe Gly Leu Thr Met Leu Phe
 145 150

<210> SEQ ID NO 27
 <211> LENGTH: 171
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (158)..(165)
 <223> OTHER INFORMATION: FLAG peptide tag
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (166)..(171)
 <223> OTHER INFORMATION: polyHis tag

<400> SEQUENCE: 27

Met Asn Pro Gln Arg Glu Ala Ala Pro Lys Ser Tyr Ala Ile Arg Asp
 1 5 10 15

Ser Arg Gln Met Val Trp Val Leu Ser Gly Asn Ser Leu Ile Ala Ala
 20 25 30

Pro Leu Ser Arg Ser Ile Lys Pro Val Thr Leu His Leu Ile Ala Cys
 35 40 45

Arg Asp Thr Glu Phe Ser Asp Lys Glu Lys Gly Asn Met Val Tyr Leu
 50 55 60

Gly Ile Lys Gly Lys Asp Leu Cys Leu Phe Cys Ala Glu Ile Gln Gly
 65 70 75 80

Lys Pro Thr Leu Gln Leu Lys Glu Lys Asn Ile Met Asp Leu Tyr Val
 85 90 95

Glu Lys Lys Ala Gln Lys Pro Phe Leu Phe Phe His Asn Lys Glu Gly
 100 105 110

Ser Thr Ser Val Phe Gln Ser Val Ser Tyr Pro Gly Trp Phe Ile Ala
 115 120 125

Thr Ser Thr Thr Ser Gly Gln Pro Ile Phe Leu Thr Lys Glu Arg Gly
 130 135 140

Ile Thr Asn Asn Thr Asn Phe Tyr Leu Asp Ser Val Glu Asp Tyr Lys
 145 150 155 160

Asp Asp Asp Asp Lys His His His His His His
 165 170

<210> SEQ ID NO 28
 <211> LENGTH: 169

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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (156)..(163)
<223> OTHER INFORMATION: FLAG peptide tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (164)..(169)
<223> OTHER INFORMATION: polyHis tag

<400> SEQUENCE: 28

Met  Gln  Arg  Glu  Ala  Ala  Pro  Lys  Ser  Tyr  Ala  Ile  Arg  Asp  Ser  Arg
 1          5          10          15

Gln  Met  Val  Trp  Val  Leu  Ser  Gly  Asn  Ser  Leu  Ile  Ala  Ala  Pro  Leu
 20          25          30

Ser  Arg  Ser  Ile  Lys  Pro  Val  Thr  Leu  His  Leu  Ile  Ala  Cys  Arg  Asp
 35          40          45

Thr  Glu  Phe  Ser  Asp  Lys  Glu  Lys  Gly  Asn  Met  Val  Tyr  Leu  Gly  Ile
 50          55          60

Lys  Gly  Lys  Asp  Leu  Cys  Leu  Phe  Cys  Ala  Glu  Ile  Gln  Gly  Lys  Pro
 65          70          75          80

Thr  Leu  Gln  Leu  Lys  Glu  Lys  Asn  Ile  Met  Asp  Leu  Tyr  Val  Glu  Lys
 85          90          95

Lys  Ala  Gln  Lys  Pro  Phe  Leu  Phe  Phe  His  Asn  Lys  Glu  Gly  Ser  Thr
100          105          110

Ser  Val  Phe  Gln  Ser  Val  Ser  Tyr  Pro  Gly  Trp  Phe  Ile  Ala  Thr  Ser
115          120          125

Thr  Thr  Ser  Gly  Gln  Pro  Ile  Phe  Leu  Thr  Lys  Glu  Arg  Gly  Ile  Thr
130          135          140

Asn  Asn  Thr  Asn  Phe  Tyr  Leu  Asp  Ser  Val  Glu  Asp  Tyr  Lys  Asp  Asp
145          150          155          160

Asp  Asp  Lys  His  His  His  His  His  His
165

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<210> SEQ ID NO 29
<211> LENGTH: 168
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (155)..(162)
<223> OTHER INFORMATION: FLAG peptide tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (163)..(168)
<223> OTHER INFORMATION: polyHis tag

<400> SEQUENCE: 29

Met  Arg  Glu  Ala  Ala  Pro  Lys  Ser  Tyr  Ala  Ile  Arg  Asp  Ser  Arg  Gln
 1          5          10          15

Met  Val  Trp  Val  Leu  Ser  Gly  Asn  Ser  Leu  Ile  Ala  Ala  Pro  Leu  Ser
 20          25          30

Arg  Ser  Ile  Lys  Pro  Val  Thr  Leu  His  Leu  Ile  Ala  Cys  Arg  Asp  Thr
 35          40          45

Glu  Phe  Ser  Asp  Lys  Glu  Lys  Gly  Asn  Met  Val  Tyr  Leu  Gly  Ile  Lys
 50          55          60

Gly  Lys  Asp  Leu  Cys  Leu  Phe  Cys  Ala  Glu  Ile  Gln  Gly  Lys  Pro  Thr
 65          70          75          80

Leu  Gln  Leu  Lys  Glu  Lys  Asn  Ile  Met  Asp  Leu  Tyr  Val  Glu  Lys  Lys
 85          90          95

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Ala Gln Lys Pro Phe Leu Phe Phe His Asn Lys Glu Gly Ser Thr Ser
      100                      105              110

Val Phe Gln Ser Val Ser Tyr Pro Gly Trp Phe Ile Ala Thr Ser Thr
      115                      120              125

Thr Ser Gly Gln Pro Ile Phe Leu Thr Lys Glu Arg Gly Ile Thr Asn
      130                      135              140

Asn Thr Asn Phe Tyr Leu Asp Ser Val Glu Asp Tyr Lys Asp Asp Asp
145                      150              155              160

Asp Lys His His His His His His
      165

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<210> SEQ ID NO 30
<211> LENGTH: 167
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (154)..(161)
<223> OTHER INFORMATION: FLAG peptide tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (162)..(167)
<223> OTHER INFORMATION: polyHis tag

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<400> SEQUENCE: 30

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Met Glu Ala Ala Pro Lys Ser Tyr Ala Ile Arg Asp Ser Arg Gln Met
 1          5          10          15

Val Trp Val Leu Ser Gly Asn Ser Leu Ile Ala Ala Pro Leu Ser Arg
 20         25         30

Ser Ile Lys Pro Val Thr Leu His Leu Ile Ala Cys Arg Asp Thr Glu
 35         40         45

Phe Ser Asp Lys Glu Lys Gly Asn Met Val Tyr Leu Gly Ile Lys Gly
 50         55         60

Lys Asp Leu Cys Leu Phe Cys Ala Glu Ile Gln Gly Lys Pro Thr Leu
 65         70         75         80

Gln Leu Lys Glu Lys Asn Ile Met Asp Leu Tyr Val Glu Lys Lys Ala
 85         90         95

Gln Lys Pro Phe Leu Phe Phe His Asn Lys Glu Gly Ser Thr Ser Val
100         105        110

Phe Gln Ser Val Ser Tyr Pro Gly Trp Phe Ile Ala Thr Ser Thr Thr
115         120        125

Ser Gly Gln Pro Ile Phe Leu Thr Lys Glu Arg Gly Ile Thr Asn Asn
130         135        140

Thr Asn Phe Tyr Leu Asp Ser Val Glu Asp Tyr Lys Asp Asp Asp Asp
145         150        155        160

Lys His His His His His His
      165

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<210> SEQ ID NO 31
<211> LENGTH: 165
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (152)..(159)
<223> OTHER INFORMATION: FLAG peptide tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (160)..(165)
<223> OTHER INFORMATION: polyHis tag

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<400> SEQUENCE: 31

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

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<210> SEQ ID NO 32
<211> LENGTH: 153
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 32

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

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<210> SEQ ID NO 33
<211> LENGTH: 183
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (170)..(177)
<223> OTHER INFORMATION: FLAG peptide tag

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<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (178)..(183)
<223> OTHER INFORMATION: polyHis tag

<400> SEQUENCE: 33
Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val Tyr
1          5          10          15
Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln
20          25          30
Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Ser
35          40          45
Asp Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro
50          55          60
Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln
65          70          75          80
Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr
85          90          95
Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu
100         105         110
Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser
115         120         125
Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys
130         135         140
Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser Tyr Asn
145         150         155         160
Thr Ala Phe Glu Leu Asn Ile Asn Asp Asp Tyr Lys Asp Asp Asp Asp
165         170         175
Lys His His His His His His
180

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<210> SEQ ID NO 34
<211> LENGTH: 166
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (153)..(160)
<223> OTHER INFORMATION: FLAG peptide tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (161)..(166)
<223> OTHER INFORMATION: polyHis tag

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<400> SEQUENCE: 34
Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln Gln
1          5          10          15
Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Ser Asp
20          25          30
Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro Glu
35          40          45
Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln Asn
50          55          60
Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr Leu
65          70          75          80
Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu Pro
85          90          95
Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser Thr
100         105         110

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-continued

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Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys Arg
    115                      120                      125

Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser Tyr Asn Thr
    130                      135                      140

Ala Phe Glu Leu Asn Ile Asn Asp Asp Tyr Lys Asp Asp Asp Asp Lys
    145                      150                      155                      160

His His His His His His
                165

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<210> SEQ ID NO 35
<211> LENGTH: 166
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (153)..(160)
<223> OTHER INFORMATION: FLAG peptide tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (161)..(166)
<223> OTHER INFORMATION: polyHis tag

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<400> SEQUENCE: 35

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```

Met Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln Gln
 1          5          10          15

Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Ser Asp
 20          25          30

Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro Glu
 35          40          45

Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln Asn
 50          55          60

Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr Leu
 65          70          75          80

Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu Pro
 85          90          95

Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser Thr
100          105          110

Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys Arg
115          120          125

Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser Tyr Asn Thr
130          135          140

Ala Phe Glu Leu Asn Ile Asn Asp Asp Tyr Lys Asp Asp Asp Asp Lys
145          150          155          160

His His His His His His
                165

```

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<210> SEQ ID NO 36
<211> LENGTH: 164
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (151)..(158)
<223> OTHER INFORMATION: FLAG peptide tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (159)..(164)
<223> OTHER INFORMATION: polyHis tag

```

```

<400> SEQUENCE: 36

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```

Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln Gln Val Trp
 1          5          10          15

```

-continued

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

<210> SEQ ID NO 37
 <211> LENGTH: 152
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 37

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

<210> SEQ ID NO 38
 <211> LENGTH: 169
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (156)..(163)
 <223> OTHER INFORMATION: FLAG peptide tag
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (164)..(169)
 <223> OTHER INFORMATION: polyHis tag

-continued

<400> SEQUENCE: 38

```

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

Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His
      20             25             30

Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg
      35             40             45

Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly
 50             55             60

Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu
65             70             75             80

Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys
      85             90             95

Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu
      100            105            110

Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp
      115            120            125

Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala
      130            135            140

Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp Asp Tyr Lys Asp Asp
145            150            155            160

Asp Asp Lys His His His His His His
      165

```

<210> SEQ ID NO 39

<211> LENGTH: 168

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (155)..(162)

<223> OTHER INFORMATION: FLAG peptide tag

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<222> LOCATION: (163)..(168)

<223> OTHER INFORMATION: polyHis tag

<400> SEQUENCE: 39

```

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

Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His Ala
      20             25             30

Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg Trp
      35             40             45

Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly Ser
 50             55             60

Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu Glu
65             70             75             80

Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys Ser
      85             90             95

Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu Ser
      100            105            110

Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp Gln
      115            120            125

Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala Pro
      130            135            140

Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp Asp Tyr Lys Asp Asp Asp

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-continued

145 150 155 160

Asp Lys His His His His His His
165

<210> SEQ ID NO 40
 <211> LENGTH: 168
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (155)..(162)
 <223> OTHER INFORMATION: FLAG peptide tag
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (163)..(168)
 <223> OTHER INFORMATION: polyHis tag

<400> SEQUENCE: 40

Met Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala Leu Lys
1 5 10 15

Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His Ala
20 25 30

Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg Trp
35 40 45

Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly Ser
50 55 60

Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu Glu
65 70 75 80

Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys Ser
85 90 95

Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu Ser
100 105 110

Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp Gln
115 120 125

Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala Pro
130 135 140

Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp Asp Tyr Lys Asp Asp Asp
145 150 155 160

Asp Lys His His His His His His
165

<210> SEQ ID NO 41
 <211> LENGTH: 166
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (153)..(160)
 <223> OTHER INFORMATION: FLAG peptide tag
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (161)..(166)
 <223> OTHER INFORMATION: polyHis tag

<400> SEQUENCE: 41

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

Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His Ala Gly Lys
20 25 30

Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg Trp Leu Asp
35 40 45

Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly Ser Gln Cys

-continued

50	55	60
Leu Ser Cys Gly Val	Gly Gln Glu Pro Thr	Leu Thr Leu Glu Pro Val
65	70	75 80
Asn Ile Met Glu Leu	Tyr Leu Gly Ala Lys	Glu Ser Lys Ser Phe Thr
	85	90 95
Phe Tyr Arg Arg Asp	Met Gly Leu Thr Ser	Ser Phe Glu Ser Ala Ala
	100	105 110
Tyr Pro Gly Trp Phe	Leu Cys Thr Val Pro	Glu Ala Asp Gln Pro Val
	115	120 125
Arg Leu Thr Gln Leu	Pro Glu Asn Gly Gly	Trp Asn Ala Pro Ile Thr
	130	135 140
Asp Phe Tyr Phe Gln	Gln Cys Asp Asp Tyr	Lys Asp Asp Asp Asp Lys
	145	150 155 160
His His His His His	His	
	165	

<210> SEQ ID NO 42
 <211> LENGTH: 165
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (152)..(159)
 <223> OTHER INFORMATION: FLAG peptide tag
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (160)..(165)
 <223> OTHER INFORMATION: polyHis tag

<400> SEQUENCE: 42

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

<210> SEQ ID NO 43
 <211> LENGTH: 154
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 43

-continued

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

Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His Ala
 20 25 30

Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg Trp
 35 40 45

Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly Ser
 50 55 60

Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu Glu
 65 70 75 80

Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys Ser
 85 90 95

Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu Ser
 100 105 110

Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp Gln
 115 120 125

Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala Pro
 130 135 140

Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
 145 150

<210> SEQ ID NO 44
 <211> LENGTH: 24
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 44

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

Lys Val Leu Tyr Leu His Asn Asn
 20

<210> SEQ ID NO 45
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 45

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

Val Leu Tyr Leu His Asn Asn
 20

<210> SEQ ID NO 46
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 46

Met Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala Leu Lys
 1 5 10 15

Val Leu Tyr Leu His Asn Asn
 20

<210> SEQ ID NO 47
 <211> LENGTH: 21
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 47

-continued

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

Tyr Leu His Asn Asn
20

<210> SEQ ID NO 48
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 48

Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala Leu Lys Val Leu Tyr
1 5 10 15

Leu His Asn Asn
20

<210> SEQ ID NO 49
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 49

Met Lys Ile Asp Thr Pro Gln Arg Gly Ser Ile Gln Asp Ile Asn His
1 5 10 15

Arg Val Trp Val Leu Gln Asp Gln
20

<210> SEQ ID NO 50
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 50

Met Ile Asp Thr Pro Gln Arg Gly Ser Ile Gln Asp Ile Asn His Arg
1 5 10 15

Val Trp Val Leu Gln Asp Gln
20

<210> SEQ ID NO 51
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 51

Met Asp Thr Pro Gln Arg Gly Ser Ile Gln Asp Ile Asn His Arg Val
1 5 10 15

Trp Val Leu Gln Asp Gln
20

<210> SEQ ID NO 52
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 52

Met Gln Arg Glu Ala Ala Pro Lys Ser Tyr Ala Ile Arg Asp Ser Arg
1 5 10 15

Gln Met Val Trp Val Leu Ser Gly Asn
20 25

<210> SEQ ID NO 53
<211> LENGTH: 24
<212> TYPE: PRT

-continued

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 53

Met Arg Glu Ala Ala Pro Lys Ser Tyr Ala Ile Arg Asp Ser Arg Gln
1 5 10 15

Met Val Trp Val Leu Ser Gly Asn
20

<210> SEQ ID NO 54

<211> LENGTH: 23

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 54

Met Glu Ala Ala Pro Lys Ser Tyr Ala Ile Arg Asp Ser Arg Gln Met
1 5 10 15

Val Trp Val Leu Ser Gly Asn
20

<210> SEQ ID NO 55

<211> LENGTH: 21

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 55

Ala Ala Pro Lys Ser Tyr Ala Ile Arg Asp Ser Arg Gln Met Val Trp
1 5 10 15

Val Leu Ser Gly Asn
20

<210> SEQ ID NO 56

<211> LENGTH: 23

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 56

Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln Gln
1 5 10 15

Val Trp Thr Leu Gln Gly Gln
20

<210> SEQ ID NO 57

<211> LENGTH: 23

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 57

Met Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln Gln
1 5 10 15

Val Trp Thr Leu Gln Gly Gln
20

<210> SEQ ID NO 58

<211> LENGTH: 21

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 58

Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln Gln Val Trp
1 5 10 15

Thr Leu Gln Gly Gln
20

-continued

<210> SEQ ID NO 59
 <211> LENGTH: 28
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 59

Met Glu Lys Ala Leu Lys Ile Asp Thr Pro Gln Gln Gly Ser Ile Gln
 1 5 10 15
 Asp Ile Asn His Arg Val Trp Val Leu Gln Asp Gln
 20 25

<210> SEQ ID NO 60
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 60

Lys Ile Asp Thr Pro Gln Gln Gly Ser Ile Gln Asp Ile Asn His Arg
 1 5 10 15
 Val Trp Val Leu Gln Asp Gln
 20

<210> SEQ ID NO 61
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 61

Met Asn Pro Gln Arg Glu Ala Ala Pro Lys Ser Tyr Ala Ile Arg Asp
 1 5 10 15
 Ser Arg Gln Met Val Trp Val Leu Ser Gly Asn
 20 25

<210> SEQ ID NO 62
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 62

Arg Glu Ala Ala Pro Lys Ser Tyr Ala Ile Arg Asp Ser Arg Gln Met
 1 5 10 15
 Val Trp Val Leu Ser Gly Asn
 20

<210> SEQ ID NO 63
 <211> LENGTH: 40
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 63

Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val Tyr
 1 5 10 15
 Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln
 20 25 30
 Gln Val Trp Thr Leu Gln Gly Gln
 35 40

<210> SEQ ID NO 64

<400> SEQUENCE: 64

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<210> SEQ ID NO 65
 <211> LENGTH: 153
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 65

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

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<210> SEQ ID NO 66
 <211> LENGTH: 164
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (154)..(161)
 <223> OTHER INFORMATION: FLAG peptide tag
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (162)..(164)
 <223> OTHER INFORMATION: polyHis tag

<400> SEQUENCE: 66

```

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

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-continued

Thr Asp Phe Gly Leu Thr Met Leu Phe Asp Tyr Lys Asp Asp Asp Asp
 145 150 155 160

Lys His His His

<210> SEQ ID NO 67
 <211> LENGTH: 153
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 67

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

<210> SEQ ID NO 68
 <211> LENGTH: 164
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (154)..(161)
 <223> OTHER INFORMATION: FLAG peptide tag
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (162)..(164)
 <223> OTHER INFORMATION: polyHis tag

<400> SEQUENCE: 68

Met Ile Asp Thr Pro Gln Arg Gly Ser Ile Gln Asp Ile Asn His Arg
 1 5 10 15
 Val Trp Val Leu Gln Asp Gln Thr Leu Ile Ala Val Pro Arg Lys Asp
 20 25 30
 Arg Met Ser Pro Val Thr Ile Ala Leu Ile Ser Cys Arg His Val Glu
 35 40 45
 Thr Leu Glu Lys Asp Arg Gly Asn Pro Ile Tyr Leu Gly Leu Asn Gly
 50 55 60
 Leu Asn Leu Cys Leu Met Cys Ala Lys Val Gly Asp Gln Pro Thr Leu
 65 70 75 80
 Gln Leu Lys Glu Lys Asp Ile Met Asp Leu Tyr Asn Gln Pro Glu Pro
 85 90 95
 Val Lys Ser Phe Leu Phe Tyr His Ser Gln Ser Gly Arg Asn Ser Thr
 100 105 110

-continued

Phe Glu Ser Val Ala Phe Pro Gly Trp Phe Ile Ala Val Ser Ser Glu
115 120 125

Gly Gly Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Lys Ala Asn Thr
130 135 140

Thr Asp Phe Gly Leu Thr Met Leu Phe Asp Tyr Lys Asp Asp Asp Asp
145 150 155 160

Lys His His His

<210> SEQ ID NO 69

<211> LENGTH: 465

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 69

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gtcctgagtg gggcgctgtg cttccgaatg aaggactcgg cattgaaggt gctttatctg    60
cataataacc agcttctagc tggagggctg catgcaggga aggtcattaa aggtgaagag    120
atcagcgtgg tccccaatcg gtggctggat gccagcctgt ccccgctcat cctgggtgtc    180
caggggtggaa gccagtgcct gtcattgtgg gtggggcagg agccgactct aacactagag    240
ccagtgaaca tcatggagct ctatcttggt gccaaaggaat ccaagagctt caccttctac    300
cggcgggaca tggggctcac ctccagcttc gagtcggctg cctaccggg ctggttctctg    360
tgacgggtgc ctgaagccga tcagcctgtc agactcacc agcttcccg gaatggtggc    420
tggaatgcc ccatcacaga cttctacttc cagcagtgtg actaa                      465
```

<210> SEQ ID NO 70

<211> LENGTH: 531

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 70

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atgctgagtg gggcgctgtg cttccgaatg aaggactcgg cattgaaggt gctttatctg    60
cataataacc agcttctagc tggagggctg catgcaggga aggtcattaa aggtgaagag    120
atcagcgtgg tccccaatcg gtggctggat gccagcctgt ccccgctcat cctgggtgtc    180
caggggtggaa gccagtgcct gtcattgtgg gtggggcagg agccgactct aacactagag    240
ccagtgaaca tcatggagct ctatcttggt gccaaaggaat ccaagagctt caccttctac    300
cggcgggaca tggggctcac ctccagcttc gagtcggctg cctaccggg ctggttctctg    360
tgacgggtgc ctgaagccga tcagcctgtc agactcacc agcttcccg gaatggtggc    420
tggaatgcc ccatcacaga cttctacttc cagcagtgtg acagatctgg cagttctgac    480
tacaaggacg acgacgacaa gggcagttct caccatcacc atcaccacta g                      531
```

<210> SEQ ID NO 71

<211> LENGTH: 462

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 71

```
aaaattgaca cacctcagcg ggggagcatt caggatatca atcatcgggt gtgggttctt    60
caggaccaga cgctcatagc agtcccagg aaggaccgta tgtctccagt cactattgcc    120
ttaatctcat gccgacatgt ggagaccctt gagaaagaca gaggggaacc catctacctg    180
ggcctgaatg gactcaatct ctgcctgatg tgtgctaaag tcggggacca gccacactg    240
cagctgaagg aaaaggatat aatggatttg tacaaccaac ccgagcctgt gaagtccttt    300
```

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ctcttctacc acagccagag tggcaggaac tccaccttcg agtctgtggc ttccctggc	360
tggttcacgc ctgtcagctc tgaaggaggc tgtcctctca tccttaccca agaactgggg	420
aaagccaaca ctactgactt tgggttaact atgctgtttt aa	462

<210> SEQ ID NO 72
 <211> LENGTH: 528
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 72

atgattgaca cacctcagcg ggggagcatt caggatatca atcatcgggt gtgggttctt	60
caggaccaga cgctcatagc agtcccagg aaggaccgta tgtctccagt cactattgcc	120
ttaatctcat gccgacatgt ggagaccctt gagaaagaca gagggaaccc catctacctg	180
ggcctgaatg gactcaatct ctgcctgatg tgtgctaaag tcggggacca gccacactg	240
cagctgaagg aaaaggatat aatggatttg tacaaccaac ccgagcctgt gaagtccttt	300
ctcttctacc acagccagag tggcaggaac tccaccttcg agtctgtggc ttccctggc	360
tggttcacgc ctgtcagctc tgaaggaggc tgtcctctca tccttaccca agaactgggg	420
aaagccaaca ctactgactt tgggttaact atgctgttta gatctggcag ttctgactac	480
aaggacgacg acgacaaggg cagttctcac catcaccatc accactag	528

<210> SEQ ID NO 73
 <211> LENGTH: 462
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 73

cgcgaggcag cacccaaate ctatgctatt cgtgattctc gacagatggg gtgggtcctg	60
agtggaaatt ctttaaatagc agctcctctt agccgcagca ttaagcctgt cactcttcat	120
ttaatagcct gtagagacac agaattcagt gacaaggaaa agggtaatat ggtttacctg	180
ggaatcaagg gaaaagatct ctgtctcttc tgtgcagaaa ttcagggcaa gcctactttg	240
cagcttaagg aaaaaaatat catggacctg tatgtggaga agaaagcaca gaagcccttt	300
ctctttttcc acaataaaga aggctccact tctgtctttc agtcagtctc ttaccctggc	360
tggttcacag ccacctccac cacatcagga cagcccatct ttctcaccaa ggagagaggc	420
ataactaata acactaactt ctacttagat tctgtggaat aa	462

<210> SEQ ID NO 74
 <211> LENGTH: 528
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 74

atggaggcag cacccaaate ctatgctatt cgtgattctc gacagatggg gtgggtcctg	60
agtggaaatt ctttaaatagc agctcctctt agccgcagca ttaagcctgt cactcttcat	120
ttaatagcct gtagagacac agaattcagt gacaaggaaa agggtaatat ggtttacctg	180
ggaatcaagg gaaaagatct ctgtctcttc tgtgcagaaa ttcagggcaa gcctactttg	240
cagcttaagg aaaaaaatat catggacctg tatgtggaga agaaagcaca gaagcccttt	300
ctctttttcc acaataaaga aggctccact tctgtctttc agtcagtctc ttaccctggc	360
tggttcacag ccacctccac cacatcagga cagcccatct ttctcaccaa ggagagaggc	420
ataactaata acactaactt ctacttagat tctgtggaag gatctggcag ttctgactac	480

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aaggacgacg acgacaaggg cagttctcac catcaccatc accactag 528

<210> SEQ ID NO 75
 <211> LENGTH: 459
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 75

tcaatgtgta aacctattac tgggactatt aatgatttga atcagcaagt gtggaccctt	60
cagggtcaga accttgtggc agttccacga agtgacagtg tgaccccagt cactgttgct	120
gttatcacat gcaagtatcc agaggtctct gagcaaggca gaggggatcc catttatctg	180
ggaatccaga atccagaaat gtgtttgtat tgtgagaagg ttggagaaca gccacattg	240
cagctaaaag agcagaagat catggatctg tatggccaac ccgagcccgt gaaacccttc	300
cttttctacc gtgccaaagac tggtaggacc tccacccttg agtctgtggc cttcccgac	360
tggttcattg cctcctccaa gagagaccag cccatcatc tgacttcaga acttgggaag	420
tcatacaaca ctgcctttga attaaatata aatgactaa	459

<210> SEQ ID NO 76
 <211> LENGTH: 528
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 76

atgtcaatgt gtaaacctat tactgggact attaatgatt tgaatcagca agtgtggacc	60
cttcagggtc agaaccttgt ggcagttcca cgaagtgaca gtgtgacccc agtcaactgtt	120
gctgttatca catgcaagta tccagaggct cttgagcaag gcagagggga tcccatttat	180
ttgggaatcc agaatccaga aatgtgtttg tattgtgaga aggttgaga acagcccaca	240
ttgcagctaa aagagcagaa gatcatggat ctgtatggcc aaccgagcc cgtgaaaccc	300
ttccttttct accgtgccaa gactggtagg acctccacc ttgagtctgt ggcttcccg	360
gactggttca ttgcctcctc caagagagac cagcccatca ttctgacttc agaacttggg	420
aagtcataca aactgcctt tgaattaaat ataaatgaca gatctggcag ttctgactac	480
aaggacgacg acgacaaggg cagttctcac catcaccatc accactag	528

<210> SEQ ID NO 77
 <211> LENGTH: 525
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 77

atgatgtgta aacctattac tgggactatt aatgatttga atcagcaagt gtggaccctt	60
cagggtcaga accttgtggc agttccacga agtgacagtg tgaccccagt cactgttgct	120
gttatcacat gcaagtatcc agaggtctct gagcaaggca gaggggatcc catttatctg	180
ggaatccaga atccagaaat gtgtttgtat tgtgagaagg ttggagaaca gccacattg	240
cagctaaaag agcagaagat catggatctg tatggccaac ccgagcccgt gaaacccttc	300
cttttctacc gtgccaaagac tggtaggacc tccacccttg agtctgtggc cttcccgac	360
tggttcattg cctcctccaa gagagaccag cccatcatc tgacttcaga acttgggaag	420
tcatacaaca ctgcctttga attaaatata aatgacagat ctggcagttc tgactacaag	480
gacgacgacg acaagggcag ttctcaccat caccatcacc actag	525

<210> SEQ ID NO 78

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<211> LENGTH: 819
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(357)
<223> OTHER INFORMATION: SUMO tag

<400> SEQUENCE: 78
atgggcagca gccatcatca tcatcatcac ggcagcggcc tggcgccgcg cggcagcgct      60
agcatgtcgg actcagaagt caatcaagaa gctaagccag aggtcaagcc agaagtcaag      120
ctgagactc acatcaattt aaaggtgtcc gatggatctt cagagatctt cttcaagatc      180
aaaaagacca ctcccttaag aagggtgatg gaagcggtcg ctaaaagaca gggtaaggaa      240
atggactcct taagattctt gtacgacggt attagaattc aagctgatca gacccttgaa      300
gatttggaca tggaggataa cgatattatt gaggtcaca gagaacagat tggtggtaaa      360
attgacacac ctacgcgggg gagcattcag gatatcaatc atcgggtgtg ggttcttcag      420
gaccagacgc tcatagcagt cccgaggaag gaccgtatgt ctccagtcac tattgcctta      480
atctcatgcc gacatgtgga gacccttgag aaagacagag ggaaccccat ctacctgggc      540
ctgaatggac tcaatctctg cctgatgtgt gctaaagtcg gggaccagcc cacactgcag      600
ctgaaggaaa aggatataat ggatttgtac aaccaaccgc agcctgtgaa gtcctttctc      660
ttctaccaca gccagagtgg caggaactcc accttcgagt ctgtggcttt cctgggetgg      720
ttcatcgctg tcagctctga aggaggtgt cctctcatcc ttaccaaga actggggaaa      780
gccaacacta ctgactttgg gttaactatg ctgttttaa                                819

```

What is claimed is:

1. An isolated IL-1F5 polypeptide that antagonizes signal transduction through IL-1Rrp2, comprising the amino acid sequence set forth in SEQ ID NO: 8, wherein the N-terminus of said IL-1F5 polypeptide starts at amino acid position one of the amino acid sequence set forth in SEQ ID NO: 8.

35 2. The isolated IL-1F5 polypeptide of claim 1 consisting of the amino acid sequence set forth in SEQ ID NO: 7 or SEQ ID NO: 8.

3. A composition comprising the polypeptide of claim 1 and a physiologically acceptable diluent, excipient or carrier.

* * * * *