US 20090098132A1

(19) United States

(12) Patent Application Publication

(10) Pub. No.: US 2009/0098132 A1

(43) Pub. Date: Apr. 16, 2009

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(54) **COMPOSITION AND METHOD FOR TREATING LUPUS NEPHRITIS**

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(21) Appl. No.: **12/235,674**

(22) Filed: **Sep. 23, 2008**

Related U.S. Application Data

(62) Division of application No. 11/355,297, filed on Feb. 15, 2006, now Pat. No. 7,491,513, which is a division of application No. 10/719,385, filed on Nov. 21, 2003, now Pat. No. 7,060,797.

(60) Provisional application No. 60/428,094, filed on Nov. 21, 2002.

Publication Classification

(51) **Int. Cl.**

A61K 39/395	(2006.01)
C12N 15/11	(2006.01)
C12N 15/00	(2006.01)
C12N 1/21	(2006.01)
C12N 5/06	(2006.01)
C12N 1/19	(2006.01)
C07K 14/00	(2006.01)
A61K 38/02	(2006.01)
C07K 16/18	(2006.01)
C12P 21/04	(2006.01)
C12Q 1/68	(2006.01)
G01N 33/566	(2006.01)

(52) **U.S. Cl.** **424/139.1**; 536/23.1; 435/320.1; 435/252.33; 435/348; 435/254.2; 435/358; 435/365; 530/350; 514/12; 530/387.9; 530/387.3; 435/69.7; 435/6; 436/501

(57) **ABSTRACT**

The present invention provides novel isolated BFLP0169 polynucleotides and polypeptides encoded by the BFLP0169 polynucleotides. Also provided are the antibodies that immunospecifically bind to a BFLP0169 polypeptide or any derivative (including fusion derivative), variant, mutant or fragment of the BFLP0169 polypeptide, polynucleotide or antibody. The invention additionally provides methods in which the BFLP0169 polypeptide, polynucleotide and antibody are utilized in the detection and treatment of a broad range of pathological states, as well as to other uses.

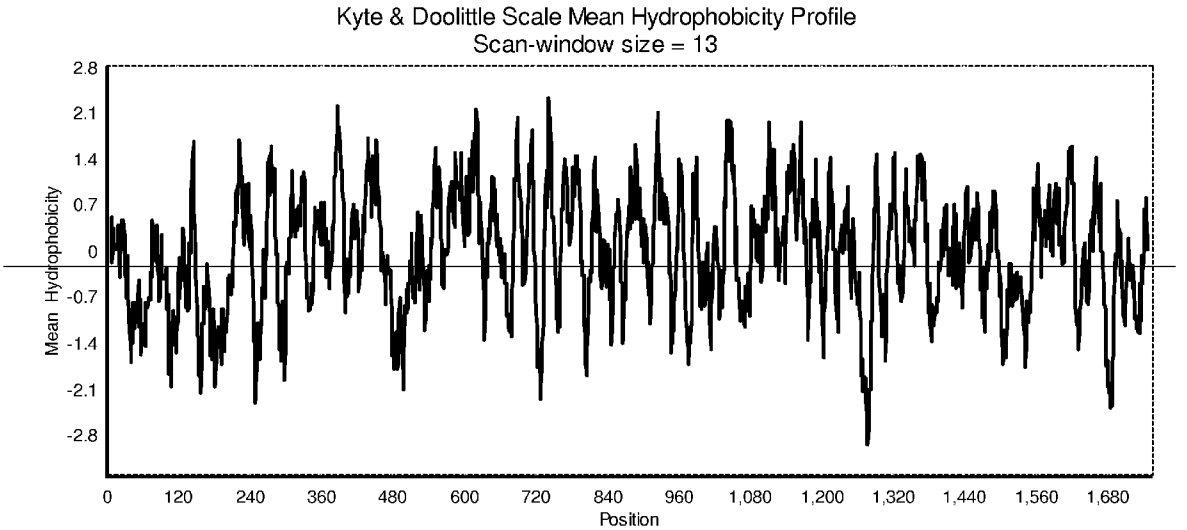


Figure 1

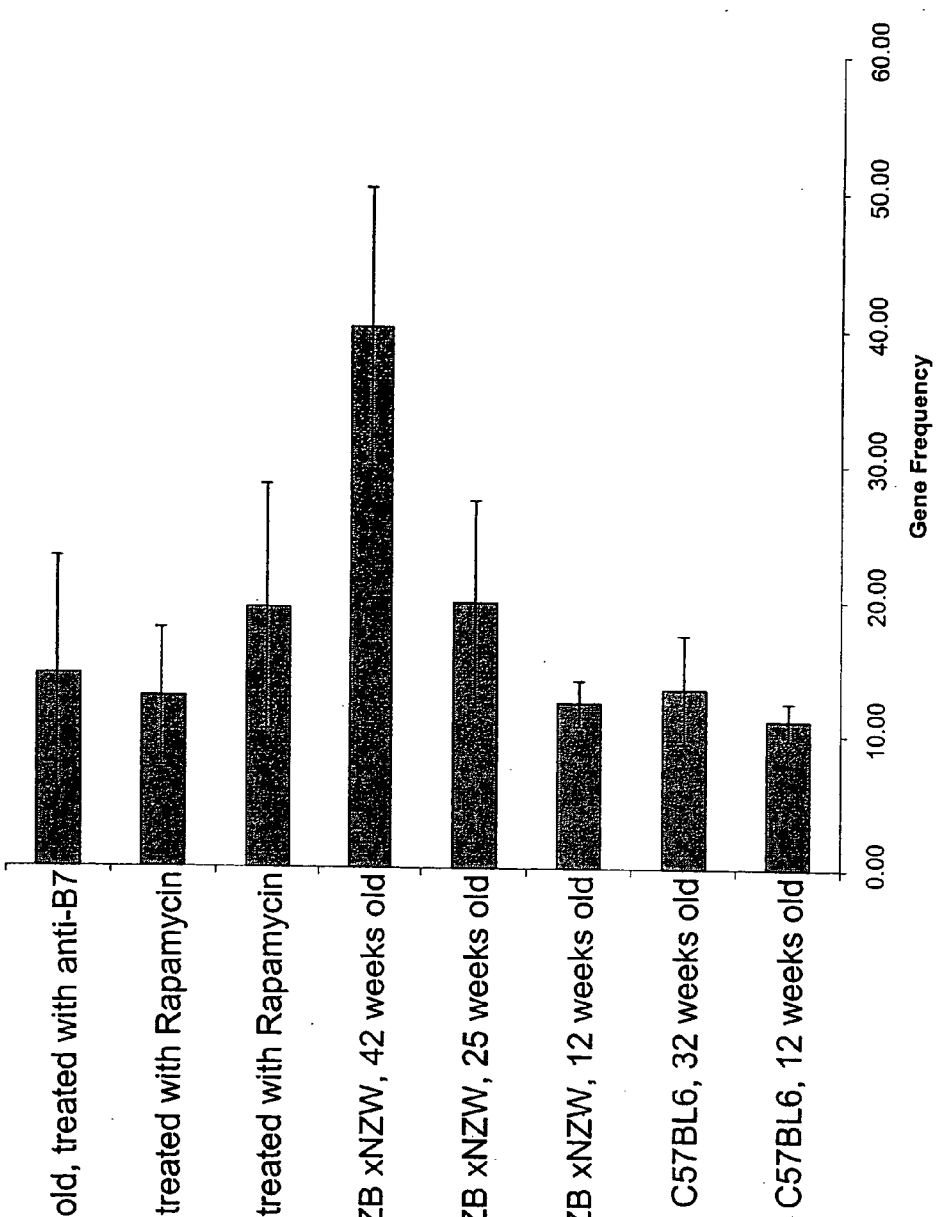
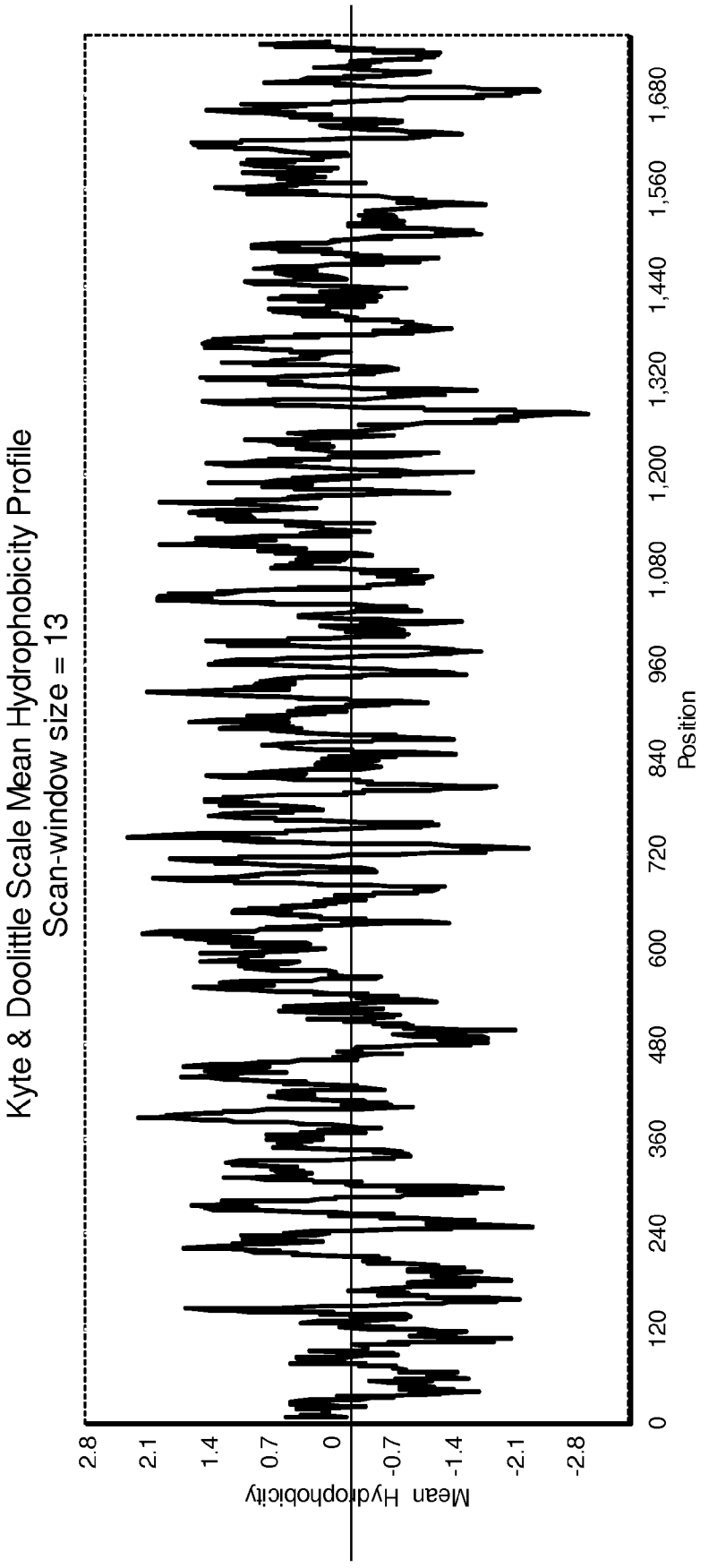

Gene Expression Levels in (NZB x NZW)F1 Kidneys of Mouse Ortholog of Human Gene BFLP0169 and the Effect of Therapy on Gene Expression Levels
NZB x NZW, 50 weeks old, treated with anti-B7
NZB x NZW, 55 weeks old, treated with Rapamycin
NZB xNZW, 42 weeks old, treated with Rapamycin
NZB xNZW, 42 weeks old
NZB xNZW, 25 weeks old
NZB xNZW, 12 weeks old
C57BL6, 32 weeks old
C57BL6, 12 weeks old
0.00
10.00
20.00
30.00
40.00
50.00
60.00
Gene Frequency

Figure 2


Kyte & Doolittle Scale Mean Hydrophobicity Profile
Scan-window size = 13
Mean Hydrophobicity
2.8
2.1
1.4
0.7
0
-0.7
-1.4
-2.1
-2.8
0
120
240
360
480
600
720
840
960
1,080
1,200
1,320
1,440
1,560
1,680
Position

COMPOSITION AND METHOD FOR TREATING LUPUS NEPHRITIS

RELATED APPLICATIONS

[0001] This application is a divisional application of U.S. patent application Ser. No. 11/355,297, filed Feb. 15, 2006, now allowed. U.S. patent application Ser. No. 11/355,297 is a divisional application of U.S. patent application Ser. No. 10/719,385, filed Nov. 21, 2003, which is now U.S. Pat. No. 7,060,797. These applications claims priority to U.S. Provisional Application No. 60/428,094, filed Nov. 21, 2002. The entire contents of these applications are incorporated herein by reference in their entireties.

FIELD OF THE INVENTION

[0002] The invention relates generally to nucleic acids and polypeptides and more specifically to nucleic acids and polypeptides encoding polypeptides useful for detecting and treating lupus nephritis, as well as for identifying therapeutic agents for treating the same.

BACKGROUND OF THE INVENTION

[0003] Lupus nephritis is an example of a "classical" autoimmune disease in which the patient's immune system attacks his/her own organs. It has been estimated that 45-75% of lupus patients eventually suffer from some form or other of kidney damage. Lupus varies greatly in severity from mild cases requiring minimal intervention to those in which significant damage occurs to vital organs such as lungs, kidneys, heart and brain, and which ultimately can be fatal. Lupus is predominantly a female disease, with an approximate female to male ratio being 9:1. In North America, it is estimated to affect 1 in 500 females mainly between the age of 20 to 40 years.

[0004] There is no known cure for lupus. Treatment is typically directed at controlling the symptoms with the hope of putting the disease into remission. Recently, the antibiotic rapamycin has been demonstrated to be an effective therapy in treating lupus nephritis in a murine model of the disease.

SUMMARY OF THE INVENTION

[0005] The invention is based, in part, upon the discovery of a gene, named BFLP0169, whose expression is increased in kidney tissue in mice with lupus nephritis; however, the expression level of the gene does not decrease markedly in response to treatment with rapamycin. This expression profile indicates that the product of the BFLP0169 gene interacts with rapamycin when this antibiotic is administered to ameliorate the symptoms of lupus nephritis. In the absence of rapamycin, the gene product is free to bring about the diseased state, and its effects can include the activation of genes required to bring about the diseased state. In the presence of rapamycin, the BFLP0169 gene product is inactive and the diseased state diminishes. Accordingly, the BFLP0169 protein is useful as a target for identifying agents that, like rapamycin, are useful in treating symptoms of lupus nephritis.

[0006] In one aspect, the invention provides an isolated nucleic acid molecule that includes the sequence of a nucleotide sequence encoding a BFLP0169 gene product. In a preferred embodiment, the nucleotide sequence includes the sequence of SEQ ID NO:1, or a fragment, homolog, analog or derivative thereof. The nucleic acid can include, e.g., a nucleic acid sequence encoding a polypeptide at least 70%, e.g., 80%, 85%, 90%, 95%, 98%, or even 99% or more identical to a polypeptide that includes the amino acid sequences of SEQ ID NO:2. The nucleic acid can be, e.g., a genomic DNA fragment, or a cDNA molecule.

[0007] Also included in the invention is a vector containing one or more of the nucleic acids described herein, and a cell containing the vectors or nucleic acids described herein.

[0008] The invention is also directed to host cells transformed with a vector comprising any of the nucleic acid molecules described above.

[0009] In another aspect, the invention includes a pharmaceutical composition that includes a BFLP0169 nucleic acid and a pharmaceutically acceptable carrier or diluent.

[0010] In a further aspect, the invention includes a substantially purified BFLP0169 polypeptide, e.g., any of the BFLP0169 polypeptides encoded by a BFLP0169 nucleic acid, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition that includes a BFLP0169 polypeptide and a pharmaceutically acceptable carrier or diluent.

[0011] In a still further aspect, the invention provides an antibody that binds specifically to a BFLP0169 polypeptide. The antibody can be, e.g., a monoclonal or polyclonal antibody, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition including BFLP0169 antibody and a pharmaceutically acceptable carrier or diluent. The invention is also directed to isolated antibodies that bind to an epitope on a polypeptide encoded by any of the nucleic acid molecules described above.

[0012] The invention also includes kits comprising in one or more containers one or more of a compound that is a BFLP0169 nucleic acid, a BFLP0169 polypeptide and/or an antibody to a BFLP0169 polypeptide. The kit is preferably provided with instructions for use. If desired, the compounds in the kits are provided along with a pharmaceutically acceptable carrier.

[0013] The invention further provides a method for producing a BFLP0169 polypeptide by providing a cell containing a BFLP0169 nucleic acid, e.g., a vector that includes a BFLP0169 nucleic acid, and culturing the cell under conditions sufficient to express the BFLP0169 polypeptide encoded by the nucleic acid. The expressed BFLP0169 polypeptide is then recovered from the cell. Preferably, the cell produces little or no endogenous BFLP0169 polypeptide. The cell can be, e.g., a prokaryotic cell or eukaryotic cell.

[0014] The invention is also directed to methods of identifying a BFLP0169 polypeptide or nucleic acid in a sample by contacting the sample with a compound that specifically binds to the polypeptide or nucleic acid, and detecting complex formation, if present.

[0015] The invention further provides methods of identifying a compound that modulates the activity of a BFLP0169 polypeptide by contacting a BFLP0169 polypeptide with a compound and determining whether the BFLP0169 polypeptide activity is modified.

[0016] The invention is also directed to compounds that modulate BFLP0169 polypeptide activity identified by contacting a BFLP0169 polypeptide with the compound and determining whether the compound modifies activity of the BFLP0169 polypeptide, binds to the BFLP0169 polypeptide, or binds to a nucleic acid molecule encoding a BFLP0169 polypeptide.

[0017] In another aspect, the invention provides a method of determining the presence of or predisposition of a BFLP0169-associated disorder in a subject. The method includes providing a sample from the subject and measuring the amount of BFLP0169 polypeptide in the subject sample. The amount of BFLP0169 polypeptide in the subject sample is then compared to the amount of BFLP0169 polypeptide in a control sample. An alteration in the amount of BFLP0169 polypeptide in the subject protein sample relative to the amount of BFLP0169 polypeptide in the control protein sample indicates the subject has a tissue proliferation-associated condition. A control sample is preferably taken from a matched individual, i.e., an individual of similar age, sex, or other general condition but who is not suspected of having a tissue proliferation-associated condition. Alternatively, the control sample may be taken from the subject at a time when the subject is not suspected of having a tissue proliferation-associated disorder. In some embodiments, the BFLP0169 is detected using a BFLP0169 antibody.

[0018] In a further aspect, the invention provides a method of determining the presence of or predisposition of a BFLP0169-associated disorder in a subject. The method includes providing a nucleic acid sample, e.g., RNA or DNA, or both, from the subject and measuring the amount of the BFLP0169 nucleic acid in the subject nucleic acid sample. The amount of BFLP0169 nucleic acid sample in the subject nucleic acid sample is then compared to the amount of a BFLP0169 nucleic acid in a control sample. An alteration in the amount of BFLP0169 nucleic acid in the sample relative to the amount of BFLP0169 in the control sample indicates the subject has a tissue proliferation-associated disorder.

[0019] In a still further aspect, the invention provides a method of treating or preventing or delaying a BFLP0169-associated disorder. The method includes administering to a subject in which such treatment or prevention or delay is desired a BFLP0169 nucleic acid, a BFLP0169 polypeptide, or a BFLP0169 antibody in an amount sufficient to treat, prevent, or delay a tissue proliferation-associated disorder in the subject. Examples of such disorders include rheumatoid arthritis and multiple sclerosis.

[0020] Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

[0021] Other features and advantages of the invention will be apparent from the following detailed description and claims.

BRIEF DESCRIPTION OF THE DRAWINGS

[0022] FIG. **1** is a histogram showing relative levels of gene expression in the mouse ortholog of the human BFLP0169 gene in NZB×NZWF1 kidneys before, during, and after rapamycin treatment, as well as in various control mouse strains and conditions.

[0023] FIG. **2** is a Kylte & Doolitle plot generated for the BFLP0169 protein.

DETAILED DESCRIPTION OF THE INVENTION

[0024] The BFLP0169 nucleic acid sequences disclosed herein were identified based on changes in expression of the gene in kidneys of a lupus nephritis model mouse as compared to expression of the gene in kidneys from non non-diseased mice. More particularly, the gene is expressed at relatively low levels in young mice and mice that do not show symptoms of lupus nephritis. Gene expression is elevated in mice with lupus nephritis, and is lower in mice that have been successfully treated with rapamycin or anti-B7 antibodies. The observation that expression levels return to normal when kidney function is normal indicates that elevated levels are related to, and diagnostic of, disease progression. Blocking the function of these genes may inhibit or retard disease progression. Expression levels can also to used to assess and compare effectiveness of various therapeutic interventions.

[0025] Accordingly, the BFLP0169 nucleic acid sequences are useful for detecting the presence of lupus nephritis in a subject. Elevated levels of BFLP0169 transcripts or polypeptides relative to levels in control samples indicate the presence of lupus nephritis in the subject. BFLP0169 nucleic acid sequences can also be used to monitor the effectiveness of treatments for lupus nephritis: a decrease in expression of BFLP0169 genes relative to levels in diseased treatments demonstrates that the treatment is effective.

[0026] The BFLP0169 sequences can additionally be used to identify therapeutic agents for treating or preventing lupus nephritis in a subject. For example, a BFLP0169 polypeptide can be contacted with a test agent. Binding of the BFLP0169 polypeptide to the test agent reveals that the test agent modulates BFLP0169 activity. The BFLP0169-binding agent can be further tested to determine if it acts to promote or inhibit lupus symptoms in a test organism (e.g., a NZB X NZW mouse). Inhibition of lupus symptoms reveals that the agent is useful for treating or preventing lupus nephritis, or symptoms associated with lupus nephritis. Additional utilities are disclosed herein.

[0027] A 5987 nucleotide sequence that includes a human BFLP0169 nucleic acid is shown in Table 1 (SEQ ID NO:1). The human sequence was identified as the human ortholog of a murine gene whose expression is increased in a NZB×NZW mouse with lupus nephritis-like symptoms.

[0028] Nucleotides 1-5259 of the sequence shown in Table 1 encode a polypeptide of 1753 amino acids, whose sequence is shown in Table 2 (SEQ ID NO:2).

TABLE 1

```
ATGATCAGAAAGAGCAAAATTACCTCTGTTCTCTCATTTTGCAGGAGCAG

TAGAGAACTGTGGACTATTCTGCTTGGAAGGTCAGCTCTGAGAGAGCTGA

GTCAGATTGAGGCAGAACTGAATAAACATTGGCGGCGATTGTTAGAGGGG

CTTTCTTACTACAAACCTCCCAGTCCAAGTTCAGCTGAAAAAGTGAAAGC

TAATAAAGATGTAGCTTCACCATTGAAGGAACTGGGTTTAAGAATCAGCA

AGTTTTTGGGTCTTGATGAAGAACAGAGTGTGCAGTTACTCCAGTGTTAC

CTGCAAGAGGACTACAGGGGTACTCGGGACTCAGTAAAGACAGTACTGCA

AGATGAGAGGCAGAGCCAGGCCTTAATCCTGAAGATTGCAGATTATTATT
```

TABLE 1-continued

ATGAAGAAAGAACCTGTATTCTTCGTTGTGTCTTACACCTTCTCACTTAC	CTGCATCTGCAGCCTGGCATACACAGAAGCAGGACAGACAGTTATCAATA
TTCCAAGATGAAAGACACCCCTATAGGGTTGAATATGCAGACTGTGTTGA	TCATGGGCATTGGCGTGGACACCATTGACATGGTGATGGCTGCTCAGCCT
TAAATTGGAGAAGGAACTAGTTTCAAAATACAGACAGCAGTTCGAAGAGC	CGAAGTGATGGGGCAGAGGGCCAGGGGCAGGGCCAGCTGCTGATCAAGAC
TTTATAAAACTGAAGCACCAACTTGGGAGACACATGGAAATCTCATGACA	AGTGAAACTGGCATTCTCCGTCACCAACAATGTTATTCGGCTGAAACCTC
GAGCGCCAAGTGTCTCGCTGGTTTGTTCAGTGCCTTCGGGAACAGTCCAT	CTTCTAATGTGGTGTCCCCCCTGGAACAGGCTCTCTCACAACATGGTGCT
GCTGCTAGAAATTATTTTCCTTTATTATGCATACTTTGAGATGGCACCCA	CATGGAAACAACCTCATTGCTGTTCTAGCCAAATACATCTACCACAAACA
GTGACTTACTTGTATTAACCAAGATGTTTAAAGAGCAAGGATTTGGTAGT	TGACCCTGCTTTGCCACGTCTTGCCATTCAGCTGCTGAAACGTCTGGCCA
AGGCAGACCAATAGGCACCTGGTGGATGAGACTATGGATCCTTTTGTAGA	CGGTGGCCCCAATGTCAGTGTATGCTTGTCTGGGCAATGATGCGGCTGCC
TCGGATTGGCTACTTCAGTGCCCTCATCCTGGTGGAGGGCATGGATATCG	ATTCGTGATGCCTTCCTGACCCGATTGCAGAGCAAAATTGAGGACATGCG
AGTCCTTGCATAAGTGTGCTTTGGATGACAGAAGAGAACTGCATCAGTTT	CATCAAAGTCATGATTCTAGAGTTCCTCACTGTTGCAGTAGAGACCCAGC
GCGCAGGATGGGCTTATTTGTCAGGATATGGACTGTTTAATGTTGACCTT	CAGGCCTCATCGAACTGTTTCTGAACCTGGAAGTTAAGGATGGCAGTGAT
TGGGGACATTCCACATCATGCCCCAGTGCTTTTGGCCTGGGCTCTCCTCC	GGCTCAAAGGAATTCAGCCTTGGGATGTGGAGCTGTCTCCATGCAGTGCT
GTCACACTCTGAACCCAGAAGAGACAAGCAGTGTGGTCCGGAAGATAGGT	GGAGCTGATTGATTCCCAACAGCAAGATCGATACTGGTGCCCACCCCTGC
GGCACAGCCATCCAGCTGAATGTGTTTCAGTACTTGACCCGATTGCTCCA	TGCATCGTGCCGCCATTGCCTTTTTGCATGCTCTGTGGCAGGATCGGAGG
GTCCCTTGCCAGTGGGGGAAATGATTGCACCACCAGCACTGCATGCATGT	GACAGTGCCATGCTGGTCCTCCGAACCAAACCCAAGTTTTGGGAAAATTT
GTGTCTATGGACTGCTCTCTTTCGTTCTGACCTCGTTGGAGCTGCACACC	AACCAGTCCGCTGTTTGGAACCCTTTCTCCTCCCTCTGAAACATCAGAGC
CTGGGCAATCAGCAGGATATAATTGATACAGCATGTGAAGTATTGGCCGA	CCAGCATCCTGGAAACCTGTGCCCTAATCATGAAGATAATTTGCTTGGAG
CCCTTCTCTTCCGGAACTGTTCTGGGGAACAGAGCCAACTTCTGGCCTTG	ATATACTATGTAGTAAAGGGTTCATTAGACCAGTCATTAAAGGATACACT
GGATCATTCTGGACAGTGTGTGTGGAATGTTTCCCCACCTTCTCTCCCCA	GAAGAAATTTTCCATCGAGAAACGCTTTGCCTACTGGTCAGGGTATGTCA
CTCCTGCAACTGCTCCGAGCCCTGGTATCAGGGAAGTCCACAGCCAAAAA	AGTCATTGGCAGTTCACGTGGCCGAAACAGAAGGCAGCAGCTGCACCTCC
GGTGTATAGCTTCTTGGATAAGATGTCTTTCTACAATGAACTTTATAAAC	TTGTTAGAGTACCAGATGCTGGTGTCCGCCTGGAGGATGCTTCTCATCAT
ACAAGCCTCATGATGTGATCTCCCATGAAGATGGAACTCTTTGGCGGAGA	TGCCACCACTCATGCAGATATAATGCACCTGACTGACTCTGTGGTGCGTC
CAAACACCCAAACTCCTTTATCCCCTTGGGGGTCAAACCAACCTTCGCAT	GCCAGCTCTTTCTTGACGTGCTTGATGGAACCAAAGCATTACTCCTAGTT
ACCTCAAGGCACTGTGGGCCAAGTAATGTTGGATGATAGGGCATACCTGG	CCAGCCTCAGTGAACTGCCTTCGCCTTGGCTCCATGAAGTGCACTCTGCT
TACGCTGGGAATACTCCTATAGCAGCTGGACCCTCTTTACCTGCGAGATT	GCTTATCCTCCTCCGGCAGTGGAAGAGAGAGTTAGGTTCTGTGGATGAAA
GAAATGTTGCTTCATGTTGTTTCAACTGCAGATGTGATTCAGCACTGCCA	TCCTTGGACCCTTGACGGAGATCCTGGAGGGAGTGCTGCAGGCCGACCAG
GCGAGTCAAACCCATCATTGATCTCGTCCATAAGGTCATCAGTACAGACC	CAACTCATGGAGAAGACCAAGGCCAAGGTGTTCTCAGCATTCATCACAGT
TGTCGATAGCAGACTGTCTCCTGCCCATCACATCTCGCATCTACATGCTG	GTTGCAAATGAAGGAGATGAAAGTAAGTGACATCCCCCAGTACTCCCAGC
CTGCAGCGGTTAACGACAGTGATCTCCCCACCTGTGGATGTCATTGCTTC	TGGTGCTGAATGTCTGTGAGACCCTCCAAGAGGAAGTGATTGCACTCTTC
TTGTGTCAACTGCTTAACTGTTTTGGCTGCCCGCAATCCAGCAAAGGTCT	GACCAGACCCGCCACAGTCTGGCATTAGGCAGTGCCACAGAGGACAAGGA
GGACTGATCTTCGTCACACAGGTTTTTTACCATTTGTGGCCCATCCTGTC	CAGCATGGAGACTGACGACTGTTCTCGGTCCCGGCACAGGGACCAGCGTG
TCCAGCCTGAGTCAGATGATTAGTGCGGAAGGGATGAATGCTGGAGGGTA	ATGGGGTGTGTGTCCTGGGCCTGCACCTGGCCAAGGAGCTGTGTGAGGTA
CGGAAACCTCTTGATGAACAGTGAACAGCCTCAGGGCGAGTATGGGGTTA	GACGAGGATGGTGACTCCTGGCTGCAGGTAACCCGCAGGCTCCCCATCCT
CTATTGCCTTTCTGCGCTTGATCACCACCCTTGTCAAGGGGCAACTTGGT	ACCCACCCTCCTCACCACTCTAGAGGTGAGCCTTCGCATGAAGCAGAACC
AGTACCCAGAGCCAAGGACTTGTACCCTGTGTAATGTTTGTGCTGAAGGA	TGCATTTCACTGAGGCCACATTGCATCTGCTCCTCACCCTGGCTCGCACT
GATGCTTCCCAGCTACCATAAGTGGCGCTACAACTCTCATGGAGTGAGGG	CAGCAGGGAGCCACAGCAGTGGCTGGAGCTGGCATCACCCAGAGCATTTG
AACAGATTGGTTGCCTGATCTTGGAGCTGATTCATGCGATACTGAACCTG	TTTGCCCCTTCTGAGTGTGTACCAGCTGAGCACCAACGGCACAGCACAGA
TGCCACGAGACAGACCTGCACAGCAGTCATACTCCCAGCCTGCAGTTTCT	CACCTAGTGCCTCTCGGAAGTCCCTGGATGCCCCCTCTTGGCCAGGAGTC

TABLE 1-continued

TACCGCCTGTCCATGTCCCTGATGGAGCAGCTGCTCAAAACTCTGCGCTA

CAACTTCCTGCCTGAGGCCCTGGACTTCGTGGGTGTCCACCAGGAGCGGA

CCTTACAGTGCCTCAACGCAGTGAGGACAGTGCAGAGTCTGGCCTGCCTG

GAGGAGGCGGACCACACCGTGGGTTTTATTCTGCAGCTCTCTAACTTCAT

GAAGGAGTGGCACTTCCACCTGCCTCAGCTCATGCGTGATATCCAGGTCA

ACCTGGGTTACTTGTGCCAGGCATGTACCTCTCTCCTGCACAGTCGAAAG

ATGCTGCAGCATTACTTACAGAACAAAAATGGGGATGGCCTCCCCTCAGC

TGTTGCCCAGCGAGTCCAGAGGCCACCGTCTGCTGCTTCTGCTGCCCCCT

CCTCCTCAAAGCAGCCCGCTGCTGACACAGAGGCATCAGAGCAGCAGGCC

TTGCACACAGTCCAGTATGGCCTTCTCAAGATCCTCAGCAAGACGCTGGC

AGCCCTGCGCCACTTCACCCCAGATGTCTGCCAGATTCTGCTGGATCAGT

CCCTGGACCTTGCTGAATACAACTTCCTGTTTGCCCTGAGCTTTACCACT

CCCACCTTTGACTCCGAAGTGGCCCCCTCCTTCGGGACCCTTCTGGCCAC

AGTGAATGTGGCCCTCAACATGCTTGGAGAGCTGGACAAGAAAAAGGAGC

CCCTCACCCAGGCAGTGGGGCTCAGCACACAGGCAGAAGGGACCAGGACG

TTAAAGTCCCTCCTGATGTTTACCATGGAAAACTGCTTCTACCTGCTCAT

CTCTCAGGCGATGCGGTACCTTAGGGACCCGGCTGTGCACCCCCGGGACA

AACAGCGGATGAAGCAGGAGCTCAGCTCTGAGTTGAGCACGCTGCTGTCC

AGCCTCTCGCGCTACTTCCGCCGGGGAGCCCCCAGCTCCCCTGCCACTGG

TGTCCTCCCCTCGCCGCAGGGCAAGTCCACCTCTCTCTCCAAAGCCAGCC

CTGAGAGTCAGGAGCCTCTGATCCAGTTGGTGCAGGCGTTTGTCCGGCAT

ATGCAAAGATAGGGCAGTGCTGTTCTGCCCACCTACCCCTCTCCACCAGC

CTACACTGCACCCTGGCTGGCAGGGGTGCTGCTGGCTGCTAGGGCCTATA

CAATGGAGGGCACCTCCTGTCACCCCCCTCCCGGAGTAGCCACGACTCCA

GCCACCACCCACTGACGTTATTTTTATACTAGATGAAGAGGTCAACAGCA

GGCATGGGGAGCCGAGTCTTCTGTGCTCAGGTCCTCACGCTGCAGACGCC

CCCTAGAGGAACTTTCCTTCCTTTCCAGCATTCCCCACAGCACTGCCGGC

CAGGGGAGAGGCGGCAGCCCAGCAGAGGGCTCTATGCACGGGTTTCAAAC

CTGTTTTCCACACTCTGTCTTTGCAGTTTTGGTAATTCTGTGGTCTATTT

ATACAGATATTAAAATCTTGTTTATAGACAGCTGTGTGATGTTTAACTTC

AAAGCCCAGGGATGACAACGTGGCTCTCAGAACCTAGAAAACTCCCCTGG

CCAGGCGCCTGGGAGTGGGGCTGCAGCCTCGGGGGAAGGCAGGTACTGAT

GGATGGCTAGTTCACCAGCATCTCCTCATTCCTGTCCTTGGGCTGAGGGT

TTGGCTGGGTGGGCGCTGTCAGATATTCCCTTCCTTGGCCTGCGCTGGTC

CTGTCCTTGACCCTGCTTTCATTGGCCCAGTGGGCTGAGCTCATCCCTGG

GTGAGCCTTTCTTGAAGCTCTGTGCCTTCCTATTTAT

(SEQ ID NO:1)

TABLE 2

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNL

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLART

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACL

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQA

LHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTT

PTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRT

LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR (SEQ ID NO:2)

[0029] BFLP0169-like nucleic acids and polypeptides of the invention (including those shown in Table 1) are referred to herein as "BFLP0169" nucleic acids and polypeptides.

[0030] A BFLP0169 nucleic acid, and the encoded polypeptide, according to the invention are useful in a variety of applications and contexts.

[0031] BFLP0169 shows homology to other proteins as shown in the BLAST results described in Table 3. KIAA0169, IMAGE: 3461492, and 3598686, and cDNA: FLJ21639 are all proteins encoded from partial reading frames (expressed sequence tags (ESTs)) found in genomic DNA. Because BFLP0169 has homology to these proteins, it is also encoded from either an entire open reading frame, or part of a larger open reading frame (EST).

TABLE 3

Blast Results for BFLP0169

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi|1136397|dbj|D79991.1|	*Homo sapiens* mRNA for KIAA0169 protein, partial cds	1745	1635/1739 (94%)	1635/1739 (94%)	0.0
gi|122046118|ref|XP_052725.6| (XM_052725)	similar to KIAA0169 protein [*Homo sapiens*]	1767	1635/1743 (93%)	1635/1743 (93%)	0.0
gi|23618434|ref|XP_130085.2| (XM_130085)	similar to KIAA0169 protein [*Homo sapiens*]	1111	949/1111 (85%)	982/1111 (87%)	0.0
gi|13529308|gb|AAH05407.1|AAH05407 (BC005407)	Unknown (protein for IMAGE:3461492) [*Homo sapiens*]	853	740/801 (92%)	740/801 (92%)	0.0
gi|19343754|gb|AAH25526.1| (BC025526)	Similar to KIAA0169 protein [*Mus musculus*]	525	411/522 (78%)	422/522 (80%)	0.0

[0032] Table 4 shows a ClustalW alignment of BFLP0169 (SEQ ID NO:2) against the proteins described above in Table 3.

TABLE 4

ClustalW Analysis of SEQ ID NO: 2

1) SEQ ID NO: 2
2) gi|1136397|dbj|D79991.1| (SEQ ID NO: 21)
3) gi|22046118|ref|XP_052725.6| (XM_052725) (SEQ ID NO: 22)
4) gi|23618434|ref|XP_130085.2| (XM_130085) (SEQ ID NO: 23)
5) gi|13529308|gb|AAH05407.1|AAH05407 (BC005407) (SEQ ID NO: 24)
6) gi|19343754|gb|AAH25526.1| (BC025526) (SEQ ID NO: 25)

```
                                  10         20         30         40         50         60
                                  ....|....|....|....|....|....|....|....|....|....|....|....|
SEQ ID NO: 2                      ----------MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG 50
gi|1136398|dbj|                   ------------------AGGPCVRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG 42
gi|22046118|ref                   MASGGGVRASGRAKMAAAAGGPCVRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG 60
gi|23618434|ref                   ------------------------------------------------------------ 1
gi|13529308|gb|                   ------------------------------------------------------------ 1
gi|19343754|gb|                   ------------------------------------------------------------ 1

                                  70         80         90         100        110        120
                                  ....|....|....|....|....|....|....|....|....|....|....|....|
SEQ ID NO: 2                      LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCYLQEDYRGTRD 110
gi|1136398|dbj|                   LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCYLQEDYRGTRD 102
gi|22046118|ref                   LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCYLQEDYRGTRD 120
gi|23618434|ref                   ------------------------------------------------------------ 1
gi|13529308|gb|                   ------------------------------------------------------------ 1
gi|19343754|gb|                   ------------------------------------------------------------ 1
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TABLE 4-continued

ClustalW Analysis of SEQ ID NO: 2

```
                                130       140       150       160       170       180
                                ....|....|....|....|....|....|....|....|....|....|....|....|
SEQ ID NO: 2                    SVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTYFQDERHPYRVEYADCVCKLE 170
gi|1136398|dbj|                 SVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTYFQDERHPYRVEYADCVCKLE 162
gi|22046118|ref                 SVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTYFQDERHPYRVEYADCVCKLE 180
gi|23618434|ref                 ------------------------------------------------------------ 1
gi|13529308|gb|                 ------------------------------------------------------------ 1
gi|19343754|gb|                 ------------------------------------------------------------ 1

                                190       200       210       220       230       240
                                ....|....|....|....|....|....|....|....|....|....|....|....|
SEQ ID NO: 2                    KELVSKYRQQFEELYKTEAPTWETHGNLMTERQVSRWFVQCLREQSMLLEIIFLYYAYFE 230
gi|1136398|dbj|                 KELVSKYRQQFEELYKTEAPTWETHGNLMTERQVSRWFVQCLREQSMLLEIIFLYYAYFE 222
gi|22046118|ref                 KELVSKYRQQFEELYKTEAPTWETHGNLMTERQVSRWFVQCLREQSMLLEIIFLYYAYFE 240
gi|23618434|ref                 ------------------------------------------------------------ 1
gi|13529308|gb|                 ------------------------------------------------------------ 1
gi|19343754|gb|                 ------------------------------------------------------------ 1

                                250       260       270       280       290       300
                                ....|....|....|....|....|....|....|....|....|....|....|....|
SEQ ID NO: 2                    MAPSDLLVLTKMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCA 290
gi|1136398|dbj|                 MAPSDLLVLTKMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCA 282
gi|22046118|ref                 MAPSDLLVLTKMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCA 300
gi|23618434|ref                 ------------------------------------------------------------ 1
gi|13529308|gb|                 ------------------------------------------------------------ 1
gi|19343754|gb|                 ------------------------------------------------------------ 1

                                310       320       330       340       350       360
                                ....|....|....|....|....|....|....|....|....|....|....|....|
SEQ ID NO: 2                    LDDRRELHQFAQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG 350
gi|1136398|dbj|                 LDDRRELHQFAQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG 342
gi|22046118|ref                 LDDRRELHQFAQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG 360
gi|23618434|ref                 ------------------------------------------------------------ 1
gi|13529308|gb|                 ------------------------------------------------------------ 1
gi|19343754|gb|                 ------------------------------------------------------------ 1

                                370       380       390       400       410       420
                                ....|....|....|....|....|....|....|....|....|....|....|....|
SEQ ID NO: 2                    GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQQDIIDT 410
gi|1136398|dbj|                 GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQQDIIDT 402
gi|22046118|ref                 GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQQDIIDT 420
gi|23618434|ref                 ------------------------------------------------------------ 1
gi|13529308|gb|                 ------------------------------------------------------------ 1
gi|19343754|gb|                 ------------------------------------------------------------ 1

                                430       440       450       460       470       480
                                ....|....|....|....|....|....|....|....|....|....|....|....|
SEQ ID NO: 2                    ACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLLRALVSGKSTAKKVYS 470
gi|1136398|dbj|                 ACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLLRALVSGKSTAKKVYS 462
gi|22046118|ref                 ACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLLRALVSGKSTAKKVYS 480
gi|23618434|ref                 ------------------------------------------------------------ 1
gi|13529308|gb|                 ------------------------------------------------------------ 1
gi|19343754|gb|                 ------------------------------------------------------------ 1

                                490       500       510       520       530       540
                                ....|....|....|....|....|....|....|....|....|....|....|....|
SEQ ID NO: 2                    FLDKMSFYNELYKHKPHDVISHEDGTLWRRQTPKLLYPLGGQTNLRIPQGTVGQVMLDDR 530
gi|1136398|dbj|                 FLDKMSFYNELYKHKPHDVISHEDGTLWRRQTPKLLYPLGGQTNLRIPQGTVGQVMLDDR 522
gi|22046118|ref                 FLDKMSFYNELYKHKPHDVISHEDGTLWRRQTPKLLYPLGGQTNLRIPQGTVGQVMLDDR 540
gi|23618434|ref                 ------------------------------------------------------------ 1
gi|13529308|gb|                 ------------------------------------------------------------ 1
gi|19343754|gb|                 ------------------------------------------------------------ 1
```

TABLE 4-continued

ClustalW Analysis of SEQ ID NO: 2

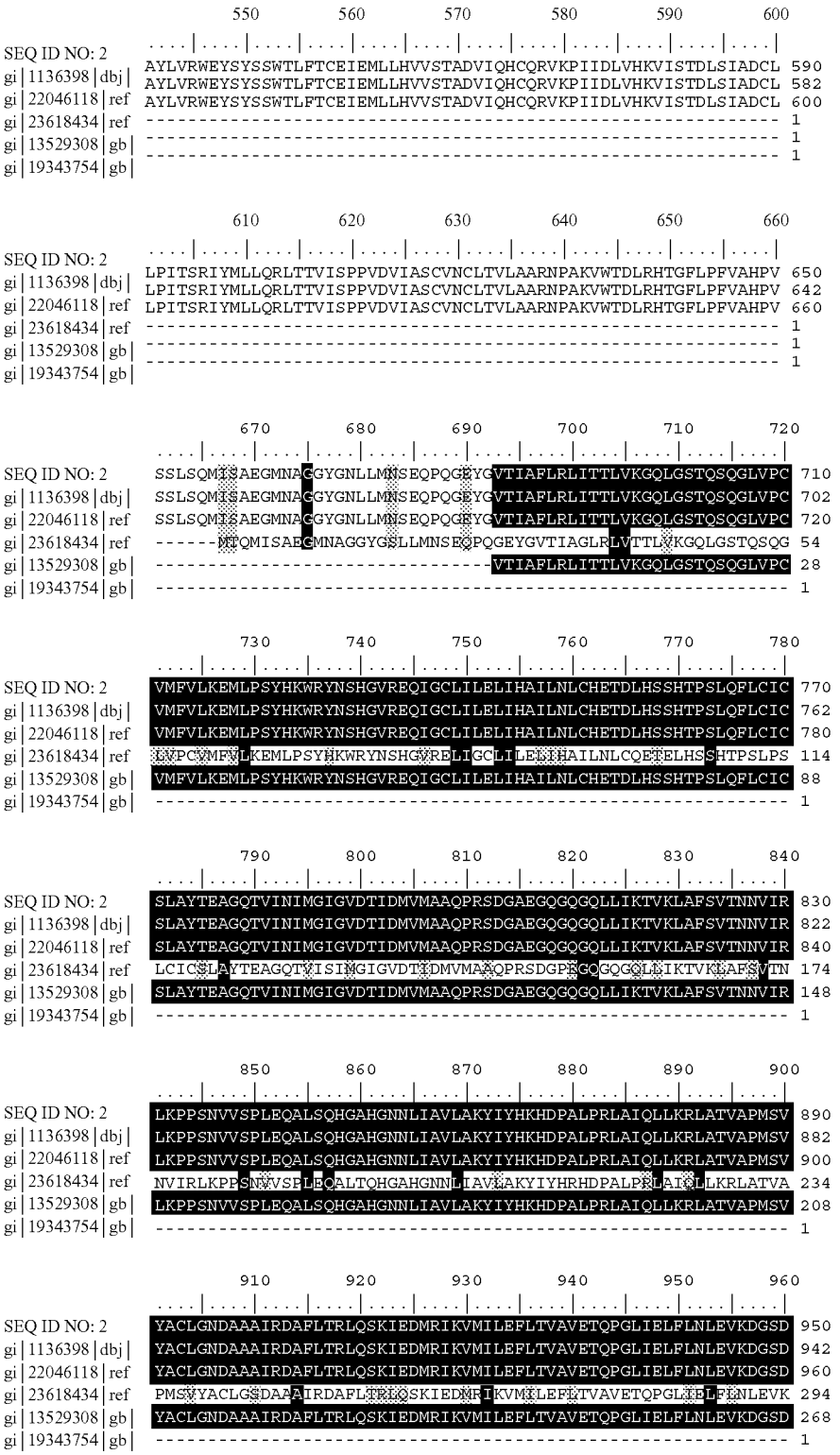

TABLE 4-continued

ClustalW Analysis of SEQ ID NO: 2

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                                970       980       990       1000      1010      1020
                                ....|....|....|....|....|....|....|....|....|....|....|....|
SEQ ID NO: 2                    GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTK 1010
gi|1136398|dbj|                 GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTK 1002
gi|22046118|ref                 GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTK 1020
gi|23618434|ref                 DGSNGSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRRDSAMLV 354
gi|13529308|gb|                 GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTK 328
gi|19343754|gb|                 ------------------------------------------------------------ 1

                                1030      1040      1050      1060      1070      1080
                                ....|....|....|....|....|....|....|....|....|....|....|....|
SEQ ID NO: 2                    PKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSLDQSLKDTLKKF 1070
gi|1136398|dbj|                 PKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSLDQSLKDTLKKF 1062
gi|22046118|ref                 PKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSLDQSLKDTLKKF 1080
gi|23618434|ref                 LKTKPKFWENLTSPLFGTLSPPSETSEPSVLETCALIMKIICLEIYYVVKGSLDQSLKDT 414
gi|13529308|gb|                 PKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSLDQSLKDTLKKF 388
gi|19343754|gb|                 ------------------------------------------------------------ 1

                                1090      1100      1110      1120      1130      1140
                                ....|....|....|....|....|....|....|....|....|....|....|....|
SEQ ID NO: 2                    SIEKRFAYWSGYVKSLAVHVAETEGSSCTSLLEYQMLVSAWRMLLIIATTHADIMHLTDS 1130
gi|1136398|dbj|                 SIEKRFAYWSGYVKSLAVHVAETEGSSCTSLLEYQMLVSAWRMLLIIATTHADIMHLTDS 1122
gi|22046118|ref                 SIEKRFAYWSGYVKSLAVHVAETEGSSCTSLLEYQMLVSAWRMLLIIATTHADIMHLTDS 1140
gi|23618434|ref                 LKKFSSEKRFAYWSGYVKSLAVYMADTEGSSCTSLLEYQMLVSAWRILLIIAASHADVMH 474
gi|13529308|gb|                 SIEKRFAYWSGYVKSLAVHVAETEGSSCTSLLEYQMLVSAWRMLLIIATTHADIMHLTDS 448
gi|19343754|gb|                 ------------------------------------------------------------ 1

                                1150      1160      1170      1180      1190      1200
                                ....|....|....|....|....|....|....|....|....|....|....|....|
SEQ ID NO: 2                    VVRRQLFLDVLDGTKALLLVPASVNCLRLGSMKCTLLLILLRQWK----RELGSVDEILG 1186
gi|1136398|dbj|                 VVRRQLFLDVLDGTKALLLVPASVNCLRLGSMKCTLLLILLRQWK----RELGSVDEILG 1178
gi|22046118|ref                 VVRRQLFLDVLDGTKALLLVPASVNCLRLGSMKCTLLLILLRQWKSILSRELGSVDEILG 1200
gi|23618434|ref                 STDMAVRRQQFLDVLDGTKALLLVAASVNCLRLGSMMCTLLLILLRQWKRELGQVDQILG 534
gi|13529308|gb|                 VVRRQLFLDVLDGTKALLLVPASVNCLRLGSMKCTLLLILLRQWK----RELGSVDEILG 504
gi|19343754|gb|                 ------------------------------------------------------------ 1

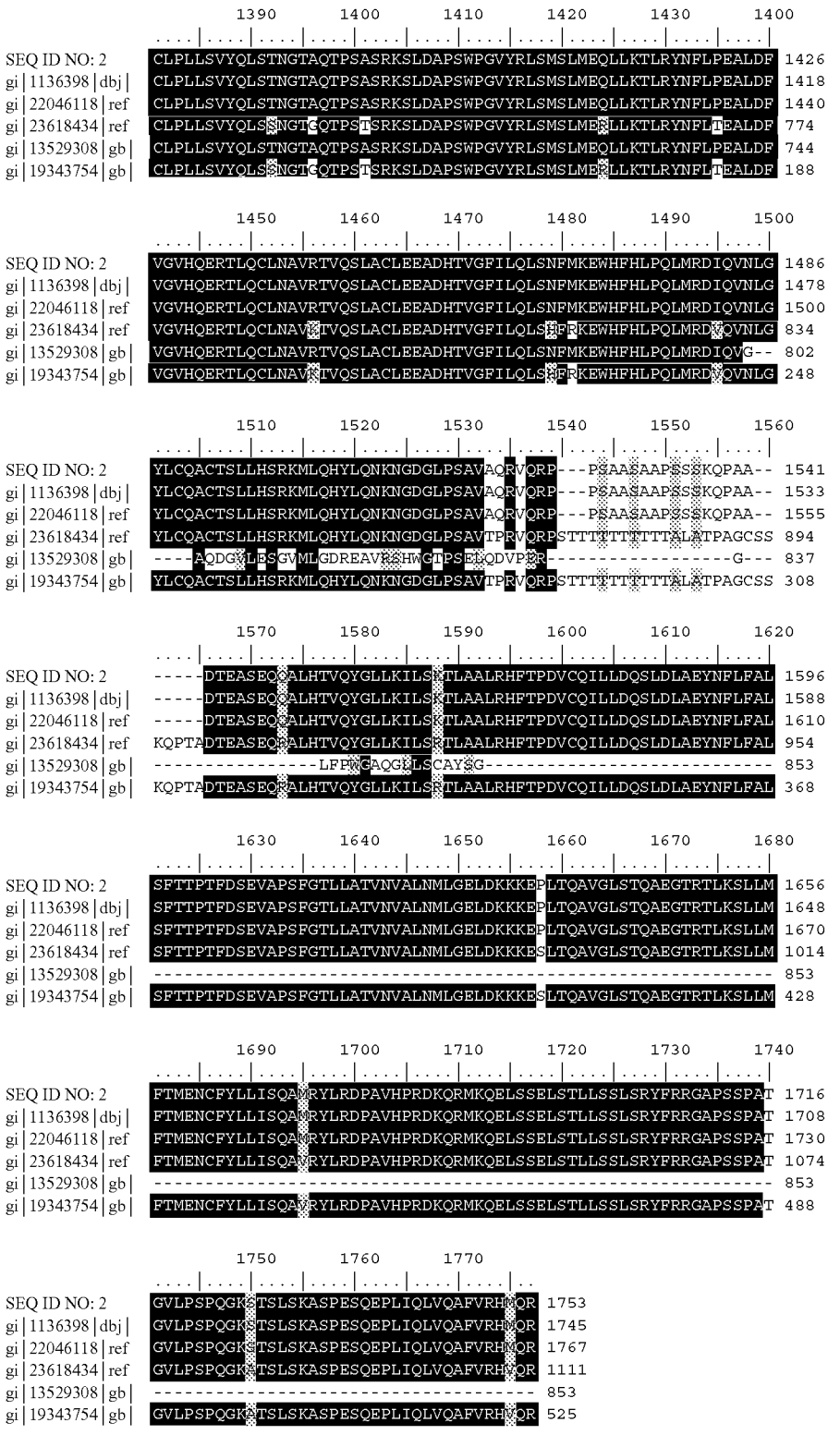
                                1210      1220      1230      1240      1250      1260
                                ....|....|....|....|....|....|....|....|....|....|....|....|
SEQ ID NO: 2                    PLTEILEGVLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEV 1246
gi|1136398|dbj|                 PLTEILEGVLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEV 1238
gi|22046118|ref                 PLTEILEGVLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEV 1260
gi|23618434|ref                 PLTEILEGVLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEV 594
gi|13529308|gb|                 PLTEILEGVLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEV 564
gi|19343754|gb|                 ------------------------------------------------------TRPLQEEV 8

                                1270      1280      1290      1300      1310      1320
                                ....|....|....|....|....|....|....|....|....|....|....|....|
SEQ ID NO: 2                    IALFDQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEVDEDGDS 1306
gi|1136398|dbj|                 IALFDQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEVDEDGDS 1298
gi|22046118|ref                 IALFDQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEVDEDGDS 1320
gi|23618434|ref                 IALFDQTRHSLASDSAAEDKDSMETDDCPRFRHRDQRDGVCVLGLHLAKELCEVDEDGDS 654
gi|13529308|gb|                 IALFDQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEVDEDGDS 624
gi|19343754|gb|                 IALFDQTRHSLASDSAAEDKDSMETDDCPRFRHRDQRDGVCVLGLHLAKELCEVDEDGDS 68

                                1330      1340      1350      1360      1370      1380
                                ....|....|....|....|....|....|....|....|....|....|....|....|
SEQ ID NO: 2                    WLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSI 1366
gi|1136398|dbj|                 WLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSI 1358
gi|22046118|ref                 WLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSI 1380
gi|23618434|ref                 WLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEAALHLLLTLARTQQGATAVAGAGITQSI 714
gi|13529308|gb|                 WLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSI 684
gi|19343754|gb|                 WLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEAALHLLLTLARTQQGATAVAGAGITQSI 128
```

TABLE 4-continued

ClustalW Analysis of SEQ ID NO: 2



[0033] Residues 1-14 of SEQ ID NO:2 are referred to herein as SEQ ID NO:20. The fragment of SEQ ID NO:21 that includes amino acids 1-6 is referred to herein as SEQ ID NO:26.

[0034] BFLP0169 Nucleic Acids

[0035] The nucleic acids of the invention include those that encode a BFLP0169 polypeptide or protein. As used herein, the terms polypeptide and protein are interchangeable.

[0036] In some embodiments, a BFLP0169 nucleic acid encodes a mature BFLP0169 polypeptide. As used herein, a "mature" form of a polypeptide or protein described herein relates to the product of a naturally occurring polypeptide or precursor form or proprotein. The naturally occurring polypeptide, precursor or proprotein includes, by way of non-limiting example, the full length gene product, encoded by the corresponding gene. Alternatively, it may be defined as the polypeptide, precursor or proprotein encoded by an open reading frame described herein. The product "mature" form arises, again by way of nonlimiting example, as a result of one or more naturally occurring processing steps that may take place within the cell in which the gene product arises. Examples of such processing steps leading to a "mature" form of a polypeptide or protein include the cleavage of the N-terminal methionine residue encoded by the initiation codon of an open reading frame, or the proteolytic cleavage of a signal peptide or leader sequence. Thus a mature form arising from a precursor polypeptide or protein that has residues 1 to N, where residue 1 is the N-terminal methionine, would have residues 2 through N remaining after removal of the N-terminal methionine. Alternatively, a mature form arising from a precursor polypeptide or protein having residues 1 to N, in which an N-terminal signal sequence from residue 1 to residue M is cleaved, would have the residues from residue M+1 to residue N remaining. Further as used herein, a "mature" form of a polypeptide or protein may arise from a step of post-translational modification other than a proteolytic cleavage event. Such additional processes include, by way of non-limiting example, glycosylation, myristoylation or phosphorylation. In general, a mature polypeptide or protein may result from the operation of only one of these processes, or a combination of any of them.

[0037] The invention includes mutant or variant nucleic acids of SEQ ID NO:1, or a fragment thereof, any of whose bases may be changed from the corresponding bases shown in SEQ ID NO:1, while still encoding a protein that maintains at least one of its BFLP0169-like activities and physiological functions (i.e., modulating angiogenesis, neuronal development). The invention further includes the complement of the nucleic acid sequence of SEQ ID NO:1, including fragments, derivatives, analogs and homologs thereof. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications.

[0038] One aspect of the invention pertains to isolated nucleic acid molecules that encode BFLP0169 proteins or biologically active portions thereof. Also included are nucleic acid fragments sufficient for use as hybridization probes to identify BFLP0169-encoding nucleic acids (e.g., BFLP0169 mRNA) and fragments for use as polymerase chain reaction (PCR) primers for the amplification or mutation of BFLP0169 nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA), RNA molecules (e.g., mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

[0039] "Probes" refer to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as about, e.g., 6,000 nt, depending on use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are usually obtained from a natural or recombinant source, are highly specific and much slower to hybridize than oligomers. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

[0040] An "isolated" nucleic acid molecule is one that is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Examples of isolated nucleic acid molecules include, but are not limited to, recombinant DNA molecules contained in a vector, recombinant DNA molecules maintained in a heterologous host cell, partially or substantially purified nucleic acid molecules, and synthetic DNA or RNA molecules. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated BFLP0169 nucleic acid molecule can contain less than about 50 kb, 25 kb, 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

[0041] A nucleic acid molecule of the present invention, e.g., a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:1, or a complement thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of SEQ ID NO:1 as a hybridization probe, BFLP0169 nucleic acid sequences can be isolated using standard hybridization and cloning techniques (e.g., as described in Sambrook et al., eds., MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989; and Ausubel, et al., eds., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, N.Y., 1993.)

[0042] A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to BFLP0169 nucleotide sequences can be prepared by standard synthetic techniques, e.g., using an automated DNA synthesizer.

[0043] As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a par-

ticular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at lease 6 contiguous nucleotides of SEQ ID NO:1, or a complement thereof. Oligonucleotides may be chemically synthesized and may be used as probes.

[0044] In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in SEQ ID NO:1, or a portion of this nucleotide sequence. A nucleic acid molecule that is complementary to the nucleotide sequence shown in SEQ ID NO:1 is one that is sufficiently complementary to the nucleotide sequence shown in SEQ ID NO:1 that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in SEQ ID NO:1, thereby forming a stable duplex.

[0045] As used herein, the term "complementary" refers to Watson-Crick or Hoogsteen base pairing between nucleotide units of a nucleic acid molecule, and the term "binding" means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, Van der Waals, hydrophobic interactions, etc. A physical interaction can be either direct or indirect. Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

[0046] Moreover, the nucleic acid molecule of the invention can comprise only a portion of the nucleic acid sequence of SEQ ID NO:1, e.g., a fragment that can be used as a probe or primer, or a fragment encoding a biologically active portion of BFLP0169. Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively, and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type.

[0047] Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the invention, in various embodiments, by at least about 70%, 80%, 85%, 90%, 95%, 98%, or even 99% identity (with a preferred identity of 80-99%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. An exemplary program is the Gap program (Wisconsin Sequence Analysis Package, Version 8 for UNIX, Genetics Computer Group, University Research Park, Madison, Wis.) using the default settings, which uses the algorithm of Smith and Waterman.

[0048] A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of a BFLP0169 polypeptide. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the present invention, homologous nucleotide sequences include nucleotide sequences encoding for a BFLP0169 polypeptide of species other than humans, including, but not limited to, mammals, and thus can include, e.g., mouse, rat, rabbit, dog, cat, cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the nucleotide sequence encoding human BFLP0169 protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in SEQ ID NO:2, as well as a polypeptide having BFLP0169 activity. Biological activities of the BFLP0169 proteins are described below. A homologous amino acid sequence does not encode the amino acid sequence of a human BFLP0169 polypeptide.

[0049] The nucleotide sequence determined from the cloning of the human BFLP0169 gene allows for the generation of probes and primers designed for use in identifying and/or cloning BFLP0169 homologues in other cell types, e.g., from other tissues, as well as BFLP0169 homologues from other mammals. The probe/primer typically comprises a substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 or more consecutive sense strand nucleotide sequence of SEQ ID NO:1; or an anti-sense strand nucleotide sequence of SEQ ID NO:1; or of a naturally occurring mutant of SEQ ID NO:1.

[0050] Probes based on the human BFLP0169 nucleotide sequence can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, e.g., the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissue which misexpress a BFLP0169 protein, such as by measuring a level of a BFLP0169-encoding nucleic acid in a sample of cells from a subject e.g., detecting BFLP0169 mRNA levels or determining whether a genomic BFLP0169 gene has been mutated or deleted.

[0051] A "polypeptide having a biologically active portion of BFLP0169" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as mea-

sured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically active portion of BFLP0169" can be prepared by isolating a portion of SEQ ID NO:1 that encodes a polypeptide having a BFLP0169 biological activity (biological activities of the BFLP0169 proteins are described below), expressing the encoded portion of BFLP0169 protein (e.g., by recombinant expression in vitro) and assessing the activity of the encoded portion of BFLP0169.

[0052] The invention also provides polymorphic forms of BFLP0169 nucleic acid sequences as well as methods of detecting polymorphic sequences in BFLP0169 sequences The polymorphic forms include genomic sequences corresponding to exons and/or introns associated with BFLP0169.

[0053] Individuals carrying polymorphic alleles of the invention may be detected at either the DNA, the RNA, or the protein level using a variety of techniques that are well known in the art. The present methods usually employ pre-characterized polymorphisms. That is, the genotyping location and nature of polymorphic forms present at a site have already been determined. The availability of this information allows sets of probes to be designed for specific identification of the known polymorphic forms.

[0054] The genomic DNA used for the diagnosis may be obtained from any nucleated cells of the body, such as those present in peripheral blood, urine, saliva, buccal samples, surgical specimen, and autopsy specimens. The DNA may be used directly or may be amplified enzymatically in vitro through use of PCR or other in vitro amplification methods such as the ligase chain reaction (LCR), strand displacement amplification (SDA), self-sustained sequence replication (3SR), prior to mutation analysis.

[0055] The detection of polymorphisms in specific DNA sequences, can be accomplished by a variety of methods including, but not limited to, restriction-fragment-length-polymorphism detection based on allele-specific restriction-endonuclease cleavage, hybridization with allele-specific oligonucleotide probes, including immobilized oligonucleotides or oligonucleotide arrays, allele-specific PCR, mismatch-repair detection (MRD), binding of MutS protein, denaturing-gradient gel electrophoresis (DGGE), single-strand-conformation-polymorphism detection, RNAase cleavage at mismatched base-pairs, chemical or enzymatic cleavage of heteroduplex DNA, methods based on allele specific primer_extension, genetic bit analysis (GBA), the oligonucleotide-ligation assay (OLA), the allele-specific ligation chain reaction (LCR), gap-LCR, radioactive and/or fluorescent DNA sequencing using standard procedures well known in the art, and peptide nucleic acid (PNA) assays.

BFLP0169 Variants

[0056] The invention further encompasses nucleic acid molecules that differ from the nucleotide sequences shown in SEQ ID NO:1 due to the degeneracy of the genetic code. These nucleic acids thus encode the same BFLP0169 protein as that encoded by the nucleotide sequence shown in SEQ ID NO:1, e.g., the polypeptide of SEQ ID NO:2. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in SEQ ID NO:2.

[0057] In addition to the human BFLP0169 nucleotide sequence shown in SEQ ID NO:1, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of BFLP0169 may exist within a population (e.g., the human population). Such genetic polymorphism in the BFLP0169 gene may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a BFLP0169 protein, preferably a mammalian BFLP0169 protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the BFLP0169 gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in BFLP0169 that are the result of natural allelic variation and that do not alter the functional activity of BFLP0169 are intended to be within the scope of the invention.

[0058] Moreover, nucleic acid molecules encoding BFLP0169 proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence of SEQ ID NO:1 are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the BFLP0169 cDNAs of the invention can be isolated based on their homology to the human BFLP0169 nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. For example, a soluble human BFLP0169 cDNA can be isolated based on its homology to human membrane-bound BFLP0169. Likewise, a membrane-bound human BFLP0169 cDNA can be isolated based on its homology to soluble human BFLP0169.

[0059] Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1. In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500 or 750 nucleotides in length. In another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

[0060] Homologs (i.e., nucleic acids encoding BFLP0169 proteins derived from species other than human) or other related sequences (e.g., paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

Thus, the present invention also includes polynucleotides capable of hybridizing under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

TABLE 4

		Stringency Conditions		
Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp)[1]	Hybridization Temperature and Buffer[H]	Wash Temperature and Buffer[H]
A	DNA:DNA	≧50	65° C.; 1xSSC -or- 42° C.; 1xSSC, 50% formamide	65° C.; 0.3xSSC
B	DNA:DNA	<50	T_B*; 1xSSC	T_B*; 1xSSC 67° C.; 0.3xSSC
C	DNA:RNA	≧50	67° C.; 1xSSC -or- 45° C.; 1xSSC, 50% formamide	
D	DNA:RNA	<50	T_D*; 1xSSC	T_D*; 1xSSC 70° C.; 0.3xSSC
E	RNA:RNA	≧50	70° C.; 1xSSC -or- 50° C.; 1xSSC, 50% formamide	
F	RNA:RNA	<50	T_F*; 1xSSC	T_f*; 1xSSC 65° C.; 1xSSC
G	DNA:DNA	≧50	65° C.; 4xSSC -or- 42° C.; 4xSSC, 50% formamide	
H	DNA:DNA	<50	T_H*; 4xSSC	T_H*; 4xSSC 67° C.; 1xSSC
I	DNA:RNA	≧50	67° C.; 4xSSC -or- 45° C.; 4xSSC, 50% formamide	
J	DNA:RNA	<50	T_J*; 4xSSC	T_J*; 4xSSC 67° C.; 1xSSC
K	RNA:RNA	≧50	70° C.; 4xSSC -or- 50° C.; 4xSSC, 50% formamide	
L	RNA:RNA	<50	T_L*; 2xSSC	T_L*; 2xSSC 50° C.; 2xSSC
M	DNA:DNA	>50	50° C.; 4xSSC -or- 40° C.; 6xSSC, 50% formamide	
N	DNA:DNA	<50	T_N*; 6xSSC	T_N*; 6xSSC 55° C.; 2xSSC
O	DNA:RNA	>50	55° C.; 4xSSC -or- 42° C.; 6xSSC, 50% formamide	
P	DNA:RNA	<50	T_P*; 6xSSC	T_P*; 6xSSC 60° C.; 2xSSC
Q	RNA:RNA	>50	60° C.; 4xSSC -or- 45° C.; 6xSSC, 50% formamide	
R	RNA:RNA	<50	T_R*; 4xSSC	T_R*; 4xSSC

[0061] 1: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

[0062] [H]:SSPE (1×SSPE is 0.15M NaCl, 10 mM NaH_2PO_4, and 1.25 mM EDTA, pH 7.4) can be substituted for SSC (1×SSC is 0.15M NaCl and 15 mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

T_B*-T_R*: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10° C. less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(° C.)=2(# of A+T bases)+4(# of G+C bases). For hybrids between 18 and 49 base pairs in length, T_m(° C.)=81.5+16.6($\log_{10}Na^+$)+0.41(% G+C)−(600/N), where N is the number of bases in the hybrid, and Na^+ is the concentration of sodium ions in the hybridization buffer (Na^+ for 1×SSC=0.165 M).

[0063] Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

[0064] A non-limiting example of stringent hybridization conditions is hybridization in a high salt buffer comprising 6×SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65° C. This hybridization is followed by one or more washes in 0.2×SSC, 0.01% BSA at 50° C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of SEQ ID NO:1 corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

[0065] In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are hybridization in 6×SSC, 5×Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55° C., followed by one or more washes in 1×SSC, 0.1% SDS at 37° C.

[0066] In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5×SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40° C., followed by one or more washes in 2×SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50° C.

Conservative Mutations

[0067] In addition to naturally-occurring allelic variants of the BFLP0169 sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequence of SEQ ID NO:1, thereby leading to changes in the amino acid sequence of the encoded BFLP0169 protein, without altering the functional ability of the BFLP0169 protein. For example, nucleotide substitutions leading to amino acid substitutions at

"non-essential" amino acid residues can be made in the sequence of SEQ ID NO:1. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of BFLP0169 without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, altering amino acid residues that are conserved among the BFLP0169 proteins of the present invention, is likely to result in loss of activity of the BFLP0169 protein.

[0068] Another aspect of the invention pertains to nucleic acid molecules encoding BFLP0169 proteins that contain changes in amino acid residues that are not essential for activity. Such BFLP0169 proteins differ in amino acid sequence from SEQ ID NO:2, yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 75% homologous to the amino acid sequence of SEQ ID NO:2. Preferably, the protein encoded by the nucleic acid is at least about 80% homologous to SEQ ID NO:2, more preferably at least about 90%, 95%, 98%, and most preferably at least about 99% homologous to SEQ ID NO:2.

[0069] An isolated nucleic acid molecule encoding a BFLP0169 protein homologous to the protein of SEQ ID NO:2 can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of SEQ ID NO:1, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

[0070] Mutations can be introduced into the nucleotide sequence of SEQ ID NO:1 by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in BFLP0169 is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a BFLP0169 coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for BFLP0169 biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:1 the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

[0071] In one embodiment, a mutant BFLP0169 protein can be assayed for (1) the ability to form protein:protein interactions with other BFLP0169 proteins, other cell-surface proteins, or biologically active portions thereof, (2) complex formation between a mutant BFLP0169 protein and a BFLP0169 receptor; (3) the ability of a mutant BFLP0169 protein to bind to an intracellular target protein or biologically active portion thereof; (e.g., avidin proteins); (4) the ability to bind BFLP0169 protein; or (5) the ability to specifically bind an anti-BFLP0169 protein antibody.

Antisense BFLP0169 Nucleic Acids

[0072] Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire BFLP0169 coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a BFLP0169 protein of SEQ ID NO:2, or antisense nucleic acids complementary to a BFLP0169 nucleic acid sequence of SEQ ID NO:1 are additionally provided.

[0073] In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding BFLP0169. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (e.g., the protein coding region of human BFLP0169 corresponds to SEQ ID NO:2). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding BFLP0169. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

[0074] Given the coding strand sequences encoding BFLP0169 disclosed herein (e.g., SEQ ID NO:1), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of BFLP0169 mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of BFLP0169 mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of BFLP0169 mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

[0075] Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galac-

tosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl)uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

[0076] The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a BFLP0169 protein to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

[0077] In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other. The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide.

[0078] Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

BFLP0169 Ribozymes and PNA Moieties

[0079] In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes) can be used to catalytically cleave BFLP0169 mRNA transcripts to thereby inhibit translation of BFLP0169 mRNA. A ribozyme having specificity for a BFLP0169-encoding nucleic acid can be designed based upon the nucleotide sequence of a BFLP0169 DNA disclosed herein (i.e., SEQ ID NO:1). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a BFLP0169-encoding mRNA. Alternatively, BFLP0169 mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules.

[0080] Alternatively, BFLP0169 gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the BFLP0169 (e.g., the BFLP0169 promoter and/or enhancers) to form triple helical structures that prevent transcription of the BFLP0169 gene in target cells.

[0081] In various embodiments, the nucleic acids of BFLP0169 can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids. As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols.

[0082] PNAs of BFLP0169 can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of BFLP0169 can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases; or as probes or primers for DNA sequence and hybridization.

[0083] In another embodiment, PNAs of BFLP0169 can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of BFLP0169 can be generated that may combine the advantageous properties of PNA and DNA.

[0084] The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane or the blood-brain barrier. In addition, oligonucleotides can be modified with hybridization triggered cleavage agents or intercalating agents. To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

BFLP0169 Interfering Nucleic Acids

[0085] Also provided by the invention is an isolated double-stranded nucleic acid (DNA or RNA) that is capable of mediating specific inhibition of BFLP0169 gene expres-

sion. In preferred embodiments, one or both strands of the double-stranded molecule is an RNA molecule. Preferably, each RNA strand has a length from 19-25, particularly from 19-23 nucleotides, more particularly from 20-22 nucleotides, and is capable of mediating BFLP0169 target-specific nucleic acid modifications, particularly RNA interference and/or DNA methylation. The double-stranded BFLP0169 molecule may be double stranded or have an overhang at one or both the 5' and/or 3' terminus. For example, the molecule may have a 3' overhang. The length of the 3'-overhang can be, e.g., 1-6 nucleotides, 2-5 nucleotides, 3-4 nucleotides, or 2 nucleotides. The length of the overhang may be the same or different for each strand. In one embodiment, dsRNAs are composed of two 21 nucleotide strands that are paired such that 1, 2, or 3 nucleotide overhangs are present on both ends of the double-stranded RNA.

[0086] The RNA strands preferably have 3'-hydroxyl groups. The 5'-terminus preferably includes a phosphate, diphosphate, triphosphate or hydroxyl group. If desired, the 3'-overhangs may be stabilized against degradation. For example, they may be selected such that they consist of purine nucleotides, particularly adenosine or guanosine nucleotides. Alternatively, pyrimidine nucleotides may be replaced with modified analogues, e.g. substitution of uridine-2 nucleotide 3' overhangs by 2'-deoxythymidine is tolerated, and does not affect the efficiency of RNA interference. The RNA molecule may contain at least one modified nucleotide analogue. The nucleotide analogues may be located at positions where the target-specific activity, e.g. the RNAi mediating activity is not substantially affected. The modified nucleotide is preferably present in a region at the 5'-end and/or the 3'-end of the double-stranded RNA molecule. In some embodiments, overhangs are stabilized by incorporating modified nucleotide analogues.

[0087] Nucleotide analogues can include sugar- or backbone-modified ribonucleotides. Other suitable nucleotides include a non-naturally occurring nucleobase instead of a naturally occurring nucleobases. For example, analogues can include uridines or cytidines modified at the 5-position, e.g. 5-(2-amino)propyl uridine, 5-bromo uridine; adenosines and guanosines modified at the 8-position, e.g. 8-bromo guanosine; deaza nucleotides, e.g. 7-deaza-adenosine; O- and N-alkylated nucleotides, e.g. N6-methyl adenosine are suitable. In preferred sugar-modified ribonucleotides the 2' OH-group is replaced by a group selected from H, OR, R, halo, SH, SR, NH_2, NHR, NR_2 or CN, wherein R is C_1-C_6 alkyl, alkenyl or alkynyl and halo is F, Cl, Br or I. In a preferred embodiment, where backbone-modified ribonucleotides are used as the phosphoester group connecting to adjacent ribonucleotides, they are replaced by a modified group, e.g. a phosphothioate group. It should be noted that the above modifications may be combined.

[0088] The BFLP0169 interfering RNA molecule can be a naturally isolated RNA molecule or can a synthetic RNA molecule. Preferably, the BFLP0169 interfering RNA molecule is substantially free from contaminants occurring in cell extracts, e.g. from *Drosophila* embryos. Further, the BFLP0169 interfering RNA molecule is preferably substantially free from any non-target-specific contaminants, particularly non-target-specific RNA molecules e.g. from contaminants occurring in cell extracts.

[0089] Isolated double-stranded BFLP0169 interfering molecules can be used for mediating BFLP0169 target-specific nucleic acid modifications, particularly RNAi, in mammalian cells, particularly in human cells.

[0090] The sequence of the double-stranded BFLP0169 interfering molecule of the present invention is of sufficient identity to a nucleic acid BFLP0169 target molecule in order to effect target-specific interference of BFLP0169 gene expression and/or DNA methylation. Preferably, the sequence has an identity of at least 50%, particularly of at least 70% to the desired target molecule in the double-stranded portion of the RNA molecule. More preferably, the identity is at least 85% and most preferably 100% in the double-stranded portion of the RNA molecule. The identity of a BFLP0169 double-stranded interfering RNA molecule to a predetermined nucleic acid target molecule, e.g. an BFLP0169 mRNA target molecule with the sequence shown in SEQ ID NO:1, may be determined using the equation: $I=(n/L)\times 100$, wherein I is the identity in percent, n is the number of identical nucleotides in the double-stranded portion of the ds RNA and the target and L is the length of the sequence overlap of the double-stranded portion of the dsRNA and the target.

[0091] Alternatively, the identity of the double-stranded RNA molecule relative to the target sequence may also be defined including the 3' overhang, particularly an overhang having a length from 1-3 nucleotides. In this case the sequence identity is preferably at least 50%, more preferably at least 70% and most preferably at least 85% to the target sequence. For example, the nucleotides from the 3' overhang and up to 2 nucleotides from the 5' and/or 3' terminus of the double strand may be modified without significant loss of activity.

[0092] A double-stranded BFLP0169 RNA molecule may be prepared by a method that includes synthesizing two RNA strands each having a length from 19-25, e.g. from 19-23 nucleotides, wherein said RNA strands are capable of forming a double-stranded RNA molecule, wherein preferably at least one strand has a 3'-overhang from 1-5 nucleotides, and (b) combining the synthesized RNA strands under conditions, wherein a double-stranded RNA molecule is formed. The double-stranded RNA molecule is capable of mediating target-specific nucleic acid modifications, particularly RNA interference and/or DNA methylation.

[0093] Methods of synthesizing RNA molecules are known in the art. The single-stranded RNAs can also be prepared by enzymatic transcription from synthetic DNA templates or from DNA plasmids isolated from recombinant bacteria. Typically, phage RNA polymerases are used such as T7, T3 or SP6 RNA polymerase.

[0094] A further aspect of the present invention relates to a method of mediating BFLP0169-specific nucleic acid modifications, particularly RNA interference and/or DNA methylation in a cell or an organism by contacting the cell or organism with the double-stranded RNA molecule of the invention under conditions wherein target-specific nucleic acid modifications may occur and mediating a target-specific nucleic acid modification effected by the double-stranded RNA towards a BFLP0169 target nucleic acid.

BFLP0169 Polypeptides

[0095] A BFLP0169 polypeptide of the invention includes the BFLP0169-like protein whose sequence is provided in SEQ ID NO:2. The invention also includes a mutant or variant

form of the disclosed BFLP0169 polypeptide, or of any of the fragments of the herein disclosed BFLP0169 polypeptide sequences.

[0096] Thus, a BFLP0169 polypeptide includes one in which any residues may be changed from the corresponding residue shown in SEQ ID NO:2 while still encoding a protein that maintains its BFLP0169-like activities and physiological functions, or a functional fragment thereof. In some embodiments, up to 20% or more of the residues may be so changed in the mutant or variant protein. In some embodiments, the BFLP0169 polypeptide according to the invention is a mature polypeptide.

Rapamycin Binding Domains

[0097] To identify regions of a BFLP0169 polypeptide sequence (e.g., a polypeptide including all or a portion of SEQ ID NO:2) containing rapamycin binding domains, the entire coding sequence, or a fragment of a BFLP0169 polypeptide sequence, is tested for its ability to bind rapamycin. Any technique known in the art for determining binding of a polypeptide to a small molecule can be used. For example, rapamycin can be labeled (i.e., with a non-radioactive label or with a radiolabel (e.g., ^{14}C, ^{32}P, ^{3}H, or ^{125}I), and mixed with a polypeptide containing some or all of a BFLP0169 polypeptide sequence. The polypeptide optionally includes a moiety that facilitates detection, e.g., the polypeptide can be a fusion polypeptide that includes a BFLP0169 sequence and a non-BFLP0169 polypeptide sequence.

[0098] A reagent specific for the polypeptide containing the BFLP0169 polypeptide sequence (e.g., an antibody specific for BFLP0169 or a probe specific for the non-BFLP0169 polypeptide in the case of a fusion polypeptide) is added to the mixture. Complexes that bind to the reagent are isolated, and the presence of label, which reveals the presence of rapamycin, is determined.

[0099] In general, a BFLP0169-like variant that preserves BFLP0169-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above.

[0100] One aspect of the invention pertains to isolated BFLP0169 proteins, and biologically active portions thereof, or derivatives, fragments, analogs or homologs thereof. Fragments can comprise contiguous stretches of SEQ ID NO:2, or interspersed segments of SEQ ID NO:2. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-BFLP0169 antibodies. In one embodiment, native BFLP0169 proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, BFLP0169 proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, a BFLP0169 protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

[0101] A "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the BFLP0169 protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of BFLP0169 protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of BFLP0169 protein having less than about 30% (by dry weight) of non-BFLP0169 protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-BFLP0169 protein, still more preferably less than about 10% of non-BFLP0169 protein, and most preferably less than about 5% non-BFLP0169 protein. When the BFLP0169 protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

[0102] The language "substantially free of chemical precursors or other chemicals" includes preparations of BFLP0169 protein in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of BFLP0169 protein having less than about 30% (by dry weight) of chemical precursors or non-BFLP0169 chemicals, more preferably less than about 20% chemical precursors or non-BFLP0169 chemicals, still more preferably less than about 10% chemical precursors or non-BFLP0169 chemicals, and most preferably less than about 5% chemical precursors or non-BFLP0169 chemicals.

[0103] Biologically active portions of a BFLP0169 protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the BFLP0169 protein, e.g., the amino acid sequence shown in SEQ ID NO:2 that include fewer amino acids than the full length BFLP0169 proteins, and exhibit at least one activity of a BFLP0169 protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the BFLP0169 protein. A biologically active portion of a BFLP0169 protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length.

[0104] A biologically active portion of a BFLP0169 protein of the present invention may contain at least one of the above-identified domains conserved between the BFLP0169 proteins. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native BFLP0169 protein.

[0105] In an embodiment, the BFLP0169 protein has an amino acid sequence shown in SEQ ID NO:2. In other embodiments, the BFLP0169 protein is substantially homologous to SEQ ID NO:2 and retains the functional activity of the protein of SEQ ID NO:2, yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail below. Accordingly, in another embodiment, the BFLP0169 protein is a protein that comprises an amino acid sequence at least about 45% homologous to the amino acid sequence of SEQ ID NO:2 and retains the functional activity of the BFLP0169 proteins of SEQ ID NO:2.

Determining Homology Between Two or More Sequences

[0106] To determine the percent homology of two amino acid sequences or of two nucleic acid sequences, the

sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in either of the sequences being compared for optimal alignment between the sequences). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (i.e., as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

[0107] The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NO:1.

[0108] The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (e.g., A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (i.e., the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region. The term "percentage of positive residues" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical and conservative amino acid substitutions, as defined above, occur in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (i.e., the window size), and multiplying the result by 100 to yield the percentage of positive residues.

Chimeric and Fusion Proteins

[0109] The invention also provides BFLP0169 chimeric or fusion proteins. As used herein, a BFLP0169 "chimeric protein" or "fusion protein" comprises a BFLP0169 polypeptide operatively linked to a non-BFLP0169 polypeptide. A "BFLP0169 polypeptide" refers to a polypeptide having an amino acid sequence corresponding to BFLP0169, whereas a "non-BFLP0169 polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the BFLP0169 protein, e.g., a protein that is different from the BFLP0169 protein and that is derived from the same or a different organism. Within a BFLP0169 fusion protein the BFLP0169 polypeptide can correspond to all or a portion of a BFLP0169 protein. An example of a BFLP0169 fusion polypeptide is one that includes amino acids 21-230 of SEQ ID NO:2 (e.g., a polypeptide that includes amino acids 1-246 or amino acids 21-246 of SEQ ID NO:2). In one embodiment, a BFLP0169 fusion protein comprises at least one biologically active portion of a BFLP0169 protein. In another embodiment, a BFLP0169 fusion protein comprises at least two biologically active portions of a BFLP0169 protein. Within the fusion protein, the term "operatively linked" is intended to indicate that the BFLP0169 polypeptide and the non-BFLP0169 polypeptide are fused in-frame to each other. The non-BFLP0169 polypeptide can be fused to the N-terminus or C-terminus of the BFLP0169 polypeptide.

[0110] For example, in one embodiment a BFLP0169 fusion protein comprises a BFLP0169 polypeptide operably linked to either an extracellular domain of a second protein, i.e., non-BFLP0169 protein, or to the transmembrane and intracellular domain of a second protein, i.e., non-BFLP0169 protein. Such fusion proteins can be further utilized in screening assays for compounds that modulate BFLP0169 activity (such assays are described in detail below).

[0111] In another embodiment, the fusion protein is a GST-BFLP0169 fusion protein in which the BFLP0169 sequences are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant BFLP0169.

[0112] In another embodiment, the fusion protein is a BFLP0169-immunoglobulin fusion protein in which the BFLP0169 sequences comprising one or more domains are fused to sequences derived from a member of the immunoglobulin protein family.

[0113] Inhibition of the BFLP0169 ligand/BFLP0169 interaction can be used therapeutically for both the treatment of proliferative and differentiative disorders, e,g., cancer, modulating (e.g., promoting or inhibiting) cell survival as well as immunomodulatory disorders, autoimmunity, transplantation, and inflammation by alteration of cyotokine and chemokine cascade mechanisms. Moreover, the BFLP0169-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-BFLP0169 antibodies in a subject, to purify BFLP0169 ligands, and in screening assays to identify molecules that inhibit the interaction of BFLP0169 with a BFLP0169 ligand.

[0114] A BFLP0169 chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence. Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A BFLP0169-encoding nucleic acid can be cloned into such an

expression vector such that the fusion moiety is linked in-frame to the BFLP0169 protein.

[0115] If desired, libraries of fragments of the BFLP0169 protein coding sequence can be used to generate a variegated population of BFLP0169 fragments for screening and subsequent selection of variants of a BFLP0169 protein.

BFLP0169 Antibodies

[0116] Also included in the invention are antibodies to BFLP0169 proteins, or fragments of BFLP0169 proteins. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab}, $F_{ab'}$ and $F_{(ab')2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG_1, IgG_2, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

[0117] An isolated BFLP0169-related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO:2, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

[0118] In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of BFLP0169-related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human BFLP0169-related protein sequence will indicate which regions of a BFLP0169-related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. A Kylte & Doolitle plot was generated for the BFLP0169 protein, and is shown in FIG. **2**.

[0119] The novel nucleic acid encoding the BFLP0169 protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods. The disclosed BFLP0169 protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated BFLP0169 epitope is from about amino acids 20 to 90. In another embodiment, a BFLP0169 epitope is from about amino acids 100 to 130. In additional embodiments, BFLP0169 epitopes are from about amino acids 140 to 220, from about amino acids 240 to 250, from about amino acids 280 to 290, from about amino acids 330 to 340, from about amino acids 370 to 380, from about amino acids 400 to 410, from about amino acids 450 to 520, from about amino acids 530 to 540, from about amino acids 640 to 650, from about amino acids 720 to 730, from about amino acids 800 to 820, from about amino acids 850 to 855, from about amino acids 900 to 910, from about amino acids 920 to 930, from about amino acids 940 to 950, from about amino acids 970 to 990, from about amino acids 1000 to 1030, from about amino acids 1060 to 1080, from about amino acids 1100 to 1110, from about amino acids 1170 to 1180, from about amino acids 1190 to 1210, from about amino acids 1250 to 1280, from about amino acids 1310 to 1320, from about amino acids 1350 to 1370, from about amino acids 1400 to 1420, from about amino acids 1430 to 1440, from about amino acids 1500 to 1560, from about amino acids 1600 to 1610, from about amino acids 1650 to 1690, from about amino acids 1700 to 1710, and from about amino acids 1720 to 1730.

[0120] Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

[0121] A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

[0122] Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof. The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product.

[0123] The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. The humanized forms of antibodies include_chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin.

[0124] The antibodies can also be human antibodies, e.g., antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique and the EBV hybridoma technique.

[0125] Human antibodies can also be produced using phage display libraries, or by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endog-

enous immunoglobulin genes have been partially or completely inactivated. Human antibodies may additionally be produced using transgenic nonhuman animals that are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen.

[0126] The invention also provides single-chain antibodies specific to an antigenic protein of the invention. In addition, methods can be adapted for the construction of F_{ab} expression libraries to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab')2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab')2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

[0127] Also provided by the invention are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. One of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

[0128] If desired, antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions.

[0129] Bispecific antibodies can be provided as full length antibodies or antibody fragments (e.g. $F(ab')_2$ bispecific antibodies).

[0130] Also within the invention are antibodies with more than two valencies (such as trispecific antibodies).

[0131] Exemplary bispecific antibodies bind to two different epitopes, at least one of which originates in the protein antigen of the invention.

[0132] The invention also includes heteroconjugate antibodies, which include two covalently joined antibodies.

[0133] The antibody of the invention can be modified to alter (e.g., enhance or diminish) its function. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The invention also includes immunoconjugates that include an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

[0134] Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), *momordica charantia* inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, and ^{186}Re.

[0135] The antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

BFLP0169 Recombinant Expression Vectors and Host Cells

[0136] Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding a BFLP0169 protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having 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 genomic sequence into which they have integrated. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively-linked. Such vectors are referred to herein as "expression vectors". "Plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

[0137] Within a recombinant expression vector, "operably-linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (e.g., in an in vitro transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). 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 (e.g., BFLP0169 proteins, mutant forms of BFLP0169 proteins, fusion proteins, etc.).

[0138] The recombinant expression vectors of the invention can be designed for expression of BFLP0169 proteins in prokaryotic or eukaryotic cells. For example, BFLP0169 proteins can be expressed in bacterial cells such as *Escherichia coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Alternatively, the recombinant

expression vector can be transcribed and translated in vitro, for example using T7 promoter regulatory sequences and T7 polymerase.

[0139] In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 and pMT2PC. When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, adenovirus 2, cytomegalovirus, and simian virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells.

[0140] In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific), lymphoid-specific promoters, in particular promoters of T cell receptors and immunoglobulins, neuron-specific promoters (e.g., the neurofilament promoter), pancreas-specific promoters, and mammary gland-specific promoters (e.g., milk whey promoter). Developmentally-regulated promoters are also encompassed, e.g., the murine hox promoters and the α-fetoprotein promoter.

[0141] The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively-linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to BFLP0169 mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced.

[0142] Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer 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 either mutation or environmental influences, 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.

[0143] A host cell can be any prokaryotic or eukaryotic cell. For example, BFLP0169 protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as human, Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

[0144] A gene that encodes a selectable marker (e.g., resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. A nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding BFLP0169 or can be introduced on a separate vector. 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).

[0145] A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (i.e., express) BFLP0169 protein. Accordingly, the invention further provides methods for producing BFLP0169 protein using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding BFLP0169 protein has been introduced) in a suitable medium such that BFLP0169 protein is produced. In another embodiment, the method further comprises isolating BFLP0169 protein from the medium or the host cell.

Transgenic BFLP0169 Animals

[0146] The host cells of the invention can also be used to produce non-human transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which BFLP0169 protein-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous BFLP0169 sequences have been introduced into their genome or homologous recombinant animals in which endogenous BFLP0169 sequences have been altered. Such animals are useful for studying the function and/or activity of BFLP0169 protein and for identifying and/or evaluating modulators of BFLP0169 protein activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous BFLP0169 gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, e.g., an embryonic cell of the animal, prior to development of the animal.

[0147] A transgenic animal of the invention can be created by introducing BFLP0169-encoding nucleic acid into the male pronuclei of a fertilized oocyte (e.g., by microinjection, retroviral infection) and allowing the oocyte to develop in a pseudopregnant female foster animal. Sequences including SEQ ID NO:1 can be introduced as a transgene into the genome of a non-human animal. Alternatively, a non-human homologue of the human BFLP0169 gene, such as a mouse BFLP0169 gene, can be isolated based on hybridization to the human BFLP0169 cDNA (described further supra) and used as a transgene. Intronic sequences and polyadenylation sig-

nals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably-linked to the BFLP0169 transgene to direct expression of BFLP0169 protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the BFLP0169 transgene in its genome and/or expression of BFLP0169 mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene-encoding BFLP0169 protein can further be bred to other transgenic animals carrying other transgenes.

[0148] To create a homologous recombinant animal, a vector is prepared which contains at least a portion of a BFLP0169 gene into which a deletion, addition or substitution has been introduced to thereby alter, e.g., functionally disrupt, the BFLP0169 gene. The BFLP0169 gene can be a human gene (e.g., the DNA of SEQ ID NO:1), but more preferably, is a non-human homologue of a human BFLP0169 gene. For example, a mouse homologue of human BFLP0169 gene of SEQ ID NO:1 can be used to construct a homologous recombination vector suitable for altering an endogenous BFLP0169 gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous BFLP0169 gene is functionally disrupted (i.e., no longer encodes a functional protein; also referred to as a "knock out" vector).

[0149] Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous BFLP0169 gene is mutated or otherwise altered but still encodes functional protein (e.g., the upstream regulatory region can be altered to thereby alter the expression of the endogenous BFLP0169 protein). In the homologous recombination vector, the altered portion of the BFLP0169 gene is flanked at its 5'- and 3'-termini by additional nucleic acid of the BFLP0169 gene to allow for homologous recombination to occur between the exogenous BFLP0169 gene carried by the vector and an endogenous BFLP0169 gene in an embryonic stem cell. The additional flanking BFLP0169 nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5'- and 3'-termini) are included in the vector. The vector is then introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced BFLP0169 gene has homologously-recombined with the endogenous BFLP0169 gene are selected.

[0150] The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously-recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously-recombined DNA by germline transmission of the transgene.

[0151] In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae*. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

[0152] Clones of the non-human transgenic animals described herein can also be produced according to the methods described in the art. In brief, a cell (e.g., a somatic cell) from the transgenic animal can be isolated and induced to exit the growth cycle and enter G_0 phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of this female foster animal will be a clone of the animal from which the cell (e.g., the somatic cell) is isolated.

Methods of Detecting BFLP0169 Nucleic Acids and Diagnosing Lupus Nephritis

[0153] Reagents that detect BFLP0169 nucleic acids and/or polypeptides can be used to detect levels of BFLP0169 RNA and/or proteins sequences in a sample. Because elevated levels of BFLP0169 RNA are found in animals with lupus nephritis, detection of enhanced levels of BFLP0169 RNA and/or BFLP0169 polypeptides indicates the presence or predisposition to lupus in the subject. In addition, lowered levels of BFLP0169 RNA in treated lupus subjects as compared to untreated lupus indicates a return to a non-lupus state. Thus, the efficacy of lupus treatment can be monitored by comparing BFLP0169 RNA or protein levels in a sample from a treated population to samples in a diseased but untreated sample, (or a sample from an individual that has been treated for a shorter period of time).

[0154] Levels of BFLP0169 RNA can be assessed by comparing levels in a test cell population, from a subject whose lupus status is unknown, to levels in a reference cell population whose lupus status is known. Thus, the test cell population will typically include at least one cell that is capable of expressing a BFLP0169 gene. By "capable of expressing" is meant that the gene is present in an intact form in the cell and can be expressed. Expression of the BFLP0169 sequence is then detected, if present, and, preferably, measured using methods known in the art. For example, the BFLP0169 sequences disclosed herein can be used to construct probes for detecting BFLP0169 RNA sequences in, e.g., northern blot hybridization analyses or methods which specifically, and, preferably, quantitatively amplify BFLP0169 specific nucleic acid sequences. Alternatively, the sequences can be used to construct primers for specifically amplifying the BFLP0169 sequences in, e.g., amplification-based detection methods such as reverse-transcription based polymerase chain reaction.

[0155] BFLP0169 expression can be also measured at the protein level, i.e., by measuring the levels of BFLP0169 polypeptides. Such methods are well known in the art and include, e.g., immunoassays based on antibodies to proteins encoded by the genes.

[0156] Expression of sequences in test and control populations of cells can be compared using any art-recognized method for comparing expression of nucleic acid sequences. Whether or not comparison of the gene expression profile in the test cell population to the reference cell population reveals the presence, or degree, of the measured parameter depends on the composition of the reference cell population. For example, if the reference cell population is composed of cells from a lupus free subject, a similar gene expression level in the test cell population and a reference cell population indicates the test cell population is from a lupus free subject. Conversely, if the reference cell population is made up of cells from a diseased subject, a similar gene expression profile between the test cell population and the reference cell population indicates the test cell population is from a subject with lupus.

[0157] In various embodiments, a BFLP0169 sequence in a test cell population is considered comparable in expression level to the expression level of the ADIPO sequence in the reference cell population if its expression level varies within a factor of 2.0, 1.5, or 1.0 fold to the level of the BFLP0169 transcript in the reference cell population. In various embodiments, a BFLP0169 sequence in a test cell population can be considered altered in levels of expression if its expression level varies from the reference cell population by more than 1.0, 1.5, 2.0 or more fold from the expression level of the corresponding BFLP0169 sequence in the reference cell population.

[0158] If desired, comparison of differentially expressed sequences between a test cell population and a reference cell population can be done with respect to a control nucleic acid whose expression is independent of the parameter or condition being measured. Expression levels of the control nucleic acid in the test and reference nucleic acid can be used to normalize signal levels in the compared populations. Suitable control nucleic acids can readily be determined by one of ordinary skill in the art.

[0159] In some embodiments, the test cell population is compared to multiple reference cell populations. Each of the multiple reference populations may differ in the known parameter. Thus, a test cell population may be compared to a first reference cell population from a subject known to have lupus, as well as a second reference population known to not have lupus.

[0160] The test cell population that is exposed can be any number of cells, i.e., one or more cells, and can be provided in vitro, in vivo, or ex vivo.

[0161] Preferably, cells in the reference cell population are derived from a tissue type as similar as possible to test cell, e.g., renal tissue. In some embodiments, the control cell is derived from the same subject as the test cell. In other embodiments, the reference cell population is derived from a plurality of cells from multiple subjects. For example, the reference cell population can be a database of expression patterns from previously tested cells.

[0162] The subject is preferably a mammal. The mammal can be, e.g., a human, non-human primate, mouse, rat, dog, cat, horse, or cow.

Pharmaceutical Compositions

[0163] The BFLP0169 nucleic acid molecules, BFLP0169 proteins, and anti-BFLP0169 antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, Ringer's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

[0164] A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, e.g., intravenous, intradermal, subcutaneous, oral (e.g., inhalation), transdermal (i.e., topical), transmucosal, and rectal administration.

[0165] Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion.

[0166] Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

[0167] Sustained-release preparations can be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides, copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods.

[0168] The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Screening and Detection Methods

[0169] The isolated nucleic acid molecules of the invention can be used to express BFLP0169 protein (e.g., via a recom-

binant expression vector in a host cell in gene therapy applications), to detect BFLP0169 mRNA (e.g., in a biological sample) or a genetic lesion in a BFLP0169 gene, and to modulate BFLP0169 activity, as described further, below. In addition, the BFLP0169 proteins can be used to screen drugs or compounds that modulate the BFLP0169 protein activity or expression as well as to treat disorders characterized by insufficient or excessive production of BFLP0169 protein or production of BFLP0169 protein forms that have decreased or aberrant activity compared to BFLP0169 wild-type protein. In addition, the anti-BFLP0169 antibodies of the invention can be used to detect and isolate BFLP0169 proteins and modulate BFLP0169 activity. For example, BFLP0169 activity includes T-cell or NK cell growth and differentiation, antibody production, and tumor growth.

[0170] The invention further pertains to novel agents identified by the screening assays described herein and uses thereof for treatments as described, supra.

Screening Assays

[0171] The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, i.e., candidate or test compounds or agents (e.g., peptides, peptidomimetics, small molecules or other drugs) that bind to BFLP0169 proteins or have a stimulatory or inhibitory effect on, e.g., BFLP0169 protein expression or BFLP0169 protein activity. The invention also includes compounds identified in the screening assays described herein.

[0172] In one embodiment, the screening assays are used to identify therapeutic agents for treating autoimmune diseases. The autoimmune disease can be, e.g., lupus, including lupus nephtitis.

[0173] In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of the membrane-bound form of a BFLP0169 protein or polypeptide or biologically-active portion thereof. The test compounds of the invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds.

[0174] A "small molecule" as used herein, is meant to refer to a composition that has a molecular weight of less than about 5 kD and most preferably less than about 4 kD. Small molecules can be, e.g., rapamycin, nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic or inorganic molecules. Libraries of chemical and/or biological mixtures, such as fungal, bacterial, or algal extracts, are known in the art and can be screened with any of the assays of the invention. The libraries of compounds may be presented in solution, or on beads, on chips, bacteria, spores, plasmids or on phage

[0175] In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of BFLP0169 protein, or a biologically-active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to a BFLP0169 protein determined. The cell, for example, can be of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the BFLP0169 protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the BFLP0169 protein or biologically-active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I, ^{35}S, ^{14}C, or ^{3}H, either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically-labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of BFLP0169 protein, or a biologically-active portion thereof, on the cell surface with a known compound which binds BFLP0169 to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a BFLP0169 protein, wherein determining the ability of the test compound to interact with a BFLP0169 protein comprises determining the ability of the test compound to preferentially bind to BFLP0169 protein or a biologically-active portion thereof as compared to the known compound.

[0176] In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of BFLP0169 protein, or a biologically-active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (e.g., stimulate or inhibit) the activity of the BFLP0169 protein or biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of BFLP0169 or a biologically-active portion thereof can be accomplished, for example, by determining the ability of the BFLP0169 protein to bind to or interact with a BFLP0169 target molecule. As used herein, a "target molecule" is a molecule with which a BFLP0169 protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses a BFLP0169 interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule associated with the internal surface of a cell membrane or a cytoplasmic molecule. A BFLP0169 target molecule can be a non-BFLP0169 molecule or a BFLP0169 protein or polypeptide of the invention In one embodiment, a BFLP0169 target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (e.g. a signal generated by binding of a compound to a membrane-bound BFLP0169 molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with BFLP0169.

[0177] Determining the ability of the BFLP0169 protein to bind to or interact with a BFLP0169 target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the BFLP0169 protein to bind to or interact with a BFLP0169 target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (i.e. intracellular Ca^{2+} diacylglycerol, IP_3, etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate,

detecting the induction of a reporter gene (comprising a BFLP0169-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, e.g., luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

[0178] In yet another embodiment, an assay of the invention is a cell-free assay comprising contacting a BFLP0169 protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to bind to the BFLP0169 protein or biologically-active portion thereof. Binding of the test compound to the BFLP0169 protein can be determined either directly or indirectly as described above. In one such embodiment, the assay comprises contacting the BFLP0169 protein or biologically-active portion thereof with a known compound which binds BFLP0169 to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a BFLP0169 protein, wherein determining the ability of the test compound to interact with a BFLP0169 protein comprises determining the ability of the test compound to preferentially bind to BFLP0169 or a biologically-active portion thereof as compared to the known compound.

[0179] In still another embodiment, an assay is a cell-free assay comprising contacting BFLP0169 protein or a biologically-active portion thereof with a test compound and determining the ability of the test compound to modulate (e.g. stimulate or inhibit) the activity of the BFLP0169 protein or a biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of BFLP0169 can be accomplished, for example, by determining the ability of the BFLP0169 protein to bind to a BFLP0169 target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of BFLP0169 protein can be accomplished by determining the ability of the BFLP0169 protein further modulate a BFLP0169 target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as described above.

[0180] In yet another embodiment, the cell-free assay comprises contacting the BFLP0169 protein or a biologically-active portion thereof with a known compound which binds BFLP0169 protein to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a BFLP0169 protein, wherein determining the ability of the test compound to interact with a BFLP0169 protein comprises determining the ability of the BFLP0169 protein to preferentially bind to or modulate the activity of a BFLP0169 target molecule.

[0181] The cell-free assays of the invention are amenable for use with both the soluble form or the membrane-bound form of BFLP0169 protein. In the case of cell-free assays comprising the membrane-bound form of BFLP0169 protein, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of BFLP0169 protein is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton® X-100, Triton® X-114, Thesit®, Isotridecypoly(ethylene glycol ether)$_n$, N-dodecyl-N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl)dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

[0182] In more than one embodiment of the above assay methods of the invention, it may be desirable to immobilize either BFLP0169 protein or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to BFLP0169 protein, or interaction of BFLP0169 protein with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For example, GST-BFLP0169 fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, Mo.) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or BFLP0169 protein, and the mixture is incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described, supra. Alternatively, the complexes can be dissociated from the matrix, and the level of BFLP0169 protein binding or activity determined using standard techniques.

[0183] Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either the BFLP0169 protein or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated BFLP0169 protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well-known within the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with BFLP0169 protein or target molecules, but which do not interfere with binding of the BFLP0169 protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or BFLP0169 protein trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the BFLP0169 protein or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the BFLP0169 protein or target molecule.

[0184] In another embodiment, modulators of BFLP0169 protein expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of BFLP0169 mRNA or protein in the cell is determined. The level of expression of BFLP0169 mRNA or protein in the presence of the candidate compound is compared to the level of expression of BFLP0169 mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of BFLP0169 mRNA or protein expression based upon this comparison. For example, when expression of BFLP0169 mRNA or protein is greater (i.e., statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate com-

pound is identified as a stimulator of BFLP0169 mRNA or protein expression. Alternatively, when expression of BFLP0169 mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of BFLP0169 mRNA or protein expression. The level of BFLP0169 mRNA or protein expression in the cells can be determined by methods described herein for detecting BFLP0169 mRNA or protein.

[0185] In yet another aspect of the invention, the BFLP0169 proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay, to identify other proteins that bind to or interact with BFLP0169 ("BFLP0169-binding proteins" or "BFLP0169-bp") and modulate BFLP0169 activity. Such BFLP0169-binding proteins are also likely to be involved in the propagation of signals by the BFLP0169 proteins as, for example, upstream or downstream elements of the BFLP0169 pathway.

[0186] The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for BFLP0169 is fused to a gene encoding the DNA binding domain of a known transcription factor (e.g., GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, in vivo, forming a BFLP0169-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (e.g., LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with BFLP0169.

[0187] The invention further pertains to novel agents identified by the aforementioned screening assays and uses thereof for treatments as described herein.

[0188] The invention will be illustrated in the following non-limiting examples.

EXAMPLE 1

Expression Patterns of Murine BFLP0169 Sequence in Disease-Free, Lupus Nephritis Simulated Disease, and Rapamycin-Treated Diseased Mice

[0189] The expression of murine BFLP0169 sequences were examined in mice that developed lupus nephritis-like symptoms in the art-recognized NZB X NZW murine model (see, e.g., Drake et al., *Genetic analysis of the NZB contribution to lupus-like autoimmune disease in (NZB×NZW)F1 mice*. Proc Natl Acad Sci U S A 91:4062-66, 1994; Finck et al., *Interleukin 6 promotes murine lupus in NZB/NZW F1 mice*, J. Clin. Invest 94:585-91, 1994; Guglielmotti et al., *Bindarit prlongs survival and reduces renal damage of NSB/W lupus mice*. Clin. Exp. Rheumatol. 16:149, 1998; Yang et al., *Dietary conjugated linoleic acid protects against end stage disease of systemic lupus erythematosus in the NZB/W F1 mouse*, Immunopharmacol. Immunotoxicol. 22:433-49, 2000. Expression in diseased mice was compared to expression of the sequences in non-diseased mice of varying ages, and in mice whose lupus nephritis-like symptoms diminished following treatment with rapamycin or anti-B7 antibodies.

[0190] Mice were obtained from Jackson Laboratories at 6 to 8 weeks of age and aged on site. Data were obtained from kidneys of mice and harvested at the indicated time point: C57BL/6 female mice at 8, and 32 weeks, F1 (NZB×NZW) female mice 12, 25, and 42 weeks, mice treated with rapamycin at 42 and 55 weeks, mice treated with antibodies to B7.1 and B7.2 at 52 weeks. Each group contained three mice.

[0191] Rapamycin treated mice received 5 mg/kg rapamycin subcutaneous injection 3 times per week for 8 weeks staring at 29 weeks of age. Control mice received injections of vehicle (methyl cellulose) on the same schedule. Effectiveness of therapy was determined by normalization of proteinuria and kidney histology (data not shown). Gene expression analysis was preformed on mice sacrificed at the end of the treatment course (36 weeks of age, data not shown), and at 42 weeks (6 weeks after treatment) and 55 weeks (20 weeks after treatment).

[0192] Mice treated with anti-B7 received 200 μg of anti-B7.1 (1G10F9 monoclonal) and 200 μg of anti-B7.2 (GL1 monoclonal) by intra-peritoneal injections 3 times per week for two weeks starting at 29 weeks of age. Gene expression analysis was performed 21 weeks after treatment.

RNA Isolation and Hybridization to Oligonucleotide Arrays

[0193] Kidneys from both male and female mice were collected and snap frozen for RNA isolation. One half each kidney was used. A longitudinal section of the left kidney and a cross section of the right kidney was used in for each individual animal.

[0194] Snap frozen mouse kidney tissue was homogenized using homogenizer suspended in RLT buffer plus 2ME for 30 to 45 seconds. Total RNA was prepared using the Qiagen Midi Kit following the manufacturer's protocol. RNA was suspended in DEPC treated H2O and quantified by OD 280.

[0195] cDNA was synthesized from 5 ug of total RNA using the Superscript Kit (BRL). cDNA was purified using phenol:cloroform:isoamyl alcohol (25:24:1) with a Phage lock gel tube following the Phage lock protocol. Supernanant was collected and cleaned up using EtOH. Sample was resuspended in DEPC treated H2O.

[0196] In vitro T7 polymerase driven transcription reactions for synthesis and biotin labeling of antisense cRNA. Qiagen RNeasy spin column purification used to purify the cRNA. GeneChip hybridization mixtures contained 15 ug fragmented cRNA, 0.5 mg/ml acetylated BSA, 0.1 mg/ml herring sperm DNA, in 1×MES buffer in a total volume of 200 ul as per manufactures instructions. Reaction mixtures were hybridized for 16 hr at 45° C. to Affymetrix Mu11 KsubA and Mu11 KsubB oligonucleotide arrays. The hybridization mixtures were removed and the arrays were washed and stained with Streptavidin R-phycoerthrin (Molecular Probes) using GeneChip Fluidics Station 400 and scanned with a Hewlett Packard GeneArray Scanner following manufactures instructions. Fluorescent data was collected and converted to gene specific difference average using MicroArray Suite software.

Analysis of Oligonucleotide Array Data

[0197] An eleven member standard curve, comprised of gene fragments derived from cloned bacterial and bacteriophage sequences were spiked into each hybridization mixture at

concentrations ranging from 0.5 pM to 150 pM representing RNA frequencies of approximately 3.3 to 1000 parts per million (ppm). The biotinylated standard curve fragments were synthesized by T7-polymerase driven IVT reactions from plasmid-based templates. The spiked biotinylated RNA fragments serve both as an internal standard to assess chip sensitivity and as standard curve to convert measured fluorescent difference averages from individual genes into RNA frequencies in ppm as described by Hill et al.

[0198] Gene expression frequencies from each individual mouse kidney were measured and the expression data subjected to statistical analysis. Frequency values determined from individual measurements for a given group of mice were averaged. Genes whose frequencies differed significantly between C57Bl6 kidneys at 12 and 32 weeks of age were classified as changing as a result of the normal aging process, and not due to a disease process.

[0199] Expression frequencies in young (disease-free), old (diseased), and effectively treated old (disease-free) F1 (NZB×NZW) mice and C57BL6 control mice of oligonucleotide sequence identified on the Affymetrix Murine 11 K chip by the qualifier aa002653_s_at are shown. This sequence represents an unknown mouse gene.

[0200] The results are shown in FIG. **1**. Shown is a histogram showing gene expression levels in kidneys from the indicated mice. Expression levels of BFLP0169 do not vary significantly between C57BL/6 kidneys at 12 weeks of age and kidney at 32 weeks of age, indicating that expression levels do not increase with age in kidneys of non-diseased mice. In (NXB×NZW)F1 kidneys, the gene is expressed at normal levels prior to disease onset (12 weeks of age). As the mice age and disease progresses, increasing expression levels are observed at 25 weeks, 36 weeks (data not shown for 36 weeks), and 42 weeks. By 55 weeks of age, the mice have died due to kidney failure. Mice treated with rapamycin for 8 weeks with treatment starting at 29 weeks of age, remain healthy past 55 weeks of age. Kidneys of mice that have received effective therapy (either rapamycin therapy or anti-B7 therapy) express normal levels of BFLP0169, and these normal levels persist in asymptomatic kidney 20 weeks after cessation of rapamycin therapy and 15 weeks after cessation of anti-B7 therapy. The observation that expression levels return to normal when kidney function is normal indicates that elevated levels are related to, and diagnostic of, disease progression. Blocking the function of these genes may inhibit or retard disease progression. Expression levels may also to used to assess and compare effectiveness of various therapeutic interventions.

EXAMPLE 2

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0201] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table 2 is shown below. For the sequence shown, the L at position 78 of the BFLP0169 sequence shown in Table 2 has been replaced by a V, which is shown in bold font.

(SEQ ID NO:3)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKE**V**GLRISKFLGLDEEQSVQLLQCY

-continued

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNL

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLART

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACL

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQA

LHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTT

PTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRT

LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR

EXAMPLE 3

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0202] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table

2 is shown below. For the sequence shown, the L at position 198 of the BFLP0169 sequence shown in Table 2 has been replaced by an I, which is shown in bold font.

(SEQ ID NO:4)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNIMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNL

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLART

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACL

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQA

LHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTT

PTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRT

LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR

EXAMPLE 4

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0203] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table 2 is shown below. For the sequence shown, the R at position 267 of the BFLP0169 sequence shown in Table 2 has been replaced by a K, which is shown in bold font.

(SEQ ID NO:5)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMTE

RQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGSR

QTNRHLVDETMDPFVD**K**IGYFSALILVEGMDIESLHKCALDDRRELHQFA

QDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIGG

TAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHTL

GNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSPL

LQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRRQ

TPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEIE

MLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYMLL

QRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPVS

SLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLGS

TQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNLC

HETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQPR

SDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGAH

GNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAAI

RDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSDG

SKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRRD

SAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLEI

YYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTSL

LEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLVP

ASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQQ

LMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALFD

QTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEVD

EDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLARTQ

QGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGVY

RLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLE

EADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRKM

LQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQAL

HTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTTP

-continued

TFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRTL

KSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLSS

LSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRHM

QR

EXAMPLE 5

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0204] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table 2 is shown below. For the sequence shown, the Q at position 355 of the BFLP0169 sequence shown in Table 2 has been replaced by an N, which is shown in bold font.

(SEQ ID NO:6)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAI**N**LNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNL

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLART

-continued

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACL

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQA

LHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTT

PTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRT

LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR

EXAMPLE 6

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0205] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table 2 is shown below. For the sequence shown, the H at position 446 of the BFLP0169 sequence shown in Table 2 has been replaced by an R, which is shown in bold font.

(SEQ ID NO:7)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFP**R**LLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNL

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

-continued

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLART

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACL

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQA

LHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTT

PTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRT

LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR

EXAMPLE 7

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0206] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table 2 is shown below. For the sequence shown, the L at position 553 of the BFLP0169 sequence shown in Table 2 has been replaced by an I, which is shown in bold font.

(SEQ ID NO:8)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMILHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNL

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

-continued

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLART

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACL

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQA

LHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTT

PTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRT

LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR

EXAMPLE 8

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0207] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table 2 is shown below. For the sequence shown, the W at position 634 of the BFLP0169 sequence shown in Table 2 has been replaced by a F, which is shown in bold font.

(SEQ ID NO:9)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

-continued

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKV**F**TDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNL

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLART

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACL

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQA

LHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTT

PTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRT

LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR

EXAMPLE 9

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0208] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table 2 is shown below. For the sequence shown, the N at position 749 of the BFLP0169 sequence shown in Table 2 has been replaced by a D, which is shown in bold font.

(SEQ ID NO:10)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

-continued

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAIL**D**L

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLART

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACL

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQA

LHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTT

PTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRT

LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR

EXAMPLE 10

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0209] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table 2 is shown below. For the sequence shown, the V at position 838 of the BFLP0169 sequence shown in Table 2 has been replaced by a M, which is shown in bold font.

(SEQ ID NO:11)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNL

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNV**M**SPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLART

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACL

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQA

LHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTT

PTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRT

LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR

EXAMPLE 11

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0210] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table 2 is shown below. For the sequence shown, the G at position 958 of the BFLP0169 sequence shown in Table 2 has been replaced by a T, which is shown in bold font.

(SEQ ID NO:12)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNL

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSL**T**MWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLART

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACL

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQA

LHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTT

-continued

PTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRT

LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR

EXAMPLE 12

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0211] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table 2 is shown below. For the sequence shown, the K at position 1084 of the BFLP0169 sequence shown in Table 2 has been replaced by a R, which is shown in bold font.

(SEQ ID NO:13)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNL

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYV**R**SLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLART

-continued

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACL

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQA

LHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTT

PTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRT

LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR

EXAMPLE 13

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0212] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table 2 is shown below. For the sequence shown, the A at position 1152 of the BFLP0169 sequence shown in Table 2 has been replaced by a S, which is shown in bold font.

(SEQ ID NO:14)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNL

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

-continued

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PSSVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLART

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACL

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQA

LHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTT

PTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRT

LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR

EXAMPLE 14

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0213] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table 2 is shown below. For the sequence shown, the I at position 1247 of the BFLP0169 sequence shown in Table 2 has been replaced by a V, which is shown in bold font.

(SEQ ID NO:15)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNL

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

-continued

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PSSVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVVALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLART

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACL

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQA

LHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTT

PTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRT

LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR

EXAMPLE 15

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0214] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table 2 is shown below. For the sequence shown, the K at position 1331 of the BFLP0169 sequence shown in Table 2 has been replaced by a R, which is shown in bold font.

(SEQ ID NO:16)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

-continued

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNL

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PSSVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRM**R**QNLHFTEATLHLLLTLART

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACL

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQA

LHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTT

PTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRT

LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR

EXAMPLE 16

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0215] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table 2 is shown below. For the sequence shown, the C at position 1449 of the BFLP0169 sequence shown in Table 2 has been replaced by a Y, which is shown in bold font.

(SEQ ID NO:17)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

-continued

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNL

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PSSVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLART

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLA**Y**L

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQA

LHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTT

PTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRT

LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR

EXAMPLE 17

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0216] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table 2 is shown below. For the sequence shown, the D at position 1542 of the BFLP0169 sequence shown in Table 2 has been replaced by a Q, which is shown in bold font.

(SEQ ID NO:18)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNL

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PSSVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLART

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACL

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAA**Q**TEASEQQA

LHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFALSFTT

PTFDSEVAPSFGTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGTRT

LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRYFRRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR

EXAMPLE 18

A Variant of the Human BFLP0169 Polypeptide Sequence Shown in Table 2

[0217] A polypeptide sequence varying by one amino acid from the BFLP0169 amino acid sequence presented in Table 2 is shown below. For the sequence shown, the F at position 1706 of the BFLP0169 sequence shown in Table 2 has been replaced by a H, which is shown in bold font.

(SEQ ID NO:19)

MIRKSKITSVLSFCRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEG

LSYYKPPSPSSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCY

LQEDYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHLLTY

FQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWETHGNLMT

ERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSDLLVLTKMFKEQGFGS

RQTNRHLVDETMDPFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQF

AQDGLICQDMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIG

GTAIQLNVFQYLTRLLQSLASGGNDCTTSTACMCVYGLLSFVLTSLELHT

LGNQQDIIDTACEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP

LLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRR

QTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEI

EMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIADCLLPITSRIYML

LQRLTTVISPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPV

SSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLG

STQSQGLVPCVMFVLKEMLPSYHKWRYNSHGVREQIGCLILELIHAILNL

CHETDLHSSHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQP

RSDGAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGA

HGNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAA

IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSD

GSKEFSLGMWSCLHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRR

DSAMLVLRTKPKFWENLTSPLFGTLSPPSETSEPSILETCALIMKIICLE

IYYVVKGSLDQSLKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTS

LLEYQMLVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV

PSSVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQ

QLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNVCETLQEEVIALF

DQTRHSLALGSATEDKDSMETDDCSRSRHRDQRDGVCVLGLHLAKELCEV

DEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHLLLTLART

QQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGV

YRLSMSLMEQLLKTLRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACL

EEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSLLHSRK

MLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAAQTEASEQQA

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-continued

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LKSLLMFTMENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLS

SLSRY**H**RRGAPSSPATGVLPSPQGKSTSLSKASPESQEPLIQLVQAFVRH

MQR

OTHER EMBODIMENTS

[0218] While the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

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<213> ORGANISM: Homo sapiens

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gccgagtctt ctgtgctcag gtcctcacgc tgcagacgcc ccctagagga actttccttc 5520

ctttccagca ttccccacag cactgccggc caggggagag gcggcagccc agcagagggc 5580

tctatgcacg ggtttcaaac ctgttttcca cactctgtct ttgcagtttt ggtaattctg 5640

tggtctattt atacagatat taaaatcttg tttatagaca gctgtgtgat gtttaacttc 5700

aaagcccagg gatgacaacg tggctctcag aacctagaaa actcccctgg ccaggcgcct 5760

gggagtgggg ctgcagcctc gggggaaggc aggtactgat ggatggctag ttcaccagca 5820

tctcctcatt cctgtccttg ggctgagggt ttggctgggt gggcgctgtc agatattccc 5880

ttccttggcc tgcgctggtc ctgtccttga ccctgctttc attggcccag tgggctgagc 5940

tcatccctgg gtgagccttt cttgaagctc tgtgccttcc tatttat 5987

<210> SEQ ID NO 2
<211> LENGTH: 1753
<212> TYPE: PRT

-continued

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 2

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Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50                  55                  60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
145                 150                 155                 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165                 170                 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180                 185                 190

Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195                 200                 205

Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210                 215                 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225                 230                 235                 240

Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245                 250                 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260                 265                 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
275                 280                 285

Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290                 295                 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305                 310                 315                 320

Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325                 330                 335

Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340                 345                 350

Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355                 360                 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys
370                 375                 380
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Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415

Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430

Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460

Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
500                 505                 510

Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540

Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala
545                 550                 555                 560

Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
595                 600                 605

Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610                 615                 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr
625                 630                 635                 640

Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645                 650                 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660                 665                 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675                 680                 685

Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
690                 695                 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705                 710                 715                 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
725                 730                 735

Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His
740                 745                 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755                 760                 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770                 775                 780

Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
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785                 790                 795                 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805                 810                 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
820                 825                 830

Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835                 840                 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850                 855                 860

His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865                 870                 875                 880

Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885                 890                 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900                 905                 910

Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
915                 920                 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930                 935                 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp
945                 950                 955                 960

Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965                 970                 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980                 985                 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995                1000                1005

Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025               1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val
1075                1080                1085

His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100

Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105               1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125                1130                1135

Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ala
1140                1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155                1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170                1175                1180

Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185               1190                1195                1200
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Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205                1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220                1225                1230

Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala
1235                1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250                1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
1265              1270                1275                1280

Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285                1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300                1305                1310

Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315                1320                1325

Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330                1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345              1350                1355                1360

Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
1365                1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380                1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395                1400                1405

Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410                1415                1420

Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425              1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr
1445                1450                1455

Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460                1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475                1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
1490                1495                1500

Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505              1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525                1530                1535

Lys Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540                1545                1550

Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555                1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570                1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
1585              1590                1595                1600
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Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605                1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620                1625                1630

Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635                1640                1645

Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650                1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665               1670                1675                1680

Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
1685                1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser
1700                1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
1715                1720                1725

Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730                1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745               1750


<210> SEQ ID NO 3
<211> LENGTH: 1753
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50                  55                  60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Val Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
145                 150                 155                 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165                 170                 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180                 185                 190

Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195                 200                 205
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Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210                 215                 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225                 230                 235                 240

Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245                 250                 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260                 265                 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
275                 280                 285

Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290                 295                 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305                 310                 315                 320

Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325                 330                 335

Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340                 345                 350

Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355                 360                 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys
370                 375                 380

Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415

Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430

Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460

Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
500                 505                 510

Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540

Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala
545                 550                 555                 560

Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
595                 600                 605
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```
Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610                 615                 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr
625                 630                 635                 640

Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645                 650                 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660                 665                 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675                 680                 685

Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
690                 695                 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705                 710                 715                 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
725                 730                 735

Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His
740                 745                 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755                 760                 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770                 775                 780

Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
785                 790                 795                 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805                 810                 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
820                 825                 830

Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835                 840                 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850                 855                 860

His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865                 870                 875                 880

Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885                 890                 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900                 905                 910

Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
915                 920                 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930                 935                 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp
945                 950                 955                 960

Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965                 970                 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980                 985                 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995                1000                1005

Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
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```
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025               1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val
1075                1080                1085

His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100

Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105               1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125                1130                1135

Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ala
1140                1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155                1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170                1175                1180

Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185               1190                1195                1200

Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205                1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220                1225                1230

Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala
1235                1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250                1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
1265               1270                1275                1280

Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285                1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300                1305                1310

Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315                1320                1325

Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330                1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345               1350                1355                1360

Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
1365                1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380                1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395                1400                1405

Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410                1415                1420
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Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425               1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr
1445               1450                1455

Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460               1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475               1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
1490               1495                1500

Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505               1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525               1530                1535

Lys Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540               1545                1550

Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555               1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570               1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
1585               1590                1595                1600

Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605               1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620               1625                1630

Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635               1640                1645

Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650               1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665               1670                1675                1680

Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
1685               1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser
1700               1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
1715               1720                1725

Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730               1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745               1750


<210> SEQ ID NO 4
<211> LENGTH: 1753
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
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20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50                  55                  60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
145                 150                 155                 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165                 170                 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180                 185                 190

Glu Thr His Gly Asn Ile Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195                 200                 205

Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210                 215                 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225                 230                 235                 240

Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245                 250                 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260                 265                 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
275                 280                 285

Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290                 295                 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305                 310                 315                 320

Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325                 330                 335

Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340                 345                 350

Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355                 360                 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys
370                 375                 380

Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415

Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430
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Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460

Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
500                 505                 510

Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540

Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala
545                 550                 555                 560

Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
595                 600                 605

Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610                 615                 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr
625                 630                 635                 640

Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645                 650                 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660                 665                 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675                 680                 685

Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
690                 695                 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705                 710                 715                 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
725                 730                 735

Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His
740                 745                 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755                 760                 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770                 775                 780

Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
785                 790                 795                 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805                 810                 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
820                 825                 830
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Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835                 840                 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850                 855                 860

His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865                 870                 875                 880

Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885                 890                 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900                 905                 910

Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
915                 920                 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930                 935                 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp
945                 950                 955                 960

Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965                 970                 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980                 985                 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995                1000                1005

Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025               1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val
1075                1080                1085

His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100

Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105               1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125                1130                1135

Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ala
1140                1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155                1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170                1175                1180

Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185               1190                1195                1200

Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205                1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220                1225                1230

Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala
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1235                1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250                1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
1265               1270                1275                1280

Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285                1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300                1305                1310

Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315                1320                1325

Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330                1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345               1350                1355                1360

Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
1365                1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380                1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395                1400                1405

Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410                1415                1420

Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425               1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr
1445                1450                1455

Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460                1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475                1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
1490                1495                1500

Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505               1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525                1530                1535

Lys Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540                1545                1550

Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555                1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570                1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
1585               1590                1595                1600

Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605                1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620                1625                1630

Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635                1640                1645
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Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650                1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665               1670                1675                1680

Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
1685                1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser
1700                1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
1715                1720                1725

Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730                1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745               1750


<210> SEQ ID NO 5
<211> LENGTH: 1752
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50                  55                  60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg Pro Tyr Arg Val Glu
145                 150                 155                 160

Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys Tyr
165                 170                 175

Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp Glu
180                 185                 190

Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe Val
195                 200                 205

Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu Tyr
210                 215                 220

Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr Lys
225                 230                 235                 240

Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His Leu
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245                 250                 255

Val Asp Glu Thr Met Asp Pro Phe Val Asp Lys Ile Gly Tyr Phe Ser
260                 265                 270

Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys Cys
275                 280                 285

Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly Leu
290                 295                 300

Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile Pro
305                 310                 315                 320

His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr Leu
325                 330                 335

Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr Ala
340                 345                 350

Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser Leu
355                 360                 365

Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys Val
370                 375                 380

Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr Leu
385                 390                 395                 400

Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala Asp
405                 410                 415

Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly Leu
420                 425                 430

Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu Ser
435                 440                 445

Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr Ala
450                 455                 460

Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu Leu
465                 470                 475                 480

Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr Leu
485                 490                 495

Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln Thr
500                 505                 510

Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp Asp
515                 520                 525

Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr Leu
530                 535                 540

Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala Asp
545                 550                 555                 560

Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val His
565                 570                 575

Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro Ile
580                 585                 590

Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile Ser
595                 600                 605

Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val Leu
610                 615                 620

Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr Gly
625                 630                 635                 640

Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met Ile
645                 650                 655
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Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met Asn
660                 665                 670

Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu Arg
675                 680                 685

Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser Gln
690                 695                 700

Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro Ser
705                 710                 715                 720

Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile Gly
725                 730                 735

Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His Glu
740                 745                 750

Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys Ile
755                 760                 765

Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile Met
770                 775                 780

Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro Arg
785                 790                 795                 800

Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys Thr
805                 810                 815

Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys Pro
820                 825                 830

Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His Gly
835                 840                 845

Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr His
850                 855                 860

Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys Arg
865                 870                 875                 880

Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn Asp
885                 890                 895

Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys Ile
900                 905                 910

Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val Ala
915                 920                 925

Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu Val
930                 935                 940

Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp Ser
945                 950                 955                 960

Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp Arg
965                 970                 975

Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu His
980                 985                 990

Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg Thr
995                1000                1005

Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr Leu
1010                1015                1020

Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys Ala
1025               1030                1035                1040

Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys Gly
1045                1050                1055
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Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile Glu
1060                1065                1070

Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val His
1075                1080                1085

Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr Gln
1090                1095                1100

Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr His
1105                1110                1115                1120

Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu Phe
1125                1130                1135

Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ala Ser
1140                1145                1150

Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu Ile
1155                1160                1165

Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile Leu
1170                1175                1180

Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln Gln
1185                1190                1195                1200

Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr Val
1205                1210                1215

Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser Gln
1220                1225                1230

Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala Leu
1235                1240                1245

Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu Asp
1250                1255                1260

Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg Asp
1265                1270                1275                1280

Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu Leu
1285                1290                1295

Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg Arg
1300                1305                1310

Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu Arg
1315                1320                1325

Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu Leu
1330                1335                1340

Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala Gly
1345                1350                1355                1360

Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu Ser
1365                1370                1375

Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu Asp
1380                1385                1390

Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met Glu
1395                1400                1405

Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu Asp
1410                1415                1420

Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala Val
1425                1430                1435                1440

Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr Val
1445                1450                1455

Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe His
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1460                1465                1470

Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu Cys
1475                1480                1485

Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His Tyr
1490                1495                1500

Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln Arg
1505               1510                1515                1520

Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser Lys
1525                1530                1535

Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His Thr
1540                1545                1550

Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala Leu
1555                1560                1565

Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser Leu
1570                1575                1580

Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr Pro
1585               1590                1595                1600

Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala Thr
1605                1610                1615

Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys Glu
1620                1625                1630

Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr Arg
1635                1640                1645

Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr Leu
1650                1655                1660

Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His Pro
1665               1670                1675                1680

Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser Thr
1685                1690                1695

Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser Ser
1700                1705                1710

Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser Leu
1715                1720                1725

Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val Gln
1730                1735                1740

Ala Phe Val Arg His Met Gln Arg
1745               1750


<210> SEQ ID NO 6
<211> LENGTH: 1753
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50                  55                  60
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Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
145                 150                 155                 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165                 170                 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180                 185                 190

Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195                 200                 205

Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210                 215                 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225                 230                 235                 240

Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245                 250                 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260                 265                 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
275                 280                 285

Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290                 295                 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305                 310                 315                 320

Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325                 330                 335

Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340                 345                 350

Ala Ile Asn Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355                 360                 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys
370                 375                 380

Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415

Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430

Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460

Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
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465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
500                 505                 510

Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540

Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala
545                 550                 555                 560

Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
595                 600                 605

Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610                 615                 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr
625                 630                 635                 640

Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645                 650                 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660                 665                 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675                 680                 685

Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
690                 695                 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705                 710                 715                 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
725                 730                 735

Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His
740                 745                 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755                 760                 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770                 775                 780

Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
785                 790                 795                 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805                 810                 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
820                 825                 830

Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835                 840                 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850                 855                 860

His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865                 870                 875                 880
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Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885                 890                 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900                 905                 910

Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
915                 920                 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930                 935                 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp
945                 950                 955                 960

Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965                 970                 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980                 985                 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995                1000                1005

Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025               1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val
1075                1080                1085

His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100

Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105               1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125                1130                1135

Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ala
1140                1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155                1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170                1175                1180

Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185               1190                1195                1200

Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205                1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220                1225                1230

Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala
1235                1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250                1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
1265               1270                1275                1280
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Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285                1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300                1305                1310

Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315                1320                1325

Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330                1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345                1350                1355                1360

Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
1365                1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380                1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395                1400                1405

Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410                1415                1420

Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425                1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr
1445                1450                1455

Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460                1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475                1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
1490                1495                1500

Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505                1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525                1530                1535

Lys Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540                1545                1550

Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555                1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570                1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
1585                1590                1595                1600

Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605                1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620                1625                1630

Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635                1640                1645

Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650                1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665                1670                1675                1680

Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
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1685                1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser
1700                1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
1715                1720                1725

Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730                1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745              1750


<210> SEQ ID NO 7
<211> LENGTH: 1753
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 7

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50                  55                  60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
145                 150                 155                 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165                 170                 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180                 185                 190

Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195                 200                 205

Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210                 215                 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225                 230                 235                 240

Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245                 250                 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260                 265                 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
275                 280                 285
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Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290                 295                 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305                 310                 315                 320

Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325                 330                 335

Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340                 345                 350

Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355                 360                 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys
370                 375                 380

Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415

Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430

Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro Arg Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460

Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
500                 505                 510

Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540

Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala
545                 550                 555                 560

Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
595                 600                 605

Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610                 615                 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr
625                 630                 635                 640

Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645                 650                 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660                 665                 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675                 680                 685

Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
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690                 695                 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705                 710                 715                 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
725                 730                 735

Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His
740                 745                 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755                 760                 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770                 775                 780

Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
785                 790                 795                 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805                 810                 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
820                 825                 830

Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835                 840                 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850                 855                 860

His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865                 870                 875                 880

Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885                 890                 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900                 905                 910

Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
915                 920                 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930                 935                 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp
945                 950                 955                 960

Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965                 970                 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980                 985                 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995                1000                1005

Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025               1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val
1075                1080                1085

His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100
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Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105               1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125               1130                1135

Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ala
1140               1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155               1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170               1175                1180

Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185               1190                1195                1200

Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205               1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220               1225                1230

Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala
1235               1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250               1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
1265               1270                1275                1280

Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285               1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300               1305                1310

Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315               1320                1325

Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330               1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345               1350                1355                1360

Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
1365               1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380               1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395               1400                1405

Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410               1415                1420

Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425               1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr
1445               1450                1455

Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460               1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475               1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
1490               1495                1500
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Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505              1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525                1530                1535

Lys Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540                1545                1550

Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555                1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570                1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
1585              1590                1595                1600

Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605                1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620                1625                1630

Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635                1640                1645

Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650                1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665              1670                1675                1680

Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
1685                1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser
1700                1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
1715                1720                1725

Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730                1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745              1750


<210> SEQ ID NO 8
<211> LENGTH: 1753
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50                  55                  60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110
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Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
145                 150                 155                 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165                 170                 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180                 185                 190

Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195                 200                 205

Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210                 215                 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225                 230                 235                 240

Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245                 250                 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260                 265                 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
275                 280                 285

Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290                 295                 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305                 310                 315                 320

Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325                 330                 335

Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340                 345                 350

Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355                 360                 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys
370                 375                 380

Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415

Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430

Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460

Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
500                 505                 510
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Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540

Leu Phe Thr Cys Glu Ile Glu Met Ile Leu His Val Val Ser Thr Ala
545                 550                 555                 560

Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
595                 600                 605

Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610                 615                 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr
625                 630                 635                 640

Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645                 650                 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660                 665                 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675                 680                 685

Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
690                 695                 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705                 710                 715                 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
725                 730                 735

Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His
740                 745                 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755                 760                 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770                 775                 780

Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
785                 790                 795                 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805                 810                 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
820                 825                 830

Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835                 840                 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850                 855                 860

His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865                 870                 875                 880

Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885                 890                 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900                 905                 910

Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
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915                 920                 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930                 935                 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp
945                 950                 955                 960

Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965                 970                 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980                 985                 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995                1000                1005

Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025               1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val
1075                1080                1085

His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100

Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105               1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125                1130                1135

Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ala
1140                1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155                1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170                1175                1180

Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185               1190                1195                1200

Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205                1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220                1225                1230

Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala
1235                1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250                1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
1265               1270                1275                1280

Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285                1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300                1305                1310

Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315                1320                1325
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Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330                1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345              1350                1355                1360

Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
1365                1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380                1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395                1400                1405

Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410                1415                1420

Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425              1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr
1445                1450                1455

Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460                1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475                1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
1490                1495                1500

Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505              1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525                1530                1535

Lys Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540                1545                1550

Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555                1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570                1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
1585              1590                1595                1600

Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605                1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620                1625                1630

Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635                1640                1645

Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650                1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665              1670                1675                1680

Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
1685                1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser
1700                1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
1715                1720                1725
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Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730                1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745              1750


<210> SEQ ID NO 9
<211> LENGTH: 1753
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50                  55                  60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
145                 150                 155                 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165                 170                 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180                 185                 190

Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195                 200                 205

Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210                 215                 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225                 230                 235                 240

Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245                 250                 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260                 265                 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
275                 280                 285

Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290                 295                 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305                 310                 315                 320

Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325                 330                 335
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Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340                 345                 350

Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355                 360                 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys
370                 375                 380

Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415

Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430

Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460

Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
500                 505                 510

Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540

Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala
545                 550                 555                 560

Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
595                 600                 605

Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610                 615                 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Phe Thr Asp Leu Arg His Thr
625                 630                 635                 640

Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645                 650                 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660                 665                 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675                 680                 685

Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
690                 695                 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705                 710                 715                 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
725                 730                 735
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Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His
740                 745                 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755                 760                 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770                 775                 780

Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
785                 790                 795                 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805                 810                 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
820                 825                 830

Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835                 840                 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850                 855                 860

His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865                 870                 875                 880

Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885                 890                 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900                 905                 910

Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
915                 920                 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930                 935                 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp
945                 950                 955                 960

Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965                 970                 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980                 985                 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995                1000                1005

Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025               1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val
1075                1080                1085

His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100

Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105               1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125                1130                1135

Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ala
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1140                1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155                1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170                1175                1180

Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185               1190                1195                1200

Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205                1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220                1225                1230

Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala
1235                1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250                1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
1265               1270                1275                1280

Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285                1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300                1305                1310

Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315                1320                1325

Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330                1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345               1350                1355                1360

Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
1365                1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380                1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395                1400                1405

Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410                1415                1420

Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425               1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr
1445                1450                1455

Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460                1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475                1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
1490                1495                1500

Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505               1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525                1530                1535

Lys Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540                1545                1550
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Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555                1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570                1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
1585              1590                1595                1600

Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605                1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620                1625                1630

Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635                1640                1645

Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650                1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665              1670                1675                1680

Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
1685                1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser
1700                1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
1715                1720                1725

Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730                1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745              1750


<210> SEQ ID NO 10
<211> LENGTH: 1753
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50                  55                  60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
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145                 150                 155                 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165                 170                 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180                 185                 190

Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195                 200                 205

Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210                 215                 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225                 230                 235                 240

Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245                 250                 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260                 265                 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
275                 280                 285

Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290                 295                 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305                 310                 315                 320

Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325                 330                 335

Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340                 345                 350

Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355                 360                 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys
370                 375                 380

Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415

Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430

Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460

Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
500                 505                 510

Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540

Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala
545                 550                 555                 560
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Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
595                 600                 605

Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610                 615                 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr
625                 630                 635                 640

Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645                 650                 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660                 665                 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675                 680                 685

Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
690                 695                 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705                 710                 715                 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
725                 730                 735

Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asp Leu Cys His
740                 745                 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755                 760                 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770                 775                 780

Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
785                 790                 795                 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805                 810                 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
820                 825                 830

Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835                 840                 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850                 855                 860

His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865                 870                 875                 880

Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885                 890                 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900                 905                 910

Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
915                 920                 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930                 935                 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp
945                 950                 955                 960
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Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965                 970                 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980                 985                 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995                1000                1005

Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025               1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val
1075                1080                1085

His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100

Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105               1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125                1130                1135

Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ala
1140                1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155                1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170                1175                1180

Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185               1190                1195                1200

Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205                1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220                1225                1230

Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala
1235                1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250                1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
1265               1270                1275                1280

Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285                1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300                1305                1310

Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315                1320                1325

Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330                1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345               1350                1355                1360

Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
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1365                1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380                1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395                1400                1405

Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410                1415                1420

Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425              1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr
1445                1450                1455

Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460                1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475                1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
1490                1495                1500

Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505              1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525                1530                1535

Lys Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540                1545                1550

Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555                1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570                1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
1585              1590                1595                1600

Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605                1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620                1625                1630

Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635                1640                1645

Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650                1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665              1670                1675                1680

Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
1685                1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser
1700                1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
1715                1720                1725

Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730                1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745              1750
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<210> SEQ ID NO 11

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<211> LENGTH: 1753
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1 5 10 15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20 25 30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35 40 45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50 55 60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65 70 75 80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85 90 95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100 105 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115 120 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130 135 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
145 150 155 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165 170 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180 185 190

Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195 200 205

Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210 215 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225 230 235 240

Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245 250 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260 265 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
275 280 285

Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290 295 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305 310 315 320

Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325 330 335

Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340 345 350

Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355 360 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys

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370                 375                 380

Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415

Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430

Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460

Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
500                 505                 510

Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540

Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala
545                 550                 555                 560

Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
595                 600                 605

Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610                 615                 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr
625                 630                 635                 640

Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645                 650                 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660                 665                 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675                 680                 685

Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
690                 695                 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705                 710                 715                 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
725                 730                 735

Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His
740                 745                 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755                 760                 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770                 775                 780
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Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
785                 790                 795                 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805                 810                 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
820                 825                 830

Pro Pro Ser Asn Val Met Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835                 840                 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850                 855                 860

His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865                 870                 875                 880

Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885                 890                 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900                 905                 910

Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
915                 920                 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930                 935                 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp
945                 950                 955                 960

Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965                 970                 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980                 985                 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995                1000                1005

Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025               1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val
1075                1080                1085

His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100

Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105               1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125                1130                1135

Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ala
1140                1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155                1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170                1175                1180
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Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185              1190                1195                1200

Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205                1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220                1225                1230

Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala
1235                1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250                1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
1265              1270                1275                1280

Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285                1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300                1305                1310

Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315                1320                1325

Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330                1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345              1350                1355                1360

Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
1365                1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380                1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395                1400                1405

Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410                1415                1420

Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425              1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr
1445                1450                1455

Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460                1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475                1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
1490                1495                1500

Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505              1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525                1530                1535

Lys Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540                1545                1550

Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555                1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570                1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
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1585                1590                1595                1600

Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605                1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620                1625                1630

Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635                1640                1645

Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650                1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665               1670                1675                1680

Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
1685                1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser
1700                1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
1715                1720                1725

Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730                1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745               1750


<210> SEQ ID NO 12
<211> LENGTH: 1753
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50                  55                  60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
145                 150                 155                 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165                 170                 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180                 185                 190
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Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195                 200                 205

Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210                 215                 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225                 230                 235                 240

Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245                 250                 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260                 265                 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
275                 280                 285

Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290                 295                 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305                 310                 315                 320

Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325                 330                 335

Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340                 345                 350

Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355                 360                 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys
370                 375                 380

Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415

Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430

Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460

Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
500                 505                 510

Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540

Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala
545                 550                 555                 560

Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
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595 600 605

Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610 615 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr
625 630 635 640

Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645 650 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660 665 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675 680 685

Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
690 695 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705 710 715 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
725 730 735

Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His
740 745 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755 760 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770 775 780

Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
785 790 795 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805 810 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
820 825 830

Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835 840 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850 855 860

His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865 870 875 880

Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885 890 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900 905 910

Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
915 920 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930 935 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Thr Met Trp
945 950 955 960

Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965 970 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980 985 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995 1000 1005

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Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025               1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val
1075                1080                1085

His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100

Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105               1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125                1130                1135

Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ala
1140                1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155                1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170                1175                1180

Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185               1190                1195                1200

Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205                1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220                1225                1230

Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala
1235                1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250                1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
1265               1270                1275                1280

Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285                1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300                1305                1310

Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315                1320                1325

Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330                1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345               1350                1355                1360

Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
1365                1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380                1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395                1400                1405
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Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410                1415                1420

Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425               1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr
1445                1450                1455

Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460                1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475                1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
1490                1495                1500

Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505               1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525                1530                1535

Lys Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540                1545                1550

Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555                1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570                1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
1585               1590                1595                1600

Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605                1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620                1625                1630

Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635                1640                1645

Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650                1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665               1670                1675                1680

Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
1685                1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser
1700                1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
1715                1720                1725

Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730                1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745               1750


<210> SEQ ID NO 13
<211> LENGTH: 1753
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 13

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15
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Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50                  55                  60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
145                 150                 155                 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165                 170                 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180                 185                 190

Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195                 200                 205

Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210                 215                 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225                 230                 235                 240

Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245                 250                 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260                 265                 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
275                 280                 285

Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290                 295                 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305                 310                 315                 320

Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325                 330                 335

Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340                 345                 350

Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355                 360                 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys
370                 375                 380

Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415
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Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430

Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460

Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
500                 505                 510

Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540

Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala
545                 550                 555                 560

Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
595                 600                 605

Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610                 615                 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr
625                 630                 635                 640

Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645                 650                 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660                 665                 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675                 680                 685

Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
690                 695                 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705                 710                 715                 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
725                 730                 735

Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His
740                 745                 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755                 760                 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770                 775                 780

Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
785                 790                 795                 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805                 810                 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
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820                 825                 830

Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835                 840                 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850                 855                 860

His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865                 870                 875                 880

Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885                 890                 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900                 905                 910

Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
915                 920                 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930                 935                 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp
945                 950                 955                 960

Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965                 970                 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980                 985                 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995                1000                1005

Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025               1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Arg Ser Leu Ala Val
1075                1080                1085

His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100

Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105               1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125                1130                1135

Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ala
1140                1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155                1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170                1175                1180

Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185               1190                1195                1200

Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205                1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220                1225                1230
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Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala
1235                1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250                1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
1265               1270                1275                1280

Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285                1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300                1305                1310

Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315                1320                1325

Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330                1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345               1350                1355                1360

Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
1365                1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380                1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395                1400                1405

Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410                1415                1420

Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425               1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr
1445                1450                1455

Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460                1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475                1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
1490                1495                1500

Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505               1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525                1530                1535

Lys Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540                1545                1550

Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555                1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570                1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
1585               1590                1595                1600

Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605                1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620                1625                1630
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Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635                1640                1645

Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650                1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665               1670                1675                1680

Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
1685                1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser
1700                1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
1715                1720                1725

Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730                1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745               1750


<210> SEQ ID NO 14
<211> LENGTH: 1753
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 14

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50                  55                  60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
145                 150                 155                 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165                 170                 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180                 185                 190

Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195                 200                 205

Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210                 215                 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225                 230                 235                 240
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Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245                 250                 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260                 265                 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
275                 280                 285

Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290                 295                 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305                 310                 315                 320

Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325                 330                 335

Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340                 345                 350

Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355                 360                 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys
370                 375                 380

Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415

Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430

Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460

Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
500                 505                 510

Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540

Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala
545                 550                 555                 560

Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
595                 600                 605

Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610                 615                 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr
625                 630                 635                 640
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Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645                 650                 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660                 665                 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675                 680                 685

Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
690                 695                 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705                 710                 715                 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
725                 730                 735

Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His
740                 745                 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755                 760                 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770                 775                 780

Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
785                 790                 795                 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805                 810                 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
820                 825                 830

Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835                 840                 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850                 855                 860

His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865                 870                 875                 880

Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885                 890                 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900                 905                 910

Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
915                 920                 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930                 935                 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp
945                 950                 955                 960

Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965                 970                 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980                 985                 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995                1000                1005

Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025                1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
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1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val
1075                1080                1085

His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100

Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105              1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125                1130                1135

Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ser
1140                1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155                1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170                1175                1180

Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185              1190                1195                1200

Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205                1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220                1225                1230

Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala
1235                1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250                1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
1265              1270                1275                1280

Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285                1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300                1305                1310

Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315                1320                1325

Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330                1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345              1350                1355                1360

Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
1365                1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380                1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395                1400                1405

Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410                1415                1420

Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425              1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr
1445                1450                1455
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Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460                1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475                1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
1490                1495                1500

Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505               1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525                1530                1535

Lys Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540                1545                1550

Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555                1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570                1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
1585               1590                1595                1600

Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605                1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620                1625                1630

Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635                1640                1645

Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650                1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665               1670                1675                1680

Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
1685                1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser
1700                1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
1715                1720                1725

Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730                1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745               1750


<210> SEQ ID NO 15
<211> LENGTH: 1753
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
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50                  55                  60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
145                 150                 155                 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165                 170                 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180                 185                 190

Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195                 200                 205

Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210                 215                 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225                 230                 235                 240

Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245                 250                 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260                 265                 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
275                 280                 285

Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290                 295                 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305                 310                 315                 320

Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325                 330                 335

Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340                 345                 350

Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355                 360                 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys
370                 375                 380

Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415

Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430

Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460
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Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
500                 505                 510

Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540

Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala
545                 550                 555                 560

Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
595                 600                 605

Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610                 615                 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr
625                 630                 635                 640

Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645                 650                 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660                 665                 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675                 680                 685

Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
690                 695                 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705                 710                 715                 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
725                 730                 735

Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His
740                 745                 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755                 760                 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770                 775                 780

Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
785                 790                 795                 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805                 810                 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
820                 825                 830

Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835                 840                 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850                 855                 860
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His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865                 870                 875                 880

Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885                 890                 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900                 905                 910

Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
915                 920                 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930                 935                 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp
945                 950                 955                 960

Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965                 970                 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980                 985                 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995                1000                1005

Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025               1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val
1075                1080                1085

His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100

Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105               1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125                1130                1135

Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ser
1140                1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155                1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170                1175                1180

Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185               1190                1195                1200

Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205                1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220                1225                1230

Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Val Ala
1235                1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250                1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
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1265                1270                1275                1280

Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285                1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300                1305                1310

Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315                1320                1325

Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330                1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345                1350                1355                1360

Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
1365                1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380                1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395                1400                1405

Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410                1415                1420

Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425                1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr
1445                1450                1455

Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460                1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475                1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
1490                1495                1500

Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505                1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525                1530                1535

Lys Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540                1545                1550

Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555                1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570                1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
1585                1590                1595                1600

Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605                1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620                1625                1630

Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635                1640                1645

Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650                1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665                1670                1675                1680
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Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
1685                1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser
1700                1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
1715                1720                1725

Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730                1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745              1750


<210> SEQ ID NO 16
<211> LENGTH: 1753
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50                  55                  60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
145                 150                 155                 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165                 170                 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180                 185                 190

Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195                 200                 205

Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210                 215                 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225                 230                 235                 240

Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245                 250                 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260                 265                 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
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275                 280                 285

Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290                 295                 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305                 310                 315                 320

Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325                 330                 335

Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340                 345                 350

Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355                 360                 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys
370                 375                 380

Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415

Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430

Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460

Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
500                 505                 510

Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540

Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala
545                 550                 555                 560

Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
595                 600                 605

Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610                 615                 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr
625                 630                 635                 640

Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645                 650                 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660                 665                 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675                 680                 685
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Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
690                 695                 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705                 710                 715                 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
725                 730                 735

Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His
740                 745                 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755                 760                 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770                 775                 780

Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
785                 790                 795                 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805                 810                 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
820                 825                 830

Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835                 840                 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850                 855                 860

His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865                 870                 875                 880

Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885                 890                 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900                 905                 910

Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
915                 920                 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930                 935                 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp
945                 950                 955                 960

Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965                 970                 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980                 985                 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995                1000                1005

Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025               1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val
1075                1080                1085
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His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100

Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105                1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125                1130                1135

Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ser
1140                1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155                1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170                1175                1180

Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185                1190                1195                1200

Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205                1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220                1225                1230

Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala
1235                1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250                1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
1265                1270                1275                1280

Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285                1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300                1305                1310

Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315                1320                1325

Arg Met Arg Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330                1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345                1350                1355                1360

Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
1365                1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380                1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395                1400                1405

Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410                1415                1420

Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425                1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr
1445                1450                1455

Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460                1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475                1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
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1490                1495                1500

Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505              1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525                1530                1535

Lys Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540                1545                1550

Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555                1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570                1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
1585              1590                1595                1600

Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605                1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620                1625                1630

Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635                1640                1645

Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650                1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665              1670                1675                1680

Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
1685                1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser
1700                1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
1715                1720                1725

Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730                1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745              1750


<210> SEQ ID NO 17
<211> LENGTH: 1753
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 17

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50                  55                  60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95
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Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
145                 150                 155                 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165                 170                 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180                 185                 190

Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195                 200                 205

Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210                 215                 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225                 230                 235                 240

Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245                 250                 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260                 265                 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
275                 280                 285

Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290                 295                 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305                 310                 315                 320

Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325                 330                 335

Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340                 345                 350

Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355                 360                 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys
370                 375                 380

Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415

Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430

Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460

Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
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500                 505                 510

Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540

Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala
545                 550                 555                 560

Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
595                 600                 605

Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610                 615                 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr
625                 630                 635                 640

Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645                 650                 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660                 665                 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675                 680                 685

Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
690                 695                 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705                 710                 715                 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
725                 730                 735

Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His
740                 745                 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755                 760                 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770                 775                 780

Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
785                 790                 795                 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805                 810                 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
820                 825                 830

Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835                 840                 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850                 855                 860

His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865                 870                 875                 880

Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885                 890                 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900                 905                 910
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Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
915                 920                 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930                 935                 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp
945                 950                 955                 960

Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965                 970                 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980                 985                 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995                1000                1005

Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025               1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val
1075                1080                1085

His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100

Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105               1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125                1130                1135

Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ser
1140                1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155                1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170                1175                1180

Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185               1190                1195                1200

Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205                1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220                1225                1230

Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala
1235                1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250                1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
1265               1270                1275                1280

Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285                1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300                1305                1310
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Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315                1320                1325

Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330                1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345              1350                1355                1360

Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
1365                1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380                1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395                1400                1405

Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410                1415                1420

Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425              1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Tyr Leu Glu Glu Ala Asp His Thr
1445                1450                1455

Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460                1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475                1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
1490                1495                1500

Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505              1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525                1530                1535

Lys Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540                1545                1550

Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555                1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570                1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
1585              1590                1595                1600

Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605                1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620                1625                1630

Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635                1640                1645

Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650                1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665              1670                1675                1680

Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
1685                1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser
1700                1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
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1715                1720                1725

Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730                1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745              1750


<210> SEQ ID NO 18
<211> LENGTH: 1753
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 18

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50                  55                  60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140

Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
145                 150                 155                 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165                 170                 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180                 185                 190

Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195                 200                 205

Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210                 215                 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225                 230                 235                 240

Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245                 250                 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260                 265                 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
275                 280                 285

Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290                 295                 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305                 310                 315                 320
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Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325                 330                 335

Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340                 345                 350

Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355                 360                 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys
370                 375                 380

Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415

Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430

Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460

Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
500                 505                 510

Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540

Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala
545                 550                 555                 560

Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
595                 600                 605

Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610                 615                 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr
625                 630                 635                 640

Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645                 650                 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660                 665                 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675                 680                 685

Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
690                 695                 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705                 710                 715                 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
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725                 730                 735

Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His
740                 745                 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755                 760                 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770                 775                 780

Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
785                 790                 795                 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805                 810                 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
820                 825                 830

Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835                 840                 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850                 855                 860

His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865                 870                 875                 880

Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885                 890                 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900                 905                 910

Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
915                 920                 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930                 935                 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp
945                 950                 955                 960

Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965                 970                 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980                 985                 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995                1000                1005

Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025               1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val
1075                1080                1085

His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100

Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105               1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125                1130                1135
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Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ser
1140                1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155                1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170                1175                1180

Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185               1190                1195                1200

Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205                1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220                1225                1230

Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala
1235                1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250                1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
1265               1270                1275                1280

Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285                1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300                1305                1310

Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315                1320                1325

Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330                1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345               1350                1355                1360

Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
1365                1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380                1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395                1400                1405

Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410                1415                1420

Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425               1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr
1445                1450                1455

Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460                1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475                1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
1490                1495                1500

Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505               1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525                1530                1535
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Lys Gln Pro Ala Ala Gln Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540                1545                1550

Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555                1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570                1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
1585               1590                1595                1600

Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605                1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620                1625                1630

Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635                1640                1645

Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650                1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665               1670                1675                1680

Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
1685                1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser
1700                1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
1715                1720                1725

Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730                1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745               1750


<210> SEQ ID NO 19
<211> LENGTH: 1753
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys Arg Ser
1               5                  10                  15

Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu
20                  25                  30

Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu Leu
35                  40                  45

Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys
50                  55                  60

Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly Leu
65                  70                  75                  80

Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln Leu
85                  90                  95

Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val
100                 105                 110

Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys
115                 120                 125

Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys Val
130                 135                 140
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Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg Val
145                 150                 155                 160

Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser Lys
165                 170                 175

Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp
180                 185                 190

Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp Phe
195                 200                 205

Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe Leu
210                 215                 220

Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu Thr
225                 230                 235                 240

Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg His
245                 250                 255

Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe
260                 265                 270

Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His Lys
275                 280                 285

Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp Gly
290                 295                 300

Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp Ile
305                 310                 315                 320

Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His Thr
325                 330                 335

Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly Thr
340                 345                 350

Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser
355                 360                 365

Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met Cys
370                 375                 380

Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His Thr
385                 390                 395                 400

Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu Ala
405                 410                 415

Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly
420                 425                 430

Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu Leu
435                 440                 445

Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser Thr
450                 455                 460

Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu
465                 470                 475                 480

Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly Thr
485                 490                 495

Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln
500                 505                 510

Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu Asp
515                 520                 525

Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr
530                 535                 540
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Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr Ala
545                 550                 555                 560

Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu Val
565                 570                 575

His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro
580                 585                 590

Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val Ile
595                 600                 605

Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr Val
610                 615                 620

Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His Thr
625                 630                 635                 640

Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln Met
645                 650                 655

Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met
660                 665                 670

Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu
675                 680                 685

Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln Ser
690                 695                 700

Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu Pro
705                 710                 715                 720

Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln Ile
725                 730                 735

Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys His
740                 745                 750

Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu Cys
755                 760                 765

Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn Ile
770                 775                 780

Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln Pro
785                 790                 795                 800

Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys
805                 810                 815

Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu Lys
820                 825                 830

Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln His
835                 840                 845

Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr
850                 855                 860

His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys
865                 870                 875                 880

Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly Asn
885                 890                 895

Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys
900                 905                 910

Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr Val
915                 920                 925

Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu
930                 935                 940

Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met Trp
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945                 950                 955                 960

Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp
965                 970                 975

Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe Leu
980                 985                 990

His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu Arg
995                1000                1005

Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr
1010                1015                1020

Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys
1025               1030                1035                1040

Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys
1045                1050                1055

Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile
1060                1065                1070

Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala Val
1075                1080                1085

His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr
1090                1095                1100

Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr Thr
1105               1110                1115                1120

His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln Leu
1125                1130                1135

Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro Ser
1140                1145                1150

Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu Leu
1155                1160                1165

Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ser Val Asp Glu Ile
1170                1175                1180

Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln
1185               1190                1195                1200

Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr
1205                1210                1215

Val Leu Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser
1220                1225                1230

Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala
1235                1240                1245

Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu
1250                1255                1260

Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg
1265               1270                1275                1280

Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu
1285                1290                1295

Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg
1300                1305                1310

Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu
1315                1320                1325

Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu
1330                1335                1340

Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala
1345               1350                1355                1360
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Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu
1365                1370                1375

Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu
1380                1385                1390

Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met
1395                1400                1405

Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu
1410                1415                1420

Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala
1425               1430                1435                1440

Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr
1445                1450                1455

Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe
1460                1465                1470

His Leu Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu
1475                1480                1485

Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His
1490                1495                1500

Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln
1505               1510                1515                1520

Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser
1525                1530                1535

Lys Gln Pro Ala Ala Gln Thr Glu Ala Ser Glu Gln Gln Ala Leu His
1540                1545                1550

Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala
1555                1560                1565

Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser
1570                1575                1580

Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr
1585               1590                1595                1600

Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala
1605                1610                1615

Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys
1620                1625                1630

Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr
1635                1640                1645

Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr
1650                1655                1660

Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His
1665               1670                1675                1680

Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser
1685                1690                1695

Thr Leu Leu Ser Ser Leu Ser Arg Tyr His Arg Arg Gly Ala Pro Ser
1700                1705                1710

Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser
1715                1720                1725

Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val
1730                1735                1740

Gln Ala Phe Val Arg His Met Gln Arg
1745               1750
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<210> SEQ ID NO 20
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

Met Ile Arg Lys Ser Lys Ile Thr Ser Val Leu Ser Phe Cys
1 5 10

<210> SEQ ID NO 21
<211> LENGTH: 1745
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 21

Ala Gly Gly Pro Cys Val Arg Ser Ser Arg Glu Leu Trp Thr Ile Leu
1 5 10 15

Leu Gly Arg Ser Ala Leu Arg Glu Leu Ser Gln Ile Glu Ala Glu Leu
20 25 30

Asn Lys His Trp Arg Arg Leu Leu Glu Gly Leu Ser Tyr Tyr Lys Pro
35 40 45

Pro Ser Pro Ser Ser Ala Glu Lys Val Lys Ala Asn Lys Asp Val Ala
50 55 60

Ser Pro Leu Lys Glu Leu Gly Leu Arg Ile Ser Lys Phe Leu Gly Leu
65 70 75 80

Asp Glu Glu Gln Ser Val Gln Leu Leu Gln Cys Tyr Leu Gln Glu Asp
85 90 95

Tyr Arg Gly Thr Arg Asp Ser Val Lys Thr Val Leu Gln Asp Glu Arg
100 105 110

Gln Ser Gln Ala Leu Ile Leu Lys Ile Ala Asp Tyr Tyr Tyr Glu Glu
115 120 125

Arg Thr Cys Ile Leu Arg Cys Val Leu His Leu Leu Thr Tyr Phe Gln
130 135 140

Asp Glu Arg His Pro Tyr Arg Val Glu Tyr Ala Asp Cys Val Asp Lys
145 150 155 160

Leu Glu Lys Glu Leu Val Ser Lys Tyr Arg Gln Gln Phe Glu Glu Leu
165 170 175

Tyr Lys Thr Glu Ala Pro Thr Trp Glu Thr His Gly Asn Leu Met Thr
180 185 190

Glu Arg Gln Val Ser Arg Trp Phe Val Gln Cys Leu Arg Glu Gln Ser
195 200 205

Met Leu Leu Glu Ile Ile Phe Leu Tyr Tyr Ala Tyr Phe Glu Met Ala
210 215 220

Pro Ser Asp Leu Leu Val Leu Thr Lys Met Phe Lys Glu Gln Gly Phe
225 230 235 240

Gly Ser Arg Gln Thr Asn Arg His Leu Val Asp Glu Thr Met Asp Pro
245 250 255

Phe Val Asp Arg Ile Gly Tyr Phe Ser Ala Leu Ile Leu Val Glu Gly
260 265 270

Met Asp Ile Glu Ser Leu His Lys Cys Ala Leu Asp Asp Arg Arg Glu
275 280 285

Leu His Gln Phe Ala Gln Asp Gly Leu Ile Cys Gln Asp Met Asp Cys
290 295 300

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Leu Met Leu Thr Phe Gly Asp Ile Pro His His Ala Pro Val Leu Leu
305                 310                 315                 320

Ala Trp Ala Leu Leu Arg His Thr Leu Asn Pro Glu Glu Thr Ser Ser
325                 330                 335

Val Val Arg Lys Ile Gly Gly Thr Ala Ile Gln Leu Asn Val Phe Gln
340                 345                 350

Tyr Leu Thr Arg Leu Leu Gln Ser Leu Ala Ser Gly Gly Asn Asp Cys
355                 360                 365

Thr Thr Ser Thr Ala Cys Met Cys Val Tyr Gly Leu Leu Ser Phe Val
370                 375                 380

Leu Thr Ser Leu Glu Leu His Thr Leu Gly Asn Gln Gln Asp Ile Ile
385                 390                 395                 400

Asp Thr Ala Cys Glu Val Leu Ala Asp Pro Ser Leu Pro Glu Leu Phe
405                 410                 415

Trp Gly Thr Glu Pro Thr Ser Gly Leu Gly Ile Ile Leu Asp Ser Val
420                 425                 430

Cys Gly Met Phe Pro His Leu Leu Ser Pro Leu Leu Gln Leu Leu Arg
435                 440                 445

Ala Leu Val Ser Gly Lys Ser Thr Ala Lys Lys Val Tyr Ser Phe Leu
450                 455                 460

Asp Lys Met Ser Phe Tyr Asn Glu Leu Tyr Lys His Lys Pro His Asp
465                 470                 475                 480

Val Ile Ser His Glu Asp Gly Thr Leu Trp Arg Arg Gln Thr Pro Lys
485                 490                 495

Leu Leu Tyr Pro Leu Gly Gly Gln Thr Asn Leu Arg Ile Pro Gln Gly
500                 505                 510

Thr Val Gly Gln Val Met Leu Asp Asp Arg Ala Tyr Leu Val Arg Trp
515                 520                 525

Glu Tyr Ser Tyr Ser Ser Trp Thr Leu Phe Thr Cys Glu Ile Glu Met
530                 535                 540

Leu Leu His Val Val Ser Thr Ala Asp Val Ile Gln His Cys Gln Arg
545                 550                 555                 560

Val Lys Pro Ile Ile Asp Leu Val His Lys Val Ile Ser Thr Asp Leu
565                 570                 575

Ser Ile Ala Asp Cys Leu Leu Pro Ile Thr Ser Arg Ile Tyr Met Leu
580                 585                 590

Leu Gln Arg Leu Thr Thr Val Ile Ser Pro Pro Val Asp Val Ile Ala
595                 600                 605

Ser Cys Val Asn Cys Leu Thr Val Leu Ala Ala Arg Asn Pro Ala Lys
610                 615                 620

Val Trp Thr Asp Leu Arg His Thr Gly Phe Leu Pro Phe Val Ala His
625                 630                 635                 640

Pro Val Ser Ser Leu Ser Gln Met Ile Ser Ala Glu Gly Met Asn Ala
645                 650                 655

Gly Gly Tyr Gly Asn Leu Leu Met Asn Ser Glu Gln Pro Gln Gly Glu
660                 665                 670

Tyr Gly Val Thr Ile Ala Phe Leu Arg Leu Ile Thr Thr Leu Val Lys
675                 680                 685

Gly Gln Leu Gly Ser Thr Gln Ser Gln Gly Leu Val Pro Cys Val Met
690                 695                 700

Phe Val Leu Lys Glu Met Leu Pro Ser Tyr His Lys Trp Arg Tyr Asn
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705                 710                 715                 720

Ser His Gly Val Arg Glu Gln Ile Gly Cys Leu Ile Leu Glu Leu Ile
725                 730                 735

His Ala Ile Leu Asn Leu Cys His Glu Thr Asp Leu His Ser Ser His
740                 745                 750

Thr Pro Ser Leu Gln Phe Leu Cys Ile Cys Ser Leu Ala Tyr Thr Glu
755                 760                 765

Ala Gly Gln Thr Val Ile Asn Ile Met Gly Ile Gly Val Asp Thr Ile
770                 775                 780

Asp Met Val Met Ala Ala Gln Pro Arg Ser Asp Gly Ala Glu Gly Gln
785                 790                 795                 800

Gly Gln Gly Gln Leu Leu Ile Lys Thr Val Lys Leu Ala Phe Ser Val
805                 810                 815

Thr Asn Asn Val Ile Arg Leu Lys Pro Pro Ser Asn Val Val Ser Pro
820                 825                 830

Leu Glu Gln Ala Leu Ser Gln His Gly Ala His Gly Asn Asn Leu Ile
835                 840                 845

Ala Val Leu Ala Lys Tyr Ile Tyr His Lys His Asp Pro Ala Leu Pro
850                 855                 860

Arg Leu Ala Ile Gln Leu Leu Lys Arg Leu Ala Thr Val Ala Pro Met
865                 870                 875                 880

Ser Val Tyr Ala Cys Leu Gly Asn Asp Ala Ala Ala Ile Arg Asp Ala
885                 890                 895

Phe Leu Thr Arg Leu Gln Ser Lys Ile Glu Asp Met Arg Ile Lys Val
900                 905                 910

Met Ile Leu Glu Phe Leu Thr Val Ala Val Glu Thr Gln Pro Gly Leu
915                 920                 925

Ile Glu Leu Phe Leu Asn Leu Glu Val Lys Asp Gly Ser Asp Gly Ser
930                 935                 940

Lys Glu Phe Ser Leu Gly Met Trp Ser Cys Leu His Ala Val Leu Glu
945                 950                 955                 960

Leu Ile Asp Ser Gln Gln Gln Asp Arg Tyr Trp Cys Pro Pro Leu Leu
965                 970                 975

His Arg Ala Ala Ile Ala Phe Leu His Ala Leu Trp Gln Asp Arg Arg
980                 985                 990

Asp Ser Ala Met Leu Val Leu Arg Thr Lys Pro Lys Phe Trp Glu Asn
995                1000                1005

Leu Thr Ser Pro Leu Phe Gly Thr Leu Ser Pro Pro Ser Glu Thr Ser
1010                1015                1020

Glu Pro Ser Ile Leu Glu Thr Cys Ala Leu Ile Met Lys Ile Ile Cys
1025               1030                1035                1040

Leu Glu Ile Tyr Tyr Val Val Lys Gly Ser Leu Asp Gln Ser Leu Lys
1045                1050                1055

Asp Thr Leu Lys Lys Phe Ser Ile Glu Lys Arg Phe Ala Tyr Trp Ser
1060                1065                1070

Gly Tyr Val Lys Ser Leu Ala Val His Val Ala Glu Thr Glu Gly Ser
1075                1080                1085

Ser Cys Thr Ser Leu Leu Glu Tyr Gln Met Leu Val Ser Ala Trp Arg
1090                1095                1100

Met Leu Leu Ile Ile Ala Thr Thr His Ala Asp Ile Met His Leu Thr
1105               1110                1115                1120
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Asp Ser Val Val Arg Arg Gln Leu Phe Leu Asp Val Leu Asp Gly Thr
1125                1130                1135

Lys Ala Leu Leu Leu Val Pro Ala Ser Val Asn Cys Leu Arg Leu Gly
1140                1145                1150

Ser Met Lys Cys Thr Leu Leu Leu Ile Leu Leu Arg Gln Trp Lys Arg
1155                1160                1165

Glu Leu Gly Ser Val Asp Glu Ile Leu Gly Pro Leu Thr Glu Ile Leu
1170                1175                1180

Glu Gly Val Leu Gln Ala Asp Gln Gln Leu Met Glu Lys Thr Lys Ala
1185               1190                1195                1200

Lys Val Phe Ser Ala Phe Ile Thr Val Leu Gln Met Lys Glu Met Lys
1205                1210                1215

Val Ser Asp Ile Pro Gln Tyr Ser Gln Leu Val Leu Asn Val Cys Glu
1220                1225                1230

Thr Leu Gln Glu Glu Val Ile Ala Leu Phe Asp Gln Thr Arg His Ser
1235                1240                1245

Leu Ala Leu Gly Ser Ala Thr Glu Asp Lys Asp Ser Met Glu Thr Asp
1250                1255                1260

Asp Cys Ser Arg Ser Arg His Arg Asp Gln Arg Asp Gly Val Cys Val
1265               1270                1275                1280

Leu Gly Leu His Leu Ala Lys Glu Leu Cys Glu Val Asp Glu Asp Gly
1285                1290                1295

Asp Ser Trp Leu Gln Val Thr Arg Arg Leu Pro Ile Leu Pro Thr Leu
1300                1305                1310

Leu Thr Thr Leu Glu Val Ser Leu Arg Met Lys Gln Asn Leu His Phe
1315                1320                1325

Thr Glu Ala Thr Leu His Leu Leu Leu Thr Leu Ala Arg Thr Gln Gln
1330                1335                1340

Gly Ala Thr Ala Val Ala Gly Ala Gly Ile Thr Gln Ser Ile Cys Leu
1345               1350                1355                1360

Pro Leu Leu Ser Val Tyr Gln Leu Ser Thr Asn Gly Thr Ala Gln Thr
1365                1370                1375

Pro Ser Ala Ser Arg Lys Ser Leu Asp Ala Pro Ser Trp Pro Gly Val
1380                1385                1390

Tyr Arg Leu Ser Met Ser Leu Met Glu Gln Leu Leu Lys Thr Leu Arg
1395                1400                1405

Tyr Asn Phe Leu Pro Glu Ala Leu Asp Phe Val Gly Val His Gln Glu
1410                1415                1420

Arg Thr Leu Gln Cys Leu Asn Ala Val Arg Thr Val Gln Ser Leu Ala
1425               1430                1435                1440

Cys Leu Glu Glu Ala Asp His Thr Val Gly Phe Ile Leu Gln Leu Ser
1445                1450                1455

Asn Phe Met Lys Glu Trp His Phe His Leu Pro Gln Leu Met Arg Asp
1460                1465                1470

Ile Gln Val Asn Leu Gly Tyr Leu Cys Gln Ala Cys Thr Ser Leu Leu
1475                1480                1485

His Ser Arg Lys Met Leu Gln His Tyr Leu Gln Asn Lys Asn Gly Asp
1490                1495                1500

Gly Leu Pro Ser Ala Val Ala Gln Arg Val Gln Arg Pro Pro Ser Ala
1505               1510                1515                1520
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Ala Ser Ala Ala Pro Ser Ser Ser Lys Gln Pro Ala Ala Asp Thr Glu
1525                1530                1535

Ala Ser Glu Gln Gln Ala Leu His Thr Val Gln Tyr Gly Leu Leu Lys
1540                1545                1550

Ile Leu Ser Lys Thr Leu Ala Ala Leu Arg His Phe Thr Pro Asp Val
1555                1560                1565

Cys Gln Ile Leu Leu Asp Gln Ser Leu Asp Leu Ala Glu Tyr Asn Phe
1570                1575                1580

Leu Phe Ala Leu Ser Phe Thr Thr Pro Thr Phe Asp Ser Glu Val Ala
1585               1590                1595                1600

Pro Ser Phe Gly Thr Leu Leu Ala Thr Val Asn Val Ala Leu Asn Met
1605                1610                1615

Leu Gly Glu Leu Asp Lys Lys Lys Glu Pro Leu Thr Gln Ala Val Gly
1620                1625                1630

Leu Ser Thr Gln Ala Glu Gly Thr Arg Thr Leu Lys Ser Leu Leu Met
1635                1640                1645

Phe Thr Met Glu Asn Cys Phe Tyr Leu Leu Ile Ser Gln Ala Met Arg
1650                1655                1660

Tyr Leu Arg Asp Pro Ala Val His Pro Arg Asp Lys Gln Arg Met Lys
1665               1670                1675                1680

Gln Glu Leu Ser Ser Glu Leu Ser Thr Leu Leu Ser Ser Leu Ser Arg
1685                1690                1695

Tyr Phe Arg Arg Gly Ala Pro Ser Ser Pro Ala Thr Gly Val Leu Pro
1700                1705                1710

Ser Pro Gln Gly Lys Ser Thr Ser Leu Ser Lys Ala Ser Pro Glu Ser
1715                1720                1725

Gln Glu Pro Leu Ile Gln Leu Val Gln Ala Phe Val Arg His Met Gln
1730                1735                1740

Arg
1745


<210> SEQ ID NO 22
<211> LENGTH: 3534
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

Met Ala Ser Gly Gly Gly Val Arg Ala Ser Gly Arg Ala Lys Met Ala
1               5                  10                  15

Ala Ala Ala Gly Gly Pro Cys Val Arg Ser Ser Arg Glu Leu Trp Thr
20                  25                  30

Ile Leu Leu Gly Arg Ser Ala Leu Arg Glu Leu Ser Gln Ile Glu Ala
35                  40                  45

Glu Leu Asn Lys His Trp Arg Arg Leu Leu Glu Gly Leu Ser Tyr Tyr
50                  55                  60

Lys Pro Pro Ser Pro Ser Ser Ala Glu Lys Val Lys Ala Asn Lys Asp
65                  70                  75                  80

Val Ala Ser Pro Leu Lys Glu Leu Gly Leu Arg Ile Ser Lys Phe Leu
85                  90                  95

Gly Leu Asp Glu Glu Gln Ser Val Gln Leu Leu Gln Cys Tyr Leu Gln
100                 105                 110

Glu Asp Tyr Arg Gly Thr Arg Asp Ser Val Lys Thr Val Leu Gln Asp
115                 120                 125
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Glu Arg Gln Ser Gln Ala Leu Ile Leu Lys Ile Ala Asp Tyr Tyr Tyr
130                 135                 140

Glu Glu Arg Thr Cys Ile Leu Arg Cys Val Leu His Leu Leu Thr Tyr
145                 150                 155                 160

Phe Gln Asp Glu Arg His Pro Tyr Arg Val Glu Tyr Ala Asp Cys Val
165                 170                 175

Asp Lys Leu Glu Lys Glu Leu Val Ser Lys Tyr Arg Gln Gln Phe Glu
180                 185                 190

Glu Leu Tyr Lys Thr Glu Ala Pro Thr Trp Glu Thr His Gly Asn Leu
195                 200                 205

Met Thr Glu Arg Gln Val Ser Arg Trp Phe Val Gln Cys Leu Arg Glu
210                 215                 220

Gln Ser Met Leu Leu Glu Ile Ile Phe Leu Tyr Tyr Ala Tyr Phe Glu
225                 230                 235                 240

Met Ala Pro Ser Asp Leu Leu Val Leu Thr Lys Met Phe Lys Glu Gln
245                 250                 255

Gly Phe Gly Ser Arg Gln Thr Asn Arg His Leu Val Asp Glu Thr Met
260                 265                 270

Asp Pro Phe Val Asp Arg Ile Gly Tyr Phe Ser Ala Leu Ile Leu Val
275                 280                 285

Glu Gly Met Asp Ile Glu Ser Leu His Lys Cys Ala Leu Asp Asp Arg
290                 295                 300

Arg Glu Leu His Gln Phe Ala Gln Asp Gly Leu Ile Cys Gln Asp Met
305                 310                 315                 320

Asp Cys Leu Met Leu Thr Phe Gly Asp Ile Pro His His Ala Pro Val
325                 330                 335

Leu Leu Ala Trp Ala Leu Leu Arg His Thr Leu Asn Pro Glu Glu Thr
340                 345                 350

Ser Ser Val Val Arg Lys Ile Gly Gly Thr Ala Ile Gln Leu Asn Val
355                 360                 365

Phe Gln Tyr Leu Thr Arg Leu Leu Gln Ser Leu Ala Ser Gly Gly Asn
370                 375                 380

Asp Cys Thr Thr Ser Thr Ala Cys Met Cys Val Tyr Gly Leu Leu Ser
385                 390                 395                 400

Phe Val Leu Thr Ser Leu Glu Leu His Thr Leu Gly Asn Gln Gln Asp
405                 410                 415

Ile Ile Asp Thr Ala Cys Glu Val Leu Ala Asp Pro Ser Leu Pro Glu
420                 425                 430

Leu Phe Trp Gly Thr Glu Pro Thr Ser Gly Leu Gly Ile Ile Leu Asp
435                 440                 445

Ser Val Cys Gly Met Phe Pro His Leu Leu Ser Pro Leu Leu Gln Leu
450                 455                 460

Leu Arg Ala Leu Val Ser Gly Lys Ser Thr Ala Lys Lys Val Tyr Ser
465                 470                 475                 480

Phe Leu Asp Lys Met Ser Phe Tyr Asn Glu Leu Tyr Lys His Lys Pro
485                 490                 495

His Asp Val Ile Ser His Glu Asp Gly Thr Leu Trp Arg Arg Gln Thr
500                 505                 510

Pro Lys Leu Leu Tyr Pro Leu Gly Gly Gln Thr Asn Leu Arg Ile Pro
515                 520                 525
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Gln Gly Thr Val Gly Gln Val Met Leu Asp Asp Arg Ala Tyr Leu Val
530                 535                 540

Arg Trp Glu Tyr Ser Tyr Ser Ser Trp Thr Leu Phe Thr Cys Glu Ile
545                 550                 555                 560

Glu Met Leu Leu His Val Val Ser Thr Ala Asp Val Ile Gln His Cys
565                 570                 575

Gln Arg Val Lys Pro Ile Ile Asp Leu Val His Lys Val Ile Ser Thr
580                 585                 590

Asp Leu Ser Ile Ala Asp Cys Leu Leu Pro Ile Thr Ser Arg Ile Tyr
595                 600                 605

Met Leu Leu Gln Arg Leu Thr Thr Val Ile Ser Pro Pro Val Asp Val
610                 615                 620

Ile Ala Ser Cys Val Asn Cys Leu Thr Val Leu Ala Ala Arg Asn Pro
625                 630                 635                 640

Ala Lys Val Trp Thr Asp Leu Arg His Thr Gly Phe Leu Pro Phe Val
645                 650                 655

Ala His Pro Val Ser Ser Leu Ser Gln Met Ile Ser Ala Glu Gly Met
660                 665                 670

Asn Ala Gly Gly Tyr Gly Asn Leu Leu Met Asn Ser Glu Gln Pro Gln
675                 680                 685

Gly Glu Tyr Gly Val Thr Ile Ala Phe Leu Arg Leu Ile Thr Thr Leu
690                 695                 700

Val Lys Gly Gln Leu Gly Ser Thr Gln Ser Gln Gly Leu Val Pro Cys
705                 710                 715                 720

Val Met Phe Val Leu Lys Glu Met Leu Pro Ser Tyr His Lys Trp Arg
725                 730                 735

Tyr Asn Ser His Gly Val Arg Glu Gln Ile Gly Cys Leu Ile Leu Glu
740                 745                 750

Leu Ile His Ala Ile Leu Asn Leu Cys His Glu Thr Asp Leu His Ser
755                 760                 765

Ser His Thr Pro Ser Leu Gln Phe Leu Cys Ile Cys Ser Leu Ala Tyr
770                 775                 780

Thr Glu Ala Gly Gln Thr Val Ile Asn Ile Met Gly Ile Gly Val Asp
785                 790                 795                 800

Thr Ile Asp Met Val Met Ala Ala Gln Pro Arg Ser Asp Gly Ala Glu
805                 810                 815

Gly Gln Gly Gln Gly Gln Leu Leu Ile Lys Thr Val Lys Leu Ala Phe
820                 825                 830

Ser Val Thr Asn Asn Val Ile Arg Leu Lys Pro Pro Ser Asn Val Val
835                 840                 845

Ser Pro Leu Glu Gln Ala Leu Ser Gln His Gly Ala His Gly Asn Asn
850                 855                 860

Leu Ile Ala Val Leu Ala Lys Tyr Ile Tyr His Lys His Asp Pro Ala
865                 870                 875                 880

Leu Pro Arg Leu Ala Ile Gln Leu Leu Lys Arg Leu Ala Thr Val Ala
885                 890                 895

Pro Met Ser Val Tyr Ala Cys Leu Gly Asn Asp Ala Ala Ala Ile Arg
900                 905                 910

Asp Ala Phe Leu Thr Arg Leu Gln Ser Lys Ile Glu Asp Met Arg Ile
915                 920                 925

Lys Val Met Ile Leu Glu Phe Leu Thr Val Ala Val Glu Thr Gln Pro
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930                 935                 940

Gly Leu Ile Glu Leu Phe Leu Asn Leu Glu Val Lys Asp Gly Ser Asp
945                 950                 955                 960

Gly Ser Lys Glu Phe Ser Leu Gly Met Trp Ser Cys Leu His Ala Val
965                 970                 975

Leu Glu Leu Ile Asp Ser Gln Gln Gln Asp Arg Tyr Trp Cys Pro Pro
980                 985                 990

Leu Leu His Arg Ala Ala Ile Ala Phe Leu His Ala Leu Trp Gln Asp
995                1000                1005

Arg Arg Asp Ser Ala Met Leu Val Leu Arg Thr Lys Pro Lys Phe Trp
1010                1015                1020

Glu Asn Leu Thr Ser Pro Leu Phe Gly Thr Leu Ser Pro Pro Ser Glu
1025               1030                1035                1040

Thr Ser Glu Pro Ser Ile Leu Glu Thr Cys Ala Leu Ile Met Lys Ile
1045                1050                1055

Ile Cys Leu Glu Ile Tyr Tyr Val Val Lys Gly Ser Leu Asp Gln Ser
1060                1065                1070

Leu Lys Asp Thr Leu Lys Lys Phe Ser Ile Glu Lys Arg Phe Ala Tyr
1075                1080                1085

Trp Ser Gly Tyr Val Lys Ser Leu Ala Val His Val Ala Glu Thr Glu
1090                1095                1100

Gly Ser Ser Cys Thr Ser Leu Leu Glu Tyr Gln Met Leu Val Ser Ala
1105               1110                1115                1120

Trp Arg Met Leu Leu Ile Ile Ala Thr Thr His Ala Asp Ile Met His
1125                1130                1135

Leu Thr Asp Ser Val Val Arg Arg Gln Leu Phe Leu Asp Val Leu Asp
1140                1145                1150

Gly Thr Lys Ala Leu Leu Leu Val Pro Ala Ser Val Asn Cys Leu Arg
1155                1160                1165

Leu Gly Ser Met Lys Cys Thr Leu Leu Leu Ile Leu Leu Arg Gln Trp
1170                1175                1180

Lys Ser Ile Leu Ser Arg Glu Leu Gly Ser Val Asp Glu Ile Leu Gly
1185               1190                1195                1200

Pro Leu Thr Glu Ile Leu Glu Gly Val Leu Gln Ala Asp Gln Gln Leu
1205                1210                1215

Met Glu Lys Thr Lys Ala Lys Val Phe Ser Ala Phe Ile Thr Val Leu
1220                1225                1230

Gln Met Lys Glu Met Lys Val Ser Asp Ile Pro Gln Tyr Ser Gln Leu
1235                1240                1245

Val Leu Asn Val Cys Glu Thr Leu Gln Glu Glu Val Ile Ala Leu Phe
1250                1255                1260

Asp Gln Thr Arg His Ser Leu Ala Leu Gly Ser Ala Thr Glu Asp Lys
1265               1270                1275                1280

Asp Ser Met Glu Thr Asp Asp Cys Ser Arg Ser Arg His Arg Asp Gln
1285                1290                1295

Arg Asp Gly Val Cys Val Leu Gly Leu His Leu Ala Lys Glu Leu Cys
1300                1305                1310

Glu Val Asp Glu Asp Gly Asp Ser Trp Leu Gln Val Thr Arg Arg Leu
1315                1320                1325

Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu Glu Val Ser Leu Arg Met
1330                1335                1340
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Lys Gln Asn Leu His Phe Thr Glu Ala Thr Leu His Leu Leu Leu Thr
1345               1350                1355                1360

Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala Val Ala Gly Ala Gly Ile
1365               1370                1375

Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu Ser Thr
1380               1385                1390

Asn Gly Thr Ala Gln Thr Pro Ser Ala Ser Arg Lys Ser Leu Asp Ala
1395               1400                1405

Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser Met Ser Leu Met Glu Gln
1410               1415                1420

Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu Pro Glu Ala Leu Asp Phe
1425               1430                1435                1440

Val Gly Val His Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala Val Arg
1445               1450                1455

Thr Val Gln Ser Leu Ala Cys Leu Glu Glu Ala Asp His Thr Val Gly
1460               1465                1470

Phe Ile Leu Gln Leu Ser Asn Phe Met Lys Glu Trp His Phe His Leu
1475               1480                1485

Pro Gln Leu Met Arg Asp Ile Gln Val Asn Leu Gly Tyr Leu Cys Gln
1490               1495                1500

Ala Cys Thr Ser Leu Leu His Ser Arg Lys Met Leu Gln His Tyr Leu
1505               1510                1515                1520

Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser Ala Val Ala Gln Arg Val
1525               1530                1535

Gln Arg Pro Pro Ser Ala Ala Ser Ala Ala Pro Ser Ser Ser Lys Gln
1540               1545                1550

Pro Ala Ala Asp Thr Glu Ala Ser Glu Gln Gln Ala Leu His Thr Val
1555               1560                1565

Gln Tyr Gly Leu Leu Lys Ile Leu Ser Lys Thr Leu Ala Ala Leu Arg
1570               1575                1580

His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser Leu Asp
1585               1590                1595                1600

Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr Pro Thr
1605               1610                1615

Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala Thr Val
1620               1625                1630

Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys Glu Pro
1635               1640                1645

Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr Arg Thr
1650               1655                1660

Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr Leu Leu
1665               1670                1675                1680

Ile Ser Gln Ala Met Arg Tyr Leu Arg Asp Pro Ala Val His Pro Arg
1685               1690                1695

Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser Thr Leu
1700               1705                1710

Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser Ser Pro
1715               1720                1725

Ala Thr Gly Val Leu Pro Ser Pro Gln Gly Lys Ser Thr Ser Leu Ser
1730               1735                1740
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Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val Gln Ala
1745               1750               1755               1760

Phe Val Arg His Met Gln Arg Met Ala Ser Gly Gly Gly Val Arg Ala
1765               1770               1775

Ser Gly Arg Ala Lys Met Ala Ala Ala Ala Gly Gly Pro Cys Val Arg
1780               1785               1790

Ser Ser Arg Glu Leu Trp Thr Ile Leu Leu Gly Arg Ser Ala Leu Arg
1795               1800               1805

Glu Leu Ser Gln Ile Glu Ala Glu Leu Asn Lys His Trp Arg Arg Leu
1810               1815               1820

Leu Glu Gly Leu Ser Tyr Tyr Lys Pro Pro Ser Pro Ser Ser Ala Glu
1825               1830               1835               1840

Lys Val Lys Ala Asn Lys Asp Val Ala Ser Pro Leu Lys Glu Leu Gly
1845               1850               1855

Leu Arg Ile Ser Lys Phe Leu Gly Leu Asp Glu Glu Gln Ser Val Gln
1860               1865               1870

Leu Leu Gln Cys Tyr Leu Gln Glu Asp Tyr Arg Gly Thr Arg Asp Ser
1875               1880               1885

Val Lys Thr Val Leu Gln Asp Glu Arg Gln Ser Gln Ala Leu Ile Leu
1890               1895               1900

Lys Ile Ala Asp Tyr Tyr Tyr Glu Glu Arg Thr Cys Ile Leu Arg Cys
1905               1910               1915               1920

Val Leu His Leu Leu Thr Tyr Phe Gln Asp Glu Arg His Pro Tyr Arg
1925               1930               1935

Val Glu Tyr Ala Asp Cys Val Asp Lys Leu Glu Lys Glu Leu Val Ser
1940               1945               1950

Lys Tyr Arg Gln Gln Phe Glu Glu Leu Tyr Lys Thr Glu Ala Pro Thr
1955               1960               1965

Trp Glu Thr His Gly Asn Leu Met Thr Glu Arg Gln Val Ser Arg Trp
1970               1975               1980

Phe Val Gln Cys Leu Arg Glu Gln Ser Met Leu Leu Glu Ile Ile Phe
1985               1990               1995               2000

Leu Tyr Tyr Ala Tyr Phe Glu Met Ala Pro Ser Asp Leu Leu Val Leu
2005               2010               2015

Thr Lys Met Phe Lys Glu Gln Gly Phe Gly Ser Arg Gln Thr Asn Arg
2020               2025               2030

His Leu Val Asp Glu Thr Met Asp Pro Phe Val Asp Arg Ile Gly Tyr
2035               2040               2045

Phe Ser Ala Leu Ile Leu Val Glu Gly Met Asp Ile Glu Ser Leu His
2050               2055               2060

Lys Cys Ala Leu Asp Asp Arg Arg Glu Leu His Gln Phe Ala Gln Asp
2065               2070               2075               2080

Gly Leu Ile Cys Gln Asp Met Asp Cys Leu Met Leu Thr Phe Gly Asp
2085               2090               2095

Ile Pro His His Ala Pro Val Leu Leu Ala Trp Ala Leu Leu Arg His
2100               2105               2110

Thr Leu Asn Pro Glu Glu Thr Ser Ser Val Val Arg Lys Ile Gly Gly
2115               2120               2125

Thr Ala Ile Gln Leu Asn Val Phe Gln Tyr Leu Thr Arg Leu Leu Gln
2130               2135               2140

Ser Leu Ala Ser Gly Gly Asn Asp Cys Thr Thr Ser Thr Ala Cys Met
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2145                2150                2155                2160

Cys Val Tyr Gly Leu Leu Ser Phe Val Leu Thr Ser Leu Glu Leu His
2165                2170                2175

Thr Leu Gly Asn Gln Gln Asp Ile Ile Asp Thr Ala Cys Glu Val Leu
2180                2185                2190

Ala Asp Pro Ser Leu Pro Glu Leu Phe Trp Gly Thr Glu Pro Thr Ser
2195                2200                2205

Gly Leu Gly Ile Ile Leu Asp Ser Val Cys Gly Met Phe Pro His Leu
2210                2215                2220

Leu Ser Pro Leu Leu Gln Leu Leu Arg Ala Leu Val Ser Gly Lys Ser
2225                2230                2235                2240

Thr Ala Lys Lys Val Tyr Ser Phe Leu Asp Lys Met Ser Phe Tyr Asn
2245                2250                2255

Glu Leu Tyr Lys His Lys Pro His Asp Val Ile Ser His Glu Asp Gly
2260                2265                2270

Thr Leu Trp Arg Arg Gln Thr Pro Lys Leu Leu Tyr Pro Leu Gly Gly
2275                2280                2285

Gln Thr Asn Leu Arg Ile Pro Gln Gly Thr Val Gly Gln Val Met Leu
2290                2295                2300

Asp Asp Arg Ala Tyr Leu Val Arg Trp Glu Tyr Ser Tyr Ser Ser Trp
2305                2310                2315                2320

Thr Leu Phe Thr Cys Glu Ile Glu Met Leu Leu His Val Val Ser Thr
2325                2330                2335

Ala Asp Val Ile Gln His Cys Gln Arg Val Lys Pro Ile Ile Asp Leu
2340                2345                2350

Val His Lys Val Ile Ser Thr Asp Leu Ser Ile Ala Asp Cys Leu Leu
2355                2360                2365

Pro Ile Thr Ser Arg Ile Tyr Met Leu Leu Gln Arg Leu Thr Thr Val
2370                2375                2380

Ile Ser Pro Pro Val Asp Val Ile Ala Ser Cys Val Asn Cys Leu Thr
2385                2390                2395                2400

Val Leu Ala Ala Arg Asn Pro Ala Lys Val Trp Thr Asp Leu Arg His
2405                2410                2415

Thr Gly Phe Leu Pro Phe Val Ala His Pro Val Ser Ser Leu Ser Gln
2420                2425                2430

Met Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly Asn Leu Leu
2435                2440                2445

Met Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr Ile Ala Phe
2450                2455                2460

Leu Arg Leu Ile Thr Thr Leu Val Lys Gly Gln Leu Gly Ser Thr Gln
2465                2470                2475                2480

Ser Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys Glu Met Leu
2485                2490                2495

Pro Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val Arg Glu Gln
2500                2505                2510

Ile Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu Asn Leu Cys
2515                2520                2525

His Glu Thr Asp Leu His Ser Ser His Thr Pro Ser Leu Gln Phe Leu
2530                2535                2540

Cys Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr Val Ile Asn
2545                2550                2555                2560
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Ile Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met Ala Ala Gln
2565                2570                2575

Pro Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln Gly Gln Leu Leu Ile
2580                2585                2590

Lys Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val Ile Arg Leu
2595                2600                2605

Lys Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala Leu Ser Gln
2610                2615                2620

His Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala Lys Tyr Ile
2625              2630                2635                2640

Tyr His Lys His Asp Pro Ala Leu Pro Arg Leu Ala Ile Gln Leu Leu
2645                2650                2655

Lys Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala Cys Leu Gly
2660                2665                2670

Asn Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg Leu Gln Ser
2675                2680                2685

Lys Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu Phe Leu Thr
2690                2695                2700

Val Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe Leu Asn Leu
2705              2710                2715                2720

Glu Val Lys Asp Gly Ser Asp Gly Ser Lys Glu Phe Ser Leu Gly Met
2725                2730                2735

Trp Ser Cys Leu His Ala Val Leu Glu Leu Ile Asp Ser Gln Gln Gln
2740                2745                2750

Asp Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala Ile Ala Phe
2755                2760                2765

Leu His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met Leu Val Leu
2770                2775                2780

Arg Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro Leu Phe Gly
2785              2790                2795                2800

Thr Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Ile Leu Glu Thr
2805                2810                2815

Cys Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr Tyr Val Val
2820                2825                2830

Lys Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys Lys Phe Ser
2835                2840                2845

Ile Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys Ser Leu Ala
2850                2855                2860

Val His Val Ala Glu Thr Glu Gly Ser Ser Cys Thr Ser Leu Leu Glu
2865              2870                2875                2880

Tyr Gln Met Leu Val Ser Ala Trp Arg Met Leu Leu Ile Ile Ala Thr
2885                2890                2895

Thr His Ala Asp Ile Met His Leu Thr Asp Ser Val Val Arg Arg Gln
2900                2905                2910

Leu Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu Leu Val Pro
2915                2920                2925

Ala Ser Val Asn Cys Leu Arg Leu Gly Ser Met Lys Cys Thr Leu Leu
2930                2935                2940

Leu Ile Leu Leu Arg Gln Trp Lys Ser Ile Leu Ser Arg Glu Leu Gly
2945              2950                2955                2960
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Ser Val Asp Glu Ile Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val
2965                2970                2975

Leu Gln Ala Asp Gln Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe
2980                2985                2990

Ser Ala Phe Ile Thr Val Leu Gln Met Lys Glu Met Lys Val Ser Asp
2995                3000                3005

Ile Pro Gln Tyr Ser Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln
3010                3015                3020

Glu Glu Val Ile Ala Leu Phe Asp Gln Thr Arg His Ser Leu Ala Leu
3025                3030                3035                3040

Gly Ser Ala Thr Glu Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Ser
3045                3050                3055

Arg Ser Arg His Arg Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu
3060                3065                3070

His Leu Ala Lys Glu Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp
3075                3080                3085

Leu Gln Val Thr Arg Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr
3090                3095                3100

Leu Glu Val Ser Leu Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala
3105                3110                3115                3120

Thr Leu His Leu Leu Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr
3125                3130                3135

Ala Val Ala Gly Ala Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu
3140                3145                3150

Ser Val Tyr Gln Leu Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser Ala
3155                3160                3165

Ser Arg Lys Ser Leu Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu
3170                3175                3180

Ser Met Ser Leu Met Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn Phe
3185                3190                3195                3200

Leu Pro Glu Ala Leu Asp Phe Val Gly Val His Gln Glu Arg Thr Leu
3205                3210                3215

Gln Cys Leu Asn Ala Val Arg Thr Val Gln Ser Leu Ala Cys Leu Glu
3220                3225                3230

Glu Ala Asp His Thr Val Gly Phe Ile Leu Gln Leu Ser Asn Phe Met
3235                3240                3245

Lys Glu Trp His Phe His Leu Pro Gln Leu Met Arg Asp Ile Gln Val
3250                3255                3260

Asn Leu Gly Tyr Leu Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg
3265                3270                3275                3280

Lys Met Leu Gln His Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro
3285                3290                3295

Ser Ala Val Ala Gln Arg Val Gln Arg Pro Pro Ser Ala Ala Ser Ala
3300                3305                3310

Ala Pro Ser Ser Ser Lys Gln Pro Ala Ala Asp Thr Glu Ala Ser Glu
3315                3320                3325

Gln Gln Ala Leu His Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser
3330                3335                3340

Lys Thr Leu Ala Ala Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile
3345                3350                3355                3360

Leu Leu Asp Gln Ser Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala
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3365                3370                3375

Leu Ser Phe Thr Thr Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe
3380                3385                3390

Gly Thr Leu Leu Ala Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu
3395                3400                3405

Leu Asp Lys Lys Lys Glu Pro Leu Thr Gln Ala Val Gly Leu Ser Thr
3410                3415                3420

Gln Ala Glu Gly Thr Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met
3425              3430                3435                3440

Glu Asn Cys Phe Tyr Leu Leu Ile Ser Gln Ala Met Arg Tyr Leu Arg
3445                3450                3455

Asp Pro Ala Val His Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu
3460                3465                3470

Ser Ser Glu Leu Ser Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg
3475                3480                3485

Arg Gly Ala Pro Ser Ser Pro Ala Thr Gly Val Leu Pro Ser Pro Gln
3490                3495                3500

Gly Lys Ser Thr Ser Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro
3505              3510                3515                3520

Leu Ile Gln Leu Val Gln Ala Phe Val Arg His Met Gln Arg
3525                3530


<210> SEQ ID NO 23
<211> LENGTH: 1111
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 23

Met Thr Gln Met Ile Ser Ala Glu Gly Met Asn Ala Gly Gly Tyr Gly
1               5                  10                  15

Ser Leu Leu Met Asn Ser Glu Gln Pro Gln Gly Glu Tyr Gly Val Thr
20                  25                  30

Ile Ala Phe Leu Arg Leu Val Thr Thr Leu Val Lys Gly Gln Leu Gly
35                  40                  45

Ser Thr Gln Ser Gln Gly Leu Val Pro Cys Val Met Phe Val Leu Lys
50                  55                  60

Glu Met Leu Pro Ser Tyr His Lys Trp Arg Tyr Asn Ser His Gly Val
65                  70                  75                  80

Arg Glu Leu Ile Gly Cys Leu Ile Leu Glu Leu Ile His Ala Ile Leu
85                  90                  95

Asn Leu Cys Gln Glu Thr Glu Leu His Ser Ser His Thr Pro Ser Leu
100                 105                 110

Pro Ser Leu Cys Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly Gln Thr
115                 120                 125

Val Ile Ser Ile Met Gly Ile Gly Val Asp Thr Ile Asp Met Val Met
130                 135                 140

Ala Ala Gln Pro Arg Ser Asp Gly Pro Glu Gly Gln Gly Gln Gly Gln
145                 150                 155                 160

Leu Leu Ile Lys Thr Val Lys Leu Ala Phe Ser Val Thr Asn Asn Val
165                 170                 175

Ile Arg Leu Lys Pro Pro Ser Asn Val Val Ser Pro Leu Glu Gln Ala
180                 185                 190
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Leu Thr Gln His Gly Ala His Gly Asn Asn Leu Ile Ala Val Leu Ala
195                 200                 205

Lys Tyr Ile Tyr His Arg His Asp Pro Ala Leu Pro Arg Leu Ala Ile
210                 215                 220

Gln Leu Leu Lys Arg Leu Ala Thr Val Ala Pro Met Ser Val Tyr Ala
225                 230                 235                 240

Cys Leu Gly Ser Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu Thr Arg
245                 250                 255

Leu Gln Ser Lys Ile Glu Asp Met Arg Ile Lys Val Met Ile Leu Glu
260                 265                 270

Phe Leu Thr Val Ala Val Glu Thr Gln Pro Gly Leu Ile Glu Leu Phe
275                 280                 285

Leu Asn Leu Glu Val Lys Asp Gly Ser Asn Gly Ser Lys Glu Phe Ser
290                 295                 300

Leu Gly Val Trp Ser Cys Leu His Val Val Leu Glu Leu Ile Asp Ser
305                 310                 315                 320

Gln Gln Gln Asp Arg Tyr Trp Cys Pro Pro Leu Leu His Arg Ala Ala
325                 330                 335

Ile Ala Phe Leu His Ala Leu Trp Gln Asp Arg Arg Asp Ser Ala Met
340                 345                 350

Leu Val Leu Arg Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr Ser Pro
355                 360                 365

Leu Phe Gly Thr Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro Ser Val
370                 375                 380

Leu Glu Thr Cys Ala Leu Ile Met Lys Ile Ile Cys Leu Glu Ile Tyr
385                 390                 395                 400

Tyr Val Val Lys Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr Leu Lys
405                 410                 415

Lys Phe Ser Ser Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr Val Lys
420                 425                 430

Ser Leu Ala Val Tyr Met Ala Asp Thr Glu Gly Ser Ser Cys Thr Ser
435                 440                 445

Leu Leu Glu Tyr Gln Met Leu Val Ser Ala Trp Arg Ile Leu Leu Ile
450                 455                 460

Ile Ala Ala Ser His Ala Asp Val Met His Leu Thr Asp Met Ala Val
465                 470                 475                 480

Arg Arg Gln Leu Phe Leu Asp Val Leu Asp Gly Thr Lys Ala Leu Leu
485                 490                 495

Leu Val Ala Ala Ser Val Asn Cys Leu Arg Leu Gly Ser Met Met Cys
500                 505                 510

Thr Leu Leu Leu Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu Gly Ala
515                 520                 525

Val Glu Lys Ile Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly Val Leu
530                 535                 540

Gln Ala Asp Gln Gln Leu Met Glu Lys Thr Lys Ala Lys Val Phe Ser
545                 550                 555                 560

Ala Phe Ile Thr Val Leu Gln Met Lys Glu Leu Arg Val Gly Asp Ile
565                 570                 575

Pro Gln Tyr Ser Gln Leu Val Leu Asn Val Cys Glu Thr Leu Gln Glu
580                 585                 590

Glu Val Ile Ala Leu Phe Asp Gln Thr Arg His Ser Leu Ala Ser Asp
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595 600 605

Ser Ala Ala Glu Asp Lys Asp Ser Met Glu Thr Asp Asp Cys Pro Arg
610 615 620

Pro Arg His Lys Asp Gln Arg Asp Gly Val Cys Val Leu Gly Leu His
625 630 635 640

Leu Ala Lys Glu Leu Cys Glu Val Asp Glu Asp Gly Asp Ser Trp Leu
645 650 655

Gln Val Thr Arg Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr Thr Leu
660 665 670

Glu Val Ser Leu Arg Met Lys Gln Asn Leu His Phe Thr Glu Ala Ala
675 680 685

Leu His Leu Leu Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala Thr Ala
690 695 700

Val Ala Gly Ala Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu Leu Ser
705 710 715 720

Val Tyr Gln Leu Ser Ser Asn Gly Thr Gly Gln Thr Pro Ser Thr Ser
725 730 735

Arg Lys Ser Leu Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg Leu Ser
740 745 750

Met Ser Leu Met Glu Arg Leu Leu Lys Thr Leu Arg Tyr Asn Phe Leu
755 760 765

Thr Glu Ala Leu Asp Phe Val Gly Val His Gln Glu Arg Thr Leu Gln
770 775 780

Cys Leu Asn Ala Val Lys Thr Val Gln Ser Leu Ala Cys Leu Glu Glu
785 790 795 800

Ala Asp His Thr Val Gly Phe Ile Leu Gln Leu Ser His Phe Arg Lys
805 810 815

Glu Trp His Phe His Leu Pro Gln Leu Met Arg Asp Val Gln Val Asn
820 825 830

Leu Gly Tyr Leu Cys Gln Ala Cys Thr Ser Leu Leu His Ser Arg Lys
835 840 845

Met Leu Gln His Tyr Leu Gln Asn Lys Asn Gly Asp Gly Leu Pro Ser
850 855 860

Ala Val Thr Pro Arg Ala Gln Arg Pro Ser Thr Thr Thr Thr Thr Thr
865 870 875 880

Thr Thr Thr Thr Ala Leu Ala Thr Pro Ala Gly Cys Ser Ser Lys Gln
885 890 895

Pro Thr Ala Asp Thr Glu Ala Ser Glu Gln Arg Ala Leu His Thr Val
900 905 910

Gln Tyr Gly Leu Leu Lys Ile Leu Ser Arg Thr Leu Ala Ala Leu Arg
915 920 925

His Phe Thr Pro Asp Val Cys Gln Ile Leu Leu Asp Gln Ser Leu Asp
930 935 940

Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu Ser Phe Thr Thr Pro Thr
945 950 955 960

Phe Asp Ser Glu Val Ala Pro Ser Phe Gly Thr Leu Leu Ala Thr Val
965 970 975

Asn Val Ala Leu Asn Met Leu Gly Glu Leu Asp Lys Lys Lys Glu Ser
980 985 990

Leu Thr Gln Ala Val Gly Leu Ser Thr Gln Ala Glu Gly Thr Arg Thr
995 1000 1005

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Leu Lys Ser Leu Leu Met Phe Thr Met Glu Asn Cys Phe Tyr Leu Leu
1010                1015                1020

Ile Ser Gln Ala Val Arg Tyr Leu Arg Asp Pro Ala Val His Pro Arg
1025               1030                1035                1040

Asp Lys Gln Arg Met Lys Gln Glu Leu Ser Ser Glu Leu Ser Thr Leu
1045                1050                1055

Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg Gly Ala Pro Ser Ser Pro
1060                1065                1070

Ala Ala Gly Val Leu Pro Ser Pro Gln Gly Lys Ala Thr Ser Leu Ser
1075                1080                1085

Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu Ile Gln Leu Val Gln Ala
1090                1095                1100

Phe Val Arg His Val Gln Arg
1105               1110


<210> SEQ ID NO 24
<211> LENGTH: 853
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 24

Val Thr Ile Ala Phe Leu Arg Leu Ile Thr Thr Leu Val Lys Gly Gln
1               5                  10                  15

Leu Gly Ser Thr Gln Ser Gln Gly Leu Val Pro Cys Val Met Phe Val
20                  25                  30

Leu Lys Glu Met Leu Pro Ser Tyr His Lys Trp Arg Tyr Asn Ser His
35                  40                  45

Gly Val Arg Glu Gln Ile Gly Cys Leu Ile Leu Glu Leu Ile His Ala
50                  55                  60

Ile Leu Asn Leu Cys His Glu Thr Asp Leu His Ser Ser His Thr Pro
65                  70                  75                  80

Ser Leu Gln Phe Leu Cys Ile Cys Ser Leu Ala Tyr Thr Glu Ala Gly
85                  90                  95

Gln Thr Val Ile Asn Ile Met Gly Ile Gly Val Asp Thr Ile Asp Met
100                 105                 110

Val Met Ala Ala Gln Pro Arg Ser Asp Gly Ala Glu Gly Gln Gly Gln
115                 120                 125

Gly Gln Leu Leu Ile Lys Thr Val Lys Leu Ala Phe Ser Val Thr Asn
130                 135                 140

Asn Val Ile Arg Leu Lys Pro Pro Ser Asn Val Val Ser Pro Leu Glu
145                 150                 155                 160

Gln Ala Leu Ser Gln His Gly Ala His Gly Asn Asn Leu Ile Ala Val
165                 170                 175

Leu Ala Lys Tyr Ile Tyr His Lys His Asp Pro Ala Leu Pro Arg Leu
180                 185                 190

Ala Ile Gln Leu Leu Lys Arg Leu Ala Thr Val Ala Pro Met Ser Val
195                 200                 205

Tyr Ala Cys Leu Gly Asn Asp Ala Ala Ala Ile Arg Asp Ala Phe Leu
210                 215                 220

Thr Arg Leu Gln Ser Lys Ile Glu Asp Met Arg Ile Lys Val Met Ile
225                 230                 235                 240

Leu Glu Phe Leu Thr Val Ala Val Glu Thr Gln Pro Gly Leu Ile Glu
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245                 250                 255

Leu Phe Leu Asn Leu Glu Val Lys Asp Gly Ser Asp Gly Ser Lys Glu
260                 265                 270

Phe Ser Leu Gly Met Trp Ser Cys Leu His Ala Val Leu Glu Leu Ile
275                 280                 285

Asp Ser Gln Gln Gln Asp Arg Tyr Trp Cys Pro Pro Leu Leu His Arg
290                 295                 300

Ala Ala Ile Ala Phe Leu His Ala Leu Trp Gln Asp Arg Arg Asp Ser
305                 310                 315                 320

Ala Met Leu Val Leu Arg Thr Lys Pro Lys Phe Trp Glu Asn Leu Thr
325                 330                 335

Ser Pro Leu Phe Gly Thr Leu Ser Pro Pro Ser Glu Thr Ser Glu Pro
340                 345                 350

Ser Ile Leu Glu Thr Cys Ala Leu Ile Met Lys Ile Ile Cys Leu Glu
355                 360                 365

Ile Tyr Tyr Val Val Lys Gly Ser Leu Asp Gln Ser Leu Lys Asp Thr
370                 375                 380

Leu Lys Lys Phe Ser Ile Glu Lys Arg Phe Ala Tyr Trp Ser Gly Tyr
385                 390                 395                 400

Val Lys Ser Leu Ala Val His Val Ala Glu Thr Glu Gly Ser Ser Cys
405                 410                 415

Thr Ser Leu Leu Glu Tyr Gln Met Leu Val Ser Ala Trp Arg Met Leu
420                 425                 430

Leu Ile Ile Ala Thr Thr His Ala Asp Ile Met His Leu Thr Asp Ser
435                 440                 445

Val Val Arg Arg Gln Leu Phe Leu Asp Val Leu Asp Gly Thr Lys Ala
450                 455                 460

Leu Leu Leu Val Pro Ala Ser Val Asn Cys Leu Arg Leu Gly Ser Met
465                 470                 475                 480

Lys Cys Thr Leu Leu Leu Ile Leu Leu Arg Gln Trp Lys Arg Glu Leu
485                 490                 495

Gly Ser Val Asp Glu Ile Leu Gly Pro Leu Thr Glu Ile Leu Glu Gly
500                 505                 510

Val Leu Gln Ala Asp Gln Gln Leu Met Glu Lys Thr Lys Ala Lys Val
515                 520                 525

Phe Ser Ala Phe Ile Thr Val Leu Gln Met Lys Glu Met Lys Val Ser
530                 535                 540

Asp Ile Pro Gln Tyr Ser Gln Leu Val Leu Asn Val Cys Glu Thr Leu
545                 550                 555                 560

Gln Glu Glu Val Ile Ala Leu Phe Asp Gln Thr Arg His Ser Leu Ala
565                 570                 575

Leu Gly Ser Ala Thr Glu Asp Lys Asp Ser Met Glu Thr Asp Asp Cys
580                 585                 590

Ser Arg Ser Arg His Arg Asp Gln Arg Asp Gly Val Cys Val Leu Gly
595                 600                 605

Leu His Leu Ala Lys Glu Leu Cys Glu Val Asp Glu Asp Gly Asp Ser
610                 615                 620

Trp Leu Gln Val Thr Arg Arg Leu Pro Ile Leu Pro Thr Leu Leu Thr
625                 630                 635                 640

Thr Leu Glu Val Ser Leu Arg Met Lys Gln Asn Leu His Phe Thr Glu
645                 650                 655
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Ala Thr Leu His Leu Leu Leu Thr Leu Ala Arg Thr Gln Gln Gly Ala
660                 665                 670

Thr Ala Val Ala Gly Ala Gly Ile Thr Gln Ser Ile Cys Leu Pro Leu
675                 680                 685

Leu Ser Val Tyr Gln Leu Ser Thr Asn Gly Thr Ala Gln Thr Pro Ser
690                 695                 700

Ala Ser Arg Lys Ser Leu Asp Ala Pro Ser Trp Pro Gly Val Tyr Arg
705                 710                 715                 720

Leu Ser Met Ser Leu Met Glu Gln Leu Leu Lys Thr Leu Arg Tyr Asn
725                 730                 735

Phe Leu Pro Glu Ala Leu Asp Phe Val Gly Val His Gln Glu Arg Thr
740                 745                 750

Leu Gln Cys Leu Asn Ala Val Arg Thr Val Gln Ser Leu Ala Cys Leu
755                 760                 765

Glu Glu Ala Asp His Thr Val Gly Phe Ile Leu Gln Leu Ser Asn Phe
770                 775                 780

Met Lys Glu Trp His Phe His Leu Pro Gln Leu Met Arg Asp Ile Gln
785                 790                 795                 800

Val Gly Ala Gln Asp Gly Val Leu Glu Ser Gly Val Met Leu Gly Asp
805                 810                 815

Arg Glu Ala Val Arg Ser His Trp Gly Thr Pro Ser Glu Leu Gln Asp
820                 825                 830

Val Pro Glu Arg Gly Leu Phe Pro Trp Gly Ala Gln Gly Leu Leu Ser
835                 840                 845

Cys Ala Tyr Ser Gly
850


<210> SEQ ID NO 25
<211> LENGTH: 525
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 25

Thr Arg Pro Leu Gln Glu Glu Val Ile Ala Leu Phe Asp Gln Thr Arg
1               5                  10                  15

His Ser Leu Ala Ser Asp Ser Ala Ala Glu Asp Lys Asp Ser Met Glu
20                  25                  30

Thr Asp Asp Cys Pro Arg Pro Arg His Lys Asp Gln Arg Asp Gly Val
35                  40                  45

Cys Val Leu Gly Leu His Leu Ala Lys Glu Leu Cys Glu Val Asp Glu
50                  55                  60

Asp Gly Asp Ser Trp Leu Gln Val Thr Arg Arg Leu Pro Ile Leu Pro
65                  70                  75                  80

Thr Leu Leu Thr Thr Leu Glu Val Ser Leu Arg Met Lys Gln Asn Leu
85                  90                  95

His Phe Thr Glu Ala Ala Leu His Leu Leu Leu Thr Leu Ala Arg Thr
100                 105                 110

Gln Gln Gly Ala Thr Ala Val Ala Gly Ala Gly Ile Thr Gln Ser Ile
115                 120                 125

Cys Leu Pro Leu Leu Ser Val Tyr Gln Leu Ser Ser Asn Gly Thr Gly
130                 135                 140

Gln Thr Pro Ser Thr Ser Arg Lys Ser Leu Asp Ala Pro Ser Trp Pro
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145                 150                 155                 160

Gly Val Tyr Arg Leu Ser Met Ser Leu Met Glu Arg Leu Leu Lys Thr
165                 170                 175

Leu Arg Tyr Asn Phe Leu Thr Glu Ala Leu Asp Phe Val Gly Val His
180                 185                 190

Gln Glu Arg Thr Leu Gln Cys Leu Asn Ala Val Lys Thr Val Gln Ser
195                 200                 205

Leu Ala Cys Leu Glu Glu Ala Asp His Thr Val Gly Phe Ile Leu Gln
210                 215                 220

Leu Ser His Phe Arg Lys Glu Trp His Phe His Leu Pro Gln Leu Met
225                 230                 235                 240

Arg Asp Val Gln Val Asn Leu Gly Tyr Leu Cys Gln Ala Cys Thr Ser
245                 250                 255

Leu Leu His Ser Arg Lys Met Leu Gln His Tyr Leu Gln Asn Lys Asn
260                 265                 270

Gly Asp Gly Leu Pro Ser Ala Val Thr Pro Arg Ala Gln Arg Pro Ser
275                 280                 285

Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Ala Leu Ala Thr Pro Ala
290                 295                 300

Gly Cys Ser Ser Lys Gln Pro Thr Ala Asp Thr Glu Ala Ser Glu Gln
305                 310                 315                 320

Arg Ala Leu His Thr Val Gln Tyr Gly Leu Leu Lys Ile Leu Ser Arg
325                 330                 335

Thr Leu Ala Ala Leu Arg His Phe Thr Pro Asp Val Cys Gln Ile Leu
340                 345                 350

Leu Asp Gln Ser Leu Asp Leu Ala Glu Tyr Asn Phe Leu Phe Ala Leu
355                 360                 365

Ser Phe Thr Thr Pro Thr Phe Asp Ser Glu Val Ala Pro Ser Phe Gly
370                 375                 380

Thr Leu Leu Ala Thr Val Asn Val Ala Leu Asn Met Leu Gly Glu Leu
385                 390                 395                 400

Asp Lys Lys Lys Glu Ser Leu Thr Gln Ala Val Gly Leu Ser Thr Gln
405                 410                 415

Ala Glu Gly Thr Arg Thr Leu Lys Ser Leu Leu Met Phe Thr Met Glu
420                 425                 430

Asn Cys Phe Tyr Leu Leu Ile Ser Gln Ala Val Arg Tyr Leu Arg Asp
435                 440                 445

Pro Ala Val His Pro Arg Asp Lys Gln Arg Met Lys Gln Glu Leu Ser
450                 455                 460

Ser Glu Leu Ser Thr Leu Leu Ser Ser Leu Ser Arg Tyr Phe Arg Arg
465                 470                 475                 480

Gly Ala Pro Ser Ser Pro Ala Ala Gly Val Leu Pro Ser Pro Gln Gly
485                 490                 495

Lys Ala Thr Ser Leu Ser Lys Ala Ser Pro Glu Ser Gln Glu Pro Leu
500                 505                 510

Ile Gln Leu Val Gln Ala Phe Val Arg His Val Gln Arg
515                 520                 525


<210> SEQ ID NO 26
<211> LENGTH: 6
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```

-continued

<400> SEQUENCE: 26

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1 5

We claim:

1. An isolated nucleic acid molecule encoding a polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of SEQ ID NO:2.

2. A vector comprising the nucleic acid molecule of claim **1**.

3. A cell including the vector of claim **2**.

4. A fusion polypeptide comprising (i) a polypeptide encoded by the nucleic acid molecule of claim **1** operably linked to (ii) a non-BFLP0169 polypeptide.

5. The fusion polypeptide of claim **4**, wherein said non-BFLP0169 polypeptide comprises at least one member selected from the group consisting of an Fc region of an immunoglobulin molecules or a FLAG epitope, a HIS tag, and a MYC tag.

6. A fusion polypeptide comprising a rapamycin-binding domain of a BFLP0169 polypeptide operably linked to a non-BFLP0169 polypeptide.

7. The fusion polypeptide of claim **6**, wherein said non-BFLP0169 polypeptide comprises at least one member selected from the group consisting of an Fc region of an immunoglobulin molecules or a FLAG epitope, a HIS tag, and a MYC tag.

8. A pharmaceutical composition comprising the fusion polypeptide of claim **6** and a pharmaceutically acceptable carrier.

9. An antibody that binds selectively to a polypeptide encoded by the nucleic acid of claim **1**.

10. The antibody of claim **9**, wherein said antibody inhibits binding of a BFLP0169 polypeptide to rapamycin.

11. The antibody of claim **9**, wherein said antibody is a polyclonal antibody.

12. The antibody of claim **9**, wherein said antibody is a monoclonal antibody.

13. The monoclonal antibody of claim **12**, wherein said monoclonal antibody is selected from the group consisting of a murine monoclonal antibody, and a humanized monoclonal antibody.

14. A method of producing a BFLP0169 polypeptide, said method comprising culturing a cell including the nucleic acid molecule of claim **1** under conditions allowing for expression of a BFLP0169 polypeptide encoded by said nucleic acid molecule.

15. A method of detecting the presence of a BFLP0169 nucleic acid molecule in a biological sample, the method comprising:

contacting the sample with a nucleic acid probe that binds specifically to a BFLP0169 nucleic acid; and

identifying the bound probe, if present,

thereby detecting the presence of BFLP0169 nucleic acid molecule in said sample.

16. A method of detecting the presence of a BFLP0169 polypeptide in a sample, the method comprising:

contacting the sample with a compound that selectively binds to said polypeptide under conditions allowing for formation of a complex between said polypeptide and said compound; and

detecting said complex, if present, thereby identifying said polypeptide in said sample.

17. A method for screening for a therapeutic agent for treating an autoimmune disorder, the method comprising:

contacting a test compound with a BFLP0169 polypeptide; and

determining if said test compound binds to said BFLP0169 polypeptide, wherein binding of said test compound to said polypeptide indicates the test compound is a therapeutic agent for an autoimmune disorder.

18. A method of treating lupus nephritis in a subject, the method comprising administering to said subject a therapeutically effective amount of an agent that inhibits activity of a BFLP0169 polypeptide in said subject.

19. A pharmaceutical composition comprising an agent that inhibits activity of a BFLP0169 polypeptide in a subject and a pharmaceutically acceptable carrier.

20. The pharmaceutical composition of claim **19**, wherein said agent is an anti-BFLP antibody.

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