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- (54) **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME**
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09/854,280, filed on May 10, 2001, which is a continuation of application No. 09/854,208, filed on May 10, 2001, which is a continuation of application No. 09/816,744, filed on Mar. 22, 2001, now Pat. No. 6,579,520, which is a continuation of application No. 09/747,259, filed on Dec. 20, 2000, now Pat. No. 6,569,645, which is a continuation of application No. 09/709,238, filed on Nov. 8, 2000, now abandoned, which is a continuation of application No. 09/664,610, filed on Sep. 18, 2000, now abandoned, which is a continuation of application No. 09/665,350, filed on

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- (52) **U.S. Cl.** **435/183**; 435/69.1; 435/320.1; 435/325; 536/23.2

(57) **ABSTRACT**

The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

GGGGCTTCGGCCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATG
AGCAGGCTCTGAAGACTAATCATTTTGTGAAGTTGTAAAAACAGAAACCTGTTAGAAATGTTGGTGGT
TTCAGCAAGGCCCTCAGTTTCCTTCCTTCAGCCCTTGTAAATTTGGACATCTGCTGCTTCATATTT
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATGCGGCAGTTTATGCAATG
CTACCATTTATGTTGTTTATAAGCAAGTTCATGCTCTGAGTCTGAAGAGAACGTTATCATCAAA
TTAAACAAGGCTGGCCTTGTAATGGAATACTGAGTTGTTTAGGACTTTCTATTGTGGCAAACTT
CCAGAAAACAACCCCTTTTGTCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT
TATATATGTTTGGTTCAGACCATCCTTTCTTACCAATGCGAGCCCAAAATCCATGGCAACAAGTC
TTCCTGGATCAGACTGTTGTTGGTTATCTGGTGGAGTAAGTGCACTTAGCATGCTGACTTGCTC
ATCAGTTTTCAGAGTGGCAATTTTGGGACTGATTAGAACAGAACTCCATTTGGAACCCCGAGG
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAAATGCTCTATGTCTATTTCTCTTTT
GGTTTTTCTGACTTACATTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA
TGGATTAACCCCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA
GAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTTCTCAGGGATTGGGGAAGG
TTCACAGAAAGTTGCTTATCTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACT
GATGAATGCTGATAATCAGGAACATGAAAGAAGCCATTTGATAGATTATCTAAAGGATATCAT
CAAGAAGACTATTAATAACACCTATGCTTATCTCTGAGAAATAAAGTCAAAGACT
ATG

Related U.S. Application Data

Sep. 18, 2000, which is a continuation of application No. 09/644,848, filed on Aug. 22, 2000, which is a continuation of application No. 09/423,844, filed on Nov. 12, 1999, now abandoned, which is a continuation of application No. 09/403,297, filed on Oct. 18, 1999, now abandoned, which is a continuation of application No. 09/397,342, filed on Sep. 15, 1999, which is a continuation of application No. 09/380,142, filed on Aug. 25, 1999, now abandoned, which is a continuation of application No. 09/380,138, filed on Aug. 25, 1999, now abandoned, which is a continuation of application No. 09/380,137, which is a continuation of application No. 09/311,832, filed on May 14, 1999, which is a continuation of application

No. 09/380,139, filed on Aug. 25, 1999, now abandoned.

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Dec. 1, 2000	(WO)		PCT/US00/32678
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Dec. 30, 1998	(KR)		1998-62142
Jun. 1, 2001	(WO)		PCT/US01/17800
May 22, 2000	(WO)		PCT/US00/14042

FIGURE 1

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATG
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGT
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTT
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTTATGCATTG
CTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAA
TTAAACAAGGCTGGCCTTGTACTTGAATACTGAGTTGTTTAGGACTTTCTATTTGTGGCAAACCTT
CCAGAAAACAACCCCTTTTGTCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT
TATATATGTTTGTTCAGACCATCCTTTCCTACCAAATGCAGCCCCAAAATCCATGGCAAACAAGTC
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTTAGCATGCTGACTTGCTC
ATCAGTTTTGCACAGTGGCAATTTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTT
GGTTTTTTCCTGACTTACATTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA
TGGATTAACCCCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA
GAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG
TTCACAGAAGTTGCTTATTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACT
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCAT
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACT
ATG

FIGURE 2

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWFFQQGLSFLPSALVIWTSAAFIIFSITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV
LCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG
MGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW
NPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR
LLSRDI

Important features:

Type II transmembrane domain:

amino acids 13-33

Other Transmembrane domains:

amino acids 54-73, 94-113, 160-180, 122-141

N-myristoylation sites.

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC
GTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTC
CTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG
GATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAG
GTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG
AGTATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGG
TTTTCATGGTGCCTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACACGA
CTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCC
CATTCTCAGCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAG
TGACTCTCATGGCTCTTCTTCTGGATTGGTGTGTCAACTGCCCATACACTTACATGTCTTACTTC
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT
CATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA
AACCATCAGGTTTCTGGGAATGATAAAAAGTGTACCACCTTCAGCATCAGGAAGTGAATCTTACT
CTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTTCTGGAAACAGCTGATCT
ATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTCAAGGGGAAATATTTAATTTTCTTGGTT
ACTTTTTCTCTATTTACTGTGTTTGGAAAATTTTCATGGCTACCATCAATATTGTTTTGATCGAGTT
GGGAAAACGGATCCTGTCAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT
GAAGTTTTGGTCCCAACACATTTCTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGAT
TGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCTTG
CTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTT
AGAATACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTTTG
ATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAACAGGCACCA
GAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAAATTTA
GATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAACAAACAAAATGCTATGGTAGC
ATTTTTACCTTCATAGCATACTCCTTCCCCGTGAGGTGATACTATGACCATGAGTAGCATCAGCCAG
AACATGAGAGGGGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG
TGTAAGGGCGGAGAGGAGCCAAGAACTAAAGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGT
CTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTTG
CCTTGAGATTGACTCATTAAAATCAGAGACTGTAACAAAAAAGGGCGGCCGCG
ACTCTAGAGTCGACCTGCAGAAGCTTGCCCGCATGGCCCACTTGTTTATTGCAGCTTATAATG

FIGURE 4

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGV
LNSSSRYPFHWMNLVCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLESCLLWLTFFMYFFWKLGBP
FPILSPKHGILSIEQLISRVGIVGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERLLQ
TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQQEVDALAEELSRQ
LPLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGKTDVPVTRGIEI
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLLAQIMGY
FVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 5

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC
 AGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT
 GTTTCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT
 TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGT
 GTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAG
 AAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCC
 TTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGGTGCATCTCTAG
 GATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTGATTGGAAGTTCCAGTGA
 GCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAAGTGCATTCCAGAA
 ATTATCACCACCAAAGATCCCATATTTCAACACTCAAAGTCAACACAAACAAGAAATTTATTGT
 CAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTACTCTC
 CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAGTTTTTATG
 GAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGA
 AGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTTGCTCTCCTCTTTGGTGCTG
 CAGCTGGTCTTGGATTTTGTATGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAT
 CAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCATA
 TGAGGAATCAAGAAAACCTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGC
 GATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTTCTTT
 CATGCTCCTTACCCTGCCCCAGCTGGGGAAATCAAAAGGGCCAAAGAACCAAGAAGAAAGTCCA
 CCCTTGGTTTCTTAAGTGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAT
 GCCCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCT
 TTCTAGCCTGGCTATGTCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAAGGAC
 CTAAACATCTCATCAGTATCCAGTGCTAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTG
 AAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGACCTTTCTTCA
 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAAAAGAAAT
 GGCAGAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAA
 GCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAAC
 ACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACA
 CTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACA
 AAAATAAAAACCTCTTATAAATTTCTATTTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT
 ACTCAGTAATTTGTTTAAAAAGTAATAAAATTCAACAAACATTTGCTGAATAGCTACTATATGTC
 AAGTGCTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCCTCAAAAAATTGCACATAGTAG
 AACGCTATCTGGGAAGCTATTTTTTTTTCAGTTTGGATATTTCTAGCTTATCTACTTCCAACTAAT
 TTTTATTTTTGCTGAGACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATT
 TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAAGTGCC
 ATTAACAAATGTATCACTAGCCCTCCTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATT
 TGTGACAAAAAATTAAAGCATTTAGAAAACCT

FIGURE 6

MARCFSLVLLLSIWTTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQQLNFTEAKEACRLLG
LSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYN
SSDTWTNSCIPEIIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR
RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVK
RYVKAFPFNTKNQOKEMIETKVVKEEKANDSNPNNEESKKTDKNPESKSPSKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 7

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCAGCCCGGC
GGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCGGGGCGG
CGGCTGCGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCCTGCTGTGCCTGCTGCTGGCGG
CGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCCGGCCCG
GCTCTCAGCTACCCGCAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGAGGTTGAGGAACTGAT
GGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA
AAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTATCACAAATGAGACCAACACAGAC
ACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAATTACAAAGATAACCAACAACCAGAC
TGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAGCC
ACGAGTGCATCATCGACGAGGACTGTGGGCCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC
ACCTGCCAGCCATGCCGGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAAGTGTGTGGAGACCA
GCTGTGTGTCTGGGGTCACTGCACCAAATGGCCACCAGGGGCAGCAATGGGACCATCTGTGACA
ACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGC
ACACCCCTGCCCCGTGGAGGGCGAGCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCAC
CTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGC
CCCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGG
GAGATCCTGCTGCCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCG
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTG
CCGCCGCTGCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAA
TAGAAATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTA
CATCTTCTTCCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCAGCT
CCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGTCTGGGAGAGTCAGGCAGGGTTAACTGCA
GGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAGACAGCCG
TTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAAACAATGTGGAGTCTCCCTC
TGATTGGTTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAACCTGGCAAAAATG
CAACAAATGAATTTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGC
AGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTCATCCAGCAGTGTGTCTCAGCTCC
TACCTCTGTGCCAGGGCAGCATTTTTCATATCCAAGATCAATTCCCTCTCTCAGCACAGCCTGGGG
AGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCT
CTCCACTACCCACACCAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGGGAT
TTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAATAATTCTCACATCCCTCTAAAAGTAAA
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGAT
ATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCA
TACAGGTTAACCTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGC
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGC
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATG
TTTTCAGGTGTATGGACTGTTGCCACCATGTATTCATCCAGAGTTCTTAAAGTTTAAAGTTGCA
CATGATTGTATAAGCATGCTTTCTTTGAGTTTTAAATTATGTATAAACATAAGTTGCATTTAGAA
ATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL
RSAVEEMEAEEAAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTGQMVFSE
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRDSECCGDQLCVWGHC
TKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRLLDLITWELEPDG
ALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQELEDLE
RSLTEEMALGEPAAAAAALLGGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 9

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCAC
GGCCCACCTTGTGAACTCCTCGTGCCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCATCCAAAG
GCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCCTGGGGCTCTTCTGGACCCTT
AACTGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTTCTACTGGGCCTT
CCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC
ACACTGGGTCAATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAGATAGCCCGGGTCATCTTG
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGCCCGCTGCATCATGTGCTGTTT
CAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCCTAAACCGCAATGCATACATCATGA
TCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTCATGCTACTCATGCGAAAC
ATTGTCAGGGTGGTTCGTCCTGGACAAAGTCACAGACCTGCTGCTGTTCTTTGGGAAGCTGCTGGT
GGTCGGAGGCGTGGGGGTCTGTCTTCTTTTTTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAG
ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCCATCATGACCTCCATCCTGGGGGCTAT
GTCATCGCCAGCGGCTTCTTCAGCGTTTTTCGGCATGTGTGTGGACACGCTCTTCCTCTGCTTCCT
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA
AGATTCTGGGCAAGAAGAACGAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG
CCCTGATCCAGGACTGCACCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGT
CTCCATTTTGTGGTAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCTGTAATCCAACACT
TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG
AAACCTCCGTCTCTATTAAAAATACAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCA
GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGA
GATCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAAACAAA
AAGATTTTATTAAAGATATTTTGTTAAC

FIGURE 10

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLEFWTL
NWVLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAFMLLMRN
IVRVVVLDKVTDLLLEFFGKLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKNEAPPDNKKRKK

Important features:

Transmembrane domains:

amino acids 57-80 (type II), 110-126, 215-231, 254-274

N-glycosylation sites.

amino acids 16-20, 27-31, 289-293

Hypothetical YBR002c family proteins.

amino acids 276-288

Ammonium transporters proteins.

amino acids 204-231

N-myristoylation sites.

amino acids 60-66, 78-84

Amidation site.

amino acids 306-310

FIGURE 11

GCCCCGCGCCCGGCGCCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGAGCCTGC
TCCCTGCTCAGCTGCGCGTCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCTGCTGCCCCGC
CAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCTCTTCTGCGGGTGCTGGTGTCCA
TCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTGCCCTGGGTGTGTGAGGAGGGGGCC
GGGATCCCCACCGTCTGCAGGGCCACATCGACTGTGGCTCCCTGCTTGGCTACCGCGCTGTCTACCG
CATGTGCTTCGCCACGGCGGCCTTCTTCTTCTTCTTTTACCCTGCTCATGCTCTGCGTGAGCAGCA
GCCGGGACCCCCGGGCTGCCATCCAGAATGGGTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTC
ACCGTGGGTGCCTTCTACATCCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCTGTGG
CTCCTTCTCTTTCATCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACAGCGGT
GGCTGGGCAAGGCCGAGGAGTGCGATTCCCGTGCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTC
TTCTACTTGCTGTGATCGCGCCGTGGCGCTGATGTTTATGTACTACACTGAGCCAGCGGCTGCCA
CGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCTGCTGTCTGC
CCAAGGTCCAGGACGCCCAGCCCAACTCGGGTCTGTGCGAGGCCTCGGTTCATCACCTCTACACCATG
TTTGTCACTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTTGCCAACCCAGCT
GGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATGCCCCGAGCATTG
TGGGCCTCATCATCTTCTCTGTGCACCTCTTCATCAGTCTGCGCTCCTCAGACCACCGGCAGGTG
AACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGT
GGCAGCCTGTGAGGGCCGGGCCTTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCC
ACTTCTGCCTGGTGCTGGCCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAG
ACCCGGAAGATGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCT
CCTCTACCTGTGGACCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTAGGAGGCAGCCTCA
CAGCCTGCCATCTGGTGCTCCTGCCACCTGGTGCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTC
CCCACACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTGCCCCTGAGCCGGGC
CTTCTAGTCGTAGTGCCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCAC
ACCCACACGGTGGAGCTGCCTCTTCTTCCCCCTCCTCCCTGTTGCCATACTCAGCATCTCGGATGAA
AGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACCTCCCACCACAG
TGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTCACGTCCCCCAGGGGACCCTGCCCCCTTCTCTG
GACTTCGTGCCTTACTGAGTCTCTAAGACTTTTTCTAATAAACAAGCCAGTGCGTGTAACAAAAA

FIGURE 12

MGACLGACSLSCASCSCGSAPCILCSCCPASRNSTVSRLI FTFFLEFLGVLVSIIMLSPGVESQL
YKLPWVCEEAGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAA FFFFFFFTLMLCVSSSRDPRAAIQ
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSWNQRWLKAE
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVSIAAVLPKV
QDAQPN SGLLQASVITLYTMEVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQAACEGRAFDNEQDGVITYSY
SFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVWKICASWAGLLLYLWTLVAPLLLRNRD
FS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 13

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCCCGTTAAGGTGTCTTCTCTTTAGGGATGGTGA
GGTTGGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAGAACG
CTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCACACAA
CTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC
TTTCTGTTTGTGTGTACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATAGAGTTAAATG
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT
TTTGATATATTTCTTCTGGCAGTTTTTCGATTTAAAGTGTTAATACTTGCATATGCTGTGTGCAG
ACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTTTACTAGCAAAAG
TGATCCTTTTCGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTGCCCATCATTTTCATTCATC
CTTGCCTGGATTGAGACGTGGTTCCTGGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA
CAGACTCCTGATAGTTTCAGGATGCTTCAGAGAGGGCAGCACTTATACCTGGTGGTCTTTCTGATG
GTCAGTTTTATTCCCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT
GAGAAACCACTTTTAGAACTATTGAGTACTACTTTTTGTAAATGTGAAAAACCCTCACAGAAAGTC
ATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTGTGACAGTAAAGTTGAAATGGTGACGTC
CACTGCTGGCTTTATTGAACAGCTAATAAAGATTTATTTATTGTAATACCTCACAAACGTTGTAC
CATATCCATGCACATTTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCATCCTCTCT
TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAGAAAGTCTTGTGCTGTATTCCCTAATC
AAAAGACTTAATATATTGAAGTAACACTTTTTTAGTAAGCAAGATACCTTTTTATTTCATTCAC
AGAATGGAATTTTTTTGTTTCATGTCTCAGATTTATTTTGTATTTCTTTTTTAACACTCTACATT
TCCCTTGTTTTTTAACTCATGCACATGTGCTCTTTGTACAGTTTTAAAAAGTGTAATAAAATCTG
ACATGTCAATGTGGCTAGTTTTATTTTCTTGTTTTGCATTATGTGTATGGCCTGAAGTGTTGGA
CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGTAAAATGTCACCAGACATTTGTATTATTT
TTATCATGAAATCATGTTTTTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGC
ACAAAATGACTTAAACCATTTCATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAATGAA
CTAAATTAAAAA

FIGURE 14

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF
VTLLWIIELNVNGGIENLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT
AVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLQPQAEENRLLIVQDASER
AALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 54-72, 100-118, 130-144, 146-166

N-myristoylation sites.

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

FIGURE 15

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTCGGGCCCCGACCCGCCAGGAAAGACTGAGG
 CCGCGGCCTGCCCCGCCCCGGCTCCCTGCGCCGCCGCCGCTCCCGGGACAGAAGATGTGCTCCAG
 GGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGGTGCAGGGCTGCCCAT
 CCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGGACCACGGTGCCC
 CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC
 AGGCAGCTTTGCCGGCCTGCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACCAGATCGCCAGCC
 TGCCACGCGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTGGACCTGACGGCCAACAGGCTG
 CATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCCTCGAGCGCCTCTACCTGGGCAAGAA
 CCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGCTCGACCGCCTCCTGGAGCTCAAGCTGC
 AGGACAACGAGCTGCGGGCACTGCCCCCGCTGCGCCTGCCCCGCCTGCTGCTGGACCTCAGC
 CACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCT
 GGCTGGTCTGGGGCTGCAGCAGCTGGAGCAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACC
 TGGATGTGTCCGACAACCACTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACG
 CGCCTGCGGCTGGCCGGCAACACCCGCATTGCCAGCTGCGGCCGAGGACCTGGCCGGCCTGGC
 TGCCCTGCAGGACTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCC
 TCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGC
 TGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTCACACTGGCCAGCCCTGAGGAGACGCGCTGCCA
 CTTCCCCGCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAG
 CCACCACCACCACAGCCACAGTGCCCAACCAGAGGCCCGTGGTGCAGGAGCCACAGCCTTGTCT
 TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCAGCCCGCCCTC
 CACTGCCCCACCGACTGTAGGGCCTGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCA
 ATGGGGGCACATGCCACCTGGGGACACGGCACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACG
 GGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCCAGCCCTACACCAGTCACGCCGAG
 GCCACCACGGTCCCTGACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGC
 AGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCG
 GGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCA
 GCTGCGGCCCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGGCCCCGGCGGGTGCCGGAGG
 GCGAGGAGGCCTGCGGGGAGGCCCATACACCCCCAGCCGTCCACTCCAACCACGCCCCAGTCACC
 CAGGCCCCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGC
 GCTGGCTGCGGTGGGGGACGCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGGCTCAGG
 ACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCTGGAACCTGGAGGGAGTGAAGGTCCCTTGGAG
 CCAGGCCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCC
 ACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAAAGCCCTACATCTAAGCCA
 GAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGTGCC
 ACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCT
 GGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCCAGCTGACGAGCC
 CTAACGTCCCCAGAACCGAGTGCCATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTC
 CCTGGGCACGGCGGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGTGGGCTCTCCAC
 TCCAGGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGC
 GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGC
 TTTAGGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCATTTATTCT
 GGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATATGAA
 GGCCTTTTGTAAAGAAAAATAAAAGATGAAGTGTGAAA

FIGURE 16

MCSRVP L L L L L L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F E N G I T
M L D A G S F A G L P G L Q L L D L S Q N Q I A S L P S G V F Q P L A N L S N L D L T A N R L H E I T N E T F R G L R R L E R L Y
L G K N R I R H I Q P G A F D T L D R L L E L K L Q D N E L R A L P P L R L P R L L L L D L S H N S L L A L E P G I L D T A N V E
A L R L A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G N T R I A Q L R P E D L
A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G P W V R E S H V T L A S P E E
T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S S S L A P T W L S P T A P A T E A P
S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E G F T G L Y C E S Q M G Q G T R P S P T P
V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L T Y R N L S G P D K R L V T L R L P A S L A E Y
T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A V H S N H A P V T Q A R E G N L P L L I A P A L A A V
L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G P L E L E G V K V P L E P G P K A T E G G G E A L P S G S E
C E V P L M G F P G P G L Q S P L H A K P Y I

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 579-599

EGF-like domain cysteine pattern signature.

amino acids 430-442

Leucine zipper pattern.

amino acids 197-219, 269-291

N-glycosylation sites.

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

Tyrosine kinase phosphorylation sites.

amino acids 124-131, 337-345

N-myristoylation sites.

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,
594-600, 640-646

FIGURE 17

[illegible]

FIGURE 18

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLDSESEL
ESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHGEPCHFPLFLDK
EYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAAKRRQMGEAEMMYQTGMKILNGSNKKSQKR
EAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMFELTEEGSPKGQTALGFLYASGLGVN
SSQAKALVYYTTFGALGGNLI AHMVLVSRL

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 195-199, 217-221, 272-276

Tyrosine kinase phosphorylation site.

amino acids 220-228

N-myristoylation sites.

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

Glycosaminoglycan attachment site.

amino acids 267-271

Microbodies C-terminal targeting signal.

amino acids 299-303

Type II fibronectin collagen-binding domain protein.

amino acids 127-169

Fructose-bisphosphate aldolase class-II protein.

amino acids 101-119

FIGURE 19

AATTCAGATTTTAAGCCCATTCTGCAGTGGAATTTTCATGAACTAGCAAGAGGACACCATCTTCTT
GTATTATACAAGAAAGGAGTGACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGG
CCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAGACATCACTG
ATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAACTTTTGAT
AAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA
AACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG
CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTGGTGT
CCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA
CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG
TTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA
TATGCAGTGGAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC
ATGCATTGAACCAGGATTGTTCAAAACAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC
TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATGGAGAAGGTTACATTGAAAAA
AGTCTAGACAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG
CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAA
GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGA
AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACT
CATTTAGATCGTGCTTATTTGGATTGCAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT
CCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCT
GTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATGA
TCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTTAAGT
ATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 20

MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESG
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNOVGEKGLWGLINNAGVPGVLAPTDWLTLEDY
REPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDSLRRDMK
AFGVHVSCTIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLDKLKGNKSYVNMD
LSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQKAELANPKAV

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 21

CTGAGGCGGCGGTAGCATGGAGGGGGAGAGTACGTGCGCGGTGCTCTCGGGCTTTGTGCTCGGCG
 CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAAGTAAAA
 GGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGA
 CATTTCAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAGGCGAAGTAAATG
 AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATTCCGT
 CGTCATTTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACCTTGCAGGAGCATTT
 TTCAAACCAAGACCTTGTTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTCTACTC
 ATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTTTTTTCACAGGGTACCTTTAGTGGTT
 GCCAATCTGGGCATGTCTGAACAACCTGGGTTATAAACTGTATCAGGTTCTGTATGTCCACTGG
 TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGG
 TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAAGTG
 GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTAAAACGAGAAATTGA
 GAAAAGGAGAGGAGCACAGATTCAGGCAGCAAGAGAGAAGAACATCCAAAAGACCCCTCAGGAGA
 ACATTTTTCTTTGTGTCAGGCATTACGGACCTTTTTTCCAAATTCTGAATTTCTTCATTCATGTGTT
 ATGTCTTTAAAAAATAGACATGTTTCTAAAAGTAGCTGTAACATAACCACCATCTCGATGTAGT
 AGACAATCTGACCTTAATGGTAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCAC
 AAATCATTAAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTA
 GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAAT
 GAGCAGCCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC
 CTACATTTTGATCCCTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAAC
 ATTTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCAATTTGTTTTTACTATGTTTACC
 TGTTTGAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTTCAAACATCA
 GATGCTTTTTATTTCCAAACCTTTTTTTCACCTTTCTACTAAGTTGTTGAGGGGAAGGCTTACACAG
 ACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT
 TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT
 GAGACCATGTCTATTAAAAAATAAAATGAAAAGCAAGAATAGCCTTATTTCAAATATGGAAA
 GAAATTTATATGAAAATTTATCTGAGTCATTAAATTTCTCCTTAAGTGATACTTTTTTAGAAGTA
 CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT
 AAAATTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGELLGEVKGEAKNSITDSQMDDVEVVYTIDIQKYI
PCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHSNQDL
VFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAV
QTHSSKFFEEEDGSLKEVHKINEMYASLQEEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLVDVNDLTL
MVEHTDIPEASPASTPQIIKHKALDLDDRWOQFKRSRLDQDKRSKANTGSSNQDKASKMSSPET
DEEIEKMKGFGEYSRSPTF

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation sites.

amino acids 75-79, 322-326

N-myristoylation site.

amino acids 184-154

Growth factor and cytokines receptors family.

amino acids 134-150

FIGURE 23

GGCACAGCCGCGCGGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCCCAA
 GCAGCGCGCAGCGAACGCCCGCCGCCGCCACACCCTCTGCGGTCCCCGCGGCGCCTGCCACCCTTCCCTCCTTCCCC
 GCGTCCCCGCTCGCCGGCCAGTCAGCTTGCCGGGTTGCTGCCCCGCGAAACCCGAGGTACACAGCCCGCGCCTCT
 GCTTCCCTGGGCGCGCGCGCCTCCACGCCCTCCTTCTCCCTGGCCCGGCGCCTGGCACCGGGGACCGTTGCCTGA
 CGCGAGGCCCAGCTCTACTTTTCGCCCCGCGTCTCCTCCGCTGCTCGCCTCTTCCACCAACTCCAACCTCCTTCTCC
 TCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCCGCTGCCGTAGCGCCGCTTCCCGTCCGGTCCCAAA
 GGTGGGAACGCGTCCGCCCGGCGCGCACCATGGCACGGTTGCGCTTGCCCGCGCTTCTCTGCACCTGGCAGTGCTC
 AGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCACGTCTTACGTGTCAAAGGCTTC
 AACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTTGAAGATCTGTCCCAGGGTTCTACCTGCTGCTCT
 CAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGATGATTTCAAAGTGTGGTCAGCGAACAGTGCAATCATTTG
 CAAGCTGTCTTTGCTTACGTTACAAGAAGTTTGATGAATTCCTCAAAGAACTACTTGAAATGCAGAGAAATCCCTG
 AATGATATGTTTGTGAAGACATATGGCCATTTATACATGCAAAATTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTG
 AAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATG
 TTCCGCCTGGTGAACCTCCAGTACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAG
 CCCTTCGGAGATGTCCCTCGCAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGTACTTTCGCTCAAGGC
 TTAGCGGTTGCGGGAGATGTCTGTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAG
 ATGATCTACTGCTCCCACTGCCGGGTCTCGTGACTGTGAAGCCATGTTACAATACTGCTCAAACATCATGAGAGGC
 TGTTTGGCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTA
 GAGGGTCCTTTCAACATTGAATCGGTCATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGAT
 AATAGTGTTCAAGTGTCTCAGAAGGTTTTCAGGGATGTGGACCCCCAAGCCCTCCAGCTGGACGAATTTCTCGT
 TCCATCTCTGAAAGTGCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCCAACCACAGCAGCTGGCACT
 AGTTTGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTCTGGTCTCCCTTCCGAGCAAC
 GTTTGCAACGATGAGAGGATGGCTGCAGGAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTAC
 CTGTTTGCACTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAAACCAGAC
 ATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG
 GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCAGAG
 TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGTCTGGGGCA
 CAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTCTCGGTTATGCAGAGAGAGTGGAGATTAATTCTCAAACCTCTGAG
 AAAAAGTGTTTCATCAAAAAGTTAAAGGCACCACTTATCACTTTTCTACCATCCTAGTGACTTTGCTTTTTAAATGAA
 TGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGCTGACTTTGTTTTCTCATTCACTTTTGGG
 AGGAAAAGGGACTGTGCATTGAGTTGGTTCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAA
 CTATAGTTAGTTGTGCATTTGTGATTTTATCACTCTATTATTTGTTTGTATGTTTTTTCTCATTTCGTTTGTGGGTT
 TTTTTTTCCAACGTGTGATCTCGCCTTGTTTCTTACAAGCAAACAGGGTCCCTTCTTGGCACGTAACATGTACGTATT
 TCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTATTTATCATGTTATCTTATTTAAAGAAAAGCCCAAAAGC

FIGURE 24

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGST
CCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGH
LYMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFRLVNSQYHFTDEYLECVSKYTE
QLKPFQDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRGL
VTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN
MQDNSVQVSQKVFQCGCPPKPLPAGRISRSISESAFSARFRPHHPEERPTTAAGTSLDRLVTDVK
EKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNNPEVQVDT
KPDILILRQIMALRVMTSKMKNAYNGNDVDFFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

Important features:

Signal peptide:

amino acids 1-22

ATP/GTP-binding site motif A (P-loop).

amino acids 515-524

N-glycosylation site.

amino acids 514-518

Glycosaminoglycan attachment sites.

amino acids 494-498, 498-502

N-myristoylation sites.

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

Glypicans proteins.

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

FIGURE 25

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACT
TACAGCTGCACCGACAGTTGCGATGAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGC
CAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATTGGTTCCTGAG
AGCCCCGAGAAGAAAATTTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCCCTGTGATCATT
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA
GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG
AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC
TTCTTCTCCCACTCACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA
TGTTTTTCAAGATCATTTTGTGTTGTTGCTCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCT
GTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCT
AGCTAGTGTCAATTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTT
AAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 26

MKVLISLLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM
TVSGLPKKQCPCDHFKNVKKTRHQRRHRKPNKHSRACQQLKQCQLRSFALPL

Important features:

Signal peptide:

amino acids 1-22

N-myristoylation sites.

amino acids 27-33, 46-52

FIGURE 27

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG
AGCTGGTCTGCCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTACCCTGCC
CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCCCCTACCTGA
TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG
ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCGGAACCGGAGC
CAACTTTTCACTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATCCCCACTTTGAGA
AGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTTGTGGTGGCTCCT
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGCTGTG
CTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGC
TCTTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTTC
GAGCCACCTGGAAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA
GAACGCCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG
GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCC
TTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTTA
GCAGAATGAGAGAAGACATTCATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG
AAACACTAGGACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTC
CCAATGTTGTCCCTTTCCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACAC
CCATGCGTCTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGAC
CCTCTCTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGG
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGAA
ACCACG

FIGURE 28

MDILVPLLQLLVLLLTPLHLMLLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSSQIKGL
TGASGKVALLELGC GTGANFQFYPPGCRVTC LDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM
RQLADGSMDV VVCTLVLC SVQSPRKVLQE VRRVLRPGGV LFFWEHVAEPYGSWAFMWQQVF EPTW
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPVGPHIMGKAVKQSFSSKALICSFPSL
QLEQATHQPIYLP LRG T

Important features:

Signal peptide:

amino acids 1-23

Leucine zipper pattern.

amino acids 10-32

N-myristoylation sites.

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

FIGURE 29

CAATGTTTGCCTATCCACCTCCCCAAGCCCCCTTACCTATGCTGCTGCTAACGCTGCTGCTGCT
GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCTCTTCTG
CCACTGACGCCCCCATCAGGGATTGGGCCTTCTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCAT
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTTA
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAAA
GTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTCAATTAAGAAATT
GTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAC
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

MLLLTLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPRG
EGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 31

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTT
 CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT
 ATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAAATCATGTCGG
 GAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCCATGATGTTTACC
 TTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTATTTTGGGATTGTTGTT
 TGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA
 CAGAAAGGGAAAATATGAAGTGCGTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGGCAGTG
 CTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCAAATCAC
 AAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCA
 TTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAACTGCAGGAGCTGCCCAGGTT
 ATGGAAGGCGGCCAAGTGAATATAAGCCCCTTTCGGGCATTCCGTACATGTGGTCGTACCATTT
 AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAG
 TGGTTACTTGTTATTTCAACAGAAGTAAAAATGATCCTCCTGATCATCCCATCCTTTTCGTCTCTC
 TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAG
 GATTCCGAGAATCATTGTGATGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT
 CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC
 AACCAGAAATGCATATACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGC
 ATTCAAAATCTTGTTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAA
 TTTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTAC
 AATCGGGCATTCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGC
 CCATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGATC
 TGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA
 AAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGAATGAGGA
 GGGAACAGAACTCCAGGCCATTGTGAGATTAGATACCCATTTAGGTATCTGTACCTGGAAAACATT
 TCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTT
 TTAAAAGACCTAATAAACCCCTATTCTTCCTCAAAA

FIGURE 32

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYTNDLSIE
LDTERENMKCVLGFAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTFA
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQOMTIA
GAVVTCYFNRSKNDDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQLKEQQHG
ALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD
FIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAHSFSLSVFETVLDALFLCFA
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

Important features:

Signal peptide:

amino acids 1-20

Putative transmembrane domains:

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

N-glycosylation sites.

amino acids 204-208, 295-299, 313-317

N-myristoylation sites.

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

FIGURE 33

[illegible]

FIGURE 34

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG
CQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWR
ESFIVLESKPKKGVTPSALTYSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVA
TPTTLPRPSPAASTTIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQRQDPSGAAFQKP
VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI
GPAGPLMGVVQYGDNPATHTNLKTHNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN
RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENKQYVVEPNFANKAVCRTNG
FYSLHVQSWFGLHKTLPVKRVCDTDLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN
LTKEFEISDTRIGAVQYTYEQRLFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALEQL
FKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARDHSFF
VDEFDNLHQYVPRIIQNICTEFNSQPRN

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 181-200

N-glycosylation sites.

amino acids 390-394, 520-524

N-myristoylation sites.

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

Amidation site.

amino acids 304-308

FIGURE 35

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGC
CAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTACACAACAGATCTGAGTGTTTTAATTAAGCATGGAAT
ACAGAAAACAACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATTCCACAGTTTTCTTAGCTCCCTGGACCC
GGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGCTCTCCGACTACTCACCCGAGTGTA
AAGAACCTTCGGCTCGCGTGCTTCTGAGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCCTTCCGAGTA
GGATGTCACTGAGATCCCTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTAC
CTCAGCCTTCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTTA
CAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTTCTGGTCATTC
TGGTGACCTCCCACCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCT
TGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGGC
ATTGTCCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGACAAGATTTTTTAGACACATATAATA
ACCTGACCTTGAAAACCATTATGGCATTTCAGGTGGGTAAGTGAAGTTTGGCCCAATGCCAAGTACGTAATG
AAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGA
GAAGTTTTTTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATATTT
CTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTATATAATGTCCAGAGAT
TTGGTGCCAAGGATCTATGAAATGATGGGTACGTAAAACCCATCAAGTTTGAAGATGTTTATGTCCGGAT
CTGTTTGAATTTATTAAAAGTGAACATTCATATCCAGAAGACACAAATCTTTTCTTTCTATATAGAATCC
ATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTT
TGGCAGGTGATGCTAAGGAACACCACATGCCATTATTAACTTCACATTCTACAAAAAGCCTAGAAGGACAG
GATACCTTGTGGAAAGTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTGAGTGTGCTGGCTT
ACACTGAACTGAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGG
CCCTTCAAAGATGATATGTGGAGGAATTAAATATAAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGG
ACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAAGGGTGTTACTGAGTTATAAGCTCA
CTAGGCTGTAAAAACAAAACAATGTAGAGTTTTATTATTGAACAATGTAGTCACTTGAAGGTTTTGTGTA
TATCTTATGTGGATTACCAATTTAAAAATATATGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATA
CTGAACAAAATTTTACCTGTTTTTGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTTCAGATTATT
ATTATTTAAAATTACTTCACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAG
TGAATCATTCTTTACATGCAAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCACTCCA
TTAATGTAAAGTCATAGGTCAATTATTGCATATCAGTAATCTCTTGGACTTTGTTAAATATTTTACTGTGGT
AATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

FIGURE 36

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMMYFYEYEPYRQDFHF
TLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EKEDKMLA
LSLEDEHLLYGDIIRQDFLDTYNNLTLKTIMAFRWVTEFCPNAKYVMKTD TDVFINTGNLVKYL
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHV
KPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR
NTTCHY

Important features:

Type II transmembrane domain:

amino acids 20-39

N-glycosylation sites.

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

Glycosaminoglycan attachment site.

amino acids 239-243

Ly-6 / u-PAR domain proteins.

amino acids 23-37

N-myristoylation site.

amino acids 271-277

FIGURE 37

CGCTCGGGCACCAGCCGCGGCAAGGATGGAGCTGGGTTGCTGGACGCAGTTGGGGCTCACTTTTCTTCAGCTCCTTCTCATC
TCGTCCTTGCCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGGAATATCATGTGTCGGGAGTGCTGTG
AATATGATCAGATTGAGTGCGCTGCCCCGGAAGAGGGGAAGTCGTGGGTATATACCATCCCTTGCTGCAGGAATGAGGAGAA
TGAGTGTGACTCCTGCCCTGATCCACCCAGGTTGTACCATCTTTGAAAAGCTGCAAGAGCTGCCGAAATGGCTCATGGGGGGGT
ACCTTGAGTACTTCTATGTGAAGGGTTCTACTGTGCAGAGTGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCCATGTG
GCCAGGTTCTGCGAGCCCCAAAGGGTCAGATTTTGTGGAAAGCTATCCCCTAAATGCTCACTGTGAATGGACCATTTCATGC
TAAACCTGGGTTTGTTCATCCAACCTAAGATTTGTTCATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAG
GTTCTGTATGGAGACAACCGCGATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAG
GATCCTCACTCCACGTCCTCTTCCACTCCGATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGC
ATGCTCCTCATCCCCTTGTTCATGACGGCAGTGCGTCTTGACAAGGCTGGATCTTACAAGTGTGCCTGCTTGGCAGGC
TATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCCTGGGGGGCCAGTCAATGGGTACCAGAAAA
TAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAATGGCACCGTGGTGTCTTCTTTTGTAAACACTCCTATGT
TCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAAATGGAGAGTGGTCAGGGAAACAGCCCATCTGCATAAAAGCCTGCCGA
GAACCAAAGATTTAGACCTGGTGAGAAGGAGAGTCTTCCGATGCAGGTTCAAGGAGACACCATTACACCAGCTAT
ACTCAGCGGCCCTCAGCAAGCAGAACTGCAGAGTGCCCCACCAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGG
ATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCCCTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGT
CTGAGGACTGGGAAGTGGAGTGGCGGGCACCATCTGCATCCCTATCTGCGGGAAAATTGAGAACATCACTGCTCCAAAGA
CCCAAGGGTTGCGCTGGCGTGGCAGGCAGCCATCTACAGGAGGACCAGCGGGGTGCATGACGGCAGCCTACACAAGGGAGC
GTGGTTCCCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTTACTGACCTGGGGAAG
GTCACCATGATCAAGACAGCAGACCTGAAGTTGTTTTGGGGAAATCTACCGGGATGATGACCGGGATGAGAAGACCATCC
AGAGCCTACAGATTTCTGCTATCATCTGCTATCCCAACTATGACCCCATCTGCTTGATGCTGACATCGCCATCCTGAAGCT
CCTAGACAAGGCCCGTATCAGCACCCGAGTCCAGCCCATCTGCCTCGCTGCCAGTCGGGATCTCAGCACTTCCTTCCAGGAG
TCCCACATCACTGTGGCTGGCTGGAATGTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGG
TGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGAGTGTCACTGATAACATGTT
CTGTGCCAGCTGGGAACCCACTGCCCCCTTCTGATATCTGCACTGCAGAGACAGGAGGCATCGCGGCTGTGCTTCCCGGGA
CGAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA
CTGCCCTTACCAAGGTGCTGCCTTTTAAAGACTGGATTGAAAGAAATATGAAATGAAGACCATGCTCATGCACCTCCTTGAGAAG
TGTTTCTGTATATCCGTCTGTACGTGTTCATTGCGTGAAGCAGTGTGGGCCTGAAGTGTGATTTGGCCTGTGAACCTGGCT
GTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAGTAGACCTCCATTGCTGGTAGGCTGATGCCGCGTCCA
CTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTCTTCAAAGAAGACCATATACAAAACCTCTCCA
CTCCACTGACCTGGTGGTCTTCCCAACTTTCAGTTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAG
GCCCCTTTGGAGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCTT
TGTGTACATGGCCACAGTACAGTCTGGTCCTTTTCCCTTCCCATCTCTTGTACACATTTTAATAAAATAAGGGTTGGCTTCT
GAACCTACAAAAA
AAAAA

FIGURE 38

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGDCMRCGQ
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGGQII
KRVCGNERPAPIQSIGSSHLVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSGNE
KRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLHQLYSAAFQKQKLSAPTK
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP
KTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL
KVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR
DLSTSFAQESHITVAGWNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLPFKDWI
ERNMK

Important features of the protein:

Signal peptide:

amino acids 1-23

EGF-like domain cysteine pattern signature.

amino acids 260-272

N-glycosylation sites.

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

N-myristoylation sites.

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,
474-480, 491-497, 638-644, 666-672

Amidation site.

amino acids 56-60

Serine proteases, trypsin family.

amino acids 489-506

CUB domain proteins profile.

amino acids 150-167

FIGURE 39

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTATTAACTGGCTTAATC
TGAAGGTTCTCAGTCAAATCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTTGGCTGG
TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGGCGCTTCTGTTGC
TGGTCTTGCCTTGGCTCAGTCCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCCTGTATTGAGAACTCTGTA
AAGGTGCCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAGACGGCTGTGCGAGCC
TCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAGACGAGCCTGGCCTAGACA
ACCCTGCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCAGTGGACTCTGGCCGGAGCAACCGAACTA
GGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTAAAAAAATAAATCGAGCTTTGAGTGTTCTTCGAA
GGACAAAGAGCGGGAGTGCAATTGCCAACCATGCCGACCAGGGCAGGGAAAATTCTGAAAACACCACTGCCCCCTGAAG
TCTTTCCAAGGTTGTACACCTGATTCCAGATGGTGAAATTACCAGCATCAAGATCAATCGAGTAGATCCCAGTGAAA
GCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGG
TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTC
ACAACTACGCTGTGCGTCTCCTGCGGCAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCCGCA
GCAGGAACAATGGACAGGCCCCGGATGCCTACAGACCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCC
CCGAGGAGCAGCTTGAATAAACTGGTGCGCAAGGTGGATGAGCCTGGGGTTTTTCATCTTCAATGTGCTGGATGGCG
GTGTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCA
GCCCAGAAAAGTGCGGCTCATCTGATTCAAGCCAGTGAAAGACGTGTTACCTCGTCGTGCCCGCCAGGTTTCGGCAGC
GGAGCCCTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACA
CTCCCAAGCCCCCTCCATCCTACAATTACTTGTATGAGAAGGTGGTAAATATCCAAAAGACCCCGGTGAATCTCTCG
GCATGACCGTCGCAGGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTATCAGTGTTGAGCCCGGAGGAG
TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTTGTGTAATGTGGATGGGGTCGAACTGACAGAGGTGAGCC
GGAGTGAGGCAGTGGCATTATTGAAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGC
CCCAGGAAGACTGCAGCAGCCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCT
GGGTCTGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTC
TGGGCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAACAAACCTTTTTTTCATCAAATCCATTGTTGAAGGAA
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTTGCTGTCAATGGTAGAAGTACATCAGGAATGA
TACATGCTTGCTTGGCAAGACTGCTGAAAGAATTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTGGCACTT
TTTTATAGAATCAATGATGGGTGAGGAAAACAGAAAAATCACAATAGGCTAAGAAGTTGAAACACTATATTTATC
TTGTGAGTTTTTATATTTTAAAGAAAAGAACATTGTAAAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTT
ACACCTCAGAAAATATGATTCAAAAAAATTAATACTACTAGTTTTTTTTTTCAGTGTGGAGGATTTCTCATTACTCTAC
AACATTGTTTATATTTTTCTATTCAATAAAAAGCCCTAAAACAATAAATGATTGATTGTATACCCCACTGAATT
CAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGTACATTATGGCCATTTTAAATTTACAGCT
AAAATATTTTTTAAATGTCATTGCTGAGAAACGTTGCTTTCATCAAACAAGAATAAATATTTTTTCAGAAGTTAAA

FIGURE 40

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPDGCASLTATAPS
PEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSEFKKINR
ALSVLRRTKSGSAVANHADQGRENSENTTAPAEVFPRLYHLIPDGEITSIKINRVDPSESLSIRLV
GGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM
REQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVFIFNVLDGGVAYRHG
QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRQSPDIFQEAGWNSNGSWSPG
PGRSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPPGGVISRDGR
IKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPP
SDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG
RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

Important features:

Signal peptide:

amino acids 1-15

N-glycosylation sites.

amino acids 108-112, 157-161, 289-293, 384-388

Tyrosine kinase phosphorylation sites.

amino acids 433-441, 492-500

N-myristoylation sites.

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,
467-473, 603-609

FIGURE 41

ACCAGGCATTGTATCTTCAGTTGTCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT
 CTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACAGTAATAAAAAACATGGGCTTCAACCTGACT
 TTCCACCTTTCTACAAATTCCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGC
 CACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCCATAAGCAAAGGAGTTTCATGGCTAATTTCC
 ATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTT
 GACAACTGTCTTCTGTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC
 TTTGGAAGAGGTACAGGCAGAAAAATCCCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG
 CTTTACAGAGGGTCGCCATCCTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAA
 CATCTGCATCCCTTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGG
 TAAAAAGTTTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAAATTGGG
 ACTGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG
 CATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTG
 GGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACACTACTGGGGAT
 GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTG
 CCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG
 GATGAAGCTCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAAT
 TAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGATTTCTGGTTTGGTGCATGACCC
 TGGATCTTTTGGTGATGTTTGGGAAGAACTGATTCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAA
 ATAGTAGCACACATTAAGAACCCTGTTACAGCTCATTGTTGAGCTGAATTTTTCTTTTTGTATTTTCT
 TAGCAGAGCTCCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGT
 CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA
 AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGAT
 AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA
 AGGTACGAAGATACAATACTGTTATTCATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGT
 GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTGGGAATGAAGA
 GGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC
 CTTACAGGGGAGGACCTGCCCAGGTATGCCTTCCAGTGATGCCACCAGAGAATACATTCTCTATTAGT
 TTTTAAAGAGTTTTTGTAAAATGATTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT
 ATTAATAATAATAATATGTCTATCAAATACCTCTGTAGTAAATGTGAAAAAGCAAAA

FIGURE 42

MGFNLT FHLSYKFRL LLLLTLC LTVVGWATS NYFVGAIQE IPKAKEFMAN FHKTLILGKGKTLTN
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYPQECKALQRVAILVPH
RNREKHLMYLLEHLHPFLQRQQLDYGIVVIHQAEKGKFNRAKLLNVGYLEALKEENWDCFI FHDV
DLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTALSREQFFKVNGFSNNYWGWGGED
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV
SVEHNPLYINITVDFWFGA

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 4-8, 220-224, 335-339

Xylose isomerase proteins.

amino acids 191-202

FIGURE 43

[illegible]

FIGURE 44

MALSSQIWAACLLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPI
CIFCCGCCHRSKCGMCCKT

Important features:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 58-59

N-myristoylation site.

amino acids 44-50

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 1-12

FIGURE 45

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC
TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT
TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTG
GACCTTCAACACAACCCCTCTTGTCACCATACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAAGTGAAG
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC
CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTCAGCAGAAACT
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATG
GTCCTCCTGTGTCTCCTGTTGGTGGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTG
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGGG
AAACTCCTAACATATGCCCCCATCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT
GGAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA
TCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCA

FIGURE 46

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP
EGGTIIVTQNRNRERVDFFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK
PKVTMGLQSNKNGTCVTNLTCCMEHGEEVDIYTWKALGQAANESHNGSILPISWRWGESDMTFIC
VARNPVS RNFS PILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE
EKKRVDICRETPNICPHSGENT EYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT
PRLFAYENVI

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 224-250

Leucine zipper pattern.

amino acids 229-251

N-glycosylation sites.

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,
291-295

FIGURE 47

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGG
ATTGAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCT
TAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCCAGGAATT
ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG
CTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCACAGTCATTGGTGCTC
TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATGTGTAATTCTCCAAGC
AACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTCATCCAGAATCCTTCAA
CTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTCAATAAACCCACCAGTAACG
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG
CTTATCCACTTCTCAGTATTTTTAGGTCTATTGCTTGTTGGAATTCTGGAGGTCCTGTTTGGGCT
CAGTCAGATAGTCATCGGTTTCCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG
TGTAGTTTAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAA

FIGURE 48

MTCCEGWTS CNGFSL LVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA
TTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNSPSNSNANCEFSL
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGL
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

Important features:

Transmembrane domains:

amino acids 10-31 (type II), 50-72, 87-110, 191-213

N-glycosylation sites.

amino acids 80-84, 132-136, 148-152, 163-167

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 223-227

N-myristoylation sites.

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 207-218

TNFR/NGFR family cysteine-rich region protein.

amino acids 4-12

FIGURE 49

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGA
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG
ATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGA
CATGGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGGAAGCCAATGACC
CATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC
TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG
CAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTCTGCCA
CTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC
TCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCT
TTCTGATCAGGAGGCTTCTTTATGAATTAACTCGCCCCACCACCCCTCA

FIGURE 50

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS
SQKQHSPVPEKAIPILITPGSATTC

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 36-59

N-myristoylation sites.

amino acids 41-47, 45-51, 84-90

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.

amino acids 54-67

FIGURE 51

[illegible]

FIGURE 52

MKFQGPLACLLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEG VGKAIGKEAGGAAGSKVS
EALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGV
GHSGAWETSGGHGIFGSQGGGLGGQGGQGNPGGLGTPWVHGYPGNSAGSFGMNPQGAPWGQGGNGGPPNF
GTNTQGAQAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGSGSQQSGSSGSGSNGDNNNGSSSSGGS
SSGSSSSGSSSGSSSGSSSGSSSGNSGSGSRGDSGSESSWGSSTGSSSGNHGSGGGNGHKPGCEKPGNE
ARGSGESGIQGFRRQGVSSNMREISKEGNRLGGSGDNYRQGSWSGGGDAVGGVNTVNSETSPGM
FNFDTEFWKNFKSKLGFINWDAINKDQRSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,
387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 53

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG
CTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT
ACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACCTGCCGCCGGCTCCAGTGTTTCC
CACAGCCCCCAAACGGAACCTGGTTTTTGGGGTCACCTGGGCCTGATCACTCCTACAGAGGAGGGC
TTGAAGGACTCGACCCAGATGTGCGCCACCTATTCCCAGGGCTTTACGGTATGGCTGGGTCCCAT
CATCCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCAATGCCTCAGCTGCCA
TTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATACTGCTG
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCCGCTTCCATTTCAACATCCT
GAAGTCCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG
CCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTA
CAGAAATGCATCTTCAGCTTTGACAGCCATTGTCAGGAGAGGGCCAGTGAATATATTGCCACCAT
CTTGGAGCTCAGTGCCCTTG TAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT
ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCTGGTG CATGACTTCACAGAC
GCTGTCATCCGGGAGCGGCGTCGCACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAA
AGCCAAGTCCAAGACTTTGGATTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACG
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCG
ACAGGAGGTGCAAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCC
AGCTGCCCTTCTTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATC
TCCCGATGCTGCACCCAGGACATTGTTCTCCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTG
CCTCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGACC
CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCCTTTCTCCGCA
GGGCCCAGGAACCTGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCTGGCGTTGAT
GCTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGCAGGAAGCTGGAATTGATCATGC
GCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCTGAATGTAGGCTTG CAGTGACTTTCTGAC
CCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGCTGTCAA

FIGURE 54

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFFPQPPKRNWFWGHLG
LITPTEEGLDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP
WLGEGILLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI
SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC
RLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLD FIDVLLLSKDEDGKALSDEDIRAEADTF
MFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENSKGRSP
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN
VGLQ

Important features:

Transmembrane domains:

amino acids 13-32 (type II), 77-102

Cytochrome P450 cysteine heme-iron ligand signature.

amino acids 461-471

N-glycosylation sites.

amino acids 112-116, 168-172

FIGURE 55

[illegible]

FIGURE 56

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIPFAR
DAVKKCFVCLA

Important features:

Signal peptide:

amino acids 1-33

Type II fibronectin collagen-binding domain protein.

amino acids 30-72

FIGURE 57

[illegible]

FIGURE 58

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDLLDG
QLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKSMDKNG
TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMWWRHLVAGGG
AGAVSRTCTAPLDRCLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIK
FMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQSSIYPMEVLKTRMALRKTGOYSGMLDCARR
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSADPGVFVLLACGTMSSTC
GQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV
VYENLKITLGVQSR

Important features:

Signal peptide:

amino acids 1-16

Putative transmembrane domains:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation sites.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC
 TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG
 CACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTCGCCTCAGCT
 GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAAACCTTTCTGATAT
 CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG
 AGCTGTCGGAGCAGGATGAAATGTTGAGAGGCCGGACAGCAGTGTTTGGCTGATCAAGTGATAGTT
 GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT
 CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG
 AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCC
 CAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACTTCTCGGAAGTCTCCAATAC
 CAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGA
 TCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG
 ACAGAATCGGAGATCAAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGT
 CTCTTCTTTCTTTGCCATCAGCTGGGCACCTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAAT
 GTGCCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC
 CACCAGATATGACCTAGTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG
 AGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAAT
 CTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTGAAGTGTGTTAAGA
 GTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT
 CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGC
 TGTAATGTTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCAC
 AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG
 GCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTC
 TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGT
 CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 6o

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTDAGTYKC
YIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVS
NTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTSEIKRRSHLQLLNSKASL
CVSSFFAISWALLPLSPYMLK

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 258-281

N-glycosylation sites.

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,
220-224

N-myristoylation sites.

amino acids 52-58, 126-132, 188-194

FIGURE 61

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCCAGGAGCTGCAGGACAAG
 CACCAGGAGCCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGT
 GGGCTACCCCCCTGGTGGTGGTTATGGGGGTCTGCCCCCTGGAGGGCCTTATGGACCACCAGCTGG
 TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCCCTCTGGAACCTCAGGAGGACCATATG
 GCGGTGCAGCTCCCGGGGGCCCCCTATGGTCAGCCACCTCCAAGTTCCTACGGTGCCCAGCAGCCT
 GGGCTTTATGGACAGGGTGGCGCCCCCTCCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC
 GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA
 ATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA
 GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGGAAGAACCTCTT
 CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC
 AAATGGGCTACAACCTGAGCCCCCAGTTACCCAGCTTCTGGTCTCCCCGCTACTGCCCACGCTCT
 GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA
 GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA
 CCATGACAGCTTCTCGGATGCTATTGACCCAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT
 TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTCTGTCCCTCTAGAAGAAC
 ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCCTGCATCATAGCCACCA
 AATAGTGAGGACCGGGGCTGAGGCCACACAGATAGGGGCCTGATGGAGGAGAGGATAGAAGTTGA
 ATGTCCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCCTTGTAATGG
 AGTTAGTGTCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAGTGTTTCATCGGCCTGTTACC
 GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAACGAGCCCATTTTCTCCAAAGTGGAAAT
 CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGAATCTGCCACACCCATAAAT
 CCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT
 CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCCCTGCCATGCTCTGCTCGGCT
 TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTTAATTTGCATTTTTTTTC
 ATTTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

FIGURE 62

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG
HPNPGMFPSGTPGGPYGGAAPGGPYGQPPPSYGAQQPGLYGQGGAPPNVDP EAYSWFQSVDSDH
SGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDR
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREK
DTAVQGNIRLSFEDFVTMTASRML

Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 147-150

Casein kinase II phosphorylation sites.

amino acids 135-138, 150-153, 202-205, 271-274

N-myristoylation sites.

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-
66, 70-75, 78-83, 83-88, 87-92, 110-115

FIGURE 63

[illegible]

FIGURE 64

MQGRVAGSCAPLGLLLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGPSNSEHPQPAL
DPRSNDLARVPLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPPEDPWQMMAAAAEDRLGEA
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRRLPRSNSLGAGGKILSQRP
PWSLIHRVLPDHPWGTILNPSVSWGGGGPGTGWGTRPMPHPEGIWGINNQPPGTSGWNINRYPGGS
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPPGVLRPPGSSWNIPAGFPNPPSPRLQWG

Important features of the protein:

Signal peptide:

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

FIGURE 65

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTC
TGGGCTGCCCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA
CTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA
TTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCATGC
AAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTGTGTCCTTCTTGGCCC
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAGCAGGCCCCCACCCTC
CTGAGTGGCAATAAATAAAATTCGGTATGCTG

FIGURE 66

MSGGLPLVLLLTLLGSSHGTGPGMTLQKLKESFLTNSSYESSFLELLEKLCLLLHLPSGTSVTL
HHARSQHHVVCNT

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 37-41

N-myristoylation sites.

amino acids 15-21, 19-25, 60-66

FIGURE 67

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGGC
CAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCC
TTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCGGGCTGGGGCTGCTTCTGGCG
CTGGGCCTGCCGTTCTTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC
AAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG
GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCAGTAGCGA
GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT
GCCTGCCCATCTAGGTCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA
GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGAAGAAGGTACTTCAA
AGACTCTGCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACTTTTATATATTTATATAAAATTAG
TAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

FIGURE 68

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSSSTSSSSSDGNLRPEAITAIIVVFS
LLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 56-80

N-glycosylation site.

amino acids 36-40

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 86-90

Tyrosine kinase phosphorylation site.

amino acids 86-94

N-myristoylation sites.

amino acids 7-13, 26-32

FIGURE 69

[illegible]

FIGURE 70

MGLFRGFVFLLVLCLLHQSNSTFIKLNNGFEDIVIVIDFSVPEDEKIIIEQIEDMVTTASTYLFE
ATEKRFFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY
IHFTPDLILLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCSAGISGRN
RVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDQVTEKASIMFMQSIDSVVEFCNEKTHNQEAP
SLQNIKCNRSTWEVISNSEDFKNTIPMVTPPPPPVFSLKISQRIVCLVLDKSGSMGGKDRLNR
MNQAAKHFLMQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTSICSGIK
YAFQVIGELHSQLDGSEVLLLTGDGEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG
SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFL
ITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR
AANSSVPPITVNAKMNKDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA
GADSFKNDBGVYSRYFTAYTENGRYSLKVRAGGANTARLKLRPPLNRAAYIPGWVVNGEIEANPP
RPEIDEDTQTTLEDFSRASGGAFVVSQVPSLPLPDQYPPSQITDLDATVHEDKIIILTWTAPGDN
FDVGKVQRYIIRISASILDLRDSFDDALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAI
KSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVI
VNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 71

CTCCTTAGGTGGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGAAAGACCATACGTCCCCGGGCAGGGGTGA
CAACAGGTGTCTCTTTTTGATCTCGTGTGTGGCTGCCTTCCTATTTCAGGAAAGACGCCAAGGTAATTTTGACCCA
GAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCCAGTTATGCCAGGATTTACTAGAGAGTGTCA
ACTCAACCAGCAAGCGGCTCCTTCGGCTTAACTTGTGGTTGGAGGAGAGAACCCTTGTGGGGCTGCGTTCTCTTAGCA
GTGCTCAGAAGTGACTTGCCCTGAGGGTGGACCAGAAGAAAGGTCCCCTCTTGCTGTGGCTGCACATCAGGAA
AGTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGCTC
CGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCCAGGGAAGCCCTTCCGTGGGGGCCCCGGCTTTGAGGGATGCC
ACCGGTTCTGGACGCATGGCTGATTCTGATGATGATGTTTCGCCGGGGGCTGCTTGCCTGGATTTCCCGGGTGGTG
GTTTTGCTGGTGTCTCTGTGCTGTCTCTGTCTGTACATGTTGGCCTGCACCCCAAAAGGTGACGAGGAGCAG
CTGGCACTGCCCAGGGCCAACAGCCCCACGGGGAAGGAGGGGTACCAGGCCCTCCTTCAGGAGTGGGAGGAGCAGAC
CGCAACTACGTGAGCAGCCTGAAGCGGCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGGAGTGAGCAGCTCAGG
AATGGGCAGTACCAAGCGAGCTGCTGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAACCCAGGCCGACCTC
CTGGCCTTCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGCAGCAGTG
CCTTTTCGATAGCTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGCCTTACCCGCCACCCCGAGGAGAAGCCTGTG
AGGAAGGACAAGCGGGATGAGTTGGTGGAAAGCCATTGAATCAGCCTTGGAGACCTGAACAATCCTGCAGAGAACAGC
CCCAATCACCGTCTTACACGGCCTCTGATTTCATAGAAGGGATCTACCGAACAGAAAGGGACAAAGGGACATTTGAT
GAGCTCACCTTCAAAGGGGACCACAAACACGAATTCAAACGGCTCATCTTATTTTCGACCATTCAGCCCCATCATGAAA
GTGAAAAATGAAAAGCTCAACATGGCCCAACAGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGGACAAGTTC
CGGCAGTTCATGCAGAATTTAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGG
AAAGAAGAAATAAATGAAGTCAAAGGAATACTTGAACACCTTCAAAGCTGCCAATTCAGGAATTTACCTTCATC
CAGCTGAATGGAGAATTTCTCGGGGAAAGGGACTTGATGTTGGAGCCCGCTTCTGGAAGGGAAGCAACGTCCTTCTC
TTTTTCTGTGATGTGGACATCTACTTCACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAAG
GTATTTTATCCAGTTCTTTTCAGTCAGTACAATCCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAA
CAGCAGCTGGTCATAAAGAAGGAACTGGATTTTGGAGAGACTTTGGATTTGGGATGACGTGTGAGTATCGGTGACAG
TTCATCAATATAGGTGGGTTTGTATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTC
CACAGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACTCTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAG
CTGACCCCGGAGCAGTACAAGATGTGCATGCAGTCCAAGGCCATGAACGAGGCATCCACCGCCAGCTGGGCATGCTG
GTGTTCAAGGCACGAGATAGAGGCTCACCTTCGCAACAGAAACAGAAGACAAGTAGCAAAAAACATGAACTCCAGAA
GAAGGATTTGGGAGACACTTTTCTTCTTTTGAATTAAGTGGCTGCAACAGAGAAAAGACTTCCATAAA
GGACGACAAAAGAATTGGACTGATGGGTGAGAGATGAGAAAAGCCTCCGATTTCTCTCTGTTGGGCTTTTACAAACAGA
AATCAAAATCTCCGCTTTGCCTGCAAAAGTAACCCAGTTGCACCTGTGAAGTGTCTGACAAAGGCAGAATGCTTGTG
AGATTATAAGCCTAATGGTGTGGAGTTTTGATGGTGTTTACAATACACTGAGACCTGTTGTTTTGTGTGCTCATTTGA
AATATTCATGATTTAAGAGCAGTTTTGTAAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGA
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAAATATCAGAAGGCAGGAGAGGATAGGCTTATTATGATACT
AGTGAGTACATTAAGTAAATAAAATGGACCAGAAAAGAAAAGAACCATAAATATCGTGTATATTTCCCCCAAGAT
TAACCAAAAATAATCTGCTTATCTTTTGGTTGCCTTTTAACTGTCTCCGTTTTTTCTTTTATTTAAAAATGCACT
TTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCCTTTGCAAGCCTTACAAGAGAGCACAGTTGGCCTAC
ATTTTTATATTTTTTAAGAAGATACTTTGAGATGCATTATGAGAACTTTCAGTTCAAAGCATCAAATGATGCCATAT
CCAAGGACATGCCAATGCTGATTCTGTGAGGCACTGAATGTGAGGCATTGAGACATAGGGAAGGAATGGTTTGTACT
AATACAGACGTACAGATACTTTCTCTGAAGAGTATTTTCGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATGAC
ACTTCTGCTTTACAGAAAAGGAACTCATTCAGACTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCATTTT
CTCCTCAGAAAGTAGGGACCGCTTTTCTTACCTGTTTAAATAAACCAGATATACCGTGTGAACCAACAATCTCTTTTC
AAAAACAGGGTCTCCTCCTGGCTTCTGGCTTCCATAAGAAGAAATGGAGAAAATATATATATATATATATATATTGT
GAAAGATCAATCCATCTGCCAGAACTAGTGGGATGGAAGTTTTTGTACATGTTATCCACCCAGGCCAGGTGGAAG
TAACTGAATTAATTTTTTAAATTAAGCAGTTCTACTCAATCACCAGATGCTTCTGAAAATGCAATTTATTACCATTT
CAAATATTTTTTAAAAATAAATACAGTTAATATAGAGTGGTTTCTTCATTCATGTGAAAATATTAGCCAGCACCAG
ATGCATGAGCTAATATCTCTTTGAGTCCTTGCTTCTGTTGCTCACAGTAACTCATTGTTTAAAGCTTCAAGAAC
ATTCAAGCTGTGGTGTGTTAAAAAATGCATTGTATTGATTTGACTGGTAGTTTAAATTTAAATTTAAACACAGG
CCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

FIGURE 72

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEW
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQV
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALET
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKV
NEKLNMAN TLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEV
KGILENTSKAANFRNF TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSE
FLNTCRLNTQPGKKVFYPVLFSQY NPGIITYGHHDAVPPLEQQLVIKKETGFWRD
FGFGMTCQYRSDFINIGGFDDLKGGWGEDVHLYR KYLHSNLIIVRTPVRGLFHLW
HEKRCMDELTPEQYKMCMQSKAMNEASHGQLGMLVFRHEIEAHL RKQKQKTSSKKT

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 315-319, 324-328

N-myristoylation sites.

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

Amidation site.

amino acids 377-381

FIGURE 74

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPDLPALQ
PHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKSPGGSEHQINSEAT
FAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP
FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLV
QNYRALQPLNQRMVFASFQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS
VVFTSAQATTEA

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 75

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGTGTC
 TCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGTCCTACA
 ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACAA
 ATTGGCCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC
 AGAGAAAGTGAAGAGAAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCTGA
 AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC
 ACGCTGGTGTCTACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCCTCGTCCC
 AGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT
 CAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGTGTTCCTTTTT
 TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATTT
 GATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGAAAAAATCGTGATTA
 ACTTTATCACCCCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA
 AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA
 GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAG
 AAAACACGGAAGGTACTTCTCTACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCGGATAAA
 ACAGTCATTGAATATGAATATGATGTCAGAACCACTGACATTTGTGCGGGGCCTGAAGAGCAGGA
 GCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG
 TCTTGGGCCCCGAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCG
 CAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGA
 TCCCCAAACTGGCAGGCTGTGTATTCTTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCG
 AGCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT
 CCAGACAGGCCACCAGGAGAAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGTATA
 TGTGCAGATGGAAAACTGATGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAG
 TCACCCCTTTGATCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTTCCAGTTTGTGAGTGT
 CTGTGAGAATTACTTATTTCTTTTCTTATTCTCATAGCACGTGTGTGATTGGTTCATGCATGTA
 GGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGTTGTTCTATGCAGAGAA
 AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTAGGTGGGTGT

FIGURE 76

MSYNGHLHQRVFKELKLLTLCSSIQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLK
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNFEDKRFFVPAEK
IVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC
DSEENTEGTSLTQQESLSRTIPDKTVIEYEYDVRTTDICAGPEEQELSLQEEVSTQGTLLESQA
ALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSSFDQDS
EGCEPSEGDGLGEEGLLSRLYEAPAPDRPPGENETYLMQFMEEWGLYVQMEN

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 77

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC
 CTGGGAAGATTGCGCGGCGCCGTGGACCTTCACCCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATC
 CAAGCCACCCTCAGTCCCCTGCACTTCTCATCCTCGGCCCAAAGTCATCAAAGAAAAGCTGAC
 ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC
 GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCCTGAAGCACATC
 ATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA
 GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCCCTGGTCAAGACCA
 TCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGAAGTGGC
 CCCACCCGCCTGGTCCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTGTGTA
 TAAGCTCTCCTTCCTGGTGAACGCCCTTAGCTAAGCAGGTTCATGAACCTCCTAGTGCCATCCCTGC
 CCAATCTAGTGAAAAACCAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGAC
 CTCCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTA
 TCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAA
 AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCG
 TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
 ATTCATGGTCCTGTTGGACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC
 TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC
 ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTT
 TCCCTCCAGTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT
 TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG
 ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA
 CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTGAAGG
 CCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCC
 TTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGG
 GTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTG
 CCTGTGAAAAA

FIGURE 78

MAGPWTFLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAMREK
PAGGIPVLGSLVNTVLKHI IWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYLGAALLDSQGVKVT
KWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPEEFMVLLDSVLPESAHLKSSIGLIN
EKAADKLGSTQIVKILTQDTPFEFFIDQGHAKVAQLIVLEVFPSSSEALRPLFTLGIEASSEAQFYT
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSQVPVSLVKALG
FEAAESSLTkdalvltpaslwkpsspvsq

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCT
CTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCAT
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGTTGGCTTCT
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC
ACCCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCCAGGCCATGATGGTGACATCCAGTGCAAT
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTCATCCTTGGAGGCCTCCTGGGATTCT
ATTCTGTGTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTCACCAGTGGTGCTGACAG
CATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAG
CTGGAATCATCCTCTGCTTTTCTGCTCATCCCAGAGAAATCGCTCCAATACTACTACGATGCCTAC
CAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA
GTTCAATTCCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTG
GGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCCTGGATCGT
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG
GCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCC
TCACCTTGCTGCTCCCCCTGCCCTAAGTCCCCAACCCCTCAACTTGAAACCCCATTCCTTAAGCCA
GGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACA
TCCCCTGACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTGGCTCTTAGCTCATT
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTC
CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGTATGACTCCACAGTGTCCA
GACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 8o

MASLGLQLVG YILG LLLG LTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD
IYSTLLGLPADIQAAQAMMVTSSAIISSLACIIISVVGMRICTVFCQESRAKDRVAVAGGVFFILGGL
LGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQRNRSNYY
DAYQAQPLATRSSPRPGQPPKVKSEFNSSYSLTG YV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 81

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTC
 CCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCCCT
 GCCCACCGCTGCTTCCTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG
 GTTGATCTGTGGCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCCTCCCGACTCCGCTCCCGG
 ACCAGCGGCCTGACCCTGGGGAAAGGATGGTCCCGAGGTGAGGGTCTCTCCTCCTTGCTGGGA
 CTCGCGCTGCTCTGGTTCCCCCTGGACTCCACGCTCGAGCCCGCCCAGACATGTTCTGCCTTTT
 CCGATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTACTTGAGGCCACAAGGCCTGATGT
 ACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCT
 GTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC
 TCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCCAGCACAAACGGGACCATGTACCAACACGGAG
 AGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCCTGCCCAACCAAGTGTGTCTCTGCAGCTGC
 ACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCGAACCAGGCTGCCAGCACCCCTCCC
 ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACA
 GTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAG
 AGAGGCCCCGGGCACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT
 CAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCT
 GTGTGCATGGCGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC
 CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC
 CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCAGAGG
 ACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTC
 CTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGC
 CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAGAGAG
 GTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAG
 GAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCACGAAGGTCACT
 GGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAG
 ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTAATAAA
 TAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 82

MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRTCSE
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKVEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELF
PSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR
HPQDPCSSDAGRKRGP GTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTY S
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPKVAGKCKICPEDKADPGHSE
ISSTRCPKAPGRVLVHTSVSPSPDNLRREFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH
SQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPGAEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

FIGURE 83

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGGCCCTCCGCTCACGCAGAGCCTCTCC
 GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCATCCGTCACCTCTCCTGTCA
 TCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGGTTCTGAGTC
 TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAG
 GACGCAGCATTCTCCTGTTTCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGTTTCTCAGGGG
 CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATC
 AAGGCAGGACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTACT
 GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCATCTGGGAGCT
 ACAGGTGTCAGCACTGGGCTCAGTTCTCTCATTTCCATCACGGGATATGTTGATAGAGACATCCAGCTAC
 TCTGTCTAGTCCCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTGGAAAGGTCCACAAGGACAGGATTTGTCC
 ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAA
 CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG
 GAGATACCTTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA
 TTTTTTGGCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGGAACCTGGACTG
 GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAG
 AGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACCTGTAACCCATAGAAAAGCTCCCCAGGAGGTG
 CCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAAACATTA
 CTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGA
 AGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTT
 ACATTAAATCCCCGTTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTTGGACTA
 TGAGTGTGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTGGTGTG
 AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCCCATAGTCATCTGC
 CCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGCAATCCCAGAGACAAGCAACAG
 TGAGTCTCTCACAGGCAACCACGCCCTTCTCCCCAGGGGTGAAATGTAGGATGAATCACATCCCACAT
 TCTTCTTTAGGGATATTAAGGTCTCTCTCCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCA
 GATGAAGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTCTGCTGCTGCTGAGCTGGGAGGGAAGAAGG
 CTGACATTACATTTAGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAG
 AACCGTCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAG
 ATCTTATTGATGACAGAGTGATCCTAATGGTTTGTTCATTATATTACACTTTCAGTAAAAAAA

FIGURE 84

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSSVVH
LYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQKAIWELQ
VSALGSVPLISITGYVDRDIQLLCQSSGWFFRPTAKWKGPQGQDLSTDSRTNRDMHGLFDVEISL
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK
FQWKIQAELDWRRKHGQAEIRDARKHAVEVTLPETAHPKLCVSDLKTVTHRKAPEVPHSEKRF
TRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLSPDHGYWVLRNLNGEHLFT
LNPRFISVFPRTPTTKIGVFLDYECGTISFFNINDQSIIYTLTCRFEGLLRPYIEYPSYNEQNGT
PIVICPVTQESEKEASWQRASAIPESTNSSESSQATTPLPRGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 85

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCTGCCCCCT
GCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTTCCGTGA
CGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATT
TACCCTGGCCCAGTAGTTCATGGCTACTGGTTCCGGGAAGGGGCAATACAGACCAGGATGCTCC
AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACCGATTCCACCTCCTTG
GGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGAAGAAGTGATGCGGGGAGA
TACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCTGTGAA
TGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAGGCACCCTGGAGTCCGGCTGCCCCC
AGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATA
GGGACCTCCGTGTCCCCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCTCATCCCACA
GCCCCAGGACCATGGCACCAGCCTCACCTGTGAGGTGACCTTCCCTGGGGCCAGCGTGACCACGA
ACAAGACCGTCCATCTCAACGTGTCCTACCCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGA
GACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTGTGCACTCCAGAGGGCCAGTCTCT
GCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGA
GAGGCCTGACCCTGTGCCCTCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCAC
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCT
GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTGACTCAGGGGTGGTTCGGGGGAGCTGGAG
CCACAGCCCTGGTCTTCCTGTCCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAA
TCGGCAAGGCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTC
AGCCTCTCAGGGGCCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCAG
CTTCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGTG
AAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG
ATGAGAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGAGAAGTCA
GAGGCTGATTCTTGTAATAAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATG
TGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCC
TCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 86

MLLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWFREG
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSVPWACEQGTPPMISWIGTSVSPLDPSTTRS
SVLTLIPQPQDHGTSLTQCQVTFPGASVTTNKTVHLNVSYPQNLTMTVFQGDGTVSTVLGNGSSL
SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPVHRLRDAAEFTCRAQNP
LGSQQVYLNVSLSQKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDGTGIE
DANAVRGSASQGPLTEPWAEDSPPDQPPPASARSSVGEGLQYASLSFQMKPWDSRGQEATDTE
YSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT
TCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTTGA
TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGACATGACCTCTG
GGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC
CAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACT
ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCAATAAGTCCCCCATGCAGCACTGG
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT
GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTTGGACTGACAACGGCC
CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCCAGAAAACAGCATCTTATTACTCACCTAT
GGCCAGCGGGAATTCAGTGCGGGATTTGTTCAAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAA
CGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG
GATACTTTCCAGAGGCCAGTCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT
GGAACATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG
TTGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAA
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA
AAAAAA

FIGURE 88

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAAT
SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYG
EGKCWTDNGPVIIPVVYDFGDAQKTASYSPYQOREFTAGFVQFRVFENNERAANALCAGMRVTGCN
TEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSSSREITEAAVLLFYR

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation site.

amino acids 163-167

Glycosaminoglycan attachment sites.

amino acids 74-78, 289-293

N-myristoylation sites.

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

FIGURE 89

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGAGAC
CGCCGCCCTTGTCCTCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGCGCCCTCTCGCTTCCTGACG
CTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTG
CCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTAGCTGGTGGCCGCGCTCT
CTGTCACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGAGTCTCCATGTTCAAC
AGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCCTTCTTCAT
ATTCGAGCGTTGGGAGTGCACTACGTATTGGTACATTTTTGTCTTCTGCAGTGCCCTTCCAGCTG
TCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAAAAGAAACCCTTCTTGATTACCTTCA
TGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCCTGGAAGAAGGAAG
GCATAGGCTTCGGTTTTCCCTCGGAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG
TCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAATAAAATATGTTTTGTAGTAACA
TTAAGACTTATATACAGTTTTAGGGGACAATTAAAAAAAAAAAA

FIGURE 90

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVTEMALFV
TVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 91

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC
TCGCTGCTGCTTCGTGTTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG
GTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT
CGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCT
GGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCCGAACCACAGCCCCC
CACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG
GCCCTGAACCTGCTCGTCAAGGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT
CCAACACAATGCCACAGGCCAGGGAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAG
AGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG
GAGTGGGAGAAGGTAGAACGGGGCCGCGGACCTCGCTTTGCACCCACGACCAGCCAAGATCTG
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCCAGCCCTTCAAAGTCGTCTGTG
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCAGATTACAACACTAC
CATAGTGATACCCCCTACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGC
TGGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCTC
AGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG
AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG
TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC
CCTTGGTTCTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACA
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGG
GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTTGTCGTGTGCTGAGCATGG
CATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC
CAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG
GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC
CGCGTGCTGTGTGTCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCG
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTCTCCCGGATCTGGATGGCGC
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGCCGAGAGCATGTGCTGGATCTGTTC
TGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGTGAAACCGCTGATTGCTGACTTT
TGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

FIGURE 92

MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDP
AKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVCPDYNHSDTPYYPSG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 93

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGGCCTGCGCTCGCC
CTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTTCTT
CTGGTTGGTGTCTCTACTGATTTGCTCCCTTGTTTGGTTTCATGGCAAGAGTCATTATTGACAACA
AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAA
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAACCC
AGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGGGCTTTGGAATCATGA
GTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTTCAT
GGAGATTCTCCTCAATTCTTCCTTTATTTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGT
ATTCTGGGGCATTGTATTTTTTGTGAGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTC
TCCTGACCCACCTGCTGGTGTGTCAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG
TCAGCATTTATAATCCTGGTGTGTCATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG
AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGAT
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACCTGTGCCT
TTTTCTGAAAATCCCTTTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 94

MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV
FSFVNTLSDSLGPSTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVLLT
HLLVSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSLKLCLLCQDKNFLLYNQSR

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 95

[illegible]

FIGURE 96

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQOQSNQVFPSLSLIPLTQM
LTLGPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE
LPQIFTSLSLIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 97

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT
CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCCTGACCATG
GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGCCAGCCTGC
AGAGCTGTCTGTGGAAGTTCCAGAAACTATGGTGGAATTTCCCTTTATACCTGACCAAGTTGC
CGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCAGGCAAGGCAACTGAG
GGCCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAGGGCCCTGGACCGAGAGGA
GCAGGCAGAGTACCAGCTACAGGTCACCCCTGGAGATGCAGGATGGACATGTCTTGTGGGGTCCAC
AGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCCATTTCTCTCAAGCCATCTAC
AGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCCCTTCCTCTTCCCTTGAGGCTTCAGACCG
GGATGAGCCAGGCACAGCCAACTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCCAGC
CTTCCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC
ACCAGCCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA
CCAGGCCTCAGGCCACCAGGCCACTGCCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGT
CCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCCTATACCCGCACCACATGGCCCAGGTA
CACTGGAGTGGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCCGGGACCCTTTGAAGTGAA
TGCAGAGGGAAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCC
AGGTGCGGGCTCAGAATTTCCATGGCGAGGACTATGCGGGCCCTCTGGAGCTGCACGTGCTGGTG
ATGGATGAGAATGACAACGTGCCATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCT
CAGTCCACCAGGTACTGAAGTGACTAGACTGTGAGCAGAGGATGCAGATGCCCCCGGCTCCCCCA
ATTCCCACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTC
CAGGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAT
CCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGTGAAG
TCGAAGTCGCAGTCACAGATATCAATGATCACGCCCCGTAGTTTCATCACTTCCCAGATTGGGCCT
ATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA
CCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACAGAAGGGACTTTTG
GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG
GCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCCC
AGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGTGATGCCACCCCCCAAGTTGG
ACCAGGAGAGCTACGAGGCCAGTGTCCCATCAGTGCCCCAGCCGGCTCTTTCCTGCTGACCATC
CAGCCCTCCGACCCCATCAGCCGAACCCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT
CTGCATTGAGAAATTCTCCGGGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGG
ACACCTACACGGTGCTTGTGGAGGCCAGGATACAGCCCTGACTCTTGCCCTGTGCCCTCCCAA
TACCTCTGCACACCCCGCCAAGACCATGGCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCT
GGCCAGTGGGCACGGTCCCTACAGCTTACCCTTGGTCCCAACCCACGGTGCAACGGGATTGGC
GCCTCCAGACTCTCAATGGTTCCCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGT
GAACACATAATCCCCGTGGTGGTCAGCCACAATGCCCAGATGTGGCAGCTCCTGGTTTCGAGTGAT
CGTGTGTCGCTGCAACGTGGAGGGGAGTGCATGCGCAAGGTGGGCGCATGAAGGGCATGCCCA
CGAAGCTGTCGGCAGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTTCCTCATCCTC
ATTTTCACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCT
GAAGGCGACTGTCTGAATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAG
TCCCCTGGGAGAGAGCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCCTCCA
TCTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAACTT
TATGGACTGCCCATGGGAGTGCTCCAAATGTCAGGGTGTGTTGCCCAATAATAAAGCCCCAGAGAA
CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 98

MVPAWLWLLCVSVQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT
EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVPHFSQAI
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSDFMQLEPRLGALALSPKG
STSLDHALERTYQLLVQVKMDQASGHQATATVEVSIIESTWVSLEPIHLAENLKVLYPHHMAQ
VHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDIAAPLELHVL
VMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSHVYQLLSPEPEDGVEGRA
FQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSSTCEVEVAVTDINDHAPEFITSQIG
PISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTEGTFGLDWEPPDSGHVRLRLCKNLSY
EAAPSHEVVVVVQSVAKLVGPGPGPGATATVTVLVERVMPPPKLDQESYEASVPISAPAGSFLLT
IQPSDPISRTLRFSLVNDSEGLWCIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALTAPVPS
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEP
REHIIPVVVSHNAQMWQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTTLVAIGIFLI
LIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 99

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCACGCCTG
 AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA
 TCTCTTCACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTAC
 ATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG
 TTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCCAATGAGACTAGCACC
 TCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG
 TGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA
 GCATAGTCACCAACTCTGAGTTCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG
 TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG
 GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCACCAACT
 CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC
 AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC
 CAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA
 CCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT
 GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG
 AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCA
 GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG
 TCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG
 GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACT
 CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCTCC
 AGTGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAACACAGCCAC
 CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA
 CCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACA
 GCCACCAACTCTGACTCCAGCACAACTCCAGTGAGGCCAGCACAGCCACCAACTCTGAGTCTAG
 CACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCA
 ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA
 ATGCACACAACTTCCCATAGTGCATCTACTGCAGTGAGTGAGGCAAAGCCTGGTGGGTCCCTGGT
 GCCGTGGGAAATCTTCCTCATCACCTGGTCTCGGTTGTGGCGGCCGTGGGGCTCTTTGCTGGGC
 TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCCT
 CATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCACAGGCCAG
 GTGGAGTCCTAACCTGGTTCTGGAGGAGACCAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA
 ACAGCGGGCCCCTGAGCAGCCCCGGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCA
 CCCAAGACCTGGTTTCTTTTCTTTCATTCATCCCAGGAGACCCCTCCAGCTTTGTTTGAGATCCTGAA
 AATCTTGAAGAAGGTATTCTTCACCTTTCTTGCCTTTACCAGACACTGGAAAGAGAATACTATAT
 TGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACACACACGACAAAGAGAAGCTGTGCTTG
 CCCCAGGGTGGGTATCTAGCTCTGAGATGAACTCAGTTATAGGAGAAAACTCCATGCTGGACTC
 CATCTGGCATTCAAATCTCCACAGTAAAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 100

MKMQKGNVLLMFGLLLHLEAATNSNETSTSA NTGSSV ISSGASTATNSGSSVTSSGVSTATISGS
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS
GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTA
TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSES
STTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNSDSSTTSS
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA
TNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESSTVSSGISTVTNSES
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA
AVGLEAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFWRPVS I
AMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 101

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCCTA
CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTACAGGTG
GGAGGCTGGAACATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCAACAAAT
GGATGATGTGATATATGCATTCCAGGGGAAGGGAAATTGTGGTGCTTCTGAACCCATGGTCAATT
AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTTGGAATCAT
GGTGTCATGGAAAGGGATTACTTTTATACTGACTCTGTTTTTGGGGAAGCTTTTTTGGAAGCATTT
TCATGCTGAGTCCCTTTTTACCTTTGATGTTTGTAACCCATCTTGGTATCGCTGGATCAACAAC
CGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAGT
GATTATAACTGGGGATGCATTTGTTTCTGGAGAAAGAAGTGTCAATTATCATGAACCATCGGACAA
GAATGGACTGGATGTTTCTGTGGAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT
TGCCTCAAAGCGAGTCTCAAAGGTGTTTCTGGATTGTGGTTGGGCCATGCAGGCTGCTGCCTATAT
CTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTTGAAGACATGATTGATTACTTTTGTG
ATATTCACGAACCACTTCAACTCCTCATATTCCCAGAAGGGACTGATCTCACAGAAAACAGCAAG
TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTTACATCCAAG
AACTACAGGCTTTACTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCTTGATGCTGTCCATG
ATATCACTGTGGCGTATCCTCACAAACATTCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT
CCCAGGGAAATCCACTTTCACGTCCACCGGTATCCAATAGACACCTCCCCACATCCAAGGAGGA
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAAGAGAGGCTGCGTTCCTTCTATCAAG
GGGAGAAGAATTTTTATTTTACCGGACAGAGTGTCAATTCACCTTGCAAGTCTGAACTCAGGGTC
CTTGTTGGTCAAATTGCTCTCTATACTGTATTGGACCCTGTTTACGCCCTGCAATGTGCCTACTCAT
ATATTTGTACAGTCTTGTTAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA
GAATATTTGGTGGACTGGAGATCATAGAACTTGCATGTTACCGACTTTTACACAAACAGCCACAT
TTAAATTCAAAGAAAAATGAGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTG
GAAATGTTCTAAACCTTTCTAAGCTCAGATGCATTTTTGCATGACTATGTCGAATATTTCTTACT
GCCATCATTATTTGTTAAAGATATTTTGCACTTAATTTTGTGGGAAAAATATTGCTACAATTTTT
TTAATCTCTGAATGTAATTTGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT
GGGCCAGAATATTATTAAACAATCATCAGGCTTTTAAA

FIGURE 102

MHSRGREIVLLNPWSINEAVSSYCTYFIKQDSKSGIMVSWKGIYFILTLFWGSFFGSIFMLSP
FLPLMFVNPSWYRWINNRLVATWLTLPVALLETMEGVKVIITGDADFVPGERSVIIMNHRTRMDWM
FLWNCLMRYSYLRLEKICLKASLKGVPFGFGWAMQAAAYIFIHRKWKDDKSHFEDMIDYFCDIHEP
LQLLIFPEGTDLTENSKSRNAFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA
YPHNIPQSEKHLLOGDFPREIHFHVHRYPIDTLPTSKEDLQLWCHKRWEEKEERLRSFYQGEKNF
YFTGQSVIPPCKSELRVLVVKLLSILYWTLEFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIEGG
LEIIEELACYRLLHKQPHLNSKKNE

Important features of the protein:

Signal peptide:

amino acids 1-22

Transmembrane domains:

amino acids 44-63, 90-108, 354-377

FIGURE 103

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC
TCCAAATCATCCATCCACCCCTGCTGTCTCATCTGTTTTTCATAGTGTGAGATCAACCCACAGGAATA
TCCATGGCTTTTTGTGCTCATTTTGGTTCTCAGTTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT
CACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTGCTCCCTCT
TTCCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAGTTCCATGCTGTGGTC
CACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAAGTGA
GTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGCTAAAAACATCACTCCCTCGG
ACATCGGCCTGTATGGGTGCTGGTTCAGTTCCCAGATTTACGATGAGGAGGCCACCTGGGAGCTG
CGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCATCGTGGGATATGTTGACGGAGGTATCCA
GTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGCCACAGCCAAGTGGAAAGGTCCACAAGGAC
AGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGA
GGTGGAAATCCAAGGTATTGATAGGAGAGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTA
TTTTACTCGGGTTACTCTGTGGTGCCCTGTGTGGTGTGTGCATGGGGATGATAATTGTTTTCTTC
AAATCCAAAGGGAAAATCCAGGCGGAACCTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAG
AGACGCCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCG
TTTCTGATCTGAAAACGTAAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGA
TTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA
CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTGCGGATGACGTAGACAGGGGGAAGAACA
ATGTGACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTC
ACATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGCTCTCCT
GGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGC
TGACATGTGAGTTTGAAGGCTTGTGAGACCCCTATATCCAGCATGCGATGTATGACGAGGAAAAG
GGGACTCCCATATTTCATATGTCCAGTGTCTGGGGATGAGACAGAGAAGACCCTGCTTAAAGGGC
CCACACACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGCCCCAGCTTCCTCT
CCGGAGCCTGCGCACAGAGAGTCAAGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCC
TGAGCCCTGCAGCAGCGGCAGTCAAGCTTCCAGATGAGGGGGGATTGGCCTGACCCCTGTGGGAG
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAA
CTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCCAGGCTCCTCATTTGCTAGTCACGG
ACAGTGATTCTGCTGCCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAAGTT
TGAGGGCACAGTGTTTGCTAATGATGTGTTTTTATATTATACATTTTCCCACCATAAACTCTGTT
TGCTTATTCCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACACC
TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTTTCACTGATTCTATAAGCCCAGCAT
TACCTGATACCAAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCC
CTCATTAACACAGACACAAAAATTTCTAAATAAAATTTTAAACAAATTAACTAAACAATATATTTA
AAGATGATATATAACTACTCAGTGTGGTTTGTCCCACAAATGCAGAGTTGGTTTAAATATTTAAAT
ATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAA

FIGURE 104

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH
LYRDGEDWESKOMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLYDVEISI
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALCGVVMGMIIVFFK
SKGKIQAELDWRRKHGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAPOEVPHSEKRF
TRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYWVLRLTTEHLYFT
FNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLCQFEGLLRPYIQHAMYDEEKG
TPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 105

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG
 TTTGTTGGGAACCCCTGGGTATCGGCCTCGTCATCTTCATATCCCTGATTGTCTGGCAGTGTGCATTGGA
 CTCACTGTTTCATTATGTGAGATATAATCAAAAGAAGACCTACAATTACTATAGCACATTGTCAATTTACAAC
 TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAATTTTACAGAAATGAGCCAGAGACTTGAAT
 CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTC
 AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGA
 AACTGTAGATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG
 ATCCTCACTCAGTTAAATTTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGGA
 ACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAGAAAGTAGAAGAGGGTGAATG
 GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTAATGCCACATGGC
 TTGTGAGTGCTGCTCACTGTTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACA
 ATAAACCTTCGAAAATGAAACGGGTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACA
 TGACTATGATATTTCTCTGCGAGGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTC
 TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAAT
 GATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACC
 TCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT
 GCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTAGAGATATCTGGTACCTTGCTGGAATAGTG
 AGCTGGGGAGATGAATGTGCGAAACCCAACAAGCCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTG
 GATTACTTCAAAAACCTGGTATCTAAGAGACAAAAGCCTCATGGAAACAGATAACATTTTTTTTTTGTTTTTTG
 GGTGTGGAGGCCATTTTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCA
 ATAAACTGTTTGCTTGATGCATGTATTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA
 GATCAACTCTGTCTATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATAATACAATATTAC
 ATTACAGCCTGTATTCAATTTGTTCTCTAGAAGTTTTGTGAGAATTTTGACTTGTGACATAAATTTGTAAT
 GCATATATACAATTTGAAGCACTCCTTTTCTCAGTTCCTCAGCTCCTCTCATTTTCAGCAAATATCCATTT
 TCAAGGTGCAGAACAAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAA
 AAGTATTAGGTGTTTTTCTTAGTGGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACA
 GCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAACCTAAGTTAAGGAAGTCCAGAAAGAAGCCAAG
 ATATATCCTTATTTTCATTTCCAAACAACCTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTGACCT
 ATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAAGCAAATATTTATTTAACATTG
 TTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 106

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYYSTLSFTTDKLY
AEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFHSTED
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL
RRIIVHEKYKHPSHDYDISLAELSSPVYTNVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS
QNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSGGPLVSSDARDIWYLAG
IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 107

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCTG
 CCCCAGATGAGCCCCCGCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCAGGGCCCAGC
 GCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTT
 ACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTACGCCCTCAA
 TCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAA
 ATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTACTTACTTTCCT
 GTGGTTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCATTGTGGGGATGTTAGGATATTG
 TGGAACGGTGAAAAGAAATCTGTGCTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCATTTTCT
 GTGTAGAAGTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTTATGGTTCCAGTACAATGGTCA
 GATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA
 TGCTTGAATTTTTTTCAGAGAGAGTTTAAAGTGTGTGGAGTAGTATATTTCACTGACTGGTTGG
 AAATGACAGAGATGGACTGGCCCCCAGATTCCCTGCTGTGTTAGAGAATTCACAGGATGTCCAAA
 CAGGCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTT
 TTTGAGAGGAACCAACAACCTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAA
 TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGG
 ACAGACCAATGATGTCTTGAAGAATGACAACCTCTCAGCACCTGTATGTCCCTCAGTAGAAGT
 GTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACT
 TTGAGATGGAGGAGTTATAAAAGAAATGTACAGAAGAAAACCACAAACTTGTTTTATTGGACT
 TGTGAATTTTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAA
 TAACACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTC
 ACCACCTGGACAATAATGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC
 TGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCA
 TCCATGCAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTACTTCTACCAA
 CTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA
 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACCTTCAATATTGGTGACT
 ACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACCTAAAAGAGCAAGCTAACACAT
 TGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGAT
 TTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCTGTATAGCATCATT
 ATTTTTAGCCTTTCTGTGTTAATAAAGCTTTACTATTCTGTCTGGGCTTATATTACACATATAAC
 TGTTATTTAAATACTTAACCACTAATTTTGAATAATACCAGTGTGATACATAGGAATCATTATTC
 AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGA
 AAGGACTTGTATGCTGTTTTTCTCCAAATGAAGACTTTTTTGCACATAAACACTTTTTAAAAA
 GCTTATCTTTGCCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTTACAGAAAA
 TAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAACATGTGACAATTTAGAGATT
 CTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAATTTTTTTACAA
 GAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTATTAT
 TTCTCAGAATATGGAAGAAAATTAATGTGTCAATAAATATTTCTAGAGAGTAA

FIGURE 108

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMDYLNNVLTTLTAETRVEEAVILTYFPVVHP
VMIAVCCFLIIVGMLGYCGTVKRNLALLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREPGTDQM
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 109

CCAAGGCCAGAGCTGTGGACACCTTATCCCACCTCATCCTCATCCTCTTCTCTGATAAAGCCCCCTACCAGTGCT
GATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCCTTAAAAAAGTGCTTGAAAGAGAAGGGGACAAAGGAACA
CCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTCCAGAAGGATGCCTCCATTCTGCTTCTCACCTG
CCTCTTCATCACAGGCACCTCCGTGTCACCCGTGGCCCTAGATCCTTGTTCTGCTTACATCAGCCTGAATGAGC
CCTGGAGGAACACTGACCACCAGTTGGATGAGTCTCAAGGTCTCCTCTATGTGACAACCATGTGAATGGGGAG
TGGTACCACCTTCACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAACCCA
CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAAGGCGACGGCATTGTGCAACGCCAGGCTTGTGCCAGCT
TCAATGGGAAGTGTCTCTGGAACACCACGGTGGAAAGTCAAGGCTTGCCCTGGAGGCTACTATGTGTATCGT
CTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGGTCATTTTATGACATCTGCAGCAGGACTGCCATGG
CAGCTGCTCAGATACCAGCGAGTGCACATGCGCTCCAGGAAGTGTGCTAGGCCCTGACAGGCAGACATGCTTTG
ATGAAAATGAATGTGAGCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCTACCGCTGT
GAGTGTGGGGTTGGCCGTGTGCTAAGAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA
TGGTGGCTGCAGCCACTCTTGCCCTGGATCTGAGAAAGGCTACCAGTGTGAATGTCCCCGGGGCCTGGTGTGT
CTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG
CTGGTTGGTGGCCTGGAGCTCTTCTGACCAACACCTCCTGCCGAGGAGTGTCCAACGGCACCCATGTCAACAT
CCTCTTCTCTCTCAAGACATGTGGTACAGTGGTCGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA
CAGGTCTACCCAAGCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTG
ACCTGCGAGTTTCCACGCCTGTACACCATTTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCCACTGGAAAT
CATGAGCCGAAATCATGGGATCTTCCCATTCACCTCTGGAGATCTTCAAGGACAATGAGTTTGAAGAGCCTTACC
GGGAAGCTCTGCCACCCCTCAAGCTTCGTGACTCCCTCTACTTTGGCATTGAGCCCCTGGTGCACGTGACCGGC
TTGGAAAGCTTGGTGGAGAGCTGCTTTGCCACCCCACTCCAAGATCGACGAGGTCTGAAATACTACCTCAT
CCGGGATGGCTGTGTTTTCAGATGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGG
TCCCTGTCTTCAAGTTTGTGGGCAAAGACCACAAGGAAGTGTCTTCTGCACTGCCGGGTCTTGTCTGTGGAGTG
TTGGACGAGCGTTCCCGCTGTGCCAGGGTTGCCACCGCGCAATGCGTCGTGGGGCAGGAGGAGAGGACTCAGC
CGGTCTACAGGGCCAGACGCTAACAGGCGGCGCGATCCGCATCGACTGGGAGGACTAGTTTCGTAGCCATACCTC
GAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTCCCCCACCGCCCTCTAAGAACATCTGCCAACAGC
TGGGTTTCAGACTTCACACTGTGAGTTCAGACTCCAGCACCAACTCACTCTGATTCTGGTCCATTCACTGGGCA
CAGGTACAGCACTGCTGAACAATGTGGCCTGGTGGGGTTTCATCTTCTAGGGTTGAAAATAAACTGTCCA
CCCAGAAAGACACTCACCCATTTCCCTCATTTCTTCTACACTTAAATACCTCGTGTATGGTGAATCAGAC
CACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCCTAGAAAAATTAAACAGTTACTGAAATTATGA
CTTAAATACCAATGACTCCTTAAATATGTAAATTATAGTTATACCTTGAAATTTCAATTCAAATGCAGACTAA
TTATAGGGAATTTGGAAGTGTATCAATAAACAGTATATAATTTT

FIGURE 110

MPPFILLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFTGMAGDAMP
TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYVYRLTKPSVCFHV
YCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV
LRSDGKTCEDVEGCHNNNGGCSHSLGSEKGYQCECPRGLVLSEDNHTCQVPVLCKSNAIEVNIIPRELVGG
LELFLTNTSCRGVSNNGTHVNILFSLKTCGTVDVVDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT
CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEPEPYREALPTLKLRLDSLYFGIEPVVHV
SGLESLVESCFATPTSKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV
LVCGVLDERSRCAQGCCHRRMRGAGGEDSAGLQGQTLTGGPIDWED

Important features of the protein:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

N-myristoylation sites.

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,
522-528, 531-537

Aspartic acid and asparagine hydroxylation site.

amino acids 197-209

ZP domain proteins.

amino acids 431-457

Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

FIGURE 111

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG
 GCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT
 CCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT
 TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCC
 ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATATAGCACTACTGAGCCTGGCGAGTATCATCATTGT
 GGTGTCTCATCAAGGTGATTCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGA
 GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC
 CCGGAAGGGCCTGCAGTGGCAGTCCGCCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC
 AGGGAAGTGGTTCTCTGCCTGTTTCGACAACTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG
 GCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAATCACAGAAAACAGCCAG
 GAGCTTCGCATGCGGAAGTCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCCTG
 TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGCCCTTGGCAGG
 TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTTCACGGCA
 GCCCCACTGCTTCAGGAAACATAACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAG
 CTTCCCATCCCTGGCTGTGGCCAAGATCATCATATTGAATTCAACCCCATGTACCCCAAAGACAATGACA
 TCGCCCTCATGAAGCTGCAGTTCCTCACTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT
 GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAA
 GATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCAATTGACAGCACACGGTGCAATGCAGACGATGCGT
 ACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGT
 GACAGTGGTGGGCCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG
 CTGCGGGGGCCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT
 GGAAGGCTGAGCTGTAATGCTGCTGCCCCCTTGCAGTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCT
 GGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCCACAGCCTCAGCAT
 TTCTTGGAGCAGCAAAGGGCCTCAATTCCTGTAAGAGACCCCTCGCAGCCAGAGGCGCCAGAGGAAGTCA
 GCAGCCCTAGCTCGGCCACACTTGGTGCTCCCAGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCT
 CAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAAAGCC
 CAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAA
 GCCTACTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT
 ACTGTTGTATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAA
 AAAA

FIGURE 112

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPII IALLSLASIIIVVVLIKVILDKYYFLCG
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN
FTEALAETACRQMGYSRAVEIGPDQDLVDVEITENSQELRMRNSSGPCLSGSLVSLHCLACGKSL
KTPRVVGEEASVDSWPWQVSIQYDKQHVCSSILDPHWVLTAAHCFRKHTDVENWKVRAGSDKL
GSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIIGWG
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCCQGDSSGGLMYQS
DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 113

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGATTA
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAAGCCACAGGAGT
TGAAGTGTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAATC
TGTTTTTTGTTCTCTTGTAAGTACCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT
GGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCCTCGAAG
CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAACTGTCTCACGTCT
GGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGTAGCTGCGGCTTTCAAGGTGGGC
CTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTTTCATAGGCGATGGCTCCCACTGCCC
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCGTGGACACCTGCTCA
GAAGCAGTGGGTGAGACATCACGCTGCCCCGCCATCTAACCTTTTCATGTCTGCACATCACCTG
ATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC
CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCATTCTCCTGGAACATGAGG
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACCTTGTGCCAAATTATGGGTGAGAAAAGATG
GAGGTGTTGGGTTATCACAAGGCATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTG
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGAT
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA
TCTGCGATCACCAGCCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCC
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG
GGCTAATGGCTCAGTGTGGCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCT
GTGCGAACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGG
CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCAAGACCAAAGGAGCTAGAGCTTGGTT
CAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCA
AACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACAT
TTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGG
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAGAATTA
TGTTTATTGTAA

FIGURE 114

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:
amino acids 1-15

FIGURE 115

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA
AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA
ATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCTAATTGTCCT
GTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT
TCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAAGTAAATA
TTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGG
CATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGTGATTCTGAATTTT
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACTTTCTTTGAACAGTCAGTG
ATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGA
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAG
ACTTTGAGGAGGAGGGAGAAGATCTTCACTTTCTGCCAACGAAAAAAAAGGGATTGAACAAAAT
GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGA
AGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTGATCCCATGCTGGATGAGAGAG
GTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTA
GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTGCTGTCATCATGCCTTG
TAACTGGTGGGTGGCCCCGATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAAC
TGCTGGCAACATATAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCCT
GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCTCTCTTCATGTTCTAATAAACTTCTACA
TTATCACCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 116

MAKNPPENCEDCHILNAAEFKSKKICKSLKICGLVFGILALTILIVLFWGSKHFWPEVPPKAYDME
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNKILEICDNVTMYWINPTLISVSE
LQDFEEEGEDLHFPAANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLD
ERGYCCIIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

Important features of the protein:

Signal peptide:

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-
242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 117

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA
 GGGCGGGCGGCCAGGATCATGTCCACCACCACATGCCAAGTGGTGGCGTTCCCTCCTGTCCATCCTGGGGCT
 GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGGACCTGTACGACAACCCCGTCACCT
 CCGTGTTCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCC
 TATTTACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCTCT
 GGGTGCCATTGGCCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG
 CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTG
 TCTGTGTTTGCCAACATGCTGGTGAATACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG
 GATGGTGCAGACTGTTTACAGCCAGGTACACATTTGGTGGCGCTCTGTTCTGGTGGGCTGGGTGCTGGAGGCC
 TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCTGGCACCAGAAGAAACCACTACAAA
 GCCGTTTCTTATCATGCCTCAGGCCACAGTGTTCCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT
 TGGGTCCAACACCAAAAAACAAGAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC
 CTTCCAAGCAGCACTATGTGTAATGTCTTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCA
 CCCAAAAACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCT
 CGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAAAA
 GCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTCAATCCTCTATTTCTTTTTTAAATATAACT
 TTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC
 TTCTCTCTAGTCAATAAACCATTGATGATCTATTTCCAGCTTATCCCCAAGAAAACCTTTTGAAAGGAAA
 GAGTAGACCCAAAGATGTATTTTCTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAA
 ACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTT
 ACACTGTGATCTTAAAGTTACCAAACCAAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTGCTG
 TTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCTCTTTCTGT
 CGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTAATTTAAGTCCTAAATATAGTTAA
 AATAAATAATGTTTGTAGTAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG
 GAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATCC
 ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGT
 TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCA
 TGGTGGCATAACCTGTAGTCCCAGCATTCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGT
 TGGGGCTGCAGTGAGCCATGATCACACCCTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA
 AATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCTTTAA

FIGURE 118

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTECRP
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSI FALKCIRIGSMEDSAKANMTLTSGIMFIVSGL
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDY
V

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 119

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGGAGTCC
 AGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTG
 GTGGTGTGGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGAGTGTGGCCTTCATT
 GAAAACAACATCGTGGTTTTTGAAAACTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA
 CATCAGGATGCAGTGC AAAATCTATGATTCCCTGCTGGCTCTTTCTCCGGACCTACAGGCAGCCAGAG
 GACTGATGTGTGCTGCTTCCGTGATGTCCTTCTTGGCTTTTCATGATGGCCATCCTTGGCATGAAATGC
 ACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT
 CATCACGGGCATGGTGGTGTCTATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATA
 ACTCAATAGTGAATGTTGCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCA
 CTGGTGTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTA
 CAGATACTCGATACCTTCCCATCGCACAAACCCAAAAAGTTATCACACCGGAAAGAGTCAACGAGCG
 TCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTTAACTTTACTATAAAGCCATGCAAATG
 ACAAAAATCTATATTACTTTCTCAAATGGACCCCAAGAACTTTGATTTACTGTTCTTAACTGCCT
 AATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTACGAGAATGAGATA
 TTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA
 CTCTTTTTTATCATTTACTTCAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAATTTCTCC
 ACGACATAGCATTATGTACATAGATGAGTGTAACATTTATATCTCACATAGAGACATGCTTATATGGT
 TTTATTTTAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA
 ATCATGGATAGGGTTGAAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCA
 TTTATAATGAAGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATAT
 GCTGTTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTT
 CTTGTGTATTAAATTAACATTTTTTAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCAAACGCTT
 TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTG
 AAAATATTTTTGTTTTTGTATTTGAAGAAGAAATGATGCATTTTGACAAGAAATCATATATGTATGGAT
 ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATA
 TGTCTTGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTCACCT
 GCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTTTTGTTCTGTGAAAAATAAATTTCCCTTCTTGTA
 CCATTTCTGTTTAGTTTTACTAAAACTGTAAATACTGTATTTTTCTGTTTATCCAAATTTGATGAA
 ACTGACAATCCAATTTGAAAGTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTT
 TATACATTTATATTAATAAATTGTACATTTTTCTAATT

FIGURE 120

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFW EGLWMNCVRQANIRMQCK
IYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG
MVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 121

GGAGAGAGGCGCGGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG
CCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCGGCAGCC
GGGAGCCATGCGACCCCAGGGCCCCGCCGCTCCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCC
TGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAG
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC
TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTCTGGGATG
GATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTAC
AAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGACATT
TACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTTCAGTGGCTCACTTCGGCTAAAATGCA
GAAATGCATGCTGTCTAGCGTTGGTATTTACATTCAATGGAGCTGAATGTTTCAGGACCTCTTCCC
ATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCACAATTAATATTCATCG
CACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG
TTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC
ATTATTGAAGAACTACCAAAATTAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTTATTATGCC
TTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG
CTAAATATGTTTACAGACCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTG
CTTCAATCAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATT
CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTCTTTTCTCTTAGTATAGCATTTTAA
AAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGT
TAAATAAAAATTATTTCCAACA

FIGURE 122

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGGKQKAQLRQREVVDLYNGMCLQGPAAGVPGR
DGSPGANVIPGTPGIPGRDGFKEGKECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAEC SGPLPIEAI IYLDQGSPEMNSTINIHRTS
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSR I IIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTGAA
 CTGGGTGCTCATCACGGGAACCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA
 ATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTTTTTTTA
 ACCGCCCCCTCCCCACCCCCCAAAAACTGTAAAGATGCAAAAACGTAATATCCATGAAGATCC
 TATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTTGTTCTTGGAG
 TGTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAGGGGTCCAATTTT
 TCTTCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGGCTGTTCATGCAACTG
 GCCCCAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTCAATG
 TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCCACTGTCTTACTGACAATG
 CTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCCAAAATGGTATATTGTGA
 ATCTCAGAAATTACAGGAGATACCCTCAAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT
 ATAACAGCCTTCAAAAACCTTAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC
 CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTTAATGGAATACGCAGACTCAAAGA
 GCTGATTTCTTAGTTCCAATAGAATCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAAT
 TACGGAACCTGGATCTGTCTTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTTCGGGGCTTG
 CGGAAGCTGCTGAGTTTACATTTACGGTCTAAGTCCCTGAGAACCATCCCTGTGCGAATATTCCA
 AGACTGCCGCAACCTGGAACCTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG
 TCTTTGCTGGCATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTTCCAAGCTCAAC
 CTGGCCCTTTTTCCAAGGTTGGTCAGCCTTCAGAACCCTTTACTTGCAAGTGAATAAAATCAGTGT
 CATAGGACAGACCATGTCCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGA
 TCGAAGCTTTTCAGTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGAT
 TCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAG
 TCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAACCTGGCTGAAAAGTT
 TTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTG
 ATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAG
 GGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAACCCCTT
 TGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCT
 TTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCCTGCTGGTTAT
 CTACGTGTCATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA
 GGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCCAGCACCCAGGAATTTTATGTA
 GATTATAAACCCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTA
 TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTGTGATAAAAAGAGCTCTTAAAGCT
 GGGAAATAAGTGGTGCTTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCC
 TTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCCTTGTCCGTTTTAGTGCATTATAATACT
 GGTCATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTT
 GAACTCCGGTTTAAATATAATACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTGCGATTT
 GTTTTAAGATAAAACTTCTTTCATAGGTAAAAA

FIGURE 124

MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGCLG
LSLRYNLSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR
PVTNLRNLDSLQNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRI FQDCRNLELLDLGYNRIRS
LARNVFAGMIRLKLHLEHNQFSKLNLA LFPRLVSLQNLYLQWNKISVIGQTMSWTWSSLQRLDL
SGNEIEAFSGPSVFQCVPNLQRLNLD SNKLTFIGQEILDSWISLNDISLAGNIWECSRNICSLVN
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE
SKPPLPPTVGATEPGPETDADA EHISFHKIIAGSVALFLSVLVILLVIYVSWKRYPASMQLQQR
SLMRRHRKKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLNGTG PCTYNKSGSRECEV

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 125

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGAGGAGGAGGAGAGGCTTTTGCCGCTG
ACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGCCGAGCT
AGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTC
GGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC
ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT
GTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAAG
ATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTTATTGGCCAGTTT
TTAGCCAATCCAACCTGACCTAGTGAAGGTTGAGATGCAAATGGAAGGAAAAAGGAAACTGGAAGG
AAAACCATTGCGATTTTCGTGGTGTACATCATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATAC
GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTA
ACCACTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC
TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA
TCAAAAGCAGAATAATGAATCAACCACGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCG
ACTGACTGCTTGATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACC
ATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAAATCAGAGAGA
TGAGTGGAGTCAGTCCATTTTAA

FIGURE 126

MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGARES
APYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEHYPLWKS
VIGGMMAGVIGQFLANPTDLVKVQMOMEGKRRKLEGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTPADVIKSRIMNQF
RDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 127

CGCGGATCGGACCCAAGCAGGTCGGCGGGCGGGCGGCAGGAGAGCGGGCCGGGCGTCAGCTCCTCGAC
CCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGGCGTGGGCCCATGGCCAGGCCCGGCATGG
AGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCCTCGGGGGGCATCGGCGCGGCCGTGGCC
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCGAGGA
GCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGGACTTTGATCCCCTACAGATGTGACCTAT
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATC
TGCATCAACAATGCTGGCTTGGCCCGGCCTGACACCCTGCTCTCAGGCAGCACCAGTGGTTGGAA
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGA
AGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTTA
CCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGGACT
GAGGCAAGAGCTTCGGGAGGCCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTGGTGG
AGACACAATTGCGCTTCAAACCTCCACGACAAGGACCCTGAGAAGGCAGCTGCCACCTATGAGCAA
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCTCAGCACCCCCGCACA
CATCCAGATTGGAGACATCCAGATGAGGCCCACGGAGCAGGTGACCTAGTGACTGTGGGAGCTCC
TCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTGCCTCTGGATTTTAGGTGTTGATTTCTGGAT
CACGGGATACCACTTCCTGTCCACACCCCGACCAGGGGCTAGAAAATTTGTTTGAGATTTTATA
TCATCTTGTCAAATTGCTTCAGTTGTAAATGTGAAAATGGGCTGGGGAAAGGAGGTGGTGTCCC
TAATTGTTTTACTTGTTAACTTGTTCTTGCGCCCTGGGCACCTGGCCTTTGTCTGCTCTCAGTG
TCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAATCCCCATCTTCTTGACCTCAACGTCTG
TGGCTCAGGGCTGGGGTGGCAGAGGGAGGCCTTCACCTTATATCTGTGTTGTTATCCAGGGCTCC
AGACTTCCTCCTCTGCCTGCCCCACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCC
AGCCCAGTCTTGGCTTCTTGTCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG
CAGAACACCAGGGCCTGGCCCAGTGGATTTTCATGGTGATCATTAATAAAGAAAAATCGCAACCAA
AAAAAAAAA

FIGURE 128

MARPGMERWRDRLALVTGASGGIGAAVARALVQQGLKVVGCA RTVG NIEELAAECKSAGYPGT LI
PYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPD TLLSGSTSGWKDMFNVNVLALSIC TR
EAYQSMKERNVDDGHIININMSGHRVLP LSVTHFY SATKYAVTALTEGLRQELREAQTHIRATC
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

Important features of the protein:

Signal peptide:

amino acids 1-17

N-myristoylation sites.

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205

Short-chain alcohol dehydrogenase.

amino acids 30-42, 104-114

FIGURE 129

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACCAT
CATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTTCAGGTGCAGAGTCTCAGTTGCCCCGGGAGC
ACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCCAGTTCTGGTTTCATGC
CAGCCTGTAAAAGGCCATGGAACTTTGGGTGAATCACCGATGCCATTTAAGAGGGTTTTCTGCCA
GGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTTCATTTTCAGTAGCCACCAGCCACCTGTGG
CCGTTGAGTGCTTGAAATGAGGGAAGTGAAGAAATTAATTTCTCATGTATTTTTCTCATTTATTTA
TTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA
TATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACATTTATTTTTTATTCTTT
TTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT
GCACCACAATGCCCAACTAATTTTTGTATTTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCAGG
CTGGCCTTGAACCTCCTGGCCTCAAACAATCCACTTGCCCTCGGCCTCCCAAAGTGTTATGATTACA
GGCGTGAGCCACCGTGCTGGCCTAAACATTTATCTTTCTTTGTGTTGGGAACCTTGAAATTAT
ACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT
ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC
AACCTCTGATCACCTCATTCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCCACATGTG
AGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTG
TTCCATCCATGTTGCTGCAAATGACAGGATTTTCGTTCTTAATTTCAATTAAATAACCACACATG
GCAAAAA

FIGURE 130

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV
KGHGTLGESPMPEFKRVFCQDGNVRSEFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

FIGURE 131

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC
 ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCCTTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG
 TCCATCTGTGTGTCGCTGCGATGCGGGTTTCATTTACTGTAATGATCGCTTTCTGACATCCATTCCAACAG
 GAATACCAGAGGATGCTACAACCTCTCTACCTTCAGAACAACCAATAAATAATGCTGGGATTCCCTTCAGAT
 TTGAAAAACTTGCTGAAAGTAGAAAGAATATACCTATACCACAACAGTTTAGATGAATTTCCCTACCAACCT
 CCCAAAGTATGTAAAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAA
 AAATTCCCTATCTGGAAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA
 TTCCGAGACAGCAACTATCTCCGACTGCTTTTCTGTCCCGTAATCACCTTAGCACAATTCCCTGGGGTTT
 GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCATCTCTTCAAG
 GTCTCACTAGTCTAAAACGCTGGTTCTAGATGGAACCTGTTGAACAATCATGGTTTAGGTGACAAAGTT
 TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATTCCTGACTGCTGCACCAGTAAACCT
 TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGCCCCAAATGCTTTTT
 CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTT
 GATGATTTGGACAATATAACACAACCTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATG
 GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAA
 AGGTTGCTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAAGC
 ACCATTCAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCAAGGACAGTGGCCAGCTCCAGTGAC
 CAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAGGGAGTCCCTCAAGAAAAA
 CAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTTCATATCTCTTGAAACTTGCTCTACCTATG
 ACTGCTTTGAGACTCAGCTGGCTTAAACTGGGCCATAGCCCGGCATTTGGATCTATAACAGAAACAATTGT
 AACAGGGGAACGCAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTCACCCTATAAAGTATGCATGGTTC
 CCATGGAAACCAGCAACCTCTACCTATTTGATGAAACTCCTGTTTGTATTGAGACTGAAACTGCACCCCTT
 CGAATGTACAACCCTACAACCACCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACC
 TTTGGCTGCCATCATTTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTTGCTTTAGTGTGTTGGTATG
 TTCATAGGAATGGATCGCTCTTCTCAAGGAACGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT
 GCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAAACTTCTTTTCAGATGTTACCAAT
 AAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAAATACACACCATATTTCCCTCCTAATGGAATGAATCTGT
 ACAAAAACAATCACAGTGAAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC
 TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATG
 GT

FIGURE 132

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCND RFLTSIPTGIPEDATTLYL
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNL PKYVKELHLQENNIRTITYDSL SKIPYL
EELHLD DNSVSAVSIEEGA FRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQDNHIN
RVPPNAFSYLRQLYRLDMSNNLSNLPQGI FDDLDNITQLILRN NPWYCGCKMKWVRDWLQSLPV
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQGQWPAPVTKQPD
IKNPKLTKDQQTGSPSRKTITITVKS VTSDTIHISWKLALPMTALRLSWLKLGHSPA FGSITET
IVTGERSEYLVTALEPDS PYKVCMPMETS NLYLFDETPVCIETETAPLRMYNPTTTLNREQEKE
PYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS
ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLYKNNHSESSSNRSYRDSGIPDS DSHSHS

Important features of the protein:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645

Amidation site.

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

FIGURE 133

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCCAGGCCACCCCAGGCTTCTTGGA
 GCCCTGCCGGGCCACTTGTCTTCAATGTCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG
 TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG
 GCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACCGCTGTGGT
 CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT
 GCGCTGGAGAGAGCCACCGTCTTCCCTAGAACAGAGGGTGCCTGAAATCAACCTGGATGGCATGGT
 GGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCGGGGAGAAGTGGGCCCAGGAGCCCCTGC
 TGCAGCCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC
 CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCAGCTGACCCCTCCAGCCCGG
 GTTTTGGAAAGCTCCCACATGCCTGGATCCACACTGATGCCTCCTTGGTGTACCCACGTTCCGGGC
 CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGGACG
 GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCGGCTGCTC
 AGGCTACTGCCTGTCCCACCACTGCTCTTCTTCTCCTCTGGGCCAGAATGAGGGGATGCACACAGG
 GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC
 AGAGCTGAGGCCATCGGATACGCCTACCCTACCCGGGACATCTTCATGGAAAACATCATGTTCTG
 TGGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA
 AACAGCAGGAAGGATGCTTCCGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA
 TATCAGCAGCATTTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGT
 TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGC
 AATTCTCTTGCTCATCCTCCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACCTGGCTAAT
 TTTTATATTTTTTTAGTAGAGACAGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT
 CTCAAGAGATCCGCCCACCTCAGGCTCCCAAAGTGTTGGGATTATAGGTGTGAGCCACCGTGTCTG
 GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC
 ATGGGGGCTCTCTCCCCTAGATGGCTGCTCCTCCCACAACACAGCCACAGCAGTGGCAGCCCTGG
 GTGGCTTCCATACATCCTGGCAGAATAACCCCCAGCAAACAGAGAGCCACACCCATCCACACCG
 CCACCACCAAGCAGCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCC
 TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG
 ATAAGCAAAGCCACCCCGACACCCAATCTTGGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG
 GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA

FIGURE 134

MSARGRWEGGGRRACRGSGLARAQGAERVTSSEQRPAMASLGLLLLLLLLLTALPPLWSSSLPGLD
TAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPLSLRV
GMLGEKLEAAIQRSLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE
RSDVCLVQLLGTGTDSSPECGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQQSQD
YINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILSQKQEGCFG
EPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQFSCILIP
SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPPTSGSQSVGL

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 39-56

Tyrosine kinase phosphorylation sites.

amino acids 149-156, 274-282

N-myristoylation sites.

amino acids 10-16, 20-26, 63-69, 208-214

Amidation site.

amino acids 10-14

Glycoprotein hormones beta chain signature 1.

amino acids 230-237

FIGURE 135

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTG
CTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGG
GAGTGGGGTCCGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGC
CTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAG
ACAGATGGGAGTTTTGTGGTTCATGATATACTTCTGGATCTTATGTAGTGGAAGTTGTATCTCC
AGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCAAGATATG
TGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT
CCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTCTAATGAACCCAATGGT
TATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATTCCAACCATGAGTTGCCTGAT
GTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTGGCAAATCTAGCAGCGGCAGCAG
TAAACAGGCAAAAGTGGGGCTGGCAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTTCGCAC
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAACCGTGTGAAGCAACTACTATAAACTT
GAGTCATCCCGACGTTGATCTCTTACAACGTGTGTATGTT
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGTAT
GAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAATTAT
ATGAACTACTATACATTATGTATATTAATTAAACATCTTAATCCAGAAATCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAA

FIGURE 136

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPDWISAA
RVLVDGEEHVGFLLKTDGSFVVHDIPSGSYVVEVVSPAYRFDVVRVDITSKGKMRARYVNYIKTSE
VVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLI FVLLPKVVNTSDPDMRREME
QSMNMLNSNHELPDVSEFMTRLFSSKSSSGKSSSGSSKTGKSGAGKRR

Important features of the protein:

Signal sequence:

amino acids 1-23

Transmembrane domain:

amino acids 161-182

N-glycosylation site.

amino acids 184-187

Glycosaminoglycan attachment sites.

amino acids 37-40, 236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 151-154

N-myristoylation sites.

amino acids 33-38, 36-41, 38-44, 229-234

Amidation site.

amino acids 238-241

ATP/GTP-binding site motif A (P-loop).

amino acids 229-236

FIGURE 137

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGA
CCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAAACAA
GTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC
CTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGC
CACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAGGCTTGGCAGT
TTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCCTAAGATGAAAGCCTCTAGTCTTGCCTTCAGC
CTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACACTCAATTTGGG
AAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGTG
TGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACA
AAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGACAGGGTATTTAA
AACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCTTTCTTA
CCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACATGCCATTGTGGGGAGGAAGCAATG
AAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC
TTTGGGGGAAGTAGACATTCTTCTGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTG
CTGCTAAGAATATTGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAA
ACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTG
CTTCCTTGCATGATTGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTT
TGTAATATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTA
ATGTATTTATTTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTG
ACTAGAGCAGGTGATGTATTTTTATACAGTAAAAAAAAAAAAACCTTGTAATTCTAGAAGAGTGG
CTAGGGGGGTTATTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGAT
ATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATTGCAC
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAG
CCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAA
AAAAAAAAAA

FIGURE 138

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGATTTCATNSHSDSELRPEIF
SSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG
FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS
SLANSFLTIKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET
E

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 139

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCAGCC
 TAGCGTGTCCACGATGCGGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCGAGGTGC
 TAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTTCGTTCTCTGCCAGAGCGGAA
 CACGGAGCGGAGCCCCCAGCGCCCCGAACCCTCGGCTGGAGCCAGTTCTAACTGGACCACGCTGCC
 ACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAGATGATTTTGTGTTTG
 GGTCAAAGGGTGTGAAATTTATGCCCTACACAACTTACCTTGTGGAAAAAGGAGCATCTCACAGT
 TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCATTGATGACGGGGAG
 CCTTCCTGGCTTTTGTGACGTCATCAGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGA
 TAAGACAAGCAAAAGCAGCTGGAAAAAGAATAGTCTTTTATGGAGATGAAACCTGGGTAAATTA
 TTCCCAAAGCATTTTGTGGAATATGATGGAACAACCTCATTTTTTCGTGTCAGATTACACAGAGGT
 GGATAATAATGTCACGAGGCATTTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAATCC
 TCCACTACCTGGGGCTGGACCACATTGGCCACATTTAGGGCCCAACAGCCCCCTGATTGGGCAG
 AAGCTGAGCGAGATGGACAGCGTGCTGATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGA
 GACGCCTTTACCCAATTTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACG
 GGGCCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCCTGCGTTTGAAAGGAAA
 CCCGGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTGGCTGCGACACTGGCGATAGC
 ACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCCAGTTGTGGAAGGAAGAC
 CAATGAGAGAGCAGTTGAGATTTTTACATTTGAATACAGTGCAGCTTAGTAACTGTTGCAAGAG
 AATGTGCCGTCATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAATGTCAGAAAGATTGCATGG
 GAACTGGATCAGACTGTACTTGGAGGAAAAGCATTCAGAAGTCTATTCAACCTGGGCTCCAAGG
 TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCAG
 TTCTCACCCCTGCTCCTGCTCAGCGTCCCACAGGCAGTGCACAGAAAGGCTGAGCTGGAAGTCCCA
 CTGTCATCTCCTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTTCGGCCGTTACGCT
 CATTGTGTGCACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGCAGGCT
 GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGGCAGTGCCCTGGAC
 AGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTGTCCCGACACAGGTG
 TTCACATCTGTGCTGTGAGGTGAGTGCCTCAGTTCTTGGAAGCTAGGTTCTGCGACTGTTAC
 CAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAA
 TCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAAGAGACAATCGGCCTGGA
 CACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCACTCATCCTGCCACCCCCAGAATGCATCCT
 GCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGACGTTTTCTGTTGGAATTCTTAGTCCTTGGCC
 TCGGACACCTTCATTTCGTTAGCTGGGGAGTGGTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCAC
 ACTCAGATCCACAGAGCCCAGGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCC
 ACCCCAACCCTGCACAGCCCTCATCCCCTCTTGGCTTGAGCCGTGAGAGGCCCTGTGCTGAGTGT
 CTGACCGAGACACTCACAGCTTTGTATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTG
 CCACGCTTGCACCTCGGGCCCCTCTGGGCTCATGCTCTCTCTCCTGCTATTGAATTAGTACCTAG
 CTGCACACAGTATGTAGTTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

FIGURE 140

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTLPPPLF
SKVVIVLIDALRDDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF
VDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWWKLFPKHFVEYDGTTSFFVSDYTEVDNNV
TRHLDKVLKRGDWDILILHYLGLDGHIGHISGPN SPLIGQKLSEMDSVLMKIHTSLQSKERETPLP
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

FIGURE 141

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAAC
TCCCTATAGAAAACAACTGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC
CCGAAGAAATTCAGCATTTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT
AGCAGTTCCAGATAAAAACTACATACGCCCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTAAAGGGGAGTTTTGTCTCTAC
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCT
GGCTGCCCCAAAAGGAATCAGCACGCCGGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCCTGGA
ACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTTCAACCAGTTTGCAA
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAACTGCCCCATTGAACGCCTTCCTCGCTA
ATTTGAACTAATTGTATAAAAACACCAAACCTGCTCACT

FIGURE 142

MLLLLLLEYNFPIENNCQHLKTTHTFRVKNLNPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEI
FFALASSLSSASAEGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFI
FYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDFENRKHIEFSFQPVCKAEMSPSEVSD

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 33-36

N-myristoylation site.
amino acids 50-55, 87-92

Interleukin-1
amino acids 37-182

FIGURE 144

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY
YAYRLGHILNSWKEQVESKTVFSMELLLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP
WMTQFSLLNKTCLEGFH

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 117-121, 139-143

N-myristoylation site.

amino acids 9-15

FIGURE 145

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGAAG
CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGGTCCA
GACGAGGGGCATCAAGCACAGAATCAAGTGAACCGGAAGGCCCTGCCCAGCACTGCCCAGATCA
CTGAGGCCCAGGTGGCTGAGAACCGCCCGGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCTGCATCAATGCCA
CCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGGAGAGGGGCGCAGGACT
TCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAAT
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT
CTTCTCCCCCAAACCCACGCGTGTCTGAAGGTGCCCAGGAGCGGCGATGCACTCGCACTGCAAA
TGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT
CCGTCACTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT
GAGAAGAACACATCAGGCACTGCGCCACCTGCTTCACAGTACTTCCCAACAACCTCTTAGAGGTAG
GTGTATTCCCGTTTTACAGATAAGGAAACTGAGGCCCAGAGAGCTGAAGTACTGCACCCAGCATC
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCTGGCTTGTCTAACCCAGGTTTTCTGCTCT
GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAAACATGTAT
CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

FIGURE 146

MRKHLSWWLATVCMLLFSHL SAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNKLHQQ
VLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWL MVK

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

FIGURE 147

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCATTT
CCTGATGATTTATAGACTCAAAGAAAACTGTTTCAGAAGCTCTCTTCTCTTCTGGCCTCCTCT
CTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG
AAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCAGTCTTAGTTTTATTTTTGAAATTT
CAACTTTCAGATTCAGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCATGATGCTGAGG
TTTGGGGT

FIGURE 148

MFRSSLLFWPPLCLLSLELLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE
GLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

FIGURE 149

GTCTCCGCGTCACAGGAACTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGACTTGAC
TCCCGCGCGCCCCAACCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGCCGCCAGTCC
CGGCCCCCTCTCCCGCCCCACACCCACCTCCTGGCTCTTCTGTTTTTACTCCTCCTTTTCATTCTATA
ACAAAAGCTACAGCTCCAGGAGCCAGCGCCGGGCTGTGACCCAAGCCGAGCGTGGAAGAATGGGGTT
CCTCGGGACCGGCACCTGGATTCTGGTGTTAGTGCTCCCGATTCAAGCTTTCCCCAACCTGGAGGAA
GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA
GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAACAAGCCAGGTGAGAGCAACTATTCTTT
TGTTGATAACTTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTA
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAAGT
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA
TCAACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAG
AAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAAACTACTTAATCTCGGCCTTATCACAGAAAGC
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCCAACAA
TTATGAGGAGGATCCCAATAAGCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG
TGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA
TTAACCTTGACAAATGGCTTGGAAGGAGAACTAAACCTACAGTGAAGACAACCTTTGAGGAACTCCA
ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTGAGAAAAAGAAGCAAAAGAGAAAGAAA
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCT
CCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCT
AGAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAA
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAA
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC
CATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGGAAATAAAGAAGATTATGACCTTT
CAAAGATGAGAGACTTCATCAATAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA
GAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAAATGGCAAAGATCCAGGAGTCTTTCAA
CTGTTTCAGAAAACATAATATAGCTTAAAACACTTCTAATTCTGTGATTAAATTTTTTGACCCAAGG
GTTATTAGAAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCC
GTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 150

MGFLGTGTWILVLVLPIQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE
VLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNTLTLTNGLE
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV
SYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLSKMRDFINKQADAYVEKGILDK
EEAEAIKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

FIGURE 151

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTCAA
GATGGTCTCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC
ATAATAACCAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGC
GTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGGAAG
CCAGTGCCTGTCTATGTGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG
AGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGGCGGGACATGGGGCTCACC
TCCAGCTTCGAGTCGGCTGCCTACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCC
TGTCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTCTACTTCC
AGCAGTGTGACT**TAG**GGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGT
GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTCTGCTCTCAGGACCCCCACGTCTGACTTAG
TGGGCACCTGACCACTTTGTCTTCTGGTTCCCAGTTTGGATAAATTCTGAGATTTGGAGCTCAGT
CCACGGTCTCTCCCCACTGGATGGTGCTACTGCTGTGGAACCTTGTA AAAACCATGTGGGGTAAA
CTGGGAATAACATGAAAAGATTTCTGTGGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCTCTGT
TAATGGTAACCTGACAAGTGTTACCCTGAGCCCCGCAGGCCAACCCTCCAGTTGAGCCTTATA
GGGTGAGTAGCTCTCCACATGAAGTCTGTCACTCACCCTGTGCAGGAGAGGGAGGTGGTCATA
GAGTCAGGGATCTATGGCCCTTGGCCCAGCCCCACCCCTTCCCTTTAATCCTGCCACTGTCTATA
TGCTACCTTTTCTATCTCTTCCCTCATCATCTTGTTGTGGGCATGAGGAGGTGGTGATGTGAGAA
GAAATGGCTCGAGCTCAGAAGATAAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAA
GATACAATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGCTCATGACATATTGAGA
AGACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAATTA AAAAGATACCTATTTATATATT
TCTTTATAGAAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTGAGGGTGGTGGCAGTAT
AGGTGATTTTTCTTTTAATTCTGTTAATTTATCTGTATTTCTTAATTTTTCTACAATGAAGATGA
ATTCTTGTATAAAAATAAGAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA
TTGTCTCAGCCTCCACTTCCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG
TTGTAGTAGTGTATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT
GTGGCTGGAATCTCTGGGTAAAGGAACCTAAAGAACAAAAATCATCTGGTAATTTCTTCTAGAAAG
GATCACAGCCCCCTGGGATTCCAAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA
ATTGTGTCCCCCTCAAATTCACATCCTTCTTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAG
GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATTCATAT
GACTGGTTTTCTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA
AAGATGAAGGCAGAGATCGGAGTTTTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC
ATCAGAAGCTTGGAAGAGGCAAAGAAGATTCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG
CTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGAATAAATTTTCGGCTGTTTTAA
GCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAAACTAATACAGCTGCTAAAATGATCCCTGT
CTCCTCGTGTTTACATTCTGTGTGTGTCCCCTCCACAATGTACCAAAGTTGTCTTTGTGACCAA
TAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTC
TACTTGAGCCCTCTCTCTCTGCCACCCACCGCCCCCAATCTATCTTGGCTCACTCGCTCTGGGGG
AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAAATGAAGTCTCCT
GCCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT
AAGTTGCTCAGTTTTGGTCTAACTTGTTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG

FIGURE 152

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEETISVVPNRWLDASLSPVILGVQGGG
QCLSCGVGQEP TLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP
VRLTQLPENGGWNAPITDFYFQQCD

N-myristoylation sites.

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

Interleukin-1 signature.

amino acids 111-131

Interleukin-1 proteins.

amino acids 8-29, 83-120, 95-134, 64-103

FIGURE 153

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAAGTTGCTCGAGTTAGAATTGTCTGCAATATGGCCGC
CCTGCAGAAATCTGTGAGCTCTTTCCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTCTCTTGG
CCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAAC
TTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA
CAACACAGACGTTCTGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT
ATCTGATGAAGCAGGTGCTGAACCTTACCCTTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTTCT
CAGCCTTATATGCAGGAGGTGGTGCCCTTCCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTTGCTGTTTATGTCTCTGAGAAAT
GCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTCCCTGCTAGAAATAA
CAATTAGATGCCCCAAAGCGATTTTTTTTAAACCAAAGGAAGATGGGAAGCCAACTCCATCATG
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTTTATA
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTCATTGTAACTGGTGTTCT
TATACACAGAAAACAATTTATTTTTTAAATAATTGTCTTTTTCCATAAAAAAGATTACTTTCCAT
TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAA
TGTATTTATTATTATTATAAGACTGCATTTTATTATATCATTTTATTAATATGGATTTATTTAT
AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT
AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGATATCCC

FIGURE 154

MAALQKSVSSFLMGTLATSCLLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL
ADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLFPPQSDRFQPYMQEVVPFLARLSNRLS
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

FIGURE 155

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT
CAGTCAGTGCCCGACTTGTGACTGAGTGTGCAGTGCCCGAGCATGTACCAGGTCAGTGCAGAGGGC
TGCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC
TGCCAGGTTTGGGGCTGGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGAT
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCCTACAGGTGGTTGCAT
TCTTGCCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCAGCTGCTGCCCCAGCAAAGGG
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCCTAGAGCCTGCTAG
GCCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCT
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGACCTGTACCACGCCCCGT
TGCCTGTGCCCCGCACTGCGTCAGCCTACAGACAGGCTCCACATGGACCCCCGGGGCAACTCGGA
GCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCCACA
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTTCCTTAGCTTGTGTGTGTGCGGCCCCGT
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTTGGGAAACCTGGAGCCAGGTGTACA
ACCACTTGCCATGAAGGGCCAGGATGCCAGATGCTTGGCCCCGTGTAAGTGCTGTCTGGAGCAG
CAGGATCCCGGGACAGGATGGGGGGCTTTGGGGAAAACCTGCACTTCTGCACATTTTGAAAAGAG
CAGCTGCTGCTTAGGGCCGCCGAAGCTGGTGTCTGTCAATTTCTCTCAGGAAAGGTTTTCAA
GTTCTGCCCATTTCTGGAGGCCACCACTCCTGTCTCTTCCTCTTTCCCATCCCCTGCTACCCTG
GCCCAGCACAGGCATTTCTAGATATTTCCCCCTTGCTGGAGAAGAAAGAGCCCCCTGGTTTTATT
TGTTTGTTTACTCATCACTCAGTGAGCATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTT
TTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTTATCCAAATAAATAT
CTTTATTTAAAAATGAAAAA

FIGURE 156

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHYSHWPSCCPSKGQDTSEELLRWSTVPVPPLEPA
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPDLYHARCLCPHCVSLQTGSHMDPRGNS
ELLYHNQTVFYRRPCHGEKGTHTKGYCLERRLYRVSLACVCVRPRVMG

Important features of the protein:

Signal peptide:

amino acids 1-32

N-glycosylation site.

amino acids 136-140

Tyrosine kinase phosphorylation site.

amino acids 127-135

N-myristoylation sites.

amino acids 44-50, 150-156

FIGURE 157

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC
GACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAAGTAGTGTGCAACAGGGGACTATTCA
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAGGCCACCAA
GATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGTGAGGTGCAATTACACAGAGG
CCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCTACATCGGCTTCCCTGTA
GAGCTGAACACAGTCTATTTTATTGGGGCCATAATATTCTAATGCAAATATGAATGAAGATGG
CCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAAA
AGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACA
GTAGAAGTGAACCTCACAACCACTCCCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCAC
TATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA
TTCCAGTGAAGTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGC
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCT
GGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCA
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT
TCTACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCA
TCACACAATTTGTTACTTCACTGAATTTCTTCAAACCATTCGAGAAGTGAGGTCATCCTTGAAA
AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCA
GCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA
GAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCCTTTAACCTTTTCTGCA
GTGATCTAAGAAGCCAGATTCATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA
AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTGAGCAGGAAAAAGATCACAAAGCCTGCCACG
ATGGCTGCTGCTCCTTGTAG

FIGURE 158

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPGLRDLRVEPVTTSVATGDYSILMNVS
WVLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFYSYIGFFVELNTVYFIGAHNIP
NANMNEDGPSMSVNFSTPGCLDHIMKYKKKCKVAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQH
STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVPFPLDNNK
SKPGGWLPLLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL
QNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHVKKQVVSAGKRSQACHD
GCCSL

Important features of the protein:

Signal peptide:

amino acids 1-14

Transmembrane domain:

amino acids 290-309

N-glycosylation sites.

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283
- 287

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 228 - 232 and 319 - 323

Casein kinase II phosphorylation sites.

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

N-myristoylation site.

amino acids 116-122

Amidation site.

amino acids 488-452

FIGURE 159

AGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT
GTCGATATTGGGGCTTGCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA
CTTTTTTCCAAAAGCCTGAGAGTTGCCCCGCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC
ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG
GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAAGTGTAGGA
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAA
GAGACCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCT
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTAAGAGGTGCATATCC
ACTCAGCTGAAGAAG

FIGURE 16o

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN
QRVMSRNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRNLGCINAQGKEDISMNSVPIQQETLVV
RRKHQGC SVSFQLEKVLVTVGCTCVTPVIHHVQ

Signal sequence:

amino acids 1-30

N-glycosylation site.

amino acids 83-87

N-myristoylation sites.

amino acids 106-111, 136-141

FIGURE 161

A C A C T G G C C A A A C A A A A C G A A A G C A C T C C G T G C T G G A A G T A G G A G G A G A G T C A G G A C T C C C A G G
 A C A G A G A G T G C A C A A A C T A C C C A G C A C A G C C C C C T C C G C C C C C T C T G G A G G C T G A A G A G G A T T C
 C A G C C C C T G C C A C C C A C A G A C A C G G G C T G A C T G G G G T G T C T G C C C C C C T T G G G G G G G G C A G C A C
 A G G G C C T C A G G C C T G G G T G C C A C C T G G C A C C T A G A A G A T G C C T G T G C C C T G G T T C T T G C T G T C C T
 T G G C A C T G G G C C G A A G C C C A G T G G T C C T T T C T C T G G A G A G G C T T G T G G G G C C T C A G G A C G C T A C C
 C A C T G C T C T C C G G G C C T C T C C T G C C G C C T C T G G G A C A G T G A C A T A C T C T G C C T G C C T G G G G A C A T
 C G T G C C T G C T C C G G G C C C C G T G C T G G C G C C T A C G C A C C T G C A G A C A G A G C T G G T G C T G A G G T G C C
 A G A A G G A G A C C G A C T G T G A C C T C T G T C T G C G T G T G G C T G T C C A C T T G G C C G T G C A T G G G C A C T G G
 G A A G A G C C T G A A G A T G A G G A A A A G T T T G G A G G A G C A G C T G A C T C A G G G G T G G A G G A G C C T A G G A A
 T G C C T C T C T C C A G G C C C A A G T C G T G C T C C T T C C A G G C C T A C C C T A C T G C C C G C T G C G T C C T G C
 T G G A G G T G C A A G T G C C T G C T G C C C T T G T G C A G T T T G G T C A G T C T G T G G G C T C T G T G G T A T A T G A C
 T G C T T C G A G G C T G C C C T A G G G A G T G A G G T A C G A A T C T G G T C C T A T A C T C A G C C C A G G T A C G A G A A
 G G A A C T C A A C C A C A C A C A G C A G C T G C C T G C C C T G C C C T G G C T C A A C G T G T C A G C A G A T G G T G A C A
 A C G T G C A T C T G G T T C T G A A T G T C T C T G A G G A G C A G C A C T T C G G C C T C T C C C T G T A C T G G A A T C A G
 G T C C A G G G C C C C C A A A A C C C C G G T G G C A C A A A A C C T G A C T G G A C C G C A G A T C A T T A C C T T G A A
 C C A C A C A G A C C T G G T T C C C T G C C T C T G T A T T C A G G T G T G G C C T C T G G A A C C T G A C T C C G T T A G G A
 C G A A C A T C T G C C C T T C A G G G A G G A C C C C G C G C A C A C C A G A A C C T C T G G C A A G C C G C C C G A C T G
 C G A C T G C T G A C C C T G C A G A G C T G G C T G C T G G A C G C A C C G T G C T C G C T G C C C G C A G A A G C G G C A C T
 G T G C T G G C G G G C T C C G G G T G G G G A C C C C T G C C A G C C A C T G G T C C C A C C G C T T T C C T G G G A G A A C G
 T C A C T G T G G A C A A G G T T C T C G A G T T C C A T T G C T G A A A G G C C A C C C T A A C C T C T G T G T T C A G G T G
 A A C A G C T C G G A G A A G C T G C A G C T G C A G G A G T G C T T G T G G G C T G A C T C C C T G G G G C C T C T C A A A G A
 C G A T G T G C T A C T G T T G G A G A C A C A G A G C C C C C A G G A C A A C A G A T C C C T C T G T G C C T T G G A A C C C A
 G T G G C T G T A C T T C A C T A C C C A G C A A A G C C T C C A C A G A G G G C A G C T C G C C T T G G A G A G T A C T T A C T A
 C A A G A C C T G C A G T C A G G C C A G T G T C T G C A G C T A T G G G A C G A T G A C T T G G G A G C G C T A T G G G C C T G
 C C C C A T G G A C A A A T A C A T C C A C A A G C G T G G G C C C T C G T G T G G C T G G C C T G C C T A C T C T T T G C C G
 C T G C G C T T T C C C T C A T C C T C C T T C T C A A A A A G G A T C A C G C G A A A G G G T G G C T G A G G C T C T T G A A A
 C A G G A C G T C C G C T C G G G G G C G G C C G C C A G G G G C C G C G C G G C T C T G C T C C T C T A C T C A G C C G A T G A
 C T C G G G T T T C G A G C G C C T G G T G G G C G C C C T G G C G T C G G C C C T G T G C C A G C T G C C G C T G C G C G T G G
 C C G T A G A C C T G T G G A G C C G T C G T G A A C T G A G C G C G C A G G G G C C C G T G G C T T G G T T T C A C G C G C A G
 C G G C G C C A G A C C C T G C A G G A G G G C G G C G T G G T G G T C T T G C T C T T C T C T C C C G G T G C G G T G G C G C T
 G T G C A G C G A G T G G C T A C A G G A T G G G G T G T C C G G G C C C G G G G C G C A C G G C C C G C A C G A C G C C T T C C
 G C G C C T C G C T C A G C T G C G T G C T G C C C G A C T T C T T G C A G G G C C G G G C G C C C G G C A G C T A C G T G G G G
 G C C T G C T T C G A C A G G C T G C T C C A C C C G G A C G C C G T A C C C G C C C T T T C C G C A C C G T G C C C G T C T T
 C A C A C T G C C C T C C C A A C T G C C A G A C T T C C T G G G G G C C C T G C A G C A G C C T C G C G C C C C G C G T C C G
 G G C G G C T C C A A G A G A G A G C G G A G C A A G T G T C C C G G G C C C T T C A G C C A G C C C T G G A T A G C T A C T T C
 C A T C C C C C G G G G A C T C C C G C G C C G G G A C G C G G G T G G G A C C A G G G G C G G G A C C T G G G G C G G G G G A
 C G G G A C T T A A A T A A A G G C A G A C G C T G T T T T C T A A A A A A

FIGURE 162

MPVPWFLLSLALGRSPVVLRLERLVGPQDATHCSPGLSCRLWSDILCLPGDIVPAPGPVLAPTHLQTELV
LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSTQAYPTARCVLLEV
QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVVSADGDNVHLVLNV
EEQHFGLSLYWNQVQGPVKPRWHKNLTGPGQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQ
LWQAARLRLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ
VNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYLLQDLQS
GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLKQDVRSGAAARG
RAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVFHAQRRQTLQEGGVVLLFSP
GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLHLPDAVPALFRTVPVFT
LPSQLPDFLGALQQPRAPRSRGLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

Signal sequence:

amino acids 1-20

Transmembrane domain.

amino acids 453-475

N-glycosylation sites.

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,
334-337, 357-360, 391-394

Glycosaminoglycan attachment site.

amino acids 583-586

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 552-555

N-myristoylation sites.

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,
692-697, 696-701, 700-705

FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGCTGACCATCTTGACTGTGGGATCCCTGGCT
GCTCACGCCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCAGTCCAGCAACTTTGA
AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA
AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTCAGCGGATCACCCGGAAGTCCTGC
AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT
GTCAGTGCGGGAGGGCCGGTCAGCCACCAAGATGACTGACAGGTTGAGCTCTCTGCAGCACACTAC
CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTGAGATGATTGTTTCATCCTA
CCCCACGCCAATCCGTGCAGGCGATGGCCACCGGCTAACCCCTGGAAGACATCTTCCATGACCTG
TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAGCAGAGAGA
ATATGAGTTCTTCGGCCTGACCCCTGACACAGAGTTCCCTTGGCACCATCATGATTTGCGTTCCCA
CCTGGGCCAAGGAGAGTGCCCCCTACATGTGCCGAGTGAAGACACTGCCAGACCGGACATGGACC
TACTCCTTCTCCGGAGCCTTCCCTGTTCTCCATGGGCTTCCCTCGTCGCAGTACTCTGCTACCTGAG
CTACAGATATGTACCAAGCCGCCTGCACCTCCCAACTCCCTGAACGTCCAGCGAGTCTGACTT
TCCAGCCGCTGCGCTTCATCCAGGAGCACGTCTGATCCCTGTCTTTGACCTCAGCGGCCCCAGC
AGTCTGGCCCAGCCTGTCCAGTACTCCAGATCAGGGTGTCTGGACCCAGGGAGCCCGCAGGAGC
TCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCCTCCAGC
CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCTATGCCCCAAACGCTGCCCCCTGAG
GTCGGGCCCCCATCCTATGCACCTCAGGTGACCCCCGAAGCTCAATTCCCATTCTACGCCCCACA
GGCCATCTCTAAGGTCCAGCCTTCCCTCCTATGCCCCCAAGCCACTCCGGACAGCTGGCCTCCCT
CCTATGGGGTATGCATGGAAGGTTCTGGCAAAGACTCCCCCACTGGGACACTTTCTAGTCTTAAA
CACCTTAGGCCTAAAGGTCAGCTTCAGAAAGAGCCACCAGCTGGAAGCTGCATGTTAGGTGGCCT
TTCTCTGCAGGAGGTGACCTCCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATTGCACCAGC
CCCTGGGGATTGTGCACAGACAGAACATCTGACCCAAATGTGCTACACAGTGGGGAGGAAGGGACA
CCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCTCCTCAGTCCAGATCGAGGGGCCACCCCATGTC
CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC
TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCCAGCCCCCTGAGACCTCAGACCTG
GAGCAGCCCACAGAACTGGATTCTCTTTTCAGAGGCCTGGCCCTGACTGTGCAGTGGGAGTCTCTG
AGGGGAATGGGAAAGGCTTGGTGCTTCCCTCCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCA
ATCCCATGCCTGCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC
AGAGGGAGTGGCATGCAGGGCCCCCTGCCATGGGTGCGCTCCTCACCGGAACAAAGCAGCATGATA
AGGACTGCAGCGGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGCGTGCTCGCTGAGCCCTG
CAAGGCAGAAATGACAGTGCAGGAGGAAATGCAGGGAAACTCCCGAGGTCCAGAGCCCCACCTC
CTAACACCATGGATTCAAAGTGCTCAGGGAATTTGCCTCTCCTTGCCCCATTCCTGGCCAGTTTC
ACAATCTAGCTCGACAGAGCATGAGGCCCCCTGCCTCTTCTGTCAATTGTTCAAAGGTGGGAAGAGA
GCCTGGAAAAGAACCAGGCCTGGAAAAGAACCAGAAGGAGGCTGGGCAGAACCAGAACAACCTGC
ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCCTGCAGCTCA
TTCCAGCCAGGGCAACTGCCTGACGTTGCACGATTTAGCTTCATTCTCTGATAGAACAAGC
GAAATGCAGGTCCACCAGGGAGGGAGACACACAAGCCTTTTCTGCAGGCAGGAGTTTCAGACCCT
ATCCTGAGAATGGGGTTTGAAAGGAAGGTGAGGGCTGTGGCCCCCTGGACGGGTACAATAACACAC
TGTACTGATGTCACAACTTTGCAAGCTCTGCCTTGGGTTGAGCCCATCTGGGCTCAAATTCAGC
CTCACCCTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCCAAGAACCTCGGTTTCCTC
ATCTGTAATGTGGGGATCATAACACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG
TCTTTAAAGTGCTTAATAGTGCCCTGGTACATGGGCAGTGCCCAATAAACGGTAGCTATTTAAAAA
AAAAAAA

FIGURE 164

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW
VAKKGCQRITRKSCNLTVETGNLTLEYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVTCIS
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMH LGGKQREYEFFGLTPDT
EFLGTIMICVPTWAKESAPYMC RVKTL PDRTWTYSFSGAFLFSMGFLVAVLCYLSYRYVTKPPAP
PNSLNVQRVLTFQPLRFIQEHVLIPVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFPFYAPQAISKVQPSSY
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLQKEPPAGSCMLGGLSLQEVTSLAM
EESQEAKSLHQPLGICTDR TSDPNVLHSGEETPQYLKGQLPLLSSVQIEGHPMSLPLQPPSGPC
SPSDQGPSPWGLLES LVC PKDEAKSPAPETSDLEQPTELDSLFRGLALTVQWES

Signal sequence.

amino acids 1-17

Transmembrane domain.

amino acids 233-250

N-glycosylation sites.

amino acids 80-83, 87-90, 172-175

N-myristoylation sites.

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

FIGURE 165

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCGCGGTGGCCACAACATGG
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGGCCAG
TCGGATCTCAGCCACGGACGGCGTTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT
GTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGTGAATTTTA
AAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAACTTTGGGCTGGA
AGTGTGTAACACAGTTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCATAAATACACGGA
AGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGGAGGAAGAGATGATT
TTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAACTGGAGGACTCTGTACCTGAAGAG
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA
ACTTGACCTGTGCCTGAGCCCGAGGCATTTCAGAGCTGATTTCAGAGGATGGAGAAGGTGCTTTCT
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCTCACACCAGCGGT
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATTCTGCACGATAA
ATTGAAAGTGCCGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCATTATT
CATTACAGCAAAGGATTTTCGTTGGCATCAAATCTAAGTTTGTTTTACAAAGATTGTTTTTTAGTA
CTAAGCTGCCTTGGCAGTTTGCATTTTGGAGCCAAACAAAAATATATTATTTCCCTTCTAAGTA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 166

MAAAPGLLFWLFLVGLALWWVPGQSDLSHGRRFSDLKVCGDEEC SMLMYRGKALEDFTGPDCRFVN
FKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADETDFVCFEGGRD
DFNSYNVEELLGSLELED SVPEESKKAEEVSQHREKSPEESRGRELDPVPEPEAFRADSEDGEGA
FSESTEGLOGQPSAQESH PHTSGPAANAQGVQSSLDTFEEILHDKLKVP GSESRTGNSSPASVER
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNL SLFYKDCF

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34

tyrosine kinase phosphorylation site.

amino acids 67-76

N-myristoylation sites.

amino acids 205-211, 225-231, 277-283

Amidation site.

amino acids 28-32

FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAGAGGCCGGGGAAGAGAAGCAAAGCGC
AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCTAACTTC
AGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGGCACAGG
CGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTCGGGCAGCTGGGCTCGGGC
GGCGGGAGTAGGGCCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTCGCGGGCTGCGCCCTG
GGCAGAGGCCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGATGAGCCGCGTGG
TCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCCGCCGCGTGGTCAGC
GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGAACT
GTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCCTGGCTTGTGAGAGTGAGGGAGGAGTCCCTCTCA
GCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG
ACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTGGAGGAATGGAGATGGGCAAACATCTGG
TGCCTGCCAGATCTCTACAGTGGTCTGATGGAAGCAATCCCAGTACCGAACTGGTACACAG
ATGAACCTTCCCTGCGGAAGTGAAAAGTGTGTTGTGATGTATCACCACCAACTGCCAATCCTGGC
CTTGGGGGTCCCTACCTTTACAGTGGAAATGATGACAGGTGTAACATGAAGCACAATTATATTTG
CAAGTATGAACCAGAGATTAATCCAACAGCCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAG
GAGACCCCATCAGAATGTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTT
ATACCAACAATACCCCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTGTTTCCAGATGCT
GCATAAAAGTAAAGGAAGAACAACAACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTA
CCAGAAAAGAAAGTGGCATGGAAGTATAATAAATCACTGACTTGGTTCCAGAAATTTGTAATTCT
GGATCTGTATAAGGAATGGCATCAGAACAAATAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGC
AAGATGAACTGTAAGCTCCCCCTTGAGGCAAATATTAAAGTAATTTTATATGCTATTATTTCA
TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGTAAAGGATGCACCCAA
ACTTCAAACCTTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTA
TGTGTGTTAGAAGCAATTCCTTTTATTTCTTTTACCTTTCATAAGTTGTTATCTAGTCAATGTAA
TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTTTGATAAAA
ATGAACTGTTCTAATATTTATTTTATGGCATCTCATTTTCAATACATGCTCTTTTGATTAAAG
AACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGT
TTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGA
AATAAGAAGCTATTTTCAATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGAT
TGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTGTAGCTTAAATTTAAACAGATT
TTGTAATAATGTAACCTTTGTTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAG
TGACATACACAATATAAATCATATGTCTTCACACGTTGCCATATAATGAGAAGCAGCTCTCTGA
GGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTTCGGGGTTTGGG
ATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTG
ACTATATTAGTATACAAAGAGGTGATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG
ACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACTACGAAATCGTGTGAAAATGGGTTGG
AACCCATCAGTGATCGCATATTCATTGATGAGGGTTTGCTTGAGATAGAAAATGCTGGCTCCTTT
CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTTCTTCTCAAGAGAAAGTTGTAACCTCT
CTGGTCTTCATATGTCCCTGTGCTCCTTTTAACCAAATAAAGAGTTCTTGTCTTCTGGGGGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 168

MSRVVSLLLGAALLCGHGAFCRRVVSQGKVCFADFKHPCYKMAYFHELSSRVSFQEARLACESE
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDFWIGLWRNGDGQTSGACPDLYQWSDGSNSQ
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAPVEK
PYLTNQPGDTHQNVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKS KGRTKTS PNQ
STLWISKSTRKESGMEV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89, 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-
145, 212-217

**SECRETED AND TRANSMEMBRANE
POLYPEPTIDES AND NUCLEIC ACIDS
ENCODING THE SAME**

**CROSS REFERENCE TO RELATED
APPLICATIONS**

[0001] This is a continuation application claiming priority under 35 USC § 120 to U.S. Ser. No. 10/006867 Filed Dec. 6, 2001, and which claims priority under 35 USC § 119 to U.S. provisional serial Nos. 60/063,435 Filed Oct. 29, 1997; 60/064,215 Filed Oct. 29, 1997; 60/082,797 Filed Apr. 22, 1998; 60/083,495 Filed Apr. 29, 1998; 60/085,579 Filed May 15, 1998; 60/087,759 Filed Jun. 2, 1998; 60/088,021 Filed Jun. 4, 1998; 60/088,029 Filed Jun. 4, 1998; 60/088,030 Filed Jun. 4, 1998; 60/088,734 Filed Jun. 10, 1998; 60/088,740 Filed Jun. 10, 1998; 60/088,811 Filed Jun. 10, 1998; 60/088,824 Filed Jun. 10, 1998; 60/088,825 Filed Jun. 10, 1998; 60/088,863 Filed Jun. 11, 1998; 60/089,105 Filed Jun. 12, 1998; 60/089,514 Filed Jun. 16, 1998; 60/089,653 Filed Jun. 17, 1998; 60/089,952 Filed Jun. 19, 1998; 60/090,246 Filed Jun. 22, 1998; 60/090,444 Filed Jun. 24, 1998; 60/090,688 Filed Jun. 25, 1998; 60/090,696 Filed Jun. 25, 1998; 60/090,862 Filed Jun. 26, 1998; 60/091,628 Filed Jul. 2, 1998; 60/096,012 Filed Aug. 10, 1998; 60/096,757 Filed Aug. 17, 1998; 60/096,949 Filed Aug. 18, 1998; 60/096,959 Filed Aug. 18, 1998; 60/097,954 Filed Aug. 26, 1998; 60/097,971 Filed Aug. 26, 1998; 60/097,979 Filed Aug. 26, 1998; 60/098,749 Filed Sep. 1, 1998; 60/099,741 Filed Sep. 10, 1998; 60/099,763 Filed Sep. 10, 1998; 60/099,792 Filed Sep. 10, 1998; 60/099,812 Filed Sep. 10, 1998; 60/099,815 Filed Sep. 10, 1998; 60/100,627 Filed Sep. 16, 1998; 60/100,662 Filed Sep. 16, 1998; 60/100,683 Filed Sep. 17, 1998; 60/100,684 Filed Sep. 17, 1998; 60/100,930 Filed Sep. 17, 1998; 60/101,279 Filed Sep. 22, 1998; 60/101,475 Filed Sep. 23, 1998; 60/101,738 Filed Sep. 24, 1998; 60/101,743 Filed Sep. 24, 1998; 60/101,916 Filed Sep. 24, 1998; 60/102,570 Filed Sep. 30, 1998; 60/103,449 Filed Oct. 6, 1998; 60/103,678 Filed Oct. 8, 1998; 60/103,679 Filed Oct. 8, 1998; 60/103,711 Filed Oct. 8, 1998; 60/105,000 Filed Oct. 20, 1998; 60/105,002 Filed Oct. 20, 1998; 60/105,881 Filed Oct. 27, 1998; 60/106,030 Filed Oct. 28, 1998; 60/106,464 Filed Oct. 30, 1998; 60/106,856 Filed Nov. 3, 1998; 60/108,807 Filed Nov. 17, 1998; 60/112,419 Filed Dec. 15, 1998; 60/112,422 Filed Dec. 15, 1998; 60/112,853 Filed Dec. 16, 1998; 60/113,011 Filed Dec. 16, 1998; 60/112,854 Filed Dec. 16, 1998; 60/113,300 Filed Dec. 22, 1998; 60/113,408 Filed Dec. 22, 1998; 60/113,430 Filed Dec. 23, 1998; 60/113,621 Filed Dec. 23, 1998; 60/114,223 Filed Dec. 30, 1998; 60/115,614 Filed Jan. 12, 1999; 60/116,527 Filed Jan. 20, 1999; 60/116,843 Filed Jan. 22, 1999; 60/119,285 Filed Feb. 9, 1999; 60/119,287 Filed Feb. 9, 1999; 60/119,525 Filed Feb. 10, 1999; 60/119,549 Filed Feb. 10, 1999; 60/120,014 Filed Feb. 11, 1999; 60/129,122 Filed Apr. 13, 1999; 60/129,674 Filed Apr. 16, 1999; 60/131,291 Filed Apr. 27, 1999; 60/138,387 Filed Jun. 9, 1999; 60/144,791 Filed Jul. 20, 1999; 60/169,495 Filed Dec. 7, 1999; 60/175,481 Filed Jan. 11, 2000; 60/191,007 Filed Mar. 21, 2000; 60/199,397 Filed Apr. 25, 2000 and which claims priority under 35 USC § 120 to U.S. patent applications and PCT International Patent Application Serial Numbers 09/380,139 Filed Aug. 25, 1999; 09/311,832 Filed May 14, 1999; 09/380,137 Filed Aug. 25, 1999, now abandoned; 09/380,138 Filed Aug. 25, 1999, now abandoned; 09/380,142 Filed Aug. 25, 1999, now abandoned; 09/397,342 Filed

Sep. 15, 1999; 09/403,297 Filed Oct. 18, 1999, now abandoned; 09/423,844 Filed Nov. 12, 1999, now abandoned; 09/644,848 Filed Aug. 22, 2000; 09/665,350 Filed Sep. 18, 2000; 09/664,610 Filed Sep. 18, 2000, now abandoned; 09/709,238 Filed Nov. 8, 2000; 09/747,259 Filed Dec. 20, 2000; 09/816,744 Filed Mar. 22, 2001; 09/854,208 Filed May 10, 2001; 09/854,280 Filed May 10, 2001; 09/870,574 Filed May 30, 2001; 09/874,503 Filed Jun. 5, 2001; 09/908,827 Filed Jul. 18, 2001; 09/869,566 Filed Feb. 19, 2002; PCT/US98/19330 Filed Sep. 16, 1998; PCT/US99/05028 Filed Mar. 8, 1999; PCT/US99/10733 Filed May 14, 1999; PCT/US99/12252 Filed Jun. 2, 1999; PCT/US99/20111 Filed Sep. 1, 1999; PCT/US99/21090 Filed Sep. 15, 1999; PCT/US99/21194 Filed Sep. 15, 1999; PCT/US99/30720 Filed Dec. 22, 1999; PCT/US00/04341 Filed Feb. 18, 2000; PCT/US00/04342 Filed Feb. 18, 2000; PCT/US00/04414 Filed Feb. 22, 2000; PCT/US00/05601 Filed Mar. 1, 2000; PCT/US00/08439 Filed Mar. 30, 2000; PCT/US00/14042 Filed May 22, 2000; PCT/US00/15264 Filed Jun. 2, 2000; PCT/US00/23522 Filed Aug. 23, 2000; PCT/US00/23328 Filed Aug. 24, 2000; PCT/US00/30873 Filed Nov. 10, 2000; PCT/US00/32678 Filed Dec. 1, 2000; PCT/US00/34956 Filed Dec. 20, 2000; PCT/US01/06520 Filed Feb. 28, 2001; PCT/US01/06666 Filed Mar. 1, 2001; PCT/US01/17443 Filed May 30, 2001; PCT/US01/17800 Filed Jun. 1, 2001; PCT/US01/19692 Filed Jun. 20, 2001; PCT/US01/21066 Filed Jun. 29, 2001; PCT/US01/21735 Filed Jul. 9, 2001, the entire disclosures of which are hereby incorporated by reference.

BACKGROUND OF INVENTION

[0002] The present invention relates generally to the identification and isolation of novel DNA and to the recombinant production of novel polypeptides.

[0003] Extracellular proteins play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted polypeptides or signaling molecules normally pass through the cellular secretory pathway to reach their site of action in the extracellular environment.

[0004] Secreted proteins have various industrial applications, including as pharmaceuticals, diagnostics, biosensors and bioreactors. Most protein drugs available at present, such as thrombolytic agents, interferons, interleukins, erythropoietins, colony stimulating factors, and various other cytokines, are secretory proteins. Their receptors, which are membrane proteins, also have potential as therapeutic or diagnostic agents. Efforts are being undertaken by both industry and academia to identify new, native secreted proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., Proc. Natl. Acad. Sci. 93:7108-7113 (1996); U.S. Pat. No. 5,536,637].

[0005] Membrane-bound proteins and receptors can play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesion molecules like selectins and integrins. For instance, transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and nerve growth factor receptor.

[0006] Membrane-bound proteins and receptor molecules have various industrial applications, including as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

[0007] Efforts are being undertaken by both industry and academia to identify new, native receptor or membrane-bound proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins.

SUMMARY OF INVENTION

[0008] In one embodiment, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

[0009] In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic

acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

[0010] In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

[0011] In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively

at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

[0012] Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

[0013] Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide probes. Such nucleic acid fragments are usually at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule frag-

ments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

[0014] In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences hereinabove identified.

[0015] In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

[0016] In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

[0017] In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

[0018] Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

[0019] In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

[0020] In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

[0021] In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

[0022] Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as hereinbefore described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

[0023] In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

[0024] In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

[0025] In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the

above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

[0026] In yet other embodiments, the invention provides oligonucleotide probes useful for isolating genomic and cDNA nucleotide sequences or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences.

[0027] In yet other embodiments, the present invention is directed to methods of using the PRO polypeptides of the present invention for a variety of uses based upon the functional biological assay data presented in the Examples below.

BRIEF DESCRIPTION OF DRAWINGS

[0028] FIG. 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO180 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA26843-1389".

[0029] FIG. 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in FIG. 1.

[0030] FIG. 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO218 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "DNA30867-1335".

[0031] FIG. 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in FIG. 3.

[0032] FIG. 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO263 cDNA, wherein SEQ ID NO:5 is a clone designated herein as "DNA34431-1177".

[0033] FIG. 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO:5 shown in FIG. 5.

[0034] FIG. 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO295 cDNA, wherein SEQ ID NO:7 is a clone designated herein as "DNA38268-1188".

[0035] FIG. 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO:7 shown in FIG. 7.

[0036] FIG. 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO874 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA40621-1440".

[0037] FIG. 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in FIG. 9.

[0038] FIG. 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO300 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA40625-1189".

[0039] FIG. 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in FIG. 11.

[0040] FIG. 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO1864 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA45409-2511".

[0041] FIG. 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:13 shown in FIG. 13.

[0042] FIG. 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO1282 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA45495-1550".

[0043] FIG. 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in FIG. 15.

[0044] FIG. 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO1063 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA49820-1427".

[0045] FIG. 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in FIG. 17.

[0046] FIG. 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO1773 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA56406-1704".

[0047] FIG. 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in FIG. 19.

[0048] FIG. 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO1013 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNA56410-1414".

[0049] FIG. 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in FIG. 21.

[0050] FIG. 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO937 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA56436-1448".

[0051] FIG. 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in FIG. 23.

[0052] FIG. 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO842 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA56855-1447".

[0053] FIG. 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in FIG. 25.

[0054] FIG. 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO1180 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA56860-1510".

[0055] FIG. 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in FIG. 27.

[0056] FIG. 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO831 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA56862-1343".

[0057] FIG. 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in FIG. 29.

[0058] FIG. 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO1115 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA56868-1478".

[0059] FIG. 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in FIG. 31.

[0060] FIG. 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO1277 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA56869-1545".

[0061] FIG. 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in FIG. 33.

[0062] FIG. 35 shows a nucleotide sequence (SEQ ID NO:35) of a native sequence PRO1074 cDNA, wherein SEQ ID NO:35 is a clone designated herein as "DNA57704-1452".

[0063] FIG. 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35 shown in FIG. 35.

[0064] FIG. 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO1344 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA58723-1588".

[0065] FIG. 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in FIG. 37.

[0066] FIG. 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO1136 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA57827-1493".

[0067] FIG. 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in FIG. 39.

[0068] FIG. 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO1109 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA58737-1473".

[0069] FIG. 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in FIG. 41.

[0070] FIG. 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO1003 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA58846-1409".

[0071] FIG. 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in FIG. 43.

[0072] FIG. 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO1138 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA58850-1495".

[0073] FIG. 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in FIG. 45.

[0074] FIG. 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO994 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA58855-1422".

[0075] FIG. 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in FIG. 47.

[0076] FIG. 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO1069 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA59211-1450".

[0077] FIG. 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in FIG. 49.

[0078] FIG. 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO1411 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA59212-1627".

[0079] FIG. 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in FIG. 51.

[0080] FIG. 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO1129 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA59213-1487".

[0081] FIG. 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in FIG. 53.

[0082] FIG. 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO1027 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA59605-1418".

[0083] FIG. 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in FIG. 55.

[0084] FIG. 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO1106 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA59609-1470".

[0085] FIG. 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in FIG. 57.

[0086] FIG. 59 shows a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO1291 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA59610-1556".

[0087] FIG. 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in FIG. 59.

[0088] FIG. 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO3573 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA59837-2545".

[0089] FIG. 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in FIG. 61.

[0090] FIG. 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO3566 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA59844-2542".

[0091] FIG. 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in FIG. 63.

[0092] FIG. 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO1098 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA59854-1459".

[0093] FIG. 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in FIG. 65.

[0094] FIG. 67 shows a nucleotide sequence (SEQ ID NO:67) of a native sequence PRO1158 cDNA, wherein SEQ ID NO:67 is a clone designated herein as "DNA60625-1507".

[0095] FIG. 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ ID NO:67 shown in FIG. 67.

[0096] FIG. 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO1124 cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA60629-1481".

[0097] FIG. 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in FIG. 69.

[0098] FIG. 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO1287 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA61755-1554".

[0099] FIG. 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in FIG. 71.

[0100] FIG. 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO1335 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA62812-1594".

[0101] FIG. 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in FIG. 73.

[0102] FIG. 75 shows a nucleotide sequence (SEQ ID NO:75) of a native sequence PRO1315 cDNA, wherein SEQ ID NO:75 is a clone designated herein as "DNA62815-1576".

[0103] FIG. 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75 shown in FIG. 75.

[0104] FIG. 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO1357 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA64881-1602".

[0105] FIG. 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in FIG. 77.

[0106] FIG. 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO1356 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA64886-1601".

[0107] FIG. 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in FIG. 79.

[0108] FIG. 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO1557 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA64902-1667".

[0109] FIG. 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in FIG. 81.

[0110] FIG. 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO1347 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA64950-1590".

[0111] FIG. 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in FIG. 83.

[0112] FIG. 85 shows a nucleotide sequence (SEQ ID NO:85) of a native sequence PRO1302 cDNA, wherein SEQ ID NO:85 is a clone designated herein as "DNA65403-1565".

[0113] FIG. 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85 shown in FIG. 85.

[0114] FIG. 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO1270 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA66308-1537".

[0115] FIG. 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in FIG. 87.

[0116] FIG. 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO1268 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA66519-1535".

[0117] FIG. 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in FIG. 89.

[0118] FIG. 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO1327 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA66521-1583".

[0119] FIG. 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in FIG. 91.

[0120] FIG. 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO1328 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA66658-1584".

[0121] FIG. 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in FIG. 93.

[0122] FIG. 95 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO1329 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA66660-1585".

[0123] FIG. 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in FIG. 95.

[0124] FIG. 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO1340 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA66663-1598".

[0125] FIG. 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in FIG. 97.

[0126] FIG. 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO1342 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA66674-1599".

[0127] FIG. 100 shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in FIG. 99.

[0128] FIG. 101 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO3579 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA68862-2546".

[0129] FIG. 102 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in FIG. 101.

[0130] FIG. 103 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO1472 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA68866-1644".

[0131] FIG. 104 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in FIG. 103.

[0132] FIG. 105 shows a nucleotide sequence (SEQ ID NO:105) of a native sequence PRO1461 cDNA, wherein SEQ ID NO:105 is a clone designated herein as "DNA68871-1638".

[0133] FIG. 106 shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ ID NO:105 shown in FIG. 105.

[0134] FIG. 107 shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO1568 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA68880-1676".

[0135] FIG. 108 shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ ID NO:107 shown in FIG. 107.

[0136] FIG. 109 shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO1753 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA68883-1691".

[0137] FIG. 110 shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in FIG. 109.

[0138] FIG. 111 shows a nucleotide sequence (SEQ ID NO:111) of a native sequence PRO1570 cDNA, wherein SEQ ID NO:111 is a clone designated herein as "DNA68885-1678".

[0139] FIG. 112 shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111 shown in FIG. 111.

[0140] FIG. 113 shows a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO1446 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "DNA71277-1636".

[0141] FIG. 114 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in FIG. 113.

[0142] FIG. 115 shows a nucleotide sequence (SEQ ID NO:115) of a native sequence PRO1565 cDNA, wherein SEQ ID NO:115 is a clone designated herein as "DNA73727-1673".

[0143] FIG. 116 shows the amino acid sequence (SEQ ID NO:116) derived from the coding sequence of SEQ ID NO:115 shown in FIG. 115.

[0144] FIG. 117 shows a nucleotide sequence (SEQ ID NO:117) of a native sequence PRO1572 cDNA, wherein SEQ ID NO:117 is a clone designated herein as "DNA73734-1680".

[0145] FIG. 118 shows the amino acid sequence (SEQ ID NO:118) derived from the coding sequence of SEQ ID NO:117 shown in FIG. 117.

[0146] FIG. 119 shows a nucleotide sequence (SEQ ID NO:119) of a native sequence PRO1573 cDNA, wherein SEQ ID NO:119 is a clone designated herein as "DNA73735-1681".

[0147] FIG. 120 shows the amino acid sequence (SEQ ID NO:120) derived from the coding sequence of SEQ ID NO:119 shown in FIG. 119.

[0148] FIG. 121 shows a nucleotide sequence (SEQ ID NO:121) of a native sequence PRO1550 cDNA, wherein SEQ ID NO:121 is a clone designated herein as "DNA76393-1664".

[0149] FIG. 122 shows the amino acid sequence (SEQ ID NO:122) derived from the coding sequence of SEQ ID NO:121 shown in FIG. 121.

[0150] FIG. 123 shows a nucleotide sequence (SEQ ID NO:123) of a native sequence PRO1693 cDNA, wherein SEQ ID NO:123 is a clone designated herein as "DNA77301-1708".

[0151] FIG. 124 shows the amino acid sequence (SEQ ID NO:124) derived from the coding sequence of SEQ ID NO:123 shown in FIG. 123.

[0152] FIG. 125 shows a nucleotide sequence (SEQ ID NO:125) of a native sequence PRO1566 cDNA, wherein SEQ ID NO:125 is a clone designated herein as "DNA77568-1626".

[0153] FIG. 126 shows the amino acid sequence (SEQ ID NO:126) derived from the coding sequence of SEQ ID NO:125 shown in FIG. 125.

[0154] FIG. 127 shows a nucleotide sequence (SEQ ID NO:127) of a native sequence PRO1774 cDNA, wherein SEQ ID NO:127 is a clone designated herein as "DNA77626-1705".

[0155] FIG. 128 shows the amino acid sequence (SEQ ID NO:128) derived from the coding sequence of SEQ ID NO:127 shown in FIG. 127.

[0156] FIG. 129 shows a nucleotide sequence (SEQ ID NO:129) of a native sequence PRO1928 cDNA, wherein SEQ ID NO:129 is a clone designated herein as "DNA81754-2532".

[0157] FIG. 130 shows the amino acid sequence (SEQ ID NO:130) derived from the coding sequence of SEQ ID NO:129 shown in FIG. 129.

[0158] FIG. 131 shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO1865 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "DNA81757-2512".

[0159] FIG. 132 shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in FIG. 131.

[0160] FIG. 133 shows a nucleotide sequence (SEQ ID NO:133) of a native sequence PRO1925 cDNA, wherein SEQ ID NO:133 is a clone designated herein as "DNA82302-2529".

[0161] FIG. 134 shows the amino acid sequence (SEQ ID NO:134) derived from the coding sequence of SEQ ID NO:133 shown in FIG. 133.

[0162] FIG. 135 shows a nucleotide sequence (SEQ ID NO:135) of a native sequence PRO1926 cDNA, wherein SEQ ID NO:135 is a clone designated herein as "DNA82340-2530".

[0163] FIG. 136 shows the amino acid sequence (SEQ ID NO:136) derived from the coding sequence of SEQ ID NO:135 shown in FIG. 135.

[0164] FIG. 137 shows a nucleotide sequence (SEQ ID NO:137) of a native sequence PRO1801 cDNA, wherein SEQ ID NO:137 is a clone designated herein as "DNA83500-2506".

[0165] FIG. 138 shows the amino acid sequence (SEQ ID NO:138) derived from the coding sequence of SEQ ID NO:137 shown in FIG. 137.

[0166] FIG. 139 shows a nucleotide sequence (SEQ ID NO:139) of a native sequence PRO4405 cDNA, wherein SEQ ID NO:139 is a clone designated herein as "DNA84920-2614".

[0167] FIG. 140 shows the amino acid sequence (SEQ ID NO:140) derived from the coding sequence of SEQ ID NO:139 shown in FIG. 139.

[0168] FIG. 141 shows a nucleotide sequence (SEQ ID NO:141) of a native sequence PRO3435 cDNA, wherein SEQ ID NO:141 is a clone designated herein as "DNA85066-2534".

[0169] FIG. 142 shows the amino acid sequence (SEQ ID NO:142) derived from the coding sequence of SEQ ID NO:141 shown in FIG. 141.

[0170] FIG. 143 shows a nucleotide sequence (SEQ ID NO:143) of a native sequence PRO3543 cDNA, wherein SEQ ID NO:143 is a clone designated herein as "DNA86571-2551".

[0171] FIG. 144 shows the amino acid sequence (SEQ ID NO:144) derived from the coding sequence of SEQ ID NO:143 shown in FIG. 143.

[0172] FIG. 145 shows a nucleotide sequence (SEQ ID NO:145) of a native sequence PRO3443 cDNA, wherein SEQ ID NO:145 is a clone designated herein as "DNA87991-2540".

[0173] FIG. 146 shows the amino acid sequence (SEQ ID NO:146) derived from the coding sequence of SEQ ID NO:145 shown in FIG. 145.

[0174] FIG. 147 shows a nucleotide sequence (SEQ ID NO:147) of a native sequence PRO3442 cDNA, wherein SEQ ID NO:147 is a clone designated herein as "DNA92238-2539".

[0175] FIG. 148 shows the amino acid sequence (SEQ ID NO:148) derived from the coding sequence of SEQ ID NO:147 shown in FIG. 147.

[0176] FIG. 149 shows a nucleotide sequence (SEQ ID NO:149) of a native sequence PRO5990 cDNA, wherein SEQ ID NO:149 is a clone designated herein as "DNA96042-2682".

[0177] FIG. 150 shows the amino acid sequence (SEQ ID NO:150) derived from the coding sequence of SEQ ID NO:149 shown in FIG. 149.

[0178] FIG. 151 shows a nucleotide sequence (SEQ ID NO:151) of a native sequence PRO4342 cDNA, wherein SEQ ID NO:151 is a clone designated herein as "DNA96787-2534".

[0179] FIG. 152 shows the amino acid sequence (SEQ ID NO:152) derived from the coding sequence of SEQ ID NO:151 shown in FIG. 151.

[0180] FIG. 153 shows a nucleotide sequence (SEQ ID NO:153) of a native sequence PRO10096 cDNA, wherein SEQ ID NO:153 is a clone designated herein as "DNA125185-2806".

[0181] FIG. 154 shows the amino acid sequence (SEQ ID NO:154) derived from the coding sequence of SEQ ID NO:153 shown in FIG. 153.

[0182] FIG. 155 shows a nucleotide sequence (SEQ ID NO:155) of a native sequence PRO10272 cDNA, wherein SEQ ID NO:155 is a clone designated herein as "DNA147531-2821".

[0183] FIG. 156 shows the amino acid sequence (SEQ ID NO:156) derived from the coding sequence of SEQ ID NO:155 shown in FIG. 155.

[0184] FIG. 157 shows a nucleotide sequence (SEQ ID NO:157) of a native sequence PRO5801 cDNA, wherein SEQ ID NO:157 is a clone designated herein as "DNA115291-2681".

[0185] FIG. 158 shows the amino acid sequence (SEQ ID NO:158) derived from the coding sequence of SEQ ID NO:157 shown in FIG. 157.

[0186] FIG. 159 shows a nucleotide sequence (SEQ ID NO:159) of a native sequence PRO20110 cDNA, wherein SEQ ID NO:159 is a clone designated herein as "DNA166819".

[0187] FIG. 160 shows the amino acid sequence (SEQ ID NO:160) derived from the coding sequence of SEQ ID NO:159 shown in FIG. 159.

[0188] FIG. 161 shows a nucleotide sequence (SEQ ID NO:161) of a native sequence PRO20040 cDNA, wherein SEQ ID NO:161 is a clone designated herein as "DNA164625-2890".

[0189] FIG. 162 shows the amino acid sequence (SEQ ID NO:162) derived from the coding sequence of SEQ ID NO:161 shown in FIG. 161.

[0190] FIG. 163 shows a nucleotide sequence (SEQ ID NO:163) of a native sequence PRO20233 cDNA, wherein SEQ ID NO:163 is a clone designated herein as "DNA165608".

[0191] FIG. 164 shows the amino acid sequence (SEQ ID NO:164) derived from the coding sequence of SEQ ID NO:163 shown in FIG. 163.

[0192] FIG. 165 shows a nucleotide sequence (SEQ ID NO:165) of a native sequence PRO19670 cDNA, wherein SEQ ID NO:165 is a clone designated herein as "DNA131639-2874".

[0193] FIG. 166 shows the amino acid sequence (SEQ ID NO:166) derived from the coding sequence of SEQ ID NO:165 shown in FIG. 165.

[0194] FIG. 167 shows a nucleotide sequence (SEQ ID NO:167) of a native sequence PRO1890 cDNA, wherein SEQ ID NO:167 is a clone designated herein as "DNA79230-2525".

[0195] FIG. 168 shows the amino acid sequence (SEQ ID NO:168) derived from the coding sequence of SEQ ID NO:167 shown in FIG. 167.

DETAILED DESCRIPTION

I. Definitions

[0196] The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the prepa-

ration of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term “PRO polypeptide” also includes variants of the PRO/number polypeptides disclosed herein.

[0197] A “native sequence PRO polypeptide” comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term “native sequence PRO polypeptide” specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (e.g., an extracellular domain sequence), naturally-occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

[0198] The PRO polypeptide “extracellular domain” or “ECD” refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

[0199] The approximate location of the “signal peptides” of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (e.g., Nielsen et al., *Prot. Eng.* 10:1-6 (1997) and von Heinje et al., *Nucl. Acids. Res.* 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal

sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

[0200] “PRO polypeptide variant” means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

[0201] “Percent (%) amino acid sequence identity” with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a

candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, Calif. or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

[0202] In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction $\frac{X}{Y}$

[0203] where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X", "Y" and "Z" each represent different hypothetical amino acid residues.

[0204] Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described

below by using the WU-BLAST-2 computer program (Altschul et al., *Methods in Enzymology* 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=11, and scoring matrix=BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

[0205] Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, Md. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask=yes, strand=all, expected occurrences=10, minimum low complexity length=15/5, multi-pass e-value=0.01, constant for multi-pass=25, dropoff for final gapped alignment=25 and scoring matrix=BLOSUM62.

[0206] In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction $\frac{X}{Y}$

[0207] where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

[0208] "PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an

extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

[0209] Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

[0210] "Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc.

and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, Calif. or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

[0211] In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } \frac{W}{Z}$$

[0212] where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides.

[0213] Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=11, and scoring matrix=BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid

molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

[0214] Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, Md. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask=yes, strand=all, expected occurrences=10, minimum low complexity length=15/5, multi-pass e-value=0.01, constant for multi-pass=25, dropoff for final gapped alignment=25 and scoring matrix=BLOSUM62.

[0215] In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } \frac{W}{Z}$$

[0216] where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

[0217] In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

[0218] "Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide in situ within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

[0219] An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

[0220] The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

[0221] Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

[0222] The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polypeptidic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

[0223] "Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that

higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., *Current Protocols in Molecular Biology*, Wiley Interscience Publishers, (1995).

[0224] “Stringent conditions” or “high stringency conditions”, as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50° C.; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42° C.; or (3) employ 50% formamide, 5×SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5×Denhardt’s solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42° C., with washes at 42° C. in 0.2×SSC (sodium chloride/sodium citrate) and 50% formamide at 55° C., followed by a high-stringency wash consisting of 0.1×SSC containing EDTA at 55° C.

[0225] “Moderately stringent conditions” may be identified as described by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and % SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37° C. in a solution comprising: 20% formamide, 5×SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5×Denhardt’s solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1×SSC at about 37-50° C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

[0226] The term “epitope tagged” when used herein refers to a chimeric polypeptide comprising a PRO polypeptide fused to a “tag polypeptide”. The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

[0227] As used herein, the term “immunoadhesin” designates antibody-like molecules which combine the binding specificity of a heterologous protein (an “adhesin”) with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is “heterologous”), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a

receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

[0228] “Active” or “activity” for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein “biological” activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an “immunological” activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

[0229] The term “antagonist” is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term “agonist” is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

[0230] “Treatment” refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

[0231] “Chronic” administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. “Intermittent” administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

[0232] “Mammal” for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

[0233] Administration “in combination with” one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

[0234] “Carriers” as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are non-toxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids;

antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEENTM, polyethylene glycol (PEG), and PLURONICSTM.

[0235] "Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies (Zapata et al., Protein Eng. 8(10): 1057-1062[1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

[0236] Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab')₂ fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

[0237] "Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V_H-V_L dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

[0238] The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

[0239] The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

[0240] Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

[0241] "Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these

domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

[0242] The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same polypeptide chain (V_H-V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

[0243] An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

[0244] An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

[0245] The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

[0246] By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Pat. No. 4,275,149.

[0247] A “liposome” is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer

formation, similar to the lipid arrangement of biological membranes.

[0248] A “small molecule” is defined herein to have a molecular weight below about 500 Daltons

TABLE 1

```
/*
 *
 * C—C increased from 12 to 15
 * Z is average of EQ
 * B is average of ND
 * match with stop is _M; stop—stop = 0; J (joker) match = 0
 */
#define _M -8 /* value of a match with a stop */
int
_day[26][26] = {
/* A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */ {2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */ {0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */ {-2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
/* D */ {0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */ {0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
/* F */ {-4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */ {1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */ {-1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
/* I */ {-1, -2, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */ {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */ {-1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */ {-2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2},
/* M */ {-1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
/* N */ {0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */ {_M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */ {1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */ {0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */ {-2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
/* S */ {1, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */ {1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
/* U */ {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */ {0, -2, -2, -2, -2, -1, -1, -1, 0, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
/* W */ {-6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
/* X */ {0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */ {-3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
/* Z */ {0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4},
};
/*
 */
#include <stdio.h>
#include <ctype.h>
#define MAXJMP 16 /* max jumps in a diag */
#define MAXGAP 24 /* don't continue to penalize gaps larger than this */
#define JMPS 1024 /* max jmps in an path */
#define MX 4 /* save if there's at least MX-1 bases since last jmp */
#define DMAT 3 /* value of matching bases */
#define DMIS 0 /* penalty for mismatched bases */
#define DINS0 8 /* penalty for a gap */
#define DINS1 1 /* penalty per base */
#define PINS0 8 /* penalty for a gap */
#define PINS1 4 /* penalty per residue */
struct jmp {
    short n[MAXJMP]; /* size of jmp (neg for dely) */
    unsigned short x[MAXJMP]; /* base no. of jmp in seq x */
    /* limits seq to 2 16 -1 */
};
struct diag {
    int score; /* score at last jmp */
    long offset; /* offset of prev block */
    short ijmp; /* current jmp index */
    struct jmp jp; /* list of jmps */
};
struct path {
    int spc; /* number of leading spaces */
    short n[JMPS]; /* size of jmp (gap) */
    int x[JMPS]; /* loc of jmp (last elem before gap) */
};
char *ofile; /* output file name */
char *namex[2]; /* seq names: getseqs() */
```

TABLE 1-continued

```

char      *prog;           /* prog name for err msgs */
char      *seqx[2];        /* seqs: getseqs() */
int        dmax;           /* best diag: nw() */
int        dmax0;          /* final diag */
int        dna;            /* set if dna: main() */
int        endgaps;        /* set if penalizing end gaps */
int        gapx, gapy;     /* total gaps in seqs */
int        len0, len1;     /* seq lens */
int        ngapx, ngapy;   /* total size of gaps */
int        smax;           /* max score: nw() */
int        *xbm;           /* bitmap for matching */
long       offset;         /* current offset in jmp file */
struct diag *dx;           /* holds diagonals */
struct path pp[2];        /* holds path for seqs */
char       *calloc(), *malloc(), *index(), *strcpy();
char       *getseq(), *g_calloc();
/* Needleman-Wunsch alignment program
 *
 * usage: progs file1 file2
 *   where file1 and file2 are two dna or two protein sequences.
 * The sequences can be in upper- or lower-case and may contain ambiguity
 * Any lines beginning with ';', '>' or '<' are ignored
 * Max file length is 65535 (limited by unsigned short x in the jmp struct)
 * A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
 * Output is in the file "align.out"
 *
 * The program may create a tmp file in /tmp to hold info about traceback.
 * Original version developed under BSD 4.3 on a vax 8650
 */
#include "nw.h"
#include "day.h"
static __dbval[26] = {
    1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};
static __pbval[26] = {
    1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
    128, 256, 0xFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
    1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
    1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};
main(ac, av)
int      ac;
char     *av[];
{
    prog = av[0];
    if(ac != 3) {
        fprintf(stderr, "usage: %s file1 file2\n", prog);
        fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        fprintf(stderr, "The sequences can be in upper- or lower-case\n");
        fprintf(stderr, "Any lines beginning with ';', '>' or '<' are ignored\n");
        fprintf(stderr, "Output is in the file \"align.out\"\n");
        exit(1);
    }
    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
    xbm = (dna)? __dbval : __pbval;
    endgaps = 0; /* 1 to penalize endgaps */
    ofile = "align.out"; /* output file */
    nw(); /* fill in the matrix, get the possible jmps */
    readjmps(); /* get the actual jmps */
    print(); /* print stats, alignment */
    cleanup(0); /* unlink any tmp files */
}
/* do the alignment, return best score: main()
 * dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
 * pro: PAM 250 values
 * When scores are equal, we prefer mismatches to any gap, prefer
 * a new gap to extending an ongoing gap, and prefer a gap in seqx
 * to a gap in seq y.
 */
nw()
{
    char      *px, *py; /* seqs and ptrs */
    int        *ndely, *dely; /* keep track of dely */

```

TABLE 1-continued

```

int      ndelx, delx;    /* keep track of delx */
int      *tmp;          /* for swapping row0, row1 */
int      mis;           /* score for each type */
int      ins0, ins1;     /* insertion penalties */
register id;             /* diagonal index */
register ij;             /* jmp index */
register *col0, *col1;    /* score for curr, last row */
register xx, yy;         /* index into seqs */
dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));
ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
ins0 = (dna)? DINS0 : PINS0;
ins1 = (dna)? DINS1 : PINS1;
smax = -10000;
if (endgaps) {
    for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
        col0[yy] = dely[yy] = col0[yy-1] - ins1;
        ndely[yy] = yy;
    }
    col0[0] = 0;    /* Waterman Bull Math Biol 84 */
}
else
    for (yy = 1; yy <= len1; yy++)
        dely[yy] = -ins0;
/* fill in match matrix
*/
for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
    /* initialize first entry in col
    */
    if (endgaps) {
        if (xx == 1)
            col1[0] = delx = -(ins0+ins1);
        else
            col1[0] = delx = col0[0]-ins1;
        ndelx = xx;
    }
    else {
        col1[0] = 0;
        delx = -ins0;
        ndelx = 0;
    }
}

for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
    mis = col0[yy-1];
    if (dna)
        mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
    else
        mis += _day[*px-'A'][*py-'A'];
    /* update penalty for del in x seq;
    * favor new del over ongong del
    * ignore MAXGAP if weighting endgaps
    */
    if (endgaps || ndely[yy] < MAXGAP) {
        if (col0[yy] - ins0 >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else {
            dely[yy] -= ins1;
            ndely[yy]++;
        }
    }
    else {
        if (col0[yy] - (ins0+ins1) >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        }
        else
            ndely[yy]++;
    }
    /* update penalty for del in y seq;
    * favor new del over ongong del
    */
    if (endgaps || ndelx < MAXGAP) {
        if (col1[yy-1] - ins0 >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;

```

...nw

TABLE 1-continued

```

    } else {
        delx -= ins1;
        ndelx++;
    }
} else {
    if (col1[yy-1] - (ins0+ins1) >= delx) {
        delx = col1[yy-1] - (ins0+ins1);
        ndelx = 1;
    } else
        ndelx++;
}
/* pick the maximum score; we're favoring
 * mis over any del and delx over dely
 */

id = xx - yy + len1 - 1;
if (mis >= delx && mis >= dely[yy])
    col1[yy] = mis;
else if (delx >= dely[yy]) {
    col1[yy] = delx;
    ij = dx[id].ijmp;
    if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
    && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
        dx[id].ijmp++;
        if (++ij >= MAXJMP) {
            writeimps(id);
            ij = dx[id].ijmp = 0;
            dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
        }
    }
    dx[id].jp.n[ij] = ndelx;
    dx[id].jp.x[ij] = xx;
    dx[id].score = delx;
}
else {
    col1[yy] = dely[yy];
    ij = dx[id].ijmp;
if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
    && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
        dx[id].ijmp++;
        if (++ij >= MAXJMP) {
            writeimps(id);
            ij = dx[id].ijmp = 0;
            dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
        }
    }
    dx[id].jp.n[ij] = ndely[yy];
    dx[id].jp.x[ij] = xx;
    dx[id].score = dely[yy];
}
if (xx == len0 && yy < len1) {
    /* last col
    */
    if (endgaps)
        col1[yy] -= ins0+ins1*(len1-yy);
    if (col1[yy] > smax) {
        smax = col1[yy];
        dmax = id;
    }
}
}
if (endgaps && xx < len0)
    col1[yy-1] -= ins0+ins1*(len0-xx);
if (col1[yy-1] > smax) {
    smax = col1[yy-1];
    dmax = id;
}
tmp = col0; col0 = col1; col1 = tmp;
}
(void) free((char *)ndely);
(void) free((char *)dely);
(void) free((char *)col0);
(void) free((char *)col1);
}

```

TABLE 1-continued

```

/*
 *
 * print() -- only routine visible outside this module
 *
 * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */
#include "nw.h"
#define SPC 3
#define P_LINE 256 /* maximum output line */
#define P_SPC 3 /* space between name or num and seq */
extern _day[26][26];
int olen; /* set output line length */
FILE *fx; /* output file */
print()
{
    int lx, ly, firstgap, lastgap; /* overlap */
    if ((fx = fopen(ofile, "w")) == 0) {
        fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
    olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
        pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
        pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) { /* trailing gap in x */
        lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
    }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
        lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
    }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}
/*
 * trace back the best path, count matches
 */
static
getmat(lx, ly, firstgap, lastgap)
{
    int lx, ly; /* "core" (minus endgaps) */
    int firstgap, lastgap; /* leading trailing overlap */
    {
        int nm, i0, i1, siz0, siz1;
        char outx[32];
        double pct;
        register n0, n1;
        register char *p0, *p1;
        /* get total matches, score
         */
        i0 = i1 = siz0 = siz1 = 0;
        p0 = seqx[0] + pp[1].spc;
        p1 = seqx[1] + pp[0].spc;
        n0 = pp[1].spc + 1;
        n1 = pp[0].spc + 1;
        nm = 0;
        while ( *p0 && *p1 ) {
            if (siz0) {
                p1++;

```

TABLE 1-continued

```

        n1++;
        siz0--;
    }
    else if (siz1) {
        p0++;
        n0++;
        siz1--;
    }
    else {
        if (xbm[*p0-'A']&xbm[*p1-'A'])
            nm++;
        if (n0++ == pp[0].x[i0])
            siz0 = pp[0].n[i0++];
        if (n1++ == pp[1].x[i1])
            siz1 = pp[1].n[i1++];
        p0++;
        p1++;
    }
}
/* pct homology:
 * if penalizing endgaps, base is the shorter seq
 * else, knock off overhangs and take shorter core
 */
if (endgaps)
    lx = (len0 < len1)? len0 : len1;
else
    lx = (lx < ly)? lx : ly;
pct = 100.*(double)nm/(double)lx;
fprintf(fx, "\n");
fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);
fprintf(fx, "< gaps in first sequence: %d", gapx);
if (gapx) {
    (void) sprintf(outx, "< (%d %s%s)",
        ngapx, (dna)? "base": "residue", (ngapx == 1)? "" : "s");
    fprintf(fx, "%s", outx);
}
fprintf(fx, ", gaps in second sequence: %d", gapy);
if (gapy) {
    (void) sprintf(outx, "< (%d %s%s)",
        ngapy, (dna)? "base": "residue", (ngapy == 1)? "" : "s");
    fprintf(fx, "%s", outx);
}
}
if (dna)
    fprintf(fx,
        "\n< score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
        smax, DMAT, DMIS, DINS0, DINS1);
else
    fprintf(fx,
        "\n< score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
        smax, PINS0, PINS1);
if (endgaps)
    fprintf(fx,
        "< endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
        firstgap, (dna)? "base": "residue", (firstgap == 1)? "" : "s",
        lastgap, (dna)? "base": "residue", (lastgap == 1)? "" : "s");
else
    fprintf(fx, "< endgaps not penalized\n");
}
static      nm;          /* matches in core -- for checking */
static      lmax;        /* lengths of stripped file names */
static      ij[2];       /* jmp index for a path */
static      nc[2];       /* number at start of current line */
static      ni[2];       /* current elem number -- for gapping */
static      siz[2];
static char *ps[2];      /* ptr to current element */
static char *po[2];      /* ptr to next output char slot */
static char out[2][P_LINE]; /* output line */
static char star[P_LINE]; /* set by stars() */
/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()
{
    int      nn;          /* char count */
    int      more;
```

TABLE 1-continued

```

register    i;
for (i = 0, lmax = 0; i < 2; i++) {
    nn = stripname(name[i]);
    if (nn > lmax)
        lmax = nn;
    nc[i] = 1;
    ni[i] = 1;
    siz[i] = ij[i] = 0;
    ps[i] = seqx[i];
    po[i] = out[i];
}
for (nn = nm = 0, more = 1; more;) {
    for (i = more = 0; i < 2; i++) {
        /*
         * do we have more of this sequence?
         */
        if (!*ps[i])
            continue;
        more++;
        if (pp[i].spc) {
            /* leading space */
            *po[i]++ = ' ';
            pp[i].spc--;
        }
        else if (siz[i]) {
            /* in a gap */
            *po[i]++ = '-';
            siz[i]--;
        }
        else {
            /* we're putting a seq element
             */
            *po[i] = *ps[i];
            if (islower(*ps[i]))
                *ps[i] = toupper(*ps[i]);
            po[i]++;
            ps[i]++;
            /*
             * are we at next gap for this seq?
             */
            if (ni[i] == pp[i].x[ij[i]]) {
                /*
                 * we need to merge all gaps
                 * at this location
                 */
                siz[i] == pp[i].n[ij[i]++];
                while (ni[i] == pp[i].x[ij[i]])
                    siz[i] += pp[i].n[ij[i]++];
            }
            ni[i]++;
        }
    }
    if (++nn == olen || !more && nn) {
        dumpblock();
        for (i = 0; i < 2; i++)
            po[i] = out[i];
        nn = 0;
    }
}
}
/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
static
dumpblock()
{
    register i;
    for (i = 0; i < 2; i++)
        *po[i]-- = '\0';

    (void) puts("\n", fx);
    for (i = 0; i < 2; i++) {
        if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
            if (i == 0)
                nums(i);
            if (i == 0 && *out[1])
                stars();
            putline(i);
            if (i == 0 && *out[1])

```

TABLE 1-continued

<pre> fprintf(fx, star); if (i == 1) nums(i); } } } } /* * put out a number line: dumpblock() */ static nums(ix) int ix; /* index in out[] holding seq line */ { char nline[P_LINE]; register i, j; register char *pn, *px, *py; for(pn = nline, i = 0; i < lmax+P_SPC; i++, pn++) *pn = ' '; for (i = nc[ix], py = out[ix]; *py; py++, pn++) { if (*py == ' ' *py == '-') *pn = ' '; else { if (i%10 == 0 (i == 1 && nc[ix] != 1)) { j = (i < 0)? -i : i; for (px = pn; j; j/= 10, px--) *px = j%10 + '0'; if (i < 0) *px = '-'; } else *pn = ' '; i++; } } *pn = '\0'; nc[ix] = i; for (pn = nline; *pn; pn++) (void) putc(*pn, fx); (void) putc('\n', fx); } /* * put out a line (name, [num], seq. [num]): dumpblock() */ static putline(ix) int ix; { int i; register char *px; for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++) (void) putc(*px, fx); for (; i < lmax+P_SPC; i++) (void) putc(' ', fx); /* these count from 1: * ni[] is current element (from 1) * nc[] is number at start of current line */ for (px = out[ix]; *px; px++) (void) putc(*px&0x7F, fx); (void) putc('\n', fx); } } /* * put a line of stars (seqs always in out[0], out[1]): dumpblock() */ static stars() { int i; register char *p0, *p1, cx, *px; if (!(*out[0] (*out[0] == ' ' && *(p0[0]) == ' ') !*out[1] (*out[1] == ' ' && *(p0[1]) == ' ')) return; px = star; for (i = lmax+P_SPC; i; i--) *px++ = ' '; for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) { </pre>		nums
	putline	
	...putline	
	stars	

TABLE 1-continued

<pre> if (isalpha(*p0) && isalpha(*p1)) { if (xbm[*p0-'A']&xbm[*p1-'A']) { cx = '*'; nm++; } else if (!dna && __day[*p0-'A'][*p1-'A'] > 0) cx = '.'; else cx = ' '; } else cx = ' '; *px++ = cx; } *px++ = '\n'; *px = '\0'; } /* * strip path or prefix from pn, return len: pr_align() */ static stripname(pn) char *pn; /* file name (may be path) */ { register char *px, *py; py = 0; for (px = pn; *px; px++) if (*px == '/') py = px + 1; if (py) (void) strcpy(pn, py); return(strlen(pn)); } /* * cleanup() -- cleanup any tmp file * getseq() -- read in seq, set dna, len, maxlen * g_calloc() -- calloc() with error checkin * readjumps() -- get the good jumps, from tmp file if necessary * writejumps() -- write a filled array of jumps to a tmp file: nw() */ #include "nw.h" #include <sys/file.h> char *jname = "/tmp/homgXXXXXX"; /* tmp file for jumps */ FILE *fj; int cleanup(); /* cleanup tmp file */ long lseek(); /* * remove any tmp file if we blow */ cleanup(i) int i; { if (fj) (void) unlink(jname); exit(i); } /* * read, return ptr to seq, set dna, len, maxlen * skip lines starting with ';', '<', or '>' * seq in upper or lower case */ char * getseq(file, len) char *file; /* file name */ int *len; /* seq len */ { char line[1024], *pseq; register char *px, *py; int natgc, tlen; FILE *fp; if ((fp = fopen(file, "r")) == 0) { fprintf(stderr, "%s: can't read %s\n", prog, file); exit(1); } tlen = natgc = 0; while (fgets(line, 1024, fp)) {</pre>		
		stripname
		cleanup
		getseq

TABLE 1-continued

```

        if (*line == ';' || *line == '<' || *line == '>')
            continue;
        for (px = line; *px != '\n'; px++)
            if (isupper(*px) || islower(*px))
                tlen++;
    }
    if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
        fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
        exit(1);
    }
    pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';

    py = pseq + 4;
    *len = tlen;
    rewind(fp);
    while (fgets(line, 1024, fp)) {
        if (*line == ';' || *line == '<' || *line == '>')
            continue;
        for (px = line; *px != '\n'; px++) {
            if (isupper(*px))
                *py++ = *px;
            else if (islower(*px))
                *py++ = toupper(*px);
            if (index("ATGCU", *(py-1)))
                natgc++;
        }
        *py++ = '\0';
        *py = '\0';
        (void) fclose(fp);
        dna = natgc > (tlen/3);
        return(pseq+4);
    }
}
char *
g__calloc(msg, nx, sz)
char *msg;          /* program, calling routine */
int nx, sz;          /* number and size of elements */
{
    char *px, *calloc();
    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
        if (*msg) {
            fprintf(stderr, "%s: g__calloc() failed %s (n= %d, sz= %d)\n", prog, msg, nx, sz);
            exit(1);
        }
    }
    return(px);
}
/*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
 */
readjmps()
{
    int fd = -1;
    int siz, i0, i1;
    register i, j, xx;
    if (fj) {
        (void) fclose(fj);
        if ((fd = open(jname, O_RDONLY, 0)) < 0) {
            fprintf(stderr, "%s: can't open() %s\n", prog, jname);
            cleanup(1);
        }
    }
    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; i++) {
        while (1) {
            for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
                ;

            if (j < 0 && dx[dmax].offset && fj) {
                (void) lseek(fd, dx[dmax].offset, 0);
                (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
                (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
                dx[dmax].ijmp = MAXJMP-1;
            }
        }
    }
}

```

...getseq

g__calloc

readjmps

...readjmps

TABLE 1-continued

```

        else
            break;
    }
    if (i >= JMPS) {
        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
        cleanup(1);
    }
    if (j >= 0) {
        siz = dx[dmax].jp.n[j];
        xx = dx[dmax].jp.x[j];
        dmax += siz;
        if (siz < 0) { /* gap in second seq */
            pp[1].n[i1] = -siz;
            xx += siz;
            /* id = xx - yy + len1 - 1
            */
            pp[1].x[i1] = xx - dmax + len1 - 1;
            gapy++;
            ngapy -= siz;
/* ignore MAXGAP when doing endgaps */
            siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
            i1++;
        }
        else if (siz > 0) { /* gap in first seq */
            pp[0].n[i0] = siz;
            pp[0].x[i0] = xx;
            gapx++;
            ngapx += siz;
/* ignore MAXGAP when doing endgaps */
            siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
            i0++;
        }
    }
    else
        break;
}
/* reverse the order of jmps
*/
for (j = 0, i0--; j < i0; j++, i0--) {
    i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
    i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
}
for (j = 0, i1--; j < i1; j++, i1--) {
    i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
    i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
}
if (fd >= 0)
    (void) close(fd);
if (fj) {
    (void) unlink(jname);
    fj = 0;
    offset = 0;
}
}

/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
writejumps(ix)
int ix;
{
    char *mktemp();
    if (!fj) {
        if (mktemp(jname) < 0) {
            fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
            cleanup(1);
        }
        if ((fj = fopen(jname, "w")) == 0) {
            fprintf(stderr, "%s: can't write %s\n", prog, jname);
            exit(1);
        }
    }
    (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
    (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
}

```

writejumps

[0249]

TABLE 2

PRO	XXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXXXYYYYYYY	(Length = 12 amino acids)

% amino acid sequence identity = (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) = 5 divided by 15 = 33.3%

[0250]

TABLE 3

PRO	XXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXXXXYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity = (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) = 5 divided by 10 = 50%

[0251]

TABLE 4

PRO-DNA	NNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity = (the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) = 6 divided by 14 = 42.9%

[0252]

TABLE 5

PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

% nucleic acid sequence identity = (the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) = 4 divided by 12 = 33.3%

II. Compositions and Methods of the Invention

[0253] A. A Full-Length PRO Polypeptides

[0254] The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

[0255] As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual

nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

[0256] B. PRO Polypeptide Variants

[0257] In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

[0258] Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Pat. No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

[0259] PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO polypeptide.

[0260] PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by poly-

merase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

[0261] In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

TABLE 6

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; lys; arg	gln
Asp (D)	glu	glu
Cys (C)	ser	ser
Gln (Q)	asn	asn
Glu (E)	asp	asp
Gly (G)	pro; ala	ala
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe; norleucine	leu
Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg
Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala; tyr	leu
Pro (P)	ala	ala
Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr; phe	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu

[0262] Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- [0263] (1) hydrophobic: norleucine, met, ala, val, leu, ile;
- [0264] (2) neutral hydrophilic: cys, ser, thr;
- [0265] (3) acidic: asp, glu;
- [0266] (4) basic: asn, gin, his, lys, arg;
- [0267] (5) residues that influence chain orientation: gly, pro; and
- [0268] (6) aromatic: trp, tyr, phe.

[0269] Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

[0270] The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al., Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

[0271] Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W. H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

[0272] C. Modifications of PRO

[0273] Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis (diazocetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimide.

[0274] Other modifications include deamidation of glutamyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T. E. Creighton, Proteins: Structure and Molecular Properties, W. H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

[0275] Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means),

and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

[0276] Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

[0277] Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 Sep. 1987, and in Aplin and Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

[0278] Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., *Arch. Biochem. Biophys.*, 259:52 (1987) and by Edge et al., *Anal. Biochem.*, 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., *Meth. Enzymol.*, 138:350 (1987).

[0279] Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Pat. Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

[0280] The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

[0281] In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl-terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., *Mol. Cell. Biol.*, 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., *Molecular and Cellular Biology*, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., *Protein Engineering*, 3(6):547-553

(1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., *BioTechnology*, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., *Science*, 255:192-194 (1992)]; an α -tubulin epitope peptide [Skinner et al., *J. Biol. Chem.*, 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., *Proc. Natl. Acad. Sci. USA*, 87:6393-6397 (1990)].

[0282] In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also U.S. Pat. No. 5,428,130 issued Jun. 27, 1995.

[0283] D. Preparation of PRO

[0284] The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., *Solid-Phase Peptide Synthesis*, W. H. Freeman Co., San Francisco, Calif. (1969); Merrifield, *J. Am. Chem. Soc.*, 85:2149-2154 (1963)]. In vitro protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, Calif.) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

[0285] 1. Isolation of DNA Encoding PRO

[0286] DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

[0287] Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual* (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., *supra*; Dieffenbach et al., *PCR Primer: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, 1995)].

[0288] The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ^{32}P -labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

[0289] Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

[0290] Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

[0291] 2. Selection and Transformation of Host Cells

[0292] Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

[0293] Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl_2 , CaPO_4 , liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 Jun. 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Pat. No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene,

polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

[0294] Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 Apr. 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype tonA; *E. coli* W3110 strain 9E4, which has the complete genotype tonA ptr3; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan^r; *E. coli* W3110 strain 37D6, which has the complete genotype tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan^r; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant degP deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Pat. No. 4,946,783 issued 7 Aug. 1990. Alternatively, in vitro methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

[0295] In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Pat. No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424) *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilum* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida*, *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 576:5259-5263 [1979]); *Schwanniomyces* such as *Schwanniomyces occidentalis* (EP 394,538 published 31 Oct. 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium* (WO 91/00357 published 10 Jan. 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983];

Tilburn et al., *Gene*, 26:205-221 [1983]; Yelton et al., *Proc. Natl. Acad. Sci. USA*, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, *EMBO J.*, 4:475-479 [1985]). Methylo-tropic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, *The Biochemistry of Methylo-trophs*, 269 (1982).

[0296] Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., *J. Gen. Virol.*, 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, *Biol. Reprod.*, 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

[0297] 3. Selection and Use of a Replicable Vector

[0298] The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

[0299] The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α -factor leaders, the latter described in U.S. Pat. No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 Apr. 1990), or the signal described in WO 90/13646 published 15 Nov. 1990. In mammalian cell expression, mammalian signal sequences

may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

[0300] Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

[0301] Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

[0302] An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980). A suitable selection gene for use in yeast is the trp 1 gene present in the yeast plasmid YRp7 [Stinchcomb et al., *Nature*, 282:39 (1979); Kingsman et al., *Gene*, 7:141 (1979); Tschemper et al., *Gene*, 10:157 (1980)]. The trp 1 gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, *Genetics*, 85:12 (1977)].

[0303] Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems [Chang et al., *Nature*, 275:615 (1978); Goeddel et al., *Nature*, 281:544 (1979)], alkaline phosphatase, a tryptophan (trp) promoter system [Goeddel, *Nucleic Acids Res.*, 8:4057 (1980); EP 36,776], and hybrid promoters such as the tac promoter [deBoer et al., *Proc. Natl. Acad. Sci. USA*, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

[0304] Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., *J. Biol. Chem.*, 255:2073 (1980)] or other glycolytic enzymes [Hess et al., *J. Adv. Enzyme Reg.*, 7:149 (1968); Holland, *Biochemistry*, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

[0305] Other yeast promoters, which are inducible promoters having the additional advantage of transcription

controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

[0306] PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 Jul. 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

[0307] Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

[0308] Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

[0309] Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., *Nature*, 293:620-625 (1981); Mantei et al., *Nature*, 281:40-46 (1979); EP 117,060; and EP 117,058.

[0310] 4. Detecting Gene Amplification/Expression

[0311] Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, *Proc. Natl. Acad. Sci. USA*, 77:5201(1980)], dot blotting (DNA analysis), or in situ hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

[0312] Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

[0313] 5. Purification of Polypeptide

[0314] Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

[0315] It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, *Methods in Enzymology*, 182 (1990); Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

[0316] E. Uses for PRO

[0317] Nucleotide sequences (or their complement) encoding PRO have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid will also be useful for the preparation of PRO polypeptides by the recombinant techniques described herein.

[0318] The full-length native sequence PRO gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length PRO cDNA or to isolate still other cDNAs (for instance, those encoding naturally-occurring variants of PRO or PRO from other species) which have a desired sequence identity to the native PRO sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO. By way of example, a screening method will comprise isolating the coding region of the PRO gene using the known DNA sequence to synthesize a selected probe of about 40 bases.

Hybridization probes may be labeled by a variety of labels, including radionucleotides such as ^{32}P or ^{35}S , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the PRO gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

[0319] Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

[0320] Other useful fragments of the PRO nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target PRO mRNA (sense) or PRO DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of PRO DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

[0321] Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. The antisense oligonucleotides thus may be used to block expression of PRO proteins. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable in vivo (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

[0322] Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

[0323] Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, CaPO_4 -mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either in vivo or ex vivo. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retro-

virus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

[0324] Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

[0325] Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

[0326] Antisense or sense RNA or DNA molecules are generally at least about 5 bases in length, about 10 bases in length, about 15 bases in length, about 20 bases in length, about 25 bases in length, about 30 bases in length, about 35 bases in length, about 40 bases in length, about 45 bases in length, about 50 bases in length, about 55 bases in length, about 60 bases in length, about 65 bases in length, about 70 bases in length, about 75 bases in length, about 80 bases in length, about 85 bases in length, about 90 bases in length, about 95 bases in length, about 100 bases in length, or more.

[0327] The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO coding sequences.

[0328] Nucleotide sequences encoding a PRO can also be used to construct hybridization probes for mapping the gene which encodes that PRO and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as in situ hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

[0329] When the coding sequences for PRO encode a protein which binds to another protein (example, where the PRO is a receptor), the PRO can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor PRO can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO or a receptor for PRO. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein

binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

[0330] Nucleic acids which encode PRO or its modified forms can also be used to generate either transgenic animals or “knock out” animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding PRO. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Pat. Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding PRO introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding PRO. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

[0331] Alternatively, non-human homologues of PRO can be used to construct a PRO “knock out” animal which has a defective or altered gene encoding PRO as a result of homologous recombination between the endogenous gene encoding PRO and altered genomic DNA encoding PRO introduced into an embryonic stem cell of the animal. For example, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques. A portion of the genomic DNA encoding PRO can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a “knock out” animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knock-

out animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO polypeptide.

[0332] Nucleic acid encoding the PRO polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve in vivo synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. “Gene therapy” includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes in vivo. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik et al., *Proc. Natl. Acad. Sci. USA* 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

[0333] There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells in vitro, or in vivo in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells in vitro include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred in vivo gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau et al., *Trends in Biotechnology* 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu et al., *J. Biol. Chem.* 262, 4429-4432 (1987); and Wagner et al., *Proc. Natl. Acad. Sci. USA* 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson et al., *Science* 256, 808-813 (1992).

[0334] The PRO polypeptides described herein may also be employed as molecular weight markers for protein electrophoresis purposes and the isolated nucleic acid sequences may be used for recombinantly expressing those markers.

[0335] The nucleic acid molecules encoding the PRO polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each PRO nucleic acid molecule of the present invention can be used as a chromosome marker.

[0336] The PRO polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the PRO polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. PRO nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

[0337] The PRO polypeptides described herein may also be employed as therapeutic agents. The PRO polypeptides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the PRO product hereof is combined in admixture with a pharmaceutically acceptable carrier vehicle. Therapeutic formulations are prepared for storage by mixing the active ingredient having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEENTM, PLURONICSTM or PEG.

[0338] The formulations to be used for in vivo administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

[0339] Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[0340] The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

[0341] Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments provide reliable guidance for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The use of interspecies scaling in toxicokinetics" In *Toxicokinetics and New Drug Development*, Yacobi et al., Eds., Pergamon Press, New York 1989, pp. 42-96.

[0342] When in vivo administration of a PRO polypeptide or agonist or antagonist thereof is employed, normal dosage

amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 μ g/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting one organ or tissue, for example, may necessitate delivery in a manner different from that to another organ or tissue.

[0343] Where sustained-release administration of a PRO polypeptide is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of the PRO polypeptide, microencapsulation of the PRO polypeptide is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon-(rhIFN-), interleukin-2, and MN rgp120. Johnson et al., *Nat. Med.*, 2:795-799 (1996); Yasuda, *Biomed. Ther.*, 27:1221-1223 (1993); Hora et al., *Bio/Technology*, 8:755-758 (1990); Cleland, "Design and Production of Single Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in *Vaccine Design: The Subunit and Adjuvant Approach*, Powell and Newman, eds, (Plenum Press: New York, 1995), pp. 439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S. Pat. No. 5,654,010.

[0344] The sustained-release formulations of these proteins were developed using poly-lactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable properties. The degradation products of PLGA, lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis, "Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.), *Biodegradable Polymers as Drug Delivery Systems* (Marcel Dekker: New York, 1990), pp. 1-41.

[0345] This invention encompasses methods of screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the PRO polypeptides encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

[0346] The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

[0347] All assays for antagonists are common in that they call for contacting the drug candidate with a PRO polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

[0348] In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction

mixture. In a particular embodiment, the PRO polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the PRO polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the PRO polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

[0349] If the candidate compound interacts with but does not bind to a particular PRO polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers (Fields and Song, *Nature* (London), 340:245-246 (1989); Chien et al., *Proc. Natl. Acad. Sci. USA*, 88:9578-9582 (1991)) as disclosed by Chevray and Nathans, *Proc. Natl. Acad. Sci. USA*, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-lac Z reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β -galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

[0350] Compounds that interfere with the interaction of a gene encoding a PRO polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the

reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

[0351] To assay for antagonists, the PRO polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence of the PRO polypeptide indicates that the compound is an antagonist to the PRO polypeptide. Alternatively, antagonists may be detected by combining the PRO polypeptide and a potential antagonist with membrane-bound PRO polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The PRO polypeptide can be labeled, such as by radioactivity, such that the number of PRO polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., *Current Protocols in Immun.*, 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the PRO polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the PRO polypeptide. Transfected cells that are grown on glass slides are exposed to labeled PRO polypeptide. The PRO polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single clone that encodes the putative receptor.

[0352] As an alternative approach for receptor identification, labeled PRO polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro-sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

[0353] In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled PRO polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

[0354] More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with PRO polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain anti-

bodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the PRO polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the PRO polypeptide.

[0355] Another potential PRO polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature PRO polypeptides herein, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix—see Lee et al., *Nucl. Acids Res.*, 6:3073 (1979); Cooney et al., *Science*, 241: 456 (1988); Dervan et al., *Science*, 251:1360 (1991)), thereby preventing transcription and the production of the PRO polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into the PRO polypeptide (antisense—Okano, *Neurochem.*, 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression (CRC Press: Boca Raton, Fla., 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed in vivo to inhibit production of the PRO polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

[0356] Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the PRO polypeptide, thereby blocking the normal biological activity of the PRO polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

[0357] Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Rossi, *Current Biology*, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published Sep. 18, 1997).

[0358] Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, supra.

[0359] These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

[0360] Diagnostic and therapeutic uses of the herein disclosed molecules may also be based upon the positive functional assay hits disclosed and described below.

[0361] F. Anti-PRO Antibodies

[0362] The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

[0363] 1. Polyclonal Antibodies

[0364] The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

[0365] 2. Monoclonal Antibodies

[0366] The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro.

[0367] The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl

transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

[0368] Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, Calif. and the American Type Culture Collection, Manassas, Va. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

[0369] The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

[0370] After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown in vivo as ascites in a mammal.

[0371] The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

[0372] The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Pat. No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Pat. No. 4,816,567; Morrison et al., supra] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted

for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

[0373] The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

[0374] In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

[0375] 3. Human and Humanized Antibodies

[0376] The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

[0377] Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Pat. No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corre-

sponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

[0378] Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Pat. Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., *Bio/Technology* 10, 779-783 (1992); Lonberg et al., *Nature* 368 856-859 (1994); Morrison, *Nature* 368, 812-13 (1994); Fishwild et al., *Nature Biotechnology* 14, 845-51 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.* 13 65-93 (1995).

[0379] The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

[0380] 4. Bispecific Antibodies

[0381] Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

[0382] Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, *Nature*, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., *EMBO J.*, 10:3655-3659 (1991).

[0383] 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. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., *Methods in Enzymology*, 121:210 (1986).

[0384] According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

[0385] Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., *Science* 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

[0386] Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al. *J. Exp. Med.* 175:217(1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

[0387] Various technique for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., *J. Immunol.* 148 (5):1547-1553(1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the

hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448(1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994). Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al. J., Immunol. 147:60(1991).

[0388] Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc γ R), such as Fc γ RI (CD64), Fc γ RII (CD32) and Fc γ RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

[0389] 5. Heteroconjugate Antibodies

[0390] Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Pat. No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Pat. No. 4,676,980.

[0391] 6. Effector Function Engineering

[0392] It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with

enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

[0393] 7. Immunoconjugates

[0394] The invention also pertains to immunoconjugates comprising 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).

[0395] Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. 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, *Phytolacca 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 . Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimide HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionuclide to the antibody. See WO 94/11026.

[0396] In another embodiment, the antibody may 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 conjugated to a cytotoxic agent (e.g., a radionuclide).

[0397] 8. Immunoliposomes

[0398] The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein et al., Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Pat. No. 5,013,556.

[0399] Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid compo-

sition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin et al., J. Biol. Chem., 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon et al., J. National Cancer Inst., 81(19): 1484 (1989).

[0400] 9. Pharmaceutical Compositions of Antibodies

[0401] Antibodies specifically binding a PRO polypeptide identified herein, as well as other molecules identified by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders in the form of pharmaceutical compositions.

[0402] If the PRO polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, e.g., Marasco et al., Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993). The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

[0403] The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nano-capsules) or in macroemulsions. Such techniques are disclosed in Remington's *Pharmaceutical Sciences*, supra.

[0404] The formulations to be used for in vivo administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

[0405] Sustained-release preparations may 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 (U.S. Pat. No. 3,773,919), 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. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37° C., resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S—S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

[0406] G. Uses for Anti-PRO Antibodies

[0407] The anti-PRO antibodies of the invention have various utilities. For example, anti-PRO antibodies may be used in diagnostic assays for PRO, e.g., detecting its expression (and in some cases, differential expression) in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, *Monoclonal Antibodies: A Manual of Techniques*, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., *Nature*, 144:945 (1962); David et al., *Biochemistry*, 13:1014 (1974); Pain et al., *J. Immunol. Meth.*, 40:219 (1981); and Nygren, *J. Histochem. and Cytochem.*, 30:407 (1982).

[0408] Anti-PRO antibodies also are useful for the affinity purification of PRO from recombinant cell culture or natural sources. In this process, the antibodies against PRO are immobilized on a suitable support, such as Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO from the antibody.

[0409] The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

[0410] All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

[0411] Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, Va.

Example 1

[0412] Extracellular Domain Homology Screening to Identify Novel Polypeptides and cDNA Encoding Therefor

[0413] The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (e.g., Dayhoff, GenBank), and proprietary databases (e.g., LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, Calif.). The search was performed using the computer program BLAST or BLAST-2 (Altschul et al., *Methods in Enzymology* 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Wash.).

[0414] Using this extracellular domain homology screen, consensus DNA sequences were assembled relative to the other identified EST sequences using phrap. In addition, the consensus DNA sequences obtained were often (but not always) extended using repeated cycles of BLAST or BLAST-2 and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

[0415] Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward and reverse PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5 kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel et al., *Current Protocols in Molecular Biology*, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

[0416] The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, Calif. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., *Science*, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

Example 2

[0417] Isolation of cDNA Clones by Amylase Screening

[0418] 1. Preparation of Oligo dT Primed cDNA Library

[0419] mRNA was isolated from a human tissue of interest using reagents and protocols from Invitrogen, San Diego, Calif. (Fast Track 2). This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, Md. (Super Script Plasmid System). In this procedure, the double stranded cDNA was sized to greater than 1000 bp and the SalI/NotI linked cDNA was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

[0420] 2. Preparation of Random Primed cDNA Library

[0421] A secondary cDNA library was generated in order to preferentially represent the 5' ends of the primary cDNA clones. Sp6 RNA was generated from the primary library (described above), and this RNA was used to generate a random primed cDNA library in the vector pSST-AMY.0 using reagents and protocols from Life Technologies (Super Script Plasmid System, referenced above). In this procedure the double stranded cDNA was sized to 500-1000 bp, linked with blunt to NotI adaptors, cleaved with SfiI, and cloned into SfiI/NotI cleaved vector. pSST-AMY.0 is a cloning vector that has a yeast alcohol dehydrogenase promoter preceding the cDNA cloning sites and the mouse amylase sequence (the mature sequence without the secretion signal) followed by the yeast alcohol dehydrogenase terminator, after the cloning sites. Thus, cDNAs cloned into this vector that are fused in frame with amylase sequence will lead to the secretion of amylase from appropriately transfected yeast colonies.

[0422] 3. Transformation and Detection

[0423] DNA from the library described in paragraph 2 above was chilled on ice to which was added electrocompetent DH10B bacteria (Life Technologies, 20 ml). The bacteria and vector mixture was then electroporated as recommended by the manufacturer. Subsequently, SOC media (Life Technologies, 1 ml) was added and the mixture was incubated at 37° C. for 30 minutes. The transformants were then plated onto 20 standard 150 mm LB plates containing ampicillin and incubated for 16 hours (37° C.). Positive colonies were scraped off the plates and the DNA was isolated from the bacterial pellet using standard protocols, e.g. CsCl-gradient. The purified DNA was then carried on to the yeast protocols below.

[0424] The yeast methods were divided into three categories: (1) Transformation of yeast with the plasmid/cDNA combined vector; (2) Detection and isolation of yeast clones secreting amylase; and (3) PCR amplification of the insert directly from the yeast colony and purification of the DNA for sequencing and further analysis.

[0425] The yeast strain used was HD56-5A (ATCC-90785). This strain has the following genotype: MAT^{alpha}, ura3-52, leu2-3, leu2-112, his3-11, his3-15, MAL⁺, SUC⁺, GAL⁺. Preferably, yeast mutants can be employed that have deficient post-translational pathways. Such mutants may have translocation deficient alleles in sec 71, sec 72, sec 62, with truncated sec 71 being most preferred. Alternatively,

antagonists (including antisense nucleotides and/or ligands) which interfere with the normal operation of these genes, other proteins implicated in this post translation pathway (e.g., SEC61p, SEC72p, SEC62p, SEC63p, TDJ1p or SSA1p-4p) or the complex formation of these proteins may also be preferably employed in combination with the amylase-expressing yeast.

[0426] Transformation was performed based on the protocol outlined by Gietz et al., Nucl. Acid. Res., 20:1425 (1992). Transformed cells were then inoculated from agar into YEPD complex media broth (100 ml) and grown overnight at 30° C. The YEPD broth was prepared as described in Kaiser et al., Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, N.Y., p. 207 (1994). The overnight culture was then diluted to about 2×10^7 cells/ml (approx. $OD_{600}=0.1$) into fresh YEPD broth (500 ml) and regrown to 1×10^7 cells/ml (approx. $OD_{600}=0.4-0.5$).

[0427] The cells were then harvested and prepared for transformation by transfer into GS3 rotor bottles in a Sorval GS3 rotor at 5,000 rpm for 5 minutes, the supernatant discarded, and then resuspended into sterile water, and centrifuged again in 50 ml falcon tubes at 3,500 rpm in a Beckman GS-6KR centrifuge. The supernatant was discarded and the cells were subsequently washed with LiAc/TE (10 ml, 10 mM Tris-HCl, 1 mM EDTA pH 7.5, 100 mM Li_2OOCCH_3), and resuspended into LiAc/TE (2.5 ml).

[0428] Transformation took place by mixing the prepared cells (100 μ l) with freshly denatured single stranded salmon testes DNA (Lofstrand Labs, Gaithersburg, Md.) and transforming DNA (1 μ g, vol. <10 μ l) in microfuge tubes. The mixture was mixed briefly by vortexing, then 40% PEG/TE (600 μ l, 40% polyethylene glycol-4000, 10 mM Tris-HCl, 1 mM EDTA, 100 mM Li_2OOCCH_3 , pH 7.5) was added. This mixture was gently mixed and incubated at 30° C. while agitating for 30 minutes. The cells were then heat shocked at 42° C. for 15 minutes, and the reaction vessel centrifuged in a microfuge at 12,000 rpm for 5-10 seconds, decanted and resuspended into TE (500 μ l, 10 mM Tris-HCl, 1 mM EDTA pH 7.5) followed by recentrifugation. The cells were then diluted into TE (1 ml) and aliquots (200 μ l) were spread onto the selective media previously prepared in 150 mm growth plates (VWR).

[0429] Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

[0430] The selective media used was a synthetic complete dextrose agar lacking uracil (SCD-Ura) prepared as described in Kaiser et al., Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, N.Y., p. 208-210 (1994). Transformants were grown at 30° C. for 2-3 days.

[0431] The detection of colonies secreting amylase was performed by including red starch in the selective growth media. Starch was coupled to the red dye (Reactive Red-120, Sigma) as per the procedure described by Biely et al., Anal. Biochem., 172:176-179 (1988). The coupled starch was incorporated into the SCD-Ura agar plates at a final concentration of 0.15% (w/v), and was buffered with potassium phosphate to a pH of 7.0 (50-100 mM final concentration).

[0432] The positive colonies were picked and streaked across fresh selective media (onto 150 mm plates) in order to obtain well isolated and identifiable single colonies. Well isolated single colonies positive for amylase secretion were detected by direct incorporation of red starch into buffered SCD-Ura agar. Positive colonies were determined by their ability to break down starch resulting in a clear halo around the positive colony visualized directly.

[0433] 4. Isolation of DNA by PCR Amplification

[0434] When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30 μ l) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5 μ l) was used as a template for the PCR reaction in a 25 μ l volume containing: 0.5 μ l KlenTaq (Clontech, Palo Alto, Calif.); 4.0 μ l 10 mM dNTP's (Perkin Elmer-Cetus); 2.5 μ l Kentaq buffer (Clontech); 0.25 μ l forward oligo 1; 0.25 μ l reverse oligo 2; 12.5 μ l distilled water. The sequence of the forward oligonucleotide 1 was:

[0435] 5'-TGTAACGACGGCCAGTTAAATA-GACCTGCAATTATTAATCT-3' (SEQ ID NO:169)

[0436] The sequence of reverse oligonucleotide 2 was:

[0437] 5'-CAGGAAACAGCTATGACCACCTG-CACACCTGCAAATCCATT-3' (SEQ ID NO:170)

[0438] PCR was then performed as follows:

a.		Denature	92° C.,	5 minutes
b.	3 cycles of:	Denature	92° C.,	30 seconds
		Anneal	59° C.,	30 seconds
		Extend	72° C.,	60 seconds
c.	3 cycles of:	Denature	92° C.,	30 seconds
		Anneal	57° C.,	30 seconds
		Extend	72° C.,	60 seconds
d.	25 cycles of:	Denature	92° C.,	30 seconds
		Anneal	55° C.,	30 seconds
		Extend	72° C.,	60 seconds
e.		Hold	4° C.	

[0439] The underlined regions of the oligonucleotides annealed to the ADH promoter region and the amylase region, respectively, and amplified a 307 bp region from vector pSST-AMY.0 when no insert was present. Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343 bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

[0440] Following the PCR, an aliquot of the reaction (5 μ l) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook et al., supra. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, Calif.).

Example 3

[0441] Isolation of cDNA Clones Using Signal Algorithm Analysis

[0442] Various polypeptide-encoding nucleic acid sequences were identified by applying a proprietary signal sequence finding algorithm developed by Genentech, Inc. (South San Francisco, Calif.) upon ESTs as well as clustered and assembled EST fragments from public (e.g., GenBank) and/or private (LIFESeq®, Incyte Pharmaceuticals, Inc., Palo Alto, Calif.) databases. The signal sequence algorithm computes a secretion signal score based on the character of the DNA nucleotides surrounding the first and optionally the second methionine codon(s) (ATG) at the 5'-end of the sequence or sequence fragment under consideration. The nucleotides following the first ATG must code for at least 35 unambiguous amino acids without any stop codons. If the first ATG has the required amino acids, the second is not examined. If neither meets the requirement, the candidate sequence is not scored. In order to determine whether the EST sequence contains an authentic signal sequence, the DNA and corresponding amino acid sequences surrounding the ATG codon are scored using a set of seven sensors (evaluation parameters) known to be associated with secretion signals. Use of this algorithm resulted in the identification of numerous polypeptide-encoding nucleic acid sequences.

Example 4

[0443] Isolation of cDNA Clones Encoding Human PRO Polypeptides

[0444] Using the techniques described in Examples 1 to 3 above, numerous full-length cDNA clones were identified as encoding PRO polypeptides as disclosed herein. These cDNAs were then deposited under the terms of the Budapest Treaty with the American Type Culture Collection, 10801 University Blvd., Manassas, Va. 20110-2209, USA (ATCC) as shown in Tabl 7 below.

TABLE 7		
Material	ATCC Dep. No.	Deposit Date
DNA26843-1389	203099	Aug. 4,1998
DNA30867-1335	209807	Apr. 28, 1998
DNA34431-1177	209399	Oct. 17, 1997
DNA38268-1188	209421	Oct. 28, 1997
DNA40621-1440	209922	Jun. 2, 1998
DNA40625-1189	209788	Apr. 21, 1998
DNA45409-2511	203579	Jan. 12,1999
DNA45495-1550	203156	Aug. 25, 1998
DNA49820-1427	209932	Jun. 2, 1998
DNA56406-1704	203478	Nov. 17, 1998
DNA56410-1414	209923	Jun. 2, 1998
DNA56436-1448	209902	May 27, 1998
DNA56855-1447	203004	Jun. 23, 1998
DNA56860-1510	209952	Jun. 9, 1998
DNA56862-1343	203174	Sep. 1, 1998
DNA56868-1478	203024	Jun. 23, 1998
DNA56869-1545	203161	Aug. 25, 1998
DNA57704-1452	209953	Jun. 9, 1998
DNA58723-1588	203133	Aug. 18, 1998
DNA57827-1493	203045	Jul. 1, 1998
DNA58737-1473	203136	Aug. 18, 1998
DNA58846-1409	209957	Jun. 9, 1998
DNA58850-1495	209956	Jun. 9, 1998
DNA58855-1422	203018	Jun. 23, 1998
DNA59211-1450	209960	Jun. 9, 1998

TABLE 7-continued

Material	ATCC Dep. No.	Deposit Date
DNA59212-1627	203245	Sep. 9, 1998
DNA59213-1487	209959	Jun. 9, 1998
DNA59605-1418	203005	Jun. 23, 1998
DNA59609-1470	209963	Jun. 9, 1998
DNA59610-1556	209990	Jun. 16, 1998
DNA59837-2545	203658	Feb. 9, 1999
DNA59844-2542	203650	Feb. 9, 1999
DNA59854-1459	209974	Jun. 16, 1998
DNA60625-1507	209975	Jun. 16, 1998
DNA60629-1481	209979	Jun. 16, 1998
DNA61755-1554	203112	Aug. 11, 1998
DNA62812-1594	203248	Sep. 9, 1998
DNA62815-1576	203247	Sep. 9, 1998
DNA64881-1602	203240	Sep. 9, 1998
DNA64886-1601	203241	Sep. 9, 1998
DNA64902-1667	203317	Oct. 6, 1998
DNA64950-1590	203224	Sep. 15, 1998
DNA65403-1565	203230	Sep. 15, 1998
DNA66308-1537	203159	Aug. 25, 1998
DNA66519-1535	203236	Sep. 15, 1998
DNA66521-1583	203225	Sep. 15, 1998
DNA66658-1584	203229	Sep. 15, 1998
DNA66660-1585	203279	Sep. 22, 1998
DNA66663-1598	203268	Sep. 22, 1998
DNA66674-1599	203281	Sep. 22, 1998
DNA68862-2546	203652	Feb. 9, 1999
DNA68866-1644	203283	Sep. 22, 1998
DNA68871-1638	203280	Sep. 22, 1998
DNA68880-1676	203319	Oct. 6, 1998
DNA68883-1691	203535	Dec. 15, 1998
DNA68885-1678	203311	Oct. 6,1998
DNA71277-1636	203285	Sep. 22, 1998
DNA73727-1673	203459	Nov. 3,1998
DNA73734-1680	203363	Oct. 20, 1998
DNA73735-1681	203356	Oct. 20, 1998
DNA76393-1664	203323	Oct. 6, 1998
DNA77301-1708	203407	Oct. 27, 1998
DNA77568-1626	203134	Aug. 18, 1998
DNA77626-1705	203536	Dec. 15, 1998
DNA81754-2532	203542	Dec. 15, 1998
DNA81757-2512	203543	Dec. 15, 1998
DNA82302-2529	203534	Dec. 15, 1998
DNA82340-2530	203547	Dec. 22, 1998
DNA83500-2506	203391	Oct. 29, 1998
DNA84920-2614	203966	Apr. 27, 1999
DNA85066-2534	203588	Jan. 12, 1999
DNA86571-2551	203660	Feb. 9, 1999
DNA87991-2540	203656	Feb. 9, 1999
DNA92238-2539	203602	Jan. 20, 1999
DNA96042-2682	PTA-382	Jul. 20, 1999
DNA96787-2534	203589	Jan. 12, 1999
DNA125185-2806	PTA-1031	Dec. 7, 1999
DNA147531-2821	PTA-1185	Jan. 11, 2000
DNA115291-2681	PTA-202	Jun. 8, 1999
DNA164625-28890	PTA-1535	Mar. 21, 2000
DNA131639-2874	PTA-1784	Apr. 25, 2000
DNA79230-2525	203549	Dec. 22, 1998

[0445] These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent

application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

[0446] The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

Example 5

[0447] Use of PRO as a Hybridization Probe

[0448] The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

[0449] DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

[0450] Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5×SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2×Denhardt's solution, and 10% dextran sulfate at 42° C. for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1×SSC and 0.1% SDS at 42° C.

[0451] DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

Example 6

[0452] Expression of PRO in *E. coli*

[0453] This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

[0454] The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., *Gene*, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

[0455] The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., *supra*. Transformants are identified by their

ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

[0456] Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

[0457] After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

[0458] PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) Ion galE rpoHts (htpRts) clpP(lacIq)). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30° C. with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH₄)₂SO₄, 0.71 g sodium citrate-2H₂O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO₄) and grown for approximately 20-30 hours at 30° C. with shaking. Samples are removed to verify expression by SDS-page analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

[0459] *E. coli* paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4° C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Ultrapure grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4° C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

[0460] The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM

cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4° C. for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

[0461] Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

[0462] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 7

[0463] Expression of PRO in Mammalian Cells

[0464] This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

[0465] The vector, pRK5 (see EP 307,247, published Mar. 15, 1989), is employed as the expression vector. Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., *supra*. The resulting vector is called pRK5-PRO.

[0466] In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 μ g pRK5-PRO DNA is mixed with about 1 μ g DNA encoding the VA RNA gene [Thimmappaya et al., *Cell*, 31:543 (1982)] and dissolved in 500 μ l of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl₂. To this mixture is added, dropwise, 500 μ l of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO₄, and a precipitate is allowed to form for 10 minutes at 25° C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37° C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

[0467] Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture

medium (alone) or culture medium containing 200 μ Ci/ml ³⁵S-cysteine and 200 μ Ci/ml ³⁵S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

[0468] In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., *Proc. Natl. Acad. Sci.*, 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μ g pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 μ g/ml bovine insulin and 0.1 μ g/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

[0469] In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as CaPO₄ or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ³⁵S-methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

[0470] Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be concentrated and purified by any selected method, such as by Ni²⁺-chelate affinity chromatography.

[0471] PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

[0472] Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

[0473] Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using

standard techniques as described in Ausubel et al., *Current Protocols of Molecular Biology*, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., *Nucl. Acids Res.* 24:9 (1774-1779) (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

[0474] Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect® (Quiagen), Dosper® or Eugene® (Boehringer Mannheim). The cells are grown as described in Lucas et al., *supra*. Approximately 3×10^{-7} cells are frozen in an ampule for further growth and production as described below.

[0475] The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 μ m filtered PS20 with 5% 0.2 μ m diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37° C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with 3×10^5 cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Pat. No. 5,122,469, issued Jun. 16, 1992 may actually be used. A 3L production spinner is seeded at 1.2×10^6 cells/mL. On day 0, the cell number pH is determined. On day 1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33° C., and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 μ m filter. The filtrate was either stored at 4° C. or immediately loaded onto columns for purification.

[0476] For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 mL Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 mL/min. at 4° C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 mL G25 Superfine (Pharmacia) column and stored at -80° C.

[0477] Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The condi-

tioned medium is pumped onto a 5 mL Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 mL fractions into tubes containing 275 μ L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

[0478] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 8

[0479] Expression of PRO in Yeast

[0480] The following method describes recombinant expression of PRO in yeast.

[0481] First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

[0482] Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

[0483] Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

[0484] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 9

[0485] Expression of PRO in Baculovirus-Infected Insect Cells

[0486] The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

[0487] The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding the mature protein if

the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

[0488] Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4-5 days of incubation at 28° C., the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., *Baculovirus expression vectors: A Laboratory Manual*, Oxford: Oxford University Press (1994).

[0489] Expressed poly-his tagged PRO can then be purified, for example, by Ni²⁺-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., *Nature*, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 μ m filter. A Ni²⁺-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A₂₈₀ with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A₂₈₀ baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni²⁺-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₁₀-tagged PRO are pooled and dialyzed against loading buffer.

[0490] Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

[0491] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 10

[0492] Preparation of Antibodies that Bind PRO

[0493] This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

[0494] Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, *supra*. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

[0495] Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, Mont.) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

[0496] After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

[0497] The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

[0498] The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

Example 11

[0499] Purification of PRO Polypeptides Using Specific Antibodies

[0500] Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

[0501] Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotech-

nology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

[0502] Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

[0503] A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (e.g., high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (e.g., a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

Example 12

[0504] Drug Screening

[0505] This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

[0506] Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with a PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

[0507] Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on Sep. 13, 1984. Briefly stated,

large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

[0508] This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

Example 13

[0509] Rational Drug Design

[0510] The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (i.e., a PRO polypeptide) or of small molecules with which they interact, e.g., agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide in vivo (c.f., Hodgson, *Bio/Technology*, 9: 19-21(1991)).

[0511] In one approach, the three-dimensional structure of the PRO polypeptide, or of a PRO polypeptide-inhibitor complex, is determined by X-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, *Biochemistry*, 31:7796-7801(1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda et al., *J. Biochem.*, 113:742-746(1993).

[0512] It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

[0513] By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to

perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to X-ray crystallography.

Example 14

[0514] Pericyte c-Fos Induction (Assay 93)

[0515] This assay shows that certain polypeptides of the invention act to induce the expression of c-fos in pericyte cells and, therefore, are useful not only as diagnostic markers for particular types of pericyte-associated tumors but also for giving rise to antagonists which would be expected to be useful for the therapeutic treatment of pericyte-associated tumors. Induction of c-fos expression in pericytes is also indicative of the induction of angiogenesis and, as such, PRO polypeptides capable of inducing the expression of c-fos would be expected to be useful for the treatment of conditions where induced angiogenesis would be beneficial including, for example, wound healing, and the like. Specifically, on day 1, pericytes are received from VEC Technologies and all but 5 ml of media is removed from flask. On day 2, the pericytes are trypsinized, washed, spun and then plated onto 96 well plates. On day 7, the media is removed and the pericytes are treated with 100 μ l of PRO polypeptide test samples and controls (positive control=DME+5% serum+/-PDGF at 500 ng/ml; negative control=protein 32). Replicates are averaged and SD/CV are determined. Fold increase over Protein 32 (buffer control) value indicated by chemiluminescence units (RLU) luminometer reading verses frequency is plotted on a histogram. Two-fold above Protein 32 value is considered positive for the assay. ASY Matrix: Growth media=low glucose DMEM=20% FBS+1 $\times$ pen strep+1 $\times$ fungizone. Assay Media=low glucose DMEM+5% FBS.

[0516] The following polypeptides tested positive in this assay: PRO1347 and PRO1340.

Example 15

[0517] Ability of PRO Polypeptides to Stimulate the Release of Proteoglycans from Cartilage (Assay 97)

[0518] The ability of various PRO polypeptides to stimulate the release of proteoglycans from cartilage tissue was tested as follows.

[0519] The metacarpophalangeal joint of 4-6 month old pigs was aseptically dissected, and articular cartilage was removed by free hand slicing being careful to avoid the underlying bone. The cartilage was minced and cultured in bulk for 24 hours in a humidified atmosphere of 95% air, 5% CO₂ in serum free (SF) media (DME/F12 1:1) with 0.1% BSA and 100U/ml penicillin and 100 μ g/ml streptomycin. After washing three times, approximately 100 mg of articular cartilage was aliquoted into micronics tubes and incubated for an additional 24 hours in the above SF media. PRO polypeptides were then added at 1% either alone or in combination with 18 ng/ml interleukin-1 α , a known stimulator of proteoglycan release from cartilage tissue. The supernatant was then harvested and assayed for the amount of proteoglycans using the 1,9-dimethyl-methylene blue (DMB) colorimetric assay (Farndale and Buttle, Biochem. Biophys. Acta 883:173-177 (1985)). A positive result in this

assay indicates that the test polypeptide will find use, for example, in the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis.

[0520] When various PRO polypeptides were tested in the above assay, the polypeptides demonstrated a marked ability to stimulate release of proteoglycans from cartilage tissue both basally and after stimulation with interleukin-1 α and at 24 and 72 hours after treatment, thereby indicating that these PRO polypeptides are useful for stimulating proteoglycan release from cartilage tissue. As such, these PRO polypeptides are useful for the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. The polypeptides testing positive in this assay are: PRO1565, PRO1693, PRO1801 and PRO10096.

Example 16

[0521] Detection of Polypeptides that Affect Glucose or FFA Uptake in Skeletal Muscle (Assay 106)

[0522] This assay is designed to determine whether PRO polypeptides show the ability to affect glucose or FFA uptake by skeletal muscle cells. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of disorders where either the stimulation or inhibition of glucose uptake by skeletal muscle would be beneficial including, for example, diabetes or hyper- or hypo-insulinemia.

[0523] In a 96 well format, PRO polypeptides to be assayed are added to primary rat differentiated skeletal muscle, and allowed to incubate overnight. Then fresh media with the PRO polypeptide and +/- insulin are added to the wells. The sample media is then monitored to determine glucose and FFA uptake by the skeletal muscle cells. The insulin will stimulate glucose and FFA uptake by the skeletal muscle, and insulin in media without the PRO polypeptide is used as a positive control, and a limit for scoring. As the PRO polypeptide being tested may either stimulate or inhibit glucose and FFA uptake, results are scored as positive in the assay if greater than 1.5 times or less than 0.5 times the insulin control.

[0524] The following PRO polypeptides tested positive as either stimulators or inhibitors of glucose and/or FFA uptake in this assay: PRO4405.

Example 17

[0525] Identification of PRO Polypeptides that Stimulate TNF- α Release in Human Blood (Assay 128)

[0526] This assay shows that certain PRO polypeptides of the present invention act to stimulate the release of TNF- α in human blood. PRO polypeptides testing positive in this assay are useful for, among other things, research purposes where stimulation of the release of TNF- α would be desired and for the therapeutic treatment of conditions wherein enhanced TNF- α release would be beneficial. Specifically, 200 μ l of human blood supplemented with 50 mM Hepes buffer (pH 7.2) is aliquotted per well in a 96 well test plate. To each well is then added 300 μ l of either the test PRO polypeptide in 50 mM Hepes buffer (at various concentrations) or 50 mM Hepes buffer alone (negative control) and the plates are incubated at 37° C. for 6 hours. The samples

are then centrifuged and 50 μ l of plasma is collected from each well and tested for the presence of TNF- α by ELISA assay. A positive in the assay is a higher amount of TNF- α in the PRO polypeptide treated samples as compared to the negative control samples.

[0527] The following PRO polypeptides tested positive in this assay: PRO263, PRO295, PRO1282, PRO1063, PRO1356, PRO3543, and PRO5990.

Example 18

[0528] Tumor Versus Normal Differential Tissue Expression Distribution

[0529] Oligonucleotide probes were constructed from some of the PRO polypeptide-encoding nucleotide sequences shown in the accompanying figures for use in quantitative PCR amplification reactions. The oligonucleotide probes were chosen so as to give an approximately 200-600 base pair amplified fragment from the 3' end of its associated template in a standard PCR reaction. The oligonucleotide probes were employed in standard quantitative PCR amplification reactions with cDNA libraries isolated from different human tumor and normal human tissue samples and analyzed by agarose gel electrophoresis so as to obtain a quantitative determination of the level of expression of the PRO polypeptide-encoding nucleic acid in the various tumor and normal tissues tested. β -actin was used as a control to assure that equivalent amounts of nucleic acid was used in each reaction. Identification of the differential expression of the PRO polypeptide-encoding nucleic acid in one or more tumor tissues as compared to one or more normal tissues of the same tissue type renders the molecule useful diagnostically for the determination of the presence or absence of tumor in a subject suspected of possessing a tumor as well as therapeutically as a target for the treatment of a tumor in a subject possessing such a tumor. These assays provided the following results.

Molecule	is more highly expressed in:	as compared to:
DNA26843-1389	normal lung rectum tumor	lung tumor normal rectum
DNA30867-1335	normal kidney	kidney tumor
DNA40621-1440	normal lung	lung tumor
DNA40625-1189	normal lung	lung tumor
DNA45409-2511	melanoma tumor	normal skin
DNA56406-1704	kidney tumor normal skin	normal kidney melanoma tumor
DNA56410-1414	normal stomach	stomach tumor
DNA56436-1448	normal skin	melanoma tumor
DNA56855-1447	normal esophagus rectum tumor	esophageal tumor normal rectum
DNA56860-1510	normal kidney rectum tumor	kidney tumor normal rectum
DNA56862-1343	kidney tumor normal lung	normal kidney lung tumor
DNA56868-1478	normal stomach normal lung	stomach tumor lung tumor
DNA56869-1545	normal esophagus normal skin	esophageal tumor melanoma tumor
DNA57704-1452	normal stomach rectum tumor	stomach tumor normal rectum
DNA58723-1588	normal stomach kidney tumor	stomach tumor normal kidney
DNA57827-1493	normal skin normal stomach	melanoma tumor stomach tumor
	normal skin	melanoma tumor

-continued

Molecule	is more highly expressed in:	as compared to:
DNA58737-1473	esophageal tumor normal stomach	normal esophagus stomach tumor
DNA58846-1409	lung tumor	normal lung
DNA58850-1495	esophageal tumor kidney tumor	normal esophagus normal kidney
DNA58855-1422	normal stomach rectum tumor	stomach tumor normal rectum
DNA59211-1450	normal kidney	kidney tumor
DNA59212-1627	normal skin	melanoma tumor
DNA59213-1487	normal stomach normal skin	stomach tumor melanoma tumor
DNA59605-1418	melanoma tumor	normal skin
DNA59609-1470	esophageal tumor	normal esophagus
DNA59610-1556	esophageal tumor lung tumor normal skin	normal esophagus normal lung melanoma tumor
DNA59837-2545	normal skin	melanoma tumor
DNA59844-2542	normal skin esophageal tumor	melanoma tumor normal esophagus
DNA59854-1459	normal esophagus stomach tumor normal lung	esophageal tumor normal stomach lung tumor
DNA60625-1507	normal lung	lung tumor
DNA60629-1481	normal esophagus normal rectum	esophageal tumor rectum tumor
DNA61755-1554	normal stomach kidney tumor	stomach tumor normal kidney
DNA62812-1594	normal stomach normal lung normal rectum normal skin	stomach tumor stomach tumor lung tumor rectum tumor
DNA62815-1576	esophageal tumor	melanoma tumor
DNA64881-1602	normal stomach normal lung	normal esophagus stomach tumor
DNA64902-1667	normal lung esophageal tumor kidney tumor	lung tumor normal esophagus normal kidney
DNA65403-1565	normal esophagus	esophageal tumor
DNA66308-1537	normal lung	lung tumor
DNA66519-1535	kidney tumor	normal kidney
DNA66521-1583	normal esophagus normal stomach normal lung normal rectum normal skin	esophageal tumor stomach tumor lung tumor rectum tumor melanoma tumor
DNA66658-1584	normal lung melanoma tumor	lung tumor normal skin
DNA66660-1585	lung tumor	normal lung
DNA66674-1599	kidney tumor normal lung	normal kidney lung tumor
DNA68862-2546	melanoma tumor	normal skin
DNA68866-1644	normal stomach	stomach tumor
DNA68871-1638	lung tumor normal skin	normal lung melanoma tumor
DNA68880-1676	normal lung normal skin	lung tumor melanoma tumor
DNA68883-1691	esophageal tumor	normal esophagus
DNA68885-1678	lung tumor	normal lung
DNA71277-1636	normal stomach	stomach tumor
DNA73734-1680	normal lung	lung tumor
DNA73735-1681	esophageal tumor normal kidney lung tumor normal skin	normal esophagus kidney tumor normal lung melanoma tumor
DNA76393-1664	esophageal tumor stomach tumor lung tumor rectum tumor	normal esophagus normal stomach normal lung normal rectum
DNA77568-1626	normal stomach lung tumor	stomach tumor normal lung
DNA77626-1705	normal rectum	rectum tumor
DNA81754-2532	normal skin	melanoma tumor
DNA81757-2512	esophageal tumor normal stomach melanoma tumor	normal esophagus stomach tumor normal skin

-continued

Molecule	is more highly expressed in:	as compared to:
DNA82302-2529	normal stomach normal lung	stomach tumor lung tumor
DNA82340-2530	normal esophagus	esophageal tumor
DNA85066-2534	lung tumor normal skin	normal lung melanoma tumor
DNA87991-2540	esophageal tumor	normal esophagus
DNA92238-2539	normal skin	melanoma tumor
DNA96787-2534	normal kidney	kidney tumor

Example 19

[0530] Identification of Receptor/Ligand Interactions

[0531] In this assay, various PRO polypeptides are tested for ability to bind to a panel of potential receptor or ligand molecules for the purpose of identifying receptor/ligand interactions. The identification of a ligand for a known receptor, a receptor for a known ligand or a novel receptor/ligand pair is useful for a variety of indications including, for example, targeting bioactive molecules (linked to the ligand or receptor) to a cell known to express the receptor or ligand, use of the receptor or ligand as a reagent to detect the presence of the ligand or receptor in a composition suspected of containing the same, wherein the composition may comprise cells suspected of expressing the ligand or receptor, modulating the growth of or another biological or immunological activity of a cell known to express or respond to the receptor or ligand, modulating the immune response of cells or toward cells that express the receptor or ligand, allowing the preparation of agonists, antagonists and/or antibodies directed against the receptor or ligand which will modulate the growth of or a biological or immunological activity of a cell expressing the receptor or ligand, and various other indications which will be readily apparent to the ordinarily skilled artisan.

[0532] The assay is performed as follows. A PRO polypeptide of the present invention suspected of being a ligand for a receptor is expressed as a fusion protein containing the Fc domain of human IgG (an immunoadhesin). Receptor-ligand binding is detected by allowing interaction of the immunoadhesin polypeptide with cells (e.g. Cos cells) expressing candidate PRO polypeptide receptors and visualization of bound immunoadhesin with fluorescent reagents directed toward the Fc fusion domain and examination by microscope. Cells expressing candidate receptors are produced by transient transfection, in parallel, of defined subsets of a library of cDNA expression vectors encoding PRO polypeptides that may function as receptor molecules. Cells are then incubated for 1 hour in the presence of the PRO polypeptide immunoadhesin being tested for possible receptor binding. The cells are then washed and fixed with paraformaldehyde. The cells are then incubated with fluorescent conjugated antibody directed against the Fc portion of the PRO polypeptide immunoadhesin (e.g. FITC conjugated goat anti-human-Fc antibody). The cells are then washed again and examined by microscope. A positive

interaction is judged by the presence of fluorescent labeling of cells transfected with cDNA encoding a particular PRO polypeptide receptor or pool of receptors and an absence of similar fluorescent labeling of similarly prepared cells that have been transfected with other cDNA or pools of cDNA. If a defined pool of cDNA expression vectors is judged to be positive for interaction with a PRO polypeptide immunoadhesin, the individual cDNA species that comprise the pool are tested individually (the pool is "broken down") to determine the specific cDNA that encodes a receptor able to interact with the PRO polypeptide immunoadhesin.

[0533] In another embodiment of this assay, an epitope-tagged potential ligand PRO polypeptide (e.g. 8 histidine "His" tag) is allowed to interact with a panel of potential receptor PRO polypeptide molecules that have been expressed as fusions with the Fc domain of human IgG (immunoadhesins). Following a 1 hour co-incubation with the epitope tagged PRO polypeptide, the candidate receptors are each immunoprecipitated with protein A beads and the beads are washed. Potential ligand interaction is determined by western blot analysis of the immunoprecipitated complexes with antibody directed towards the epitope tag. An interaction is judged to occur if a band of the anticipated molecular weight of the epitope tagged protein is observed in the western blot analysis with a candidate receptor, but is not observed to occur with the other members of the panel of potential receptors.

[0534] Using these assays, the following receptor/ligand interactions have been herein identified:

[0535] (1) PRO10272 binds to PRO5801.

[0536] (2) PRO20110 binds to the human IL-17 receptor (Yao et al., *Cytokine* 9(11):794-800 (1997); also herein designated as PRO1) and to PRO20040.

[0537] (3) PRO10096 binds to PRO20233.

[0538] (4) PRO19670 binds to PRO1890.

[0539] The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

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Lys	Gln	Val	His	Ala	Leu	Ser	Pro	Glu	Glu	Asn	Val	Ile	Ile	Lys
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Leu	Asn	Lys	Ala	Gly	Leu	Val	Leu	Gly	Ile	Leu	Ser	Cys	Leu	Gly
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Leu	Ser	Ile	Val	Ala	Asn	Phe	Gln	Lys	Thr	Thr	Leu	Phe	Ala	Ala
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His	Val	Ser	Gly	Ala	Val	Leu	Thr	Phe	Gly	Met	Gly	Ser	Leu	Tyr
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His	Ser	Gly	Asn	Phe	Gly	Thr	Asp	Leu	Glu	Gln	Lys	Leu	His	Trp
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Tyr	Ile	Arg	Asp	Phe	Gln	Lys	Ile	Ser	Leu	Arg	Val	Glu	Ala	Asn
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Leu	His	Gly	Leu	Thr	Leu	Tyr	Asp	Thr	Ala	Pro	Cys	Pro	Ile	Asn
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Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu	95	100	105
His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe	110	115	120
Met Tyr Phe Phe Trp Lys Leu Gly Asp Pro Phe Pro Ile Leu Ser	125	130	135
Pro Lys His Gly Ile Leu Ser Ile Glu Gln Leu Ile Ser Arg Val	140	145	150
Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu Ser Gly Phe Gly	155	160	165
Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe Leu Arg Asn	170	175	180
Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu Leu Gln	185	190	195
Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met Ala	200	205	210
Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser	215	220	225
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Glu Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala	260	265	270
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Gly Ile Gln Phe Asp Val Lys Phe Trp Ser Gln His Ile Ser Phe	335	340	345
Ile Leu Val Gly Ile Ile Ile Val Thr Ser Ile Arg Gly Leu Leu	350	355	360
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Ser Ile Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser
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Lys Lys Ala Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala
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Cys Arg Leu Leu Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu
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Thr Ala Leu Lys Ala Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val
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Gly Asp Gly Phe Val Val Ile Ser Arg Ile Ser Pro Asn Pro Lys
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Cys Gly Lys Asn Gly Val Gly Val Leu Ile Trp Lys Val Pro Val
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Thr Asn Ser Cys Ile Pro Glu Ile Ile Thr Thr Lys Asp Pro Ile
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Pro	Thr	Thr	Thr	Pro	Pro	Ala	Pro	Ala	Ser	Thr	Ser	Ile	Pro	Arg
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Thr	Met	Ser	Thr	Glu	Thr	Glu	Pro	Phe	Val	Glu	Asn	Lys	Ala	Ala
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gggctgtgct gtgccttcca gagagcctg ctgttccctg tgtgcacacc	850
cctgcccgtg gagggcgagc tttgccatga ccccgccagc cggcttcttg	900
acctcatcac ctgggagcta gagcctgatg gagccttga ccgatgccct	950
tgtgccagtg gcctcctctg ccagcccccac agccacagcc tgggtgatgt	1000
gtgcaagccg accttcgtgg ggagccgtga ccaagatggg gagatcctgc	1050
tgccagaga ggtccccgat gagtatgaag ttggcagctt catggaggag	1100
gtgcgccagg agctggagga cctggagagg agcctgactg aagagatggc	1150
gctgggggag cctgcggtg ccgccgtgc actgctggga ggggaagaga	1200
tttagatctg gaccaggctg tgggtagatg tgcaatagaa atagctaatt	1250
tatttcccca ggtgtgtgct ttaggcgtgg gctgaccagg cttcttctca	1300
catcttcttc ccagtaagtt tcccctctgg cttgacagca tgagggtgtg	1350
tgcatttggt cagctcccc aggctgttct ccaggcttca cagtctggtg	1400
cttgggagag tcaggcaggg ttaaactgca ggagcagttt gccaccctg	1450
tccagattat tggctgcttt gcctctacca gttggcagac agcgtttgt	1500
tctacatggc tttgataatt gtttgagggg aggagatgga aacaatgtgg	1550
agtctccctc tgattggttt tggggaaatg tggagaagag tgccctgctt	1600
tgcaaacatc aacctggcaa aaatgcaaca aatgaatttt ccacgcagtt	1650
ctttccatgg gcataggtaa gctgtgcctt cagctgttgc agatgaaatg	1700
ttctgttcc cctgcattac atgtgtttat tcattccagca gtgttgctca	1750
gctcctacct ctgtgccagg gcagcatttt catatccaag atcaattccc	1800
tctctcagca cagcctgggg agggggtcat tgttctctc gtccatcagg	1850
gatctcagag gctcagagac tgcaagctgc ttgccaagt cacacagcta	1900
gtgaagacca gagcagtttc atctggttgt gactctaagc tcagtgtctc	1950
ctccactacc ccacaccagc cttggtgcca ccaaaagtgc tccccaaaag	2000
gaaggagaat gggatttttc ttgaggcatg cacatctgga attaaggtca	2050
aactaattct cacatccctc taaaagttaa ctactgttag gaacagcagt	2100
gttctcacag tgtggggcag ccgtccttct aatgaagaca atgatattga	2150
cactgtccct ctttggcagt tgcattagta actttgaaag gtatatgact	2200
gagcgtagca tacagggtta cctgcagaaa cagtacttag gtaattgtag	2250
ggcgaggatt ataaatgaaa ttgcaaaat cacttagcag caactgaaga	2300
caattatcaa ccacgtggag aaaatcaaac cgagcagggc tgtgtgaaac	2350
atggttgtaa tatgcgactg cgaacactga actctacgcc actccacaaa	2400
tgatgttttc aggtgtcatg gactgttgcc accatgtatt catccagagt	2450
tcttaaagtt taaagttgca catgattgta taagcatgct ttctttgagt	2500
tttaaatat gtataaacat aagttgcatt tagaaatcaa gcataaatca	2550
cttcaactgc aaaaaaaaa aaaaaaaaa aaaaaa	2586

<210> SEQ ID NO 8

<211> LENGTH: 350

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<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 8

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Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala
 1          5          10          15

Ala Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala
20          25          30

Pro Val Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala
35          40          45

Thr Leu Asn Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp
50          55          60

Thr Gln His Lys Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu
65          70          75

Glu Ala Ala Ala Lys Ala Ser Ser Glu Val Asn Leu Ala Asn Leu
80          85          90

Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr Lys Val Gly
95          100         105

Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile Thr Asn
110         115         120

Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr Ser
125         130         135

Val Gly Asp Glu Glu Gly Arg Arg Ser His Glu Cys Ile Ile Asp
140         145         150

Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln Phe Ala Ser Phe Gln
155         160         165

Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met Leu Cys Thr Arg
170         175         180

Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp Gly His Cys
185         190         195

Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys Asp Asn
200         205         210

Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly
215         220         225

Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
230         235         240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu
245         250         255

Leu Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly
260         265         270

Leu Leu Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys
275         280         285

Pro Thr Phe Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu
290         295         300

Pro Arg Glu Val Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu
305         310         315

Glu Val Arg Gln Glu Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu
320         325         330

Glu Met Ala Leu Gly Glu Pro Ala Ala Ala Ala Ala Ala Leu Leu
335         340         345

Gly Gly Glu Glu Ile
350

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<210> SEQ ID NO 9
<211> LENGTH: 1395
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 9

cggacgcgtg ggcggacgcg tgggggctgt gagaaagtgc caataaatac	50
atcatgcaac cccacggccc accttgtaga ctctctgtgc ccagggctga	100
tgtgcgtctt ccagggtac tcatccaaag gcctaatacca acgttctgtc	150
ttcaatctgc aaatctatgg ggtcctgggg ctcttctgga cccttaactg	200
ggtactggcc ctgggccaat gcgtcctcgc tggagccttt gcctccttct	250
actgggcctt ccacaagccc caggacatcc ctacottccc cttaatctct	300
gccttcaccc gcacactccg ttaccacact gggtcattgg catttgagc	350
cctcatcctg acccttgtag agatagcccc ggtcatcttg gagtatattg	400
accacaagct cagaggagtg cagaaccctg tagcccgctg catcatgtgc	450
tgtttcaagt gctgcctctg gtgtctggaa aaatttatca agttcctaaa	500
ccgcaatgca tacatcatga tcgccatcta cgggaagaat ttctgtgtct	550
cagccaaaaa tgcgttcattg ctactcatgc gaaacattgt cagggtggtc	600
gtcctggaca aagtcacaga cctgtgctg ttctttggga agctgctggg	650
ggtcggaggc gtgggggtcc tgtccttctt ttttttctcc ggtcgcatcc	700
cggggctggg taaagacttt aagagcccc acctcaacta ttactggctg	750
cccattcatg cctccatcct gggggcctat gtcatcgcca gcggcttctt	800
cagcgttttc ggcatgtgtg tggacacgct ctctctctgc ttcttggaag	850
acctggagcg gaacaacggc tccctggacc ggccacta catgtccaag	900
agccttctaa agattctggg caagaagaac gaggcgcccc cggacaacaa	950
gaagagggaag aagtgcagc tccggccctg atccaggact gcacccacc	1000
cccaccgtcc agccatccaa cctcacttcg ccttacaggt ctccattttg	1050
tggtaaaaaa aggttttagg ccaggcgccg tggctcacgc ctgtaatacca	1100
acacttttag aggtgagggc gggcggtatc cctgagtcag gatttcgaga	1150
ccagcctggc caacatggtg aaacctccgt ctctattaaa aatacaaaaa	1200
ttagccgaga gtggtggcat gcacctgtca tcccagctac tcgggaggct	1250
gaggcaggag aatcgcttga acccgggagg cagaggttgc agtgagccga	1300
gatcgcgcca ctgcactcca acctgggtga cagactctgt ctccaaaaca	1350
aaacaaacaa acaaaaagat ttatttaaag atattttgtt aactc	1395

<210> SEQ ID NO 10
<211> LENGTH: 321
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 10

Arg	Thr	Arg	Gly	Arg	Thr	Arg	Gly	Gly	Cys	Glu	Lys	Val	Pro	Ile
1					5				10					15

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

<210> SEQ ID NO 11
<211> LENGTH: 1901
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 11

gccccgcgcc	cggcgcggg	cgccgaagc	cgggagccac	cgccatggg	50
gcctgcctgg	gagcctgtc	cctgtcagc	tgcgcgtcct	gcctctgcgg	100
ctctgcccc	tgcatcctgt	gcagctgtg	ccccgccagc	cgcaactcca	150

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ccgtgagcgg cctcatcttc acgttcttcc tcttcctggg ggtgctggtg	200
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc	250
ctgggtgtgt gaggaggggg cgggatccc caccgtcctg cagggccaca	300
tcgactgtgg ctccctgctt ggctaccgag ctgtctaccg catgtgcttc	350
gccacggcgg ccttcttctt cttctttttc accctgctca tgctctgcgt	400
gagcagcagc cgggaccccc gggctgcat ccagaatggg ttttggttct	450
ttaagtctct gatcctgggt ggctcaccg tgggtgcctt ctacatccct	500
gacggctcct tcaccaacat ctggtttctac ttcggcgtcg tgggtcctt	550
cctcttcata ctcatccagc tgggtgctgt catcgacttt gcgcactcct	600
ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg	650
tacgcaggcc tcttcttctt cactctcctc ttctacttgc tgctgatcgc	700
ggccgtggcg ctgatgttca tgtactacac tgagccagc ggcgtccacg	750
agggcaaggt cttcatcagc ctcaacctca cctctgtgt ctgcgtgtcc	800
atcgctgtgt tcctgcccac ggtccaggac gccagccca actcgggtct	850
gctgcaggcc tcggtcatca ccctctacac catgtttgtc acctggtcag	900
ccctatccag tatccctgaa cagaaatgca accccattt gccaacccag	950
ctgggcaacg agacagtgtt ggcaggcccc gagggctatg agaccagtg	1000
gtgggatgcc ccgagcattg tgggcctcat catcttcctc ctgtgcaccc	1050
tcttcatcag tctgcgtccc tcagaccacc ggcaggtgaa cagcctgatg	1100
cagaccgagg agtgcccacc tatgctagac gccacacagc agcagcagca	1150
gcaggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg	1200
tcacctacag ctactccttc ttccacttct gcctgggtgt ggcctcactg	1250
cacgtcatga tgacgtctac caactggtac aagcccggtg agaccggaa	1300
gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg	1350
cagggctgct cctctacctg tggaccctgg tagccccact cctcctgcgc	1400
aaccgcgact tcagctgagg cagcctcaca gcctgccatc tgggtgcctcc	1450
tgccacctgg tgctctcgg ctcggtgaca gccaacctgc cccctcccca	1500
caccaatcag ccaggctgag cccccacccc tgccccagct ccaggacctg	1550
cccctgagcc gggccttcta gtcgtagtgc cttcagggtc cgaggagcat	1600
caggctcctg cagagcccca tccccccgcc acaccacac ggtggagctg	1650
cctcttctct cccctcctcc ctgttgccca tactcagcat ctcgatgaa	1700
agggctccct tgtcctcagg ctccacggga gcggggctgc tggagagagc	1750
ggggaactcc caccacagtg gggcatccgg cactgaagcc ctgggtgttc	1800
tggtcacgtc cccagggga ccctgcccc ttcttggaact tcgtgcctta	1850
ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa	1900
a	1901

<210> SEQ ID NO 12

<211> LENGTH: 457

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<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 12

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Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser
 1           5           10           15

Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro
 20           25           30

Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe
 35           40           45

Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly
 50           55           60

Val Glu Ser Gln Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly
 65           70           75

Ala Gly Ile Pro Thr Val Leu Gln Gly His Ile Asp Cys Gly Ser
 80           85           90

Leu Leu Gly Tyr Arg Ala Val Tyr Arg Met Cys Phe Ala Thr Ala
 95           100          105

Ala Phe Phe Phe Phe Phe Phe Thr Leu Leu Met Leu Cys Val Ser
 110          115          120

Ser Ser Arg Asp Pro Arg Ala Ala Ile Gln Asn Gly Phe Trp Phe
 125          130          135

Phe Lys Phe Leu Ile Leu Val Gly Leu Thr Val Gly Ala Phe Tyr
 140          145          150

Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe Tyr Phe Gly Val
 155          160          165

Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val Leu Leu Ile
 170          175          180

Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys Ala Glu
 185          190          195

Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe Thr
 200          205          210

Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe
 215          220          225

Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe
 230          235          240

Ile Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala
 245          250          255

Val Leu Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu
 260          265          270

Gln Ala Ser Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser
 275          280          285

Ala Leu Ser Ser Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro
 290          295          300

Thr Gln Leu Gly Asn Glu Thr Val Val Ala Gly Pro Glu Gly Tyr
 305          310          315

Glu Thr Gln Trp Trp Asp Ala Pro Ser Ile Val Gly Leu Ile Ile
 320          325          330

Phe Leu Leu Cys Thr Leu Phe Ile Ser Leu Arg Ser Ser Asp His
 335          340          345

Arg Gln Val Asn Ser Leu Met Gln Thr Glu Glu Cys Pro Pro Met
 350          355          360

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Leu Asp Ala Thr Gln Gln Gln Gln Gln Val Ala Ala Cys Glu
365 370 375

Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr
380 385 390

Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met
395 400 405

Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr Arg Lys Met
410 415 420

Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp
425 430 435

Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu
440 445 450

Leu Arg Asn Arg Asp Phe Ser
455

<210> SEQ ID NO 13
<211> LENGTH: 1572
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 13

cgggccagcc tggggcggcc ggccaggaac caccggttaa ggtgtcttct	50
ctttagggat ggtgaggttg gaaaaagact cctgtaacct tcctccagga	100
tgaaccacct gccagaagac atggagaacg ctctcaccgg gagccagagc	150
tcccatgctt ctctgcgcaa tatccattcc atcaaccca cacaactcat	200
ggccaggatt gagtccatg aaggaaggga aaagaaaggc atatctgatg	250
tcaggaggac tttctgtttg ttgtgcacct ttgacctctt attcgtaaca	300
ttactgtgga taatagagtt aaatgtgaat ggaggcattg agaacacatt	350
agagaaggag gtgatgcagt atgactacta ttcttcatat ttgatatat	400
ttcttctggc agtttttcga tttaaagtgt taatacttgc atatgctgtg	450
tgcagactgc gccattggtg ggcaatagcg ttgacaacgg cagtgaccag	500
tgccctttta ctagcaaaaag tgatcccttc gaagcttttc tctcaagggg	550
cttttggtta tgtgctgccc atcatttcac tcacccctgc ctggattgag	600
acgtgggtcc tggatttcaa agtgttacct caagaagcag aagaagaaaa	650
cagactcctg atagtccagg atgcttcaga gagggcagca cttataacctg	700
gtggctcttc tgatggtcag ttttattccc ctctgaatc cgaagcagga	750
tctgaagaag ctgaagaaaa acaggacagt gagaaccac ttttagaact	800
atgagtacta cttttgttaa atgtgaaaa ccctcacaga aagtcacga	850
ggcaaaaaga ggcaggcagt ggagtctccc tgtcgacagt aaagttgaaa	900
tggtgacgtc cactgctggc tttattgaac agctaataaa gatttattta	950
ttgtaatacc tcacaaacgt tgtaccatat ccatgcacat ttagttgcct	1000
gcctgtggct ggtaaggtaa tgtcatgatt catcctctct tcagtgagac	1050
tgagcctgat gtgttaacaa atagggtgaag aaagtcttgt gctgtattcc	1100
taatcaaaag acttaataata ttgaagtaac acttttttag taagcaagat	1150

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acctttttat ttcaattcac agaatggaat ttttttgttt catgtctcag	1200
atattttttg tatttctttt ttaacactct acatttcctt tgttttttta	1250
ctcatgcaca tgtgctcttt gtacagtttt aaaaagtgtataaaaatctg	1300
acatgtcaat gtggctagtt ttatttttct tgttttgcat tatgtgtatg	1350
gcctgaagtgt ttggacttgc aaaaggggaa gaaaggaatt gcgaatacat	1400
gtaaaatgtc accagacatt tgtattattt ttatcatgaa atcatgtttt	1450
tctctgattg ttctgaaatg ttctaaatac tcttattttg aatgcacaaa	1500
atgacttaaa ccattcatat catgtttcct ttgcgttcag ccaatttcaa	1550
ttaaaatgaa ctaaattaaa aa	1572

<210> SEQ ID NO 14

<211> LENGTH: 234

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 14

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

<210> SEQ ID NO 15

-continued

<211> LENGTH: 2768

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 15

actcgaacgc agttgcttcg ggaccagga cccctcggg ccgacccgc	50
caggaaagac tgaggccgcg gcctgccccg cccggctccc tgcgcgcgcg	100
ccgcctcccg ggacagaaga tgtgtcccag ggtccctctg ctgctgccgc	150
tgtccttct actggccctg gggcctgggg tgcagggtg cccatccggc	200
tgccagtga gccagccaca gacagtcttc tgcactgcc gccaggggac	250
cacggtgcc cgagactgc caccgcacac ggtggggctg tacgtctttg	300
agaacggcat caccatgctc gacgcaggca gctttgccg cctgccgggc	350
ctgcagctcc tggacctgtc acagaaccag atcgccagcc tgcccagcgg	400
ggtcttccag cactcgcca acctcagcaa cctggacctg acggccaaca	450
ggctgcatga aatcaccaat gagaccttc gtggcctgcg gcgcctcgag	500
cgcctctacc tgggcaagaa ccgcctccgc cacatccagc ctggtgcctt	550
cgacacgctc gaccgcctcc tggagctcaa gctgcaggac aacgagctgc	600
gggcactgcc cccgctgcgc ctgccccgcc tegtgtgtgt ggacctcagc	650
cacaacagcc tcctggccct ggagcccgcc atcctggaca ctgccaacgt	700
ggagggcgtg cggctggctg gtctggggct gcagcagctg gacgaggggc	750
tcttcagcgc cttgcgcaac ctccacgacc tggatgtgtc cgacaaccag	800
ctggagcgag tgccacctgt gatccgaggc ctccggggcc tgacgcgcct	850
gcggctggcc ggcaacaccc gcattgcccc gctgcggccc gaggacctgg	900
ccggcctggc tgccctgcag gagctggatg tgagcaacct aagcctgcag	950
gccctgcctg gcgacctctc gggcctcttc cccgcctgc ggtgtgtggc	1000
agctgccgcg aacccttca actgcgtgtg cccctcagc tggtttgccc	1050
cctgggtgcg cgagagccac gtcacactgg ccagccctga ggagacgcgc	1100
tgccacttcc cgccaagaa cgctggcccg ctgctcctgg agcttgacta	1150
cgccgacttt ggtgcccag ccaccaccac cacagccaca gtgccacca	1200
cgaggcccggt ggtgcgggag cccacagcct tgtcttctag cttggctcct	1250
acctggctta gccccacagc gccggccact gagccccca gccgcacctc	1300
cactgcccca ccgactgtag ggctgtccc ccagccccag gactgcccac	1350
cgctccactg cctcaatggg ggcacatgcc acctggggac acggcaccac	1400
ctggcggtgt tgtgccccga aggttcacg ggctgtact gtgagagcca	1450
gatggggcag gggacacggc ccagccctac accagtacg ccgaggccac	1500
cacggtccct gaccctgggc atcgagccgg tgagcccccac ctccctgcgc	1550
gtggggctgc agcgctacct ccaggggagc tccgtgcagc tcaggagcct	1600
ccgtctcacc tatcgcaacc tatcgggccc tgataagcgg ctggtgacgc	1650
tgcgactgcc tgcctcgctc gctgagtaca cggtcaccca gctgcggccc	1700
aacgccactt actccgtctg tgtcatgcct ttggggcccg ggcgggtgcc	1750

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ggagggcgag gaggcctgcg gggaggccca tacaccccca gccgtccact      1800
ccaaccacgc ccagtcacc caggcccgcg agggcaacct gccgtcctc      1850
attgcgcccg ccctggccgc ggtgctcctg gccgcgctgg ctgcggtggg      1900
ggcagcctac tgtgtgcggc gggggcgggc catggcagca gcggctcagg      1950
acaaagggca ggtggggcca ggggctgggc ccctggaact ggagggagtg      2000
aaggtccctt tggagccagg ccggaaggca acagaggcggt gtggagaggc      2050
cctgccacgc gggctctgagt gtgaggtgcc actcatgggc tccccagggc      2100
ctggcctcca gtcaccctc caccgaaagc cctacatcta agccagagag      2150
agacagggca gctggggccg ggctctcagc cagtgagatg gccagccccc      2200
tctctgtgcc acaccacgta agttctcagt cccaacctcg gggatgtgtg      2250
cagacagggc tgtgtgacca cagctgggco ctgttccctc tggacctcgg      2300
tctctctatc tgtgagatgc tgtggcccag ctgacgagcc ctaacgtccc      2350
cagaaccgag tgcctatgag gacagtgtcc gccctgccct ccgcaactgt      2400
cagtcctctg gcacggcggg ccctgccatg tgctggtaac gcatgcctgg      2450
gtcctgtctg gctctccac tccaggcgga ccctgggggc cagtgaagga      2500
agctcccgga aagagcagag ggagagcggg taggcggctg tgtgactcta      2550
gtcttggccc caggaagcga aggaacaaaa gaaactggaa aggaagatgc      2600
tttaggaaca tgttttgctt ttttaaaata tataatatta taagagatcc      2650
tttccatttt attctgggaa gatgtttttc aaactcagag acaaggactt      2700
tggtttttgt aagacaaacg atgatatgaa ggccttttgt aagaaaaaat      2750
aaaagatgaa gtgtgaaa      2768

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<210> SEQ ID NO 16

<211> LENGTH: 673

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 16

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

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Ile Arg His Ile Gln Pro Gly Ala Phe Asp Thr Leu Asp Arg Leu	140	145	150
Leu Glu Leu Lys Leu Gln Asp Asn Glu Leu Arg Ala Leu Pro Pro	155	160	165
Leu Arg Leu Pro Arg Leu Leu Leu Leu Asp Leu Ser His Asn Ser	170	175	180
Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala Asn Val Glu	185	190	195
Ala Leu Arg Leu Ala Gly Leu Gly Leu Gln Gln Leu Asp Glu Gly	200	205	210
Leu Phe Ser Arg Leu Arg Asn Leu His Asp Leu Asp Val Ser Asp	215	220	225
Asn Gln Leu Glu Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly	230	235	240
Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu	245	250	255
Arg Pro Glu Asp Leu Ala Gly Leu Ala Ala Leu Gln Glu Leu Asp	260	265	270
Val Ser Asn Leu Ser Leu Gln Ala Leu Pro Gly Asp Leu Ser Gly	275	280	285
Leu Phe Pro Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe	290	295	300
Asn Cys Val Cys Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu	305	310	315
Ser His Val Thr Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe	320	325	330
Pro Pro Lys Asn Ala Gly Arg Leu Leu Leu Glu Leu Asp Tyr Ala	335	340	345
Asp Phe Gly Cys Pro Ala Thr Thr Thr Thr Ala Thr Val Pro Thr	350	355	360
Thr Arg Pro Val Val Arg Glu Pro Thr Ala Leu Ser Ser Ser Leu	365	370	375
Ala Pro Thr Trp Leu Ser Pro Thr Ala Pro Ala Thr Glu Ala Pro	380	385	390
Ser Pro Pro Ser Thr Ala Pro Pro Thr Val Gly Pro Val Pro Gln	395	400	405
Pro Gln Asp Cys Pro Pro Ser Thr Cys Leu Asn Gly Gly Thr Cys	410	415	420
His Leu Gly Thr Arg His His Leu Ala Cys Leu Cys Pro Glu Gly	425	430	435
Phe Thr Gly Leu Tyr Cys Glu Ser Gln Met Gly Gln Gly Thr Arg	440	445	450
Pro Ser Pro Thr Pro Val Thr Pro Arg Pro Pro Arg Ser Leu Thr	455	460	465
Leu Gly Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu	470	475	480
Gln Arg Tyr Leu Gln Gly Ser Ser Val Gln Leu Arg Ser Leu Arg	485	490	495
Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr	500	505	510

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

<210> SEQ ID NO 17
<211> LENGTH: 1672
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 17

gcagcggcga ggcggcgggtg gtggctgagt ccgtgggtggc agaggcgaag	50
gcgacagctc atgcgggtcc ggatagggct gacgctgctg ctgtgtgcgg	100
tgctgctgag cttggcctcg gcgtcctcgg atgaagaagg cagccaggat	150
gaatccttag attccaagac tactttgaca tcagatgagt cagtaaagga	200
ccatactact gcaggcagag tagttgctgg tcaaatatth cttgattcag	250
aagaatctga attagaatcc tctattcaag aagaggaaga cagcctcaag	300
agccaagagg gggaaagtgt cacagaagat atcagctttc tagagtctcc	350
aaatccagaa aacaaggact atgaagagcc aaagaaagta cggaaaccag	400
ctttgaccgc cattgaaggc acagcacatg gggagccctg ccacttcctt	450
tttcttttcc tagataagga gtatgatgaa tgtacatcag atgggaggga	500
agatggcaga ctgtggtgtg ctacaaccta tgactacaaa gcagatgaaa	550
agtggggctt ttgtgaaact gaagaagagg ctgctaagag acggcagatg	600
caggaagcag aaatgatgta tcaaactgga atgaaatcc ttaatggaag	650
caataagaaa agccaaaaaa gagaagcata tcggtatctc caaaaggcag	700
caagcatgaa ccataccaaa gccctggaga gagtgtcata tgctctttta	750
tttggtgatt acttgccaca gaatatccag gcagcgagag agatgtttga	800
gaagctgact gaggaaggct ctccaaggg acagactgct cttggctttc	850
tgatgcctc tggacttggg gttaattcaa gtcaggcaaa ggctcttgta	900

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tattatacat ttggagctct tgggggcaat ctaatagccc acatggtttt 950
ggtaagtaga ctttagtgga aggctaataa tattaacatc agaagaattt 1000
gtggtttata gcggccacaa ctttttcagc tttcatgac cagatttgct 1050
tgtattaaga ccaaatattc agttgaactt cttcaaatt cttgttaatg 1100
gatataacac atggaatcta catgtaaatg aaagttgggtg gagtccacaa 1150
tttttcttta aaatgattag ttggctgat tgcccctaaa aagagagatc 1200
tgataaatgg ctctttttta attttctctg agttggaatt gtcagaatca 1250
ttttttacat tagattatca taattttaaa aatttttctt tagtttttca 1300
aaattttgta aatggtggct atagaaaaac aacatgaaat attatacaat 1350
attttgcaac aatgccctaa gaattgttaa aattcatgga gttatttggtg 1400
cagaatgact ccagagagct ctactttctg ttttttactt ttcatgattg 1450
gctgtcttcc catttattct ggtcatttat tgctagtgc actgtgcctg 1500
cttcagtag tctcattttc cctattttgc taatttgta ctttttctt 1550
gctaatttgg aagattaact cttttttaat aaaattatgt ctaagattaa 1600
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
aaaaaaaaa aaaaaaaaaa aa 1672

<210> SEQ ID NO 18

<211> LENGTH: 301

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 18

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

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

<210> SEQ ID NO 19
<211> LENGTH: 1508
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 19

aattcagatt ttaagcccat tctgcagtgg aatttcatga actagcaaga	50
ggacaccatc ttcttgtatt atacaagaaa ggagtgtacc tatcacacac	100
agggggaaaa atgctctttt ggggtgctagg cctcctaatc ctctgtggtt	150
ttctgtggag tcgtaaagga aaactaaaga ttgaagacat cactgataag	200
tacattttta tcaactggatg tgactcgggc tttggaaact tggcagccag	250
aacttttgat aaaaagggat ttcattgtaat cgctgcctgt ctgactgaat	300
caggatcaac agctttaaag gcagaaacct cagagagact tcgtactgtg	350
cttctggatg tgaccgacct agagaatgtc aagaggactg cccagtgggt	400
gaagaaccaa gttggggaga aaggtctctg gggctctgac aataatgctg	450
gtgttcccgg cgtgctggct cccactgact ggctgacact agaggactac	500
agagaaccta ttgaagtga cctgtttgga ctcactcagt tgacactaaa	550
tatgcttcct ttggtcaaga aagctcaagg gagagttatt aatgtctcca	600
gtgttgaggg tcgccttgca atcgttggag ggggctatac tccatccaaa	650
tatgcagtgg aaggtttcaa tgacagctta agacgggaca tgaaagcttt	700
tggtgtgcac gtctcatgca ttgaaccagg attgttcaa acaaacttgg	750
cagatccagt aaaggtaatt gaaaaaaac tcgccatttg ggagcagctg	800
tctccagaca tcaaacaaca atatggagaa gggtacattg aaaaaagtct	850
agacaaactg aaaggcaata aatcctatgt gaacatggac ctctctccgg	900
tggtagagtg catggaccac gctctaacaa gtctcttccc taagactcat	950
tatgccgctg gaaaagatgc caaaattttc tggatacctc tgtctcacat	1000
gccagcagct ttgcaagact ttttattgtt gaaacagaaa gcagagctgg	1050

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ctaatacccaa ggcagtgatga ctacagctaac cacaatatgtc tcctccaggc 1100
tatgaaattg gccgatttca agaacacatc tccttttcaa ccccatctct 1150
tatctgctcc aacctggact catttagatc gtgcttattt ggattgcaaa 1200
aggagatccc accatcgctg gtggtatccc agggtcctctg ctcaagtttt 1250
ctttgaaaag gagggtctga atggtacatc acataggcaa gtcctgccct 1300
gtatttaggc ttgacctgct tgggtgatg taagggaaat tgaaagactt 1350
gcccattcaa aatgatcttt accgtggcct gcccctgct tatggctccc 1400
agcatttaca gtaacttgat aatgttaagt atcatctctt atctaaatat 1450
taaaagataa gtcaacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaa 1508

<210> SEQ ID NO 20

<211> LENGTH: 319

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 20

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

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Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser
245 250 255
Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His
260 265 270
Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys
275 280 285
Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala
290 295 300
Leu Gln Asp Phe Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn
305 310 315
Pro Lys Ala Val

<210> SEQ ID NO 21
<211> LENGTH: 1849
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 21

ctgaggcggc ggtagcatgg agggggagag tacgtcggcg gtgctctcgg 50
gctttgtgct cggcgccactc gctttccagc acctcaacac ggactcggac 100
acggaagggtt ttcttcttgg ggaagtaaaa ggtgaagcca agaacagcat 150
tactgattcc caaatggatg atgttgaagt tgtttatata attgacattc 200
agaaatatat tccatgctat cagcttttta gcttttataa ttcttcaggc 250
gaagtaaatg agcaagcact gaagaaaata ttatcaaatg tcaaaaagaa 300
tgtggtaggt tggtaacaaat tccgtcgtca ttcagatcag atcatgacgt 350
ttagagagag gctgcttcac aaaaacttgc aggagcattt ttcaaaccaa 400
gaccttggtt ttctgctatt aacaccaagt ataataacag aaagctgctc 450
tactcatcga ctggaacatt ccttatataa acctcaaaaa ggactttttc 500
acagggtaacc tttagtgggt gccaatctgg gcatgtctga acaactgggt 550
tataaaactg tatcaggttc ctgtatgtcc actggtttta gccgagcagt 600
acaaacacac agctctaata tttttgaaga agatggatcc ttaaaggagg 650
tacataagat aaatgaaatg tatgcttcat tacaagagga attaaagagt 700
atatgcaaaa aagtgaaga cagtgaacaa gcagtagata aactagtaaa 750
ggatgtaaac agattaaaac gagaaattga gaaaaggaga ggagcacaga 800
ttcaggcagc aagagagaag aacatccaaa aagaccctca ggagaacatt 850
tttctttgtc aggcattacg gacctttttt ccaaattctg aatttcttca 900
ttcatgtgtt atgtctttta aaaatagaca tgtttctaaa agtagctgta 950
actacaacca ccatctcgat gtagtagaca atctgacctt aatggtagaa 1000
cacactgaca ttctgaagc tagtccagct agtacaccac aaatcattaa 1050
gcataaagcc ttagacttag atgacagatg gcaattcaag agatctcggg 1100
tgtagatata acaagacaaa cgatctaaag caaatactgg tagtagtaac 1150
caagataaag catccaaaat gagcagccca gaaacagatg aagaaattga 1200
aaagatgaag ggttttggtg aatattcacg gtctoctaca ttttgatcct 1250

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tttaacctta caaggagatt tttttatttg gctgatgggt aaagccaaac	1300
atttctattg tttttactat gttgagctac ttgcagtaag ttcatttggt	1350
tttactatgt tcacctgttt gcagtaatac acagataact cttagtgcac	1400
ttacttcaca aagtactttt tcaaacatca gatgctttta tttccaaacc	1450
tttttttcac ctttcactaa gttgttgagg ggaaggctta cacagacaca	1500
ttcttttagaa ttgaaaagt gagaccaggc acagtggctc acacctgtaa	1550
ttccagcact tagggaagac aagtcaggag gattgattga agctaggagt	1600
tagagaccag cctgggcaac gtattgagac catgtctatt aaaaaataaa	1650
atggaaaagc aagaatagcc ttattttcaa aatatggaaa gaaatttata	1700
tgaaaattta tctgagtcat taaaattctc cttaagtgat acttttttag	1750
aagtacatta tggctagagt tgccagataa aatgctggat atcatgcaat	1800
aaatttgcaa aacatcatct aaaatttaaa aaaaaaaaaa aaaaaaaaaa	1849

<210> SEQ ID NO 22

<211> LENGTH: 409

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 22

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

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Leu Lys Ser Ile Cys Lys Lys Val Glu Asp Ser Glu Gln Ala Val
230 235 240
Asp Lys Leu Val Lys Asp Val Asn Arg Leu Lys Arg Glu Ile Glu
245 250 255
Lys Arg Arg Gly Ala Gln Ile Gln Ala Ala Arg Glu Lys Asn Ile
260 265 270
Gln Lys Asp Pro Gln Glu Asn Ile Phe Leu Cys Gln Ala Leu Arg
275 280 285
Thr Phe Phe Pro Asn Ser Glu Phe Leu His Ser Cys Val Met Ser
290 295 300
Leu Lys Asn Arg His Val Ser Lys Ser Ser Cys Asn Tyr Asn His
305 310 315
His Leu Asp Val Val Asp Asn Leu Thr Leu Met Val Glu His Thr
320 325 330
Asp Ile Pro Glu Ala Ser Pro Ala Ser Thr Pro Gln Ile Ile Lys
335 340 345
His Lys Ala Leu Asp Leu Asp Asp Arg Trp Gln Phe Lys Arg Ser
350 355 360
Arg Leu Leu Asp Thr Gln Asp Lys Arg Ser Lys Ala Asn Thr Gly
365 370 375
Ser Ser Asn Gln Asp Lys Ala Ser Lys Met Ser Ser Pro Glu Thr
380 385 390
Asp Glu Glu Ile Glu Lys Met Lys Gly Phe Gly Glu Tyr Ser Arg
395 400 405

Ser Pro Thr Phe

<210> SEQ ID NO 23
<211> LENGTH: 2651
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 23

ggcacagccg cgcgggcgag ggcagagtca gccgagccga gtccagcccg 50
acgagcggac cagcgcaggg cagcccaagc agcgcgcagc gaacgcccgc 100
cgccgcccac accctctgcg gtccccgcgg cgcctgccac ccttccctcc 150
ttccccgcgt ccccgctcgc ccggccagtc agcttgccgg gttcgtgcc 200
ccgcgaaacc ccgaggtcac cagcccgcg cctctgettcc ctgggccgcg 250
cgccgcctcc acgcccctct tctcccctgg cccggcgccct ggcaccgggg 300
accgttgccct gacgcgaggc ccagctctac ttttcgcccc gcgtctcctc 350
cgctgctcg cctcttccac caactccaac tccttctccc tccagctcca 400
ctcgctagtc cccgactccg ccagccctcg gcccgctgcc gtagcgccgc 450
ttcccgctcg gtcccaaagg tgggaacgcg tccgccccgg cccgcacccat 500
ggcacggttc ggcttgcccg cgcttctctg caccctggca gtgctcagcg 550
ccgcgctgct ggctgccgag ctcaagtcca aaagttgctc ggaagtgcga 600
cgtctttacg tgtccaaagg cttcaacaag aacgatgccc cctccacga 650
gatcaacggt gatcatttga agatctgtcc ccagggttct acctgctgct 700
ctcaagagat ggaggagaag tacagcctgc aaagtaaaga tgatttcaaa 750

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agtgtggcca gcgaacagtg caatcatttg caagctgtct ttgcttcacg	800
ttacaagaag tttgatgaat tcttcaaaga actacttgaa aatgcagaga	850
aatccctgaa tgatatgttt gtgaagacat atggccattt atacatgcaa	900
aattctgagc tatttaaaga tctcttcgta gagttgaaac gttactacgt	950
gggtgggaaat gtgaacctgg aagaaatgct aaatgacttc tgggctcgcc	1000
tcctggagcg gatgttcgcg ctggtgaact ccagtagcca ctttacagat	1050
gagtatctgg aatgtgtgag caagtatacg gagcagctga agcccttcgg	1100
agatgtccct cgcaaatga agctccaggt tactcgtgct tttgtagcag	1150
cccgtacttt cgctcaaggc ttagcggttg cgggagatgt cgtgagcaag	1200
gtctccgtgg taaacccac agcccagtg acccatgccc tgttgaagat	1250
gatctactgc tcccactgcc ggggtctcgt gactgtgaag ccatgttaca	1300
actactgctc aaacatcatg agaggctgtt tggccaacca aggggatctc	1350
gattttgaat ggaacaattt catagatgct atgctgatgg tggcagagag	1400
gctagagggg ctttcaaca ttgaatcggg catggatccc atcgatgtga	1450
agattttctga tgctattatg aacatgcagg ataatagtgt tcaagtgtct	1500
cagaaggttt tccagggatg tggaccccc aagcccctcc cagctggacg	1550
aatttctcgt tccatctctg aaagtgcctt cagtgtctgc ttcagaccac	1600
atcaccccca ggaacgcca accacagcag ctggcactag tttggaccga	1650
ctggttactg atgtcaagga gaaactgaaa caggccaaga aattctggtc	1700
ctcccttcgc agcaacgttt gcaacgatga gaggatggct gcaggaaacg	1750
gcaatgagga tgactgttgg aatgggaaa gcaaaagcag gtacctgttt	1800
gcagtgcagc gaaatggatt agccaaccag ggcaacaacc cagaggtcca	1850
ggttgacacc agcaaaccag acatactgat cttcgtcaa atcatggctc	1900
ttcagtgatg gaccagcaag atgaagaatg catacaatgg gaacgacgtg	1950
gacttctttg atatcagtga tgaaagtatg ggagaaggaa gtggaagtgg	2000
ctgtgagtat cagcagtgcc cttcagagtt tgactacaat gccactgacc	2050
atgtctggga gagtgccaat gagaagccg acagtgtggt gtccgtcct	2100
ggggcacagg cctacctcct cactgtcttc tgcattctgt tcctggttat	2150
gcagagagag tggagataat tctcaaacctc tgagaaaaag tgttcacaa	2200
aaagttaaaa ggcaccagtt atcacttttc taccatccta gtgactttgc	2250
tttttaaatg aatggacaac aatgtacagt ttttactatg tggccactgg	2300
tttaagaagt gctgactttg ttttctcatt cagttttggg aggaaaagg	2350
actgtgcatt gatttggttc ctgctcccc aaaccatgtt aaacgtggct	2400
aacagtgtag gtacagaact atagttagtt gtgcatttgt gattttatca	2450
ctctattatt tgtttgtatg ttttttctc atttcgtttg tgggtttttt	2500
tttccaactg tgatctcgcc ttgtttctta caagcaaac agggccctt	2550
cttggcacgt aacatgtacg tttttctgaa atattaaata gctgtacaga	2600
agcagggtttt atttatcatg ttatcttatt aaaagaaaa gcccaaaaag	2650

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2651

<210> SEQ ID NO 24

<211> LENGTH: 556

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 24

Met Ala Arg Phe Gly Leu Pro Ala Leu Leu Cys Thr Leu Ala Val
1 5 10 15

Leu Ser Ala Ala Leu Leu Ala Ala Glu Leu Lys Ser Lys Ser Cys
20 25 30

Ser Glu Val Arg Arg Leu Tyr Val Ser Lys Gly Phe Asn Lys Asn
35 40 45

Asp Ala Pro Leu His Glu Ile Asn Gly Asp His Leu Lys Ile Cys
50 55 60

Pro Gln Gly Ser Thr Cys Cys Ser Gln Glu Met Glu Glu Lys Tyr
65 70 75

Ser Leu Gln Ser Lys Asp Asp Phe Lys Ser Val Val Ser Glu Gln
80 85 90

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

Asp Glu Phe Phe Lys Glu Leu Leu Glu Asn Ala Glu Lys Ser Leu
110 115 120

Asn Asp Met Phe Val Lys Thr Tyr Gly His Leu Tyr Met Gln Asn
125 130 135

Ser Glu Leu Phe Lys Asp Leu Phe Val Glu Leu Lys Arg Tyr Tyr
140 145 150

Val Val Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp
155 160 165

Ala Arg Leu Leu Glu Arg Met Phe Arg Leu Val Asn Ser Gln Tyr
170 175 180

His Phe Thr Asp Glu Tyr Leu Glu Cys Val Ser Lys Tyr Thr Glu
185 190 195

Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Leu Gln
200 205 210

Val Thr Arg Ala Phe Val Ala Ala Arg Thr Phe Ala Gln Gly Leu
215 220 225

Ala Val Ala Gly Asp Val Val Ser Lys Val Ser Val Val Asn Pro
230 235 240

Thr Ala Gln Cys Thr His Ala Leu Leu Lys Met Ile Tyr Cys Ser
245 250 255

His Cys Arg Gly Leu Val Thr Val Lys Pro Cys Tyr Asn Tyr Cys
260 265 270

Ser Asn Ile Met Arg Gly Cys Leu Ala Asn Gln Gly Asp Leu Asp
275 280 285

Phe Glu Trp Asn Asn Phe Ile Asp Ala Met Leu Met Val Ala Glu
290 295 300

Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile
305 310 315

Asp Val Lys Ile Ser Asp Ala Ile Met Asn Met Gln Asp Asn Ser
320 325 330

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Val	Gln	Val	Ser	Gln	Lys	Val	Phe	Gln	Gly	Cys	Gly	Pro	Pro	Lys
			335						340					345
Pro	Leu	Pro	Ala	Gly	Arg	Ile	Ser	Arg	Ser	Ile	Ser	Glu	Ser	Ala
			350						355					360
Phe	Ser	Ala	Arg	Phe	Arg	Pro	His	His	Pro	Glu	Glu	Arg	Pro	Thr
			365						370					375
Thr	Ala	Ala	Gly	Thr	Ser	Leu	Asp	Arg	Leu	Val	Thr	Asp	Val	Lys
			380						385					390
Glu	Lys	Leu	Lys	Gln	Ala	Lys	Lys	Phe	Trp	Ser	Ser	Leu	Pro	Ser
			395						400					405
Asn	Val	Cys	Asn	Asp	Glu	Arg	Met	Ala	Ala	Gly	Asn	Gly	Asn	Glu
			410						415					420
Asp	Asp	Cys	Trp	Asn	Gly	Lys	Gly	Lys	Ser	Arg	Tyr	Leu	Phe	Ala
			425						430					435
Val	Thr	Gly	Asn	Gly	Leu	Ala	Asn	Gln	Gly	Asn	Asn	Pro	Glu	Val
			440						445					450
Gln	Val	Asp	Thr	Ser	Lys	Pro	Asp	Ile	Leu	Ile	Leu	Arg	Gln	Ile
			455						460					465
Met	Ala	Leu	Arg	Val	Met	Thr	Ser	Lys	Met	Lys	Asn	Ala	Tyr	Asn
			470						475					480
Gly	Asn	Asp	Val	Asp	Phe	Phe	Asp	Ile	Ser	Asp	Glu	Ser	Ser	Gly
			485						490					495
Glu	Gly	Ser	Gly	Ser	Gly	Cys	Glu	Tyr	Gln	Gln	Cys	Pro	Ser	Glu
			500						505					510
Phe	Asp	Tyr	Asn	Ala	Thr	Asp	His	Ala	Gly	Lys	Ser	Ala	Asn	Glu
			515						520					525
Lys	Ala	Asp	Ser	Ala	Gly	Val	Arg	Pro	Gly	Ala	Gln	Ala	Tyr	Leu
			530						535					540
Leu	Thr	Val	Phe	Cys	Ile	Leu	Phe	Leu	Val	Met	Gln	Arg	Glu	Trp
			545						550					555

Arg

<210> SEQ ID NO 25
<211> LENGTH: 870
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 25

ctcgccctca aatgggaacg ctggcctggg actaaagcat agaccaccag	50
gctgagtatc ctgacctgag tcatccccag ggatcaggag cctccagcag	100
ggaaccttcc attatattct tcaagcaact tacagctgca cgcacagttg	150
cgatgaaagt tctaattctt tccctcctcc tgttgctgcc actaatgctg	200
atgtccatgg tctctagcag cctgaatcca ggggtcgcca gaggccacag	250
ggaccgaggg caggcttcta ggagatggct ccaggaaggc ggccaagaat	300
gtgagtgcaa agattggttc ctgagagccc cgagaagaaa attcatgaca	350
gtgtctgggc tgccaaagaa gcagtgcctt tgtgatcatt tcaagggcaa	400
tgtgaagaaa acaagacacc aaaggcacca cagaaagcca aacaagcatt	450
ccagagcctg ccagcaattt ctcaacaat gtcagctaag aagctttgct	500

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ctgcctttgt aggagctctg agcgcccaact cttccaatta aacattctca	550
gccaagaaga cagtgagcac acctaccaga cactcttctt ctcccacctc	600
actctcccac tgtacccacc cctaaatcat tccagtgtc tcaaaaagca	650
tgtttttcaa gatcattttg ttgtgtgtc tctctagtgt cttcttctct	700
cgtcagtctt agcctgtgcc ctccccttac ccaggcttag gcttaattac	750
ctgaaagatt ccaggaaaact gtagcttcct agctagtgtc atttaacctt	800
aatgcaatc aggaaagtag caaacagaag tcaataaata tttttaaatg	850
tcaaaaaaaaa aaaaaaaaaa	870

<210> SEQ ID NO 26
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 26

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

<210> SEQ ID NO 27
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 27

ggacgccagc gcctgcagag gctgagcagg gaaaaagcca gtgccccagc	50
ggaagcacag ctgagagctg gtctgccatg gacatcctgg tcccactcct	100
gcagctgtgt gtgtgtcttc ttacctgtcc cctgcacctc atggctctgc	150
tgggtgtgtg gcagcccctg tgcaaaagct acttccccta cctgatggcc	200
gtgctgactc ccaagagcaa ccgcaagatg gagagcaaga aacgggagct	250
cttcagccag ataaaggggc ttacaggagc ctccgggaaa gtggccctac	300
tggagctggg ctgcggaacc ggagccaact ttcagttcta cccaccgggc	350
tgcagggtca cctgcctaga cccaaatccc cactttgaga agttcctgac	400
aaagagcatg gctgagaaca ggcacctcca atatgagcgg tttgtggtgg	450
ctcctggaga ggacatgaga cagctggctg atggctccat ggatgtggtg	500

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gtctgcactc tgggtgctgtg ctctgtgcag agcccaagga aggtcctgca	550
ggaggtccgg agagtactga gaccgggagg tgtgctcttt ttctgggagc	600
atgtggcaga accatatgga agctgggcct tcatgtggca gcaagttttc	650
gagcccacct ggaaacacat tggggatggc tgctgcctca ccagagagac	700
ctggaaggat cttgagaacg ccagtttctc cgaaatccaa atggaacgac	750
agccccctcc cttgaagtgg ctacctgttg ggccccacat catgggaaag	800
gctgtcaaac aatctttccc aagctccaag gcaactcattt gctccttccc	850
cagcctccaa ttagaacaag ccaccacca gcctatctat cttccactga	900
gagggaccta gcagaatgag agaagacatt catgtaccac ctactagtcc	950
ctctctcccc aacctctgcc agggcaatct ctaacttcaa tccgccttc	1000
gacagtga aaagctctact tctacgtga ccagggagg aaacactagg	1050
accctgttgt atcctcaact gcaagtttct ggactagtct cccaacgttt	1100
gcctcccaat gttgtccctt tccttcgttc ccatggtaaa gctcctctcg	1150
ctttcctcct gaggctacac ccatgcgtct ctaggaactg gtcacaaaag	1200
tcatggtgcc tgcacccctg ccaagccccc ctgaccctct ctccccacta	1250
ccaccttctt cctgagctgg gggcaccagg gagaatcaga gatgctgggg	1300
atgccagagc aagactcaaa gaggcagagg ttttgttctc aaatatTTTT	1350
taataaatag acgaaaccac g	1371

<210> SEQ ID NO 28

<211> LENGTH: 277

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 28

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

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Pro Gly Gly Val Leu Phe Phe Trp Glu His Val Ala Glu Pro Tyr
170 175 180

Gly Ser Trp Ala Phe Met Trp Gln Gln Val Phe Glu Pro Thr Trp
185 190 195

Lys His Ile Gly Asp Gly Cys Cys Leu Thr Arg Glu Thr Trp Lys
200 205 210

Asp Leu Glu Asn Ala Gln Phe Ser Glu Ile Gln Met Glu Arg Gln
215 220 225

Pro Pro Pro Leu Lys Trp Leu Pro Val Gly Pro His Ile Met Gly
230 235 240

Lys Ala Val Lys Gln Ser Phe Pro Ser Ser Lys Ala Leu Ile Cys
245 250 255

Ser Phe Pro Ser Leu Gln Leu Glu Gln Ala Thr His Gln Pro Ile
260 265 270

Tyr Leu Pro Leu Arg Gly Thr
275

<210> SEQ ID NO 29
<211> LENGTH: 494
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 29

caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50

aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100

gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150

gattgggcct tctttccccc ttcttctctg tgtctcctgc ctcatcggcc 200

tgcccatgacc tgcagccaag ccagagcccg tggggaaggg gagaaagtgg 250

gggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300

ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350

atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400

cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450

taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> SEQ ID NO 30
<211> LENGTH: 73
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 30

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Lys Gly
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

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<210> SEQ ID NO 31	
<211> LENGTH: 1660	
<212> TYPE: DNA	
<213> ORGANISM: Homo Sapien	
<400> SEQUENCE: 31	
gtttgaattc cttcaactat acccacagtc caaaagcaga ctactgtgt	50
cccaggctac cagttcctcc aagcaagtca tttcccttat ttaaccgatg	100
tgcccccaaa acacctgagt gctactccct atttgcattc gttttgataa	150
atgatgttga caccctccac cgaattctaa gtggaatcat gtcgggaaga	200
gatacaatcc ttggcctgtg tatcctcgca ttgacctgtt ctttggccat	250
gatgtttacc ttcagattca tcaccaccct tctgggtcac attttcattt	300
cattgggttat tttgggattg ttgtttgtct gcggtgtttt atggtggctg	350
tattatgact ataccaacga cctcagcata gaattggaca cagaaaggga	400
aaatatgaag tgcgtgctgg ggtttgctat cgtatccaca ggcattcacg	450
cagtgcctgt cgtcttgatt ttgtttctca gaaagagaat aaaattgaca	500
gttagagctt tccaaatcac aaataaagcc atcagcagtg ctcccttcct	550
gctgttccag ccactgtgga catttgccat cctcattttc tctgggtcc	600
tctgggtggc tgtgctgctg agcctgggaa ctgcaggagc tgcccagggt	650
atggaaggcg gccaaagtga atataagccc ctttcgggca ttoggtacat	700
gtggctgtac catttaattg gcctcatctg gactagttaa ttcattcctg	750
cgtgccagca aatgactata gctggggcag tggttacttg ttatttcaac	800
agaagtaaaa atgatcctcc tgatcatccc atcctttcgt ctctctccat	850
tctcttcttc taccatcaag gaaccgttgt gaaagggta tttttaatct	900
ctgtggtgag gattccgaga atcattgtca tgtacatgca aaacgcactg	950
aaagaacagc agcatggtgc attgtccagg tacctgttcc gatgctgcta	1000
ctgctgtttc tgggtgtctg acaaatacct gctccatctc aaccagaatg	1050
catatactac aactgctatt aatgggacag atttctgtac atcagcaaaa	1100
gatgcattca aaatcttgtc caagaactca agtcacttta catctattaa	1150
ctgctttgga gacttcataa tttttctagg aaagggtta gtggtgtgtt	1200
tcactgtttt tggaggactc atggctttta actacaatcg ggcattccag	1250
gtgtgggcag tccctctgtt attggtagct tttttgcct acttagtagc	1300
ccatagtttt ttatctgtgt ttgaaactgt gctggatgca cttttcctgt	1350
gttttctgtg tgatctggaa acaaatgatg gatcgtcaga aaagccctac	1400
tttatggatc aagaatttct gagtttcgta aaaaggagca acaaattaaa	1450
caatgcaagg gcacagcagg acaagcactc attaaggaat gaggagggaa	1500
cagaactcca ggccattgtg agatagatac ccatttaggt atctgtacct	1550
ggaaaacatt tccttctaag agccatttac agaatagaag atgagaccac	1600
tagagaaaaa ttagtgaatt tttttttaa agacctata aacctattc	1650
ttcctcaaaa	1660

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<210> SEQ ID NO 32

<211> LENGTH: 445

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 32

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Met Ser Gly Arg Asp Thr Ile Leu Gly Leu Cys Ile Leu Ala Leu
 1           5           10           15

Ala Leu Ser Leu Ala Met Met Phe Thr Phe Arg Phe Ile Thr Thr
 20           25           30

Leu Leu Val His Ile Phe Ile Ser Leu Val Ile Leu Gly Leu Leu
 35           40           45

Phe Val Cys Gly Val Leu Trp Trp Leu Tyr Tyr Asp Tyr Thr Asn
 50           55           60

Asp Leu Ser Ile Glu Leu Asp Thr Glu Arg Glu Asn Met Lys Cys
 65           70           75

Val Leu Gly Phe Ala Ile Val Ser Thr Gly Ile Thr Ala Val Leu
 80           85           90

Leu Val Leu Ile Phe Val Leu Arg Lys Arg Ile Lys Leu Thr Val
 95           100          105

Glu Leu Phe Gln Ile Thr Asn Lys Ala Ile Ser Ser Ala Pro Phe
110           115          120

Leu Leu Phe Gln Pro Leu Trp Thr Phe Ala Ile Leu Ile Phe Phe
125           130          135

Trp Val Leu Trp Val Ala Val Leu Leu Ser Leu Gly Thr Ala Gly
140           145          150

Ala Ala Gln Val Met Glu Gly Gly Gln Val Glu Tyr Lys Pro Leu
155           160          165

Ser Gly Ile Arg Tyr Met Trp Ser Tyr His Leu Ile Gly Leu Ile
170           175          180

Trp Thr Ser Glu Phe Ile Leu Ala Cys Gln Gln Met Thr Ile Ala
185           190          195

Gly Ala Val Val Thr Cys Tyr Phe Asn Arg Ser Lys Asn Asp Pro
200           205          210

Pro Asp His Pro Ile Leu Ser Ser Leu Ser Ile Leu Phe Phe Tyr
215           220          225

His Gln Gly Thr Val Val Lys Gly Ser Phe Leu Ile Ser Val Val
230           235          240

Arg Ile Pro Arg Ile Ile Val Met Tyr Met Gln Asn Ala Leu Lys
245           250          255

Glu Gln Gln His Gly Ala Leu Ser Arg Tyr Leu Phe Arg Cys Cys
260           265          270

Tyr Cys Cys Phe Trp Cys Leu Asp Lys Tyr Leu Leu His Leu Asn
275           280          285

Gln Asn Ala Tyr Thr Thr Thr Ala Ile Asn Gly Thr Asp Phe Cys
290           295          300

Thr Ser Ala Lys Asp Ala Phe Lys Ile Leu Ser Lys Asn Ser Ser
305           310          315

His Phe Thr Ser Ile Asn Cys Phe Gly Asp Phe Ile Ile Phe Leu
320           325          330

Gly Lys Val Leu Val Val Cys Phe Thr Val Phe Gly Gly Leu Met
335           340          345

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Ala	Phe	Asn	Tyr	Asn	Arg	Ala	Phe	Gln	Val	Trp	Ala	Val	Pro	Leu
				350					355					360
Leu	Leu	Val	Ala	Phe	Phe	Ala	Tyr	Leu	Val	Ala	His	Ser	Phe	Leu
				365					370					375
Ser	Val	Phe	Glu	Thr	Val	Leu	Asp	Ala	Leu	Phe	Leu	Cys	Phe	Ala
				380					385					390
Val	Asp	Leu	Glu	Thr	Asn	Asp	Gly	Ser	Ser	Glu	Lys	Pro	Tyr	Phe
				395					400					405
Met	Asp	Gln	Glu	Phe	Leu	Ser	Phe	Val	Lys	Arg	Ser	Asn	Lys	Leu
				410					415					420
Asn	Asn	Ala	Arg	Ala	Gln	Gln	Asp	Lys	His	Ser	Leu	Arg	Asn	Glu
				425					430					435
Glu	Gly	Thr	Glu	Leu	Gln	Ala	Ile	Val	Arg					
				440					445					

<210> SEQ ID NO 33
<211> LENGTH: 2773
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 33

gttcgattag	ctcctctgag	aagaagagaa	aaggttcttg	gacctctccc	50
tgtttcttcc	ttagaataat	ttgtatggga	tttgtgatgc	aggaaagcct	100
aagggaaaaa	gaatattcat	tctgtgtggt	gaaaaatttt	tgaaaaaaa	150
attgccttct	tcaaacaagg	gtgtcattct	gatatttatg	aggactgttg	200
ttctcactat	gaaggcatct	gttattgaaa	tgttccttgt	tttgctgggtg	250
actggagtac	attcaaacaa	agaaacggca	aagaagatta	aaaggcccaa	300
gttcactgtg	cctcagatca	actgcgatgt	caaagccgga	aagatcatcg	350
atcctgagtt	cattgtgaaa	tgtccagcag	gatgccaaga	ccccaataac	400
catgtttatg	gcactgacgt	gtatgcatcc	tactccagtg	tgtgtggcgc	450
tgccgtacac	agtgggtgtg	ttgataattc	aggagggaaa	atacttgttc	500
ggaagggttg	tggacagtct	ggttacaaag	ggagtatttc	caacggtgtc	550
caatcgttat	ccctaccacg	atggagagaa	tcctttatcg	tcttagaaaag	600
taaaccctaa	aagggtgtaa	cctaccctac	agctcttaca	tactcatcat	650
cgaaaagtcc	agctgcccac	gcaggtgaga	ccacaaaagc	ctatcagagg	700
ccacctattc	cagggacaac	tgcacagccg	gtcactctga	tgcagcttct	750
ggctgtcact	gtagctgtgg	ccacccccac	caccttgcca	aggccatccc	800
cttctgctgc	ttctaccacc	agcatcccca	gaccacaatc	agtgggccac	850
aggagccagg	agatggatct	ctggtccact	gccacctaca	caagcagcca	900
aaacaggccc	agagctgata	caggatatca	aaggcaagat	ccttcaggag	950
ctgccttcca	gaaacctggt	ggagcggatg	tcagcctggg	acttgttcca	1000
aaagaagaat	tgagcacaca	gtctttggag	ccagtatccc	tgggagatcc	1050
aaactgcaaa	attgacttgt	cgtttttaat	tgatggggagc	accagcattg	1100
gcaaacggcg	attccgaatc	cagaagcagc	tcctggctga	tgttgcccaa	1150

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gctcttgaca ttggccctgc cgggccactg atgggtgttg tccagtatgg	1200
agacaaccct gctactcact ttaacctcaa gacacacacg aattctcgag	1250
atctgaagac agccatagag aaaattactc agagaggagg actttcta	1300
gtaggtcggg ccatctcctt tgtgaccaag aacttctttt ccaaagccaa	1350
tggaaacaga agcggggctc ccaatgtggt ggtggtgatg gtggatggct	1400
ggccacgga caaagtggag gaggcttcaa gacttgcgag agagtcagga	1450
atcaacattt tcttcacac cattgaaggt gctgctgaaa atgagaagca	1500
gtatgtggtg gagcccaact ttgcaacaa ggccgtgtgc agaacaacg	1550
gcttctactc gctccacgtg cagagctggt ttggcctcca caagacctg	1600
cagcctctg tgaagcgggt ctgcgacact gaccgcctgg cctgcagcaa	1650
gacctgcttg aactcggctg acattggctt cgtcatcgac ggctccagca	1700
gtgtggggac gggcaacttc cgcaccgtcc tccagtttgt gaccaacctc	1750
accaagagat ttgagatttc cgacacggac acgcgcatcg gggccgtgca	1800
gtacacctac gaacagcggc tggagtttgg gttcgacaag tacagcagca	1850
agcctgacat cctcaacgcc atcaagaggg tgggctactg gagtgtggc	1900
accagcagc gggctgccat caacttcgcc ctggagcagc tcttcaagaa	1950
gtccaagccc aacaagagga agttaatgat cctcatcacc gacgggaggt	2000
cctacgacga cgtccggatc ccagccatgg ctgcccattc gaagggagt	2050
atcacctatg cgataggcgt tgctgggct gcccaagagg agctagaagt	2100
cattgccact caccgccca gagaccactc cttctttgtg gacgagtgtg	2150
acaacctcca tcagtatgtc ccaggatca tccagaacat ttgtacagag	2200
ttcaactcac agcctcggaa ctgaattcag agcaggcaga gcaccagcaa	2250
gtgctgcttt actaactgac gtgttgacc accccaccgc ttaatggggc	2300
acgcacgggt catcaagtct tgggcagggc atggagaaac aaatgtcttg	2350
ttattattct ttgccatcat gctttttcat attccaaaac ttggagtac	2400
aaagatgatc acaaactgat agaatgagcc aaaaggctac atcatgttga	2450
gggtgctgga gattttacat ttgacaatt gttttcaaaa taaatgttcg	2500
gaatacagtg cagcccttac gacaggctta cgtagagctt ttgtgagatt	2550
tttaagtgtg tatttctgat ttgaactctg taaccctcag caagtttcat	2600
ttttgtcatg acaatgtagg aattgctgaa ttaaatgttt agaaggatga	2650
aaaataaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	2700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	2750
aaaaaaaaaa aaaaaaaaaa aag	2773

<210> SEQ ID NO 34

<211> LENGTH: 678

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 34

Met	Arg	Thr	Val	Val	Leu	Thr	Met	Lys	Ala	Ser	Val	Ile	Glu	Met
1					5				10					15

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Phe	Leu	Val	Leu	Leu	Val	Thr	Gly	Val	His	Ser	Asn	Lys	Glu	Thr	20	25	30
Ala	Lys	Lys	Ile	Lys	Arg	Pro	Lys	Phe	Thr	Val	Pro	Gln	Ile	Asn	35	40	45
Cys	Asp	Val	Lys	Ala	Gly	Lys	Ile	Ile	Asp	Pro	Glu	Phe	Ile	Val	50	55	60
Lys	Cys	Pro	Ala	Gly	Cys	Gln	Asp	Pro	Lys	Tyr	His	Val	Tyr	Gly	65	70	75
Thr	Asp	Val	Tyr	Ala	Ser	Tyr	Ser	Ser	Val	Cys	Gly	Ala	Ala	Val	80	85	90
His	Ser	Gly	Val	Leu	Asp	Asn	Ser	Gly	Gly	Lys	Ile	Leu	Val	Arg	95	100	105
Lys	Val	Ala	Gly	Gln	Ser	Gly	Tyr	Lys	Gly	Ser	Tyr	Ser	Asn	Gly	110	115	120
Val	Gln	Ser	Leu	Ser	Leu	Pro	Arg	Trp	Arg	Glu	Ser	Phe	Ile	Val	125	130	135
Leu	Glu	Ser	Lys	Pro	Lys	Lys	Gly	Val	Thr	Tyr	Pro	Ser	Ala	Leu	140	145	150
Thr	Tyr	Ser	Ser	Ser	Lys	Ser	Pro	Ala	Ala	Gln	Ala	Gly	Glu	Thr	155	160	165
Thr	Lys	Ala	Tyr	Gln	Arg	Pro	Pro	Ile	Pro	Gly	Thr	Thr	Ala	Gln	170	175	180
Pro	Val	Thr	Leu	Met	Gln	Leu	Leu	Ala	Val	Thr	Val	Ala	Val	Ala	185	190	195
Thr	Pro	Thr	Thr	Leu	Pro	Arg	Pro	Ser	Pro	Ser	Ala	Ala	Ser	Thr	200	205	210
Thr	Ser	Ile	Pro	Arg	Pro	Gln	Ser	Val	Gly	His	Arg	Ser	Gln	Glu	215	220	225
Met	Asp	Leu	Trp	Ser	Thr	Ala	Thr	Tyr	Thr	Ser	Ser	Gln	Asn	Arg	230	235	240
Pro	Arg	Ala	Asp	Pro	Gly	Ile	Gln	Arg	Gln	Asp	Pro	Ser	Gly	Ala	245	250	255
Ala	Phe	Gln	Lys	Pro	Val	Gly	Ala	Asp	Val	Ser	Leu	Gly	Leu	Val	260	265	270
Pro	Lys	Glu	Glu	Leu	Ser	Thr	Gln	Ser	Leu	Glu	Pro	Val	Ser	Leu	275	280	285
Gly	Asp	Pro	Asn	Cys	Lys	Ile	Asp	Leu	Ser	Phe	Leu	Ile	Asp	Gly	290	295	300
Ser	Thr	Ser	Ile	Gly	Lys	Arg	Arg	Phe	Arg	Ile	Gln	Lys	Gln	Leu	305	310	315
Leu	Ala	Asp	Val	Ala	Gln	Ala	Leu	Asp	Ile	Gly	Pro	Ala	Gly	Pro	320	325	330
Leu	Met	Gly	Val	Val	Gln	Tyr	Gly	Asp	Asn	Pro	Ala	Thr	His	Phe	335	340	345
Asn	Leu	Lys	Thr	His	Thr	Asn	Ser	Arg	Asp	Leu	Lys	Thr	Ala	Ile	350	355	360
Glu	Lys	Ile	Thr	Gln	Arg	Gly	Gly	Leu	Ser	Asn	Val	Gly	Arg	Ala	365	370	375
Ile	Ser	Phe	Val	Thr	Lys	Asn	Phe	Phe	Ser	Lys	Ala	Asn	Gly	Asn	380	385	390

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Arg	Ser	Gly	Ala	Pro	Asn	Val	Val	Val	Val	Met	Val	Asp	Gly	Trp
				395						400				405
Pro	Thr	Asp	Lys	Val	Glu	Glu	Ala	Ser	Arg	Leu	Ala	Arg	Glu	Ser
				410					415					420
Gly	Ile	Asn	Ile	Phe	Phe	Ile	Thr	Ile	Glu	Gly	Ala	Ala	Glu	Asn
				425					430					435
Glu	Lys	Gln	Tyr	Val	Val	Glu	Pro	Asn	Phe	Ala	Asn	Lys	Ala	Val
				440					445					450
Cys	Arg	Thr	Asn	Gly	Phe	Tyr	Ser	Leu	His	Val	Gln	Ser	Trp	Phe
				455					460					465
Gly	Leu	His	Lys	Thr	Leu	Gln	Pro	Leu	Val	Lys	Arg	Val	Cys	Asp
				470					475					480
Thr	Asp	Arg	Leu	Ala	Cys	Ser	Lys	Thr	Cys	Leu	Asn	Ser	Ala	Asp
				485					490					495
Ile	Gly	Phe	Val	Ile	Asp	Gly	Ser	Ser	Ser	Val	Gly	Thr	Gly	Asn
				500					505					510
Phe	Arg	Thr	Val	Leu	Gln	Phe	Val	Thr	Asn	Leu	Thr	Lys	Glu	Phe
				515					520					525
Glu	Ile	Ser	Asp	Thr	Asp	Thr	Arg	Ile	Gly	Ala	Val	Gln	Tyr	Thr
				530					535					540
Tyr	Glu	Gln	Arg	Leu	Glu	Phe	Gly	Phe	Asp	Lys	Tyr	Ser	Ser	Lys
				545					550					555
Pro	Asp	Ile	Leu	Asn	Ala	Ile	Lys	Arg	Val	Gly	Tyr	Trp	Ser	Gly
				560					565					570
Gly	Thr	Ser	Thr	Gly	Ala	Ala	Ile	Asn	Phe	Ala	Leu	Glu	Gln	Leu
				575					580					585
Phe	Lys	Lys	Ser	Lys	Pro	Asn	Lys	Arg	Lys	Leu	Met	Ile	Leu	Ile
				590					595					600
Thr	Asp	Gly	Arg	Ser	Tyr	Asp	Asp	Val	Arg	Ile	Pro	Ala	Met	Ala
				605					610					615
Ala	His	Leu	Lys	Gly	Val	Ile	Thr	Tyr	Ala	Ile	Gly	Val	Ala	Trp
				620					625					630
Ala	Ala	Gln	Glu	Glu	Leu	Glu	Val	Ile	Ala	Thr	His	Pro	Ala	Arg
				635					640					645
Asp	His	Ser	Phe	Phe	Val	Asp	Glu	Phe	Asp	Asn	Leu	His	Gln	Tyr
				650					655					660
Val	Pro	Arg	Ile	Ile	Gln	Asn	Ile	Cys	Thr	Glu	Phe	Asn	Ser	Gln
				665					670					675
Pro	Arg	Asn												

<210> SEQ ID NO 35
<211> LENGTH: 2095
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 35

ccgagcacag gagattgcct gcgtttagga ggtggctgcg ttgtgggaaa	50
agctatcaag gaagaaattg ccaaaccatg tctttttttc tgttttcaga	100
gtagttcaca acagatctga gtgttttaat taagcatgga atacagaaaa	150
caacaaaaaa cttaagcttt aatttcacatc ggaattccac agttttctta	200
gtcccttgga cccggttgac ctgttggcto ttcccgctgg ctgctctatc	250

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acgtgggtgct ctccgactac tcaccccgag tgtaaagaac cttcggtctg	300
cgtgcttctg agctgctgtg gatggcctcg gctctctgga ctgtccttcc	350
gagtaggatg tcaactgagat ccctcaaatg gagcctcctg ctgctgtcac	400
tcctgagttt ctttgtgatg tggtagctca gccttcccca ctacaatgtg	450
atagaacgcg tgaactggat gtacttctat gagtatgagc cgatttacag	500
acaagacttt cacttcacac ttcgagagca ttcaaactgc tctcatcaaa	550
atccattttt ggtcattctg gtgacctccc acccttcaga tgtgaaagcc	600
aggcaggcca ttagagttac ttggggtgaa aaaaagtctt ggtggggata	650
tgaggttctt acatttttct tattaggcca agaggctgaa aaggaagaca	700
aaatgttggc attgtcctta gaggatgaac accttcttta tggtgacata	750
atccgacaag atttttttaga cacatataat aacctgacct tgaaaacct	800
tatggcattc aggtgggtaa ctgagttttg cccaatgcc aagtacgtaa	850
tgaagacaga cactgatgtt ttcataata ctggcaattt agtgaagtat	900
cttttaaacc taaaccactc agagaagttt ttcacagggt atcctcta	950
tgataattat tcctatagag gattttacca aaaaacccat atttcttacc	1000
aggagtatcc tttcaagggt ttccctccat actgcagtgg gttgggttat	1050
ataatgtcca gagatttggg gccaaagatc tatgaaatga tgggtcacgt	1100
aaaaccatc aagtttgaag atgtttatgt cgggatctgt ttgaatttat	1150
taaaagtga cattcatatt ccagaagaca caaatctttt ctttctatat	1200
agaatccatt tggatgtctg tcaactgaga cgtgtgattg cagccatgg	1250
ctttcttcc aaggagatca tcaacttttg gcaggatcatg ctaaggaaca	1300
ccacatgcca ttattaactt cacattctac aaaaagccta gaaggacagg	1350
ataccttgtg gaaagtgtta aataaagtag gtactgtgga aaattcatgg	1400
ggaggtcagt gtgctggcct acactgaact gaaactcatg aaaaaccag	1450
actggagact ggagggttac acttgtgatt tattagtcag gcccttcaaa	1500
gatgatatgt ggaggaatta aatataaagg aattggaggt ttttgctaaa	1550
gaaattaata ggaccaaaca atttggacat gtcattctgt agactagaat	1600
ttcttaaaag ggtgttactg agttataagc tcaactaggct gtaaaaaaa	1650
aacaatgtag agttttatct attgaacaat gtagtcactt gaaggttttg	1700
tgtatatctt atgtggatta ccaatttaaa aatatatgta gttctgtgtc	1750
aaaaaacttc ttactgaag ttatactgaa caaaatttta cctgtttttg	1800
gtcattttata aagtacttca agatgttgca gtatttcaca gttattatta	1850
tttaaaatta cttcaacttt gtgtttttta atgttttgac gatttcaata	1900
caagataaaa aggatagtga atcattcttt acatgcaaac attttccagt	1950
tacttaactg atcagtttat tattgataca tcaactccatt aatgtaaagt	2000
cataggtcatt tattgcatat cagtaatctc ttggactttg ttaaatattt	2050
tactgtggta atatagagaa gaattaaagc aagaaaatct gaaaa	2095

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<210> SEQ ID NO 36

<211> LENGTH: 331

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 36

Met	Ala	Ser	Ala	Leu	Trp	Thr	Val	Leu	Pro	Ser	Arg	Met	Ser	Leu
1				5					10					15

Arg	Ser	Leu	Lys	Trp	Ser	Leu	Leu	Leu	Leu	Ser	Leu	Leu	Ser	Phe
			20						25					30

Phe	Val	Met	Trp	Tyr	Leu	Ser	Leu	Pro	His	Tyr	Asn	Val	Ile	Glu
			35						40					45

Arg	Val	Asn	Trp	Met	Tyr	Phe	Tyr	Glu	Tyr	Glu	Pro	Ile	Tyr	Arg
			50						55					60

Gln	Asp	Phe	His	Phe	Thr	Leu	Arg	Glu	His	Ser	Asn	Cys	Ser	His
			65						70					75

Gln	Asn	Pro	Phe	Leu	Val	Ile	Leu	Val	Thr	Ser	His	Pro	Ser	Asp
			80						85					90

Val	Lys	Ala	Arg	Gln	Ala	Ile	Arg	Val	Thr	Trp	Gly	Glu	Lys	Lys
			95						100					105

Ser	Trp	Trp	Gly	Tyr	Glu	Val	Leu	Thr	Phe	Phe	Leu	Leu	Gly	Gln
			110						115					120

Glu	Ala	Glu	Lys	Glu	Asp	Lys	Met	Leu	Ala	Leu	Ser	Leu	Glu	Asp
			125						130					135

Glu	His	Leu	Leu	Tyr	Gly	Asp	Ile	Ile	Arg	Gln	Asp	Phe	Leu	Asp
			140						145					150

Thr	Tyr	Asn	Asn	Leu	Thr	Leu	Lys	Thr	Ile	Met	Ala	Phe	Arg	Trp
			155						160					165

Val	Thr	Glu	Phe	Cys	Pro	Asn	Ala	Lys	Tyr	Val	Met	Lys	Thr	Asp
			170						175					180

Thr	Asp	Val	Phe	Ile	Asn	Thr	Gly	Asn	Leu	Val	Lys	Tyr	Leu	Leu
			185						190					195

Asn	Leu	Asn	His	Ser	Glu	Lys	Phe	Phe	Thr	Gly	Tyr	Pro	Leu	Ile
			200						205					210

Asp	Asn	Tyr	Ser	Tyr	Arg	Gly	Phe	Tyr	Gln	Lys	Thr	His	Ile	Ser
			215						220					225

Tyr	Gln	Glu	Tyr	Pro	Phe	Lys	Val	Phe	Pro	Pro	Tyr	Cys	Ser	Gly
			230						235					240

Leu	Gly	Tyr	Ile	Met	Ser	Arg	Asp	Leu	Val	Pro	Arg	Ile	Tyr	Glu
			245						250					255

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

Gly	Ile	Cys	Leu	Asn	Leu	Leu	Lys	Val	Asn	Ile	His	Ile	Pro	Glu
			275						280					285

Asp	Thr	Asn	Leu	Phe	Phe	Leu	Tyr	Arg	Ile	His	Leu	Asp	Val	Cys
			290						295					300

Gln	Leu	Arg	Arg	Val	Ile	Ala	Ala	His	Gly	Phe	Ser	Ser	Lys	Glu
			305						310					315

Ile	Ile	Thr	Phe	Trp	Gln	Val	Met	Leu	Arg	Asn	Thr	Thr	Cys	His
			320						325					330

Tyr

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<210> SEQ ID NO 37

<211> LENGTH: 2846

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 37

cgctcgggca ccagccgcgg caaggatgga gctgggttgc tggacgcagt	50
tggggctcac ttttcttcag ctcttctca tctcgtcctt gccaaagagag	100
tacacagtca ttaatgaagc ctgccctgga gcagagtgga atatcatgtg	150
tcgggagatgc tgtgaatatg atcagattga gtgcgtctgc cccggaaaga	200
gggaagtctg ggggtatacc atcccttgct gcaggaatga ggagaatgag	250
tgtgactcct gcctgatcca ccaggttgt accatcttg aaaactgcaa	300
gagctgccga aatggctcat ggggggttac cttggatgac ttctatgtga	350
aggggttcta ctgtgcagag tgccgagcag gctggtacgg aggagactgc	400
atgcgatgtg gccaggttct gcgagcccca aagggtcaga ttttgttga	450
aagctatccc ctaaagtctc actgtgaatg gaccattcat gctaaacctg	500
ggtttgtcat ccaactaaga tttgtcatgt tgagtctgga gtttgactac	550
atgtgccagt atgactatgt tgaggttcgt gatggagaca accgcgatgg	600
ccagatcatc aagcgtgtct gtggcaacga gcggccagct cctatccaga	650
gcataaggatc ctactccac gtctcttcc actccgatgg ctccaagaat	700
tttgacggtt tccatgccat ttatgaggag atcacagcat gctcctcatc	750
cccttgtttc catgacggca cgtgcgtcct tgacaaggct ggatcttaca	800
agtggtcctg cttggcaggc tatactgggc agcgtgtga aaatctcctt	850
gaagaaagaa actgctcaga ccctgggggc ccagtcaatg ggtaccagaa	900
aataacaggg ggcctgggc ttatcaacgg acgccatgct aaaattggca	950
ccgtggtgtc tttcttttgt aacaactcct atgttcttag tggcaatgag	1000
aaaagaactt gccagcagaa tggagagtgg tcagggaaac agcccatctg	1050
cataaaagcc tgccgagaac caaagatttc agacctggtg agaaggagag	1100
ttcttccgat gcaggttcag tcaagggaga caccattaca ccagctatac	1150
tcagcggcct tcagcaagca gaaactgcag agtgccccta ccaagaagcc	1200
agcccttccc tttggagatc tgcccatggg ataccaacat ctgcataccc	1250
agctccagta tgagtgcata tcacccttct accgccgctt gggcagcagc	1300
aggaggacat gtctgaggac tgggaagtgg agtgggctgg caccatcctg	1350
catccctatc tgcgggaaaa ttgagaacat cactgctcca aagacccaag	1400
ggttgcgctg gccgtggcag gcagccatct acaggaggac cagcggggtg	1450
catgacggca gcctacacaa gggagcgtgg ttcctagtct gcagcgggtg	1500
cctggtgaat gagcgactg tgggtggtgg tgcccactgt gttactgacc	1550
tggggaaggt caccatgata aagacagcag acctgaaagt tgttttgggg	1600
aaattctacc gggatgatga ccgggatgag aagaccatcc agagcctaca	1650
gatttctgct atcattctgc atcccaacta tgaccccatc ctgcttgatg	1700
ctgacatcgc catcctgaag ctctagaca aggcccgat cagcaccgca	1750

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gtccagccca tctgcctcgc tgccagtcgg gatctcagca cttccttcca 1800
ggagtcccac atcactgtgg ctggctggaa tgtcctggca gacgtgagga 1850
gccctggctt caagaacgac aactgcgcct ctgggggtgg cagtgtggtg 1900
gactcgtgc tgtgtgagga gcagcatgag gacatggca tcccagtgag 1950
tgtcactgat aacatgttct gtgccagctg ggaaccact gcccttctg 2000
atatctgcac tgcagagaca ggaggcatcg cggctgtgtc cttcccgga 2050
cgagcatctc ctgagccacg ctggcatctg atgggactgg tcagctggag 2100
ctatgataaa acatgcagcc acaggctctc cactgccttc accaaggtgc 2150
tgccttttaa agactggatt gaaagaaata tgaatgaac catgctcatg 2200
cactccttga gaagtgttct tgtatatccg tctgtacgtg tgtcattgcg 2250
tgaagcagtg tgggcctgaa gtgtgatttg gctgtgaac ttggctgtgc 2300
cagggtctct gacttcaggg acaaaactca gtgaagggtg agtagacctc 2350
cattgctggt aggtgatgc cgcgtccact actaggacag ccaattggaa 2400
gatgccaggg cttgcaagaa gtaagtctct tcaaagaaga ccatatacaa 2450
aacctctcca ctccactgac ctgggtgtct tccccaactt tcagttatac 2500
gaatgccatc agcttgacca gggaagatct gggcttcatg aggcccttt 2550
tgaggctctc aagtctaga gagctgcctg tgggacagcc cagggcagca 2600
gagctgggat gtggtgcatg ctttgtgtga catggccaca gtacagtctg 2650
gtccttttcc ttcccatctc cttgtacaca ttttaataaa ataagggttg 2700
gtctctgaac tacaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2750
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2800
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2846

<210> SEQ ID NO 38

<211> LENGTH: 720

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 38

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

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Tyr Gly Gly Asp Cys Met Arg Cys Gly Gln Val Leu Arg Ala Pro	125	130	135
Lys Gly Gln Ile Leu Leu Glu Ser Tyr Pro Leu Asn Ala His Cys	140	145	150
Glu Trp Thr Ile His Ala Lys Pro Gly Phe Val Ile Gln Leu Arg	155	160	165
Phe Val Met Leu Ser Leu Glu Phe Asp Tyr Met Cys Gln Tyr Asp	170	175	180
Tyr Val Glu Val Arg Asp Gly Asp Asn Arg Asp Gly Gln Ile Ile	185	190	195
Lys Arg Val Cys Gly Asn Glu Arg Pro Ala Pro Ile Gln Ser Ile	200	205	210
Gly Ser Ser Leu His Val Leu Phe His Ser Asp Gly Ser Lys Asn	215	220	225
Phe Asp Gly Phe His Ala Ile Tyr Glu Glu Ile Thr Ala Cys Ser	230	235	240
Ser Ser Pro Cys Phe His Asp Gly Thr Cys Val Leu Asp Lys Ala	245	250	255
Gly Ser Tyr Lys Cys Ala Cys Leu Ala Gly Tyr Thr Gly Gln Arg	260	265	270
Cys Glu Asn Leu Leu Glu Glu Arg Asn Cys Ser Asp Pro Gly Gly	275	280	285
Pro Val Asn Gly Tyr Gln Lys Ile Thr Gly Gly Pro Gly Leu Ile	290	295	300
Asn Gly Arg His Ala Lys Ile Gly Thr Val Val Ser Phe Phe Cys	305	310	315
Asn Asn Ser Tyr Val Leu Ser Gly Asn Glu Lys Arg Thr Cys Gln	320	325	330
Gln Asn Gly Glu Trp Ser Gly Lys Gln Pro Ile Cys Ile Lys Ala	335	340	345
Cys Arg Glu Pro Lys Ile Ser Asp Leu Val Arg Arg Arg Val Leu	350	355	360
Pro Met Gln Val Gln Ser Arg Glu Thr Pro Leu His Gln Leu Tyr	365	370	375
Ser Ala Ala Phe Ser Lys Gln Lys Leu Gln Ser Ala Pro Thr Lys	380	385	390
Lys Pro Ala Leu Pro Phe Gly Asp Leu Pro Met Gly Tyr Gln His	395	400	405
Leu His Thr Gln Leu Gln Tyr Glu Cys Ile Ser Pro Phe Tyr Arg	410	415	420
Arg Leu Gly Ser Ser Arg Arg Thr Cys Leu Arg Thr Gly Lys Trp	425	430	435
Ser Gly Arg Ala Pro Ser Cys Ile Pro Ile Cys Gly Lys Ile Glu	440	445	450
Asn Ile Thr Ala Pro Lys Thr Gln Gly Leu Arg Trp Pro Trp Gln	455	460	465
Ala Ala Ile Tyr Arg Arg Thr Ser Gly Val His Asp Gly Ser Leu	470	475	480
His Lys Gly Ala Trp Phe Leu Val Cys Ser Gly Ala Leu Val Asn	485	490	495

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Glu	Arg	Thr	Val	Val	Val	Ala	Ala	His	Cys	Val	Thr	Asp	Leu	Gly
			500						505					510
Lys	Val	Thr	Met	Ile	Lys	Thr	Ala	Asp	Leu	Lys	Val	Val	Leu	Gly
			515						520					525
Lys	Phe	Tyr	Arg	Asp	Asp	Asp	Arg	Asp	Glu	Lys	Thr	Ile	Gln	Ser
			530						535					540
Leu	Gln	Ile	Ser	Ala	Ile	Ile	Leu	His	Pro	Asn	Tyr	Asp	Pro	Ile
			545						550					555
Leu	Leu	Asp	Ala	Asp	Ile	Ala	Ile	Leu	Lys	Leu	Leu	Asp	Lys	Ala
			560						565					570
Arg	Ile	Ser	Thr	Arg	Val	Gln	Pro	Ile	Cys	Leu	Ala	Ala	Ser	Arg
			575						580					585
Asp	Leu	Ser	Thr	Ser	Phe	Gln	Glu	Ser	His	Ile	Thr	Val	Ala	Gly
			590						595					600
Trp	Asn	Val	Leu	Ala	Asp	Val	Arg	Ser	Pro	Gly	Phe	Lys	Asn	Asp
			605						610					615
Thr	Leu	Arg	Ser	Gly	Val	Val	Ser	Val	Val	Asp	Ser	Leu	Leu	Cys
			620						625					630
Glu	Glu	Gln	His	Glu	Asp	His	Gly	Ile	Pro	Val	Ser	Val	Thr	Asp
			635						640					645
Asn	Met	Phe	Cys	Ala	Ser	Trp	Glu	Pro	Thr	Ala	Pro	Ser	Asp	Ile
			650						655					660
Cys	Thr	Ala	Glu	Thr	Gly	Gly	Ile	Ala	Ala	Val	Ser	Phe	Pro	Gly
			665						670					675
Arg	Ala	Ser	Pro	Glu	Pro	Arg	Trp	His	Leu	Met	Gly	Leu	Val	Ser
			680						685					690
Trp	Ser	Tyr	Asp	Lys	Thr	Cys	Ser	His	Arg	Leu	Ser	Thr	Ala	Phe
			695						700					705
Thr	Lys	Val	Leu	Pro	Phe	Lys	Asp	Trp	Ile	Glu	Arg	Asn	Met	Lys
			710						715					720

<210> SEQ ID NO 39
<211> LENGTH: 2571
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 39

ggttcctaca tcctctcatc tgagaatcag agagcataat cttcttacgg	50
gcccgtgatt tattaacgtg gcttaatctg aaggttctca gtcaaattct	100
ttgtgatcta ctgattgtgg gggcatggca aggtttgctt aaaggagctt	150
ggctggtttg ggcccttgta gctgacagaa ggtggccagg gagaatgcag	200
cacactgctc ggagaatgaa ggcgcttctg ttgctggtct tgccttggtc	250
cagtctgctt aactacattg acaatgtggg caacctgcac ttcctgtatt	300
cagaactctg taaaggtgcc tcccactacg gcctgaccaa agataggaag	350
aggcgctcac aagatggctg tccagacggc tgtgcgagcc tcacagccac	400
ggctccctcc ccagaggttt ctgcagctgc caccatctcc ttaatgacag	450
acgagcctgg cctagacaac cctgcctacg tgtcctcggc agaggacggg	500
cagccagcaa tcagcccagt ggactctggc cggagcaacc gaactagggc	550
acggcccttt gagagatcca ctattagaag cagatcattt aaaaaataa	600

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atcgagcttt gagtgttctt cgaaggacaa agagcgggag tgcagttgcc	650
aaccatgccg accagggcag ggaaaattct gaaaacacca ctgcccctga	700
agtctttcca aggttgtacc acctgattcc agatggtgaa attaccagca	750
tcaagatcaa tcgagtagat cccagtgaag gcctctctat taggctggtg	800
ggaggtagcg aaacccact ggtccatctc attatccaac acatttatcg	850
tgatggggtg atcgccagag acggccggct actgccagga gacatcattc	900
taaaggatcaa cgggatggac atcagcaatg tccctcacia ctacgctgtg	950
cgtctcctcg ggcagccctg ccaggtgctg tggtgactg tgatgcgtga	1000
acagaagtgc cgcagcagga acaatggaca ggccccgat gcctacagac	1050
cccagatga cagctttcat gtgattctca acaaaagtag ccccgaggag	1100
cagcttgga taaaactggt gcgcaagggt gatgagcctg gggttttcat	1150
cttcaatgtg ctggatggcg gtgtggcata tcgacatggt cagcttgagg	1200
agaatgacgg tgtgttagcc atcaatggac atgatcttcg atatggcagc	1250
ccagaaagtg cggctcatct gattcaggcc agtgaaagac gtgttcacct	1300
cgtcgtgtcc cgccagggtc ggcagcggag ccctgacatc tttcaggaag	1350
ccggctggaa cagcaatggc agctgggtccc cagggccagg ggagaggagc	1400
aacactccca agccctccca tcctacaatt acttgatcat agaagggtgt	1450
aaatatccaa aaagaccccg gtgaatctct cggcatgacc gtcgcagggg	1500
gagcatcaca tagagaatgg gatttgctca tctatgtcat cagtgttgag	1550
cccgaggagg tcataagcag agatggaaga ataaaaacag gtgacatttt	1600
gttgaatgtg gatggggtcg aactgacaga ggtcagccgg agtgaggcag	1650
tggcattatt gaaaagaaca tcctcctcga tagtactcaa agcttttgaa	1700
gtcaagagt atgagcccca ggaagactgc agcagcccag cagccctgga	1750
ctccaaacc aacatggccc caccagtgta ctggtcccca tcctgggtca	1800
tggtgctgga attaccacgg tgcctgtata actgtaaaga tattgtatta	1850
cgaagaaca cagctggaag tctgggcttc tgcattgtag gaggttatga	1900
agaatacaat ggaacaaac cttttttcat caaatccatt gttgaaggaa	1950
caccagcata caatgatgga agaattagat gtggtgatat tcttcttgct	2000
gtcaatggtg gaagtacatc aggaatgata catgcttgct tggcaagact	2050
gctgaaagaa cttaaaggaa gaattactct aactattggt tcttgccctg	2100
gcactttttt atagaatcaa tgatgggtca gaggaaca gaaaaatcac	2150
aaataggcta agaagttgaa aactatatt tatctgtca gtttttata	2200
ttaaagaaag aatacattgt aaaaatgtca ggaaaagtat gatcatctaa	2250
tgaaagccag ttacacctca gaaaatatga ttccaaaaaa attaaaacta	2300
ctagtttttt ttcagtgtgg aggattttctc attactctac aacattgttt	2350
atattttttc tattcaataa aaagccctaa aacaactaaa atgattgatt	2400
tgtatacccc actgaattca agctgattta aatttaaaat ttggtatatg	2450
ctgaagtctg ccaagggtac attatggcca tttttaattt acagctaaaa	2500

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tatttttttaa aatgcattgc tgagaaacgt tgctttcatc aaacaagaat 2550

aaatatatttt cagaagttaa a 2571

<210> SEQ ID NO 40

<211> LENGTH: 632

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 40

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

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

<210> SEQ ID NO 41
<211> LENGTH: 1964
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 41

accaggcatt gtatcttcag ttgtcatcaa gttcgcaatc agattggaaa	50
agctcaactt gaagctttct tgccctgcagt gaagcagaga gatagatatt	100

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attcacgtaa taaaaaacat gggcttcaac ctgactttcc acctttccta	150
caaattccga ttactgttgc tgttgacttt gtgcctgaca gtgggtgggt	200
gggccaccag taactacttc gtgggtgcca ttcaagagat tcctaaagca	250
aaggagtcca tggctaattt ccataagacc ctcatTTTtg ggaaggga	300
aactctgact aatgaagcat ccacgaagaa ggtagaactt gacaactgtc	350
cttctgtgtc tccttacctc agaggccaga gcaagctcat tttcaacca	400
gatctcactt tggaagaggt acaggcagaa aatcccaaag tgtccagagg	450
ccggtatcgc cctcaggaat gtaaagcttt acagagggtc gccatcctcg	500
ttccccaccg gaacagagag aaacacctga tgtacctgct ggaacatctg	550
catcccttcc tgcagaggca gcagctggat tatggcatct acgtcatcca	600
ccaggctgaa ggtaaaaagt ttaatcgagc caaactcttg aatgtgggct	650
atctagaagc cctcaaggaa gaaaattggg actgctttat attocacgat	700
gtggacctgg tacccgagaa tgactttaac ctttacaagt gtgaggagca	750
tcccaagcat ctggtggttg gcaggaacag cactgggtac aggttacgtt	800
acagtggata ttttgggggt gttactgccc taagcagaga gcagtttttc	850
aagggtgaatg gattctctaa caactactgg ggatggggag gcgaagacga	900
tgacctcaga ctcagggttg agctccaaag aatgaaaatt tcccgcccc	950
tgccgtgaagt gggtaaatat acaatgggtc tccacactag agacaaaggc	1000
aatgagggtga acgcagaacg gatgaagctc ttacaccaag tgtcacgagt	1050
ctggagaaca gatgggttga gtagtgttc ttataaatta gtatctgtgg	1100
aacacaatcc tttatatatc aacatcacag tggatttctg gtttggtgca	1150
tgaccctgga tcttttgggtg atgtttggaa gaactgattc tttgtttgca	1200
ataatttttg cctagagact tcaaatagta gcacacatta agaacctgtt	1250
acagctcatt gttgagctga atttttcctt tttgtatttt cttagcagag	1300
ctcctggtga tgtagagtat aaaacagttg taacaagaca gctttcttag	1350
tcattttgat catgagggtt aaatattgta atatggatac ttgaaggact	1400
ttatataaaa ggatgactca aaggataaaa tgaacgctat ttgaggactc	1450
tggttgaagg agatttatTT aaatttgaag taatatatta tgggataaaa	1500
ggccacagga aataagactg ctgaatgtct gagagaacca gagttgttct	1550
cgtccaaggt agaaaggtac gaagatacaa tactgttatt catTTTcct	1600
gtacaatcat ctgtgaagtg gtggtgtcag gtgagaaggc gtccacaaaa	1650
gaggggagaa aaggcgacga atcaggacac agtgaacttg ggaatgaaga	1700
ggtagcagga ggggtgagtg tcggctgcaa aggcagcagt agctgagctg	1750
gttgacagtg ctgtagcct tcaggggagg acctgccag gtatgccttc	1800
cagtgatgcc caccagagaa tacattctct attagttttt aaagagtttt	1850
tgtaaaatga ttttgtacaa gtaggatag aattagcagt ttacaagttt	1900
acatattaac taataataaa tatgtctatc aaatacctct gtagtaaaat	1950
gtgaaaaagc aaaa	1964

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<210> SEQ ID NO 42

<211> LENGTH: 344

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 42

Met	Gly	Phe	Asn	Leu	Thr	Phe	His	Leu	Ser	Tyr	Lys	Phe	Arg	Leu
1				5					10					15
Leu	Leu	Leu	Leu	Thr	Leu	Cys	Leu	Thr	Val	Val	Gly	Trp	Ala	Thr
				20					25					30
Ser	Asn	Tyr	Phe	Val	Gly	Ala	Ile	Gln	Glu	Ile	Pro	Lys	Ala	Lys
				35					40					45
Glu	Phe	Met	Ala	Asn	Phe	His	Lys	Thr	Leu	Ile	Leu	Gly	Lys	Gly
				50					55					60
Lys	Thr	Leu	Thr	Asn	Glu	Ala	Ser	Thr	Lys	Lys	Val	Glu	Leu	Asp
				65					70					75
Asn	Cys	Pro	Ser	Val	Ser	Pro	Tyr	Leu	Arg	Gly	Gln	Ser	Lys	Leu
				80					85					90
Ile	Phe	Lys	Pro	Asp	Leu	Thr	Leu	Glu	Glu	Val	Gln	Ala	Glu	Asn
				95					100					105
Pro	Lys	Val	Ser	Arg	Gly	Arg	Tyr	Arg	Pro	Gln	Glu	Cys	Lys	Ala
				110					115					120
Leu	Gln	Arg	Val	Ala	Ile	Leu	Val	Pro	His	Arg	Asn	Arg	Glu	Lys
				125					130					135
His	Leu	Met	Tyr	Leu	Leu	Glu	His	Leu	His	Pro	Phe	Leu	Gln	Arg
				140					145					150
Gln	Gln	Leu	Asp	Tyr	Gly	Ile	Tyr	Val	Ile	His	Gln	Ala	Glu	Gly
				155					160					165
Lys	Lys	Phe	Asn	Arg	Ala	Lys	Leu	Leu	Asn	Val	Gly	Tyr	Leu	Glu
				170					175					180
Ala	Leu	Lys	Glu	Glu	Asn	Trp	Asp	Cys	Phe	Ile	Phe	His	Asp	Val
				185					190					195
Asp	Leu	Val	Pro	Glu	Asn	Asp	Phe	Asn	Leu	Tyr	Lys	Cys	Glu	Glu
				200					205					210
His	Pro	Lys	His	Leu	Val	Val	Gly	Arg	Asn	Ser	Thr	Gly	Tyr	Arg
				215					220					225
Leu	Arg	Tyr	Ser	Gly	Tyr	Phe	Gly	Gly	Val	Thr	Ala	Leu	Ser	Arg
				230					235					240
Glu	Gln	Phe	Phe	Lys	Val	Asn	Gly	Phe	Ser	Asn	Asn	Tyr	Trp	Gly
				245					250					255
Trp	Gly	Gly	Glu	Asp	Asp	Asp	Leu	Arg	Leu	Arg	Val	Glu	Leu	Gln
				260					265					270
Arg	Met	Lys	Ile	Ser	Arg	Pro	Leu	Pro	Glu	Val	Gly	Lys	Tyr	Thr
				275					280					285
Met	Val	Phe	His	Thr	Arg	Asp	Lys	Gly	Asn	Glu	Val	Asn	Ala	Glu
				290					295					300
Arg	Met	Lys	Leu	Leu	His	Gln	Val	Ser	Arg	Val	Trp	Arg	Thr	Asp
				305					310					315
Gly	Leu	Ser	Ser	Cys	Ser	Tyr	Lys	Leu	Val	Ser	Val	Glu	His	Asn
				320					325					330

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Pro Leu Tyr Ile Asn Ile Thr Val Asp Phe Trp Phe Gly Ala
335 340

<210> SEQ ID NO 43
<211> LENGTH: 485
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 43
gctcaagacc cagcagtggg acagccagac agacggcacg atggcactga 50
gtctccagat ctgggcccgt tgcctcctgc tcctcctcct cctcgccagc 100
ctgaccagtg gctctgtttt cccacaacag acgggacaac ttgcagagct 150
gcaaccccag gacagagctg gagccagggc cagctggatg cccatgttcc 200
agaggcgaag gaggcgagac acccacttcc ccatctgcat tttctgctgc 250
ggctgctgtc atcgatcaaa gtgtgggatg tgctgcaaga cgtagaacct 300
acctgccctg ccccgctccc ctcccttcct tatttattcc tgctgcccc 350
gaacataggt ctggaataa aatggctggt tctttgttt tccaaaaaaa 400
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 485

<210> SEQ ID NO 44
<211> LENGTH: 84
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 44
Met Ala Leu Ser Ser Gln Ile Trp Ala Ala Cys Leu Leu Leu Leu
1 5 10 15
Leu Leu Leu Ala Ser Leu Thr Ser Gly Ser Val Phe Pro Gln Gln
20 25 30
Thr Gly Gln Leu Ala Glu Leu Gln Pro Gln Asp Arg Ala Gly Ala
35 40 45
Arg Ala Ser Trp Met Pro Met Phe Gln Arg Arg Arg Arg Arg Asp
50 55 60
Thr His Phe Pro Ile Cys Ile Phe Cys Cys Gly Cys Cys His Arg
65 70 75
Ser Lys Cys Gly Met Cys Cys Lys Thr
80

<210> SEQ ID NO 45
<211> LENGTH: 1076
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 45
gtggcttcat ttcagtggct gacttcaga gagcaatatg gctgggtccc 50
caacatgcct caccctcatc tatatccttt ggcagctcac agggtcagca 100
gcctctggac ccgtgaaaga gctggtcggt tccgttggtg gggccgtgac 150
tttccccctg aagtccaaag taaagcaagt tgactctatt gtctggacct 200
tcaacacaac ccctcttgct accatacagc cagaaggggg cactatcata 250

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gtgacccaaa atcgtaatag ggagagagta gacttcccag atggaggcta	300
ctccctgaag ctacagaaac tgaagaagaa tgactcaggg atctactatg	350
tggggatata cagctcatca ctccagcagc cctccaccca ggagtacgtg	400
ctgcatgtct acgagcacct gtcaaagcct aaagtcacca tgggtctgca	450
gagcaataag aatggcacct gtgtgaccaa tctgacatgc tgcattggaac	500
atggggaaga ggatgtgatt tatacctgga aggccctggg gcaagcagcc	550
aatgagtccc ataatgggtc catcctcccc atctcctgga gatggggaga	600
aagtgatatg accttcattc gcgttgccag gaaccctgtc agcagaaact	650
tctcaagccc catccttgcc aggaagctct gtgaagggtc tgctgatgac	700
ccagattcct ccatggtcct cctgtgtctc ctgttggtgc ccctcctgct	750
cagtctcttt gtactggggc tatttctttg gtttctgaag agagagagac	800
aagaagagta cattgaagag aagaagagag tggacatttg tcgggaaact	850
cctaacatat gccccattc tggagagaac acagagtacg acacaatccc	900
tcacactaat agaacaatcc taaaggaaga tccagcaaat acggtttact	950
ccactgtgga aataccgaaa aagatggaaa atccccactc actgctcacg	1000
atgccagaca caccaaggct atttgcttat gagaatgtta tctagacagc	1050
agtgcactcc cctaagtctc tgctca	1076

<210> SEQ ID NO 46
<211> LENGTH: 335
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 46

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

-continued

Ala Leu Gly Gln Ala Ala Asn Glu Ser His Asn Gly Ser Ile Leu
170 175 180

Pro Ile Ser Trp Arg Trp Gly Glu Ser Asp Met Thr Phe Ile Cys
185 190 195

Val Ala Arg Asn Pro Val Ser Arg Asn Phe Ser Ser Pro Ile Leu
200 205 210

Ala Arg Lys Leu Cys Glu Gly Ala Ala Asp Asp Pro Asp Ser Ser
215 220 225

Met Val Leu Leu Cys Leu Leu Leu Val Pro Leu Leu Leu Ser Leu
230 235 240

Phe Val Leu Gly Leu Phe Leu Trp Phe Leu Lys Arg Glu Arg Gln
245 250 255

Glu Glu Tyr Ile Glu Glu Lys Lys Arg Val Asp Ile Cys Arg Glu
260 265 270

Thr Pro Asn Ile Cys Pro His Ser Gly Glu Asn Thr Glu Tyr Asp
275 280 285

Thr Ile Pro His Thr Asn Arg Thr Ile Leu Lys Glu Asp Pro Ala
290 295 300

Asn Thr Val Tyr Ser Thr Val Glu Ile Pro Lys Lys Met Glu Asn
305 310 315

Pro His Ser Leu Leu Thr Met Pro Asp Thr Pro Arg Leu Phe Ala
320 325 330

Tyr Glu Asn Val Ile
335

<210> SEQ ID NO 47
<211> LENGTH: 766
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 47

ggctcgagcg tttctgagcc aggggtgacc atgacctgct gcgaaggatg 50

gacatcctgc aatggattca gcctgctggt tctactgctg ttaggagtag 100

ttctcaatgc gatacctcta attgtcagct tagttgagga agaccaattt 150

tctcaaaacc ccatctcttg ctttgagtgg tgggtcccag gaattatag 200

agcagggtctg atggccattc cagcaacaac aatgtccttg acagcaagaa 250

aaagagcgtg ctgcaacaac agaactggaa tgtttctttc atcatttttc 300

agtgatgatca cagtcattgg tgctctgtat tgcagtgtga tatccatcca 350

ggctctctta aaaggtcctc tcatgtgtaa ttctccaagc aacagtaatg 400

ccaattgtga attttcattg aaaaacatca gtgacattca tccagaatcc 450

ttcaacttgc agtgggtttt caatgactct tgtgcacctc ctactggttt 500

caataaacc accagtaacg acaccatggc gagtggctgg agagcatcta 550

gtttccactt cgattctgaa gaaaacaaac ataggcttat ccacttctca 600

gtatttttag gtctattgct tgttggaatt ctggaggtcc tgtttgggct 650

cagtcagata gtcatcgggt tccttggtg tctgtgtgga gtctctaagc 700

gaagaagtca aattgtgtag tttaatggga ataaaatgta agtatcagta 750

gtttgaaaaa aaaaaa 766

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<210> SEQ ID NO 48
<211> LENGTH: 229
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 48

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

<210> SEQ ID NO 49
<211> LENGTH: 636
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 49

atccgtttctc tgcgctgccca gctcaggtga gccctcgcca aggtgacctc 50
gcagagacct ggtgaaggag cagtgaaggaa cctgcagagt cacacagttg 100
ctgaccaatt gagctgtgag cctggagcag atccgtgggc tgcagacccc 150
cgccccagtg cctctcccc tgcagccctg cccctcgaac tgtgacatgg 200
agagagtgac cctggccctt ctectactgg caggcctgac tgccttgga 250
gccaatgacc catttgccaa taaagacgat cccttctact atgactggaa 300

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aaacctgcag ctgagcggac tgatctgcgg agggctcctg gccattgctg	350
ggatcgcggc agttctgagt ggcaaatgca aatacaagag cagccagaag	400
cagcacagtc ctgtacctga gaaggccatc ccactcatca ctccaggctc	450
tgccactact tgctgagcac aggactggcc tccagggatg gcctgaagcc	500
taacactggc cccagcacc tcctcccctg ggaggcctta tcctcaagga	550
aggactttct tccaagggca ggctgttagg cccctttctg atcaggaggc	600
ttctttatga attaaactcg cccaccacc ccctca	636

<210> SEQ ID NO 50
<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 50

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

<210> SEQ ID NO 51
<211> LENGTH: 1734
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 51

gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca	50
gaccagaggg gagggaggac agggagtctg aaggaggagg acagaggagg	100
gcacagagac gcagagcaag gccggcaagg aggagaccct ggtgggagga	150
agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc	200
cctggcctgc ctctgctgg ccctctgcct gggcagtggt gaggtggcc	250
ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt	300
ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg	350
caaagaggcc ggaggggcag ctggctctaa agtcagttag gcccttgcc	400
aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt	450
ggcgacagc atgctttggg caacagggtc ggggaagcag cccatgctct	500
gggaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac	550
acggagcaga tgctgtccgc ggctcctggc aggggggtgcc tggccacagt	600
ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaaggtgg	650
ccttgagggc cagggccagg gcaatcctgg aggtctgggt actccgtggg	700

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tccacggata ccccggaac tcagcaggca gctttggaat gaatcctcag	750
ggagctccct ggggtcaagg aggcaatgga gggccaccaa actttgggac	800
caacactcag ggagctgtgg ccagcctgg ctatggttca gtgagagcca	850
gcaaccagaa tgaaggggtgc acgaatcccc caccatctgg ctgaggtgga	900
ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtg	950
cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca	1000
gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc	1050
agtgtgtgca gcagtggcaa cagtgtgtgc agcagaggtg acagcggcag	1100
tgagtcctcc tggggatcca gcaccggctc ctctccggc aaccacggtg	1150
ggagcggcgg aggaaatgga cataaaccgg ggtgtgaaaa gccagggaat	1200
gaagcccgcg ggagcgggga atctgggatt cagggttca gaggacagg	1250
agtttccagc aacatgaggg aaataagcaa agagggcaat cgctccttg	1300
gaggctctgg agacaattat cgggggcaag ggtcgagctg ggcagtgga	1350
ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc	1400
tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg	1450
gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc	1500
ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact	1550
ccctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg	1600
aaataaacct tagctgcccc acaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1650
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa	1734

<210> SEQ ID NO 52
<211> LENGTH: 440
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 52

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

-continued

Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile
140 145 150

Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro
155 160 165

Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser
170 175 180

Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln
185 190 195

Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly
200 205 210

Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln
215 220 225

Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly
230 235 240

Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser
245 250 255

Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly
260 265 270

Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser
275 280 285

Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser
290 295 300

Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly
305 310 315

Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His
320 325 330

Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly
335 340 345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn
350 355 360

Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser
365 370 375

Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
380 385 390

Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser
395 400 405

Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
410 415 420

Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg
425 430 435

Ser Ser Arg Ile Pro
440

<210> SEQ ID NO 53
<211> LENGTH: 1676
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 53

ggagaagagg ttgtgtggga caagctgctc cgcacagaag gatgtcgctg 50

ctgagcctgc cctggctggg cctcagaccg gtggcaatgt ccccatggct 100

-continued

actcctgctg ctgggttggt gctcctggct actcgccgc atcctggctt	150
ggacctatgc cttctataac aactgccgc ggctccagt tttccacag	200
ccccaaaaa ggaactggtt ttggggtcac ctgggcctga tcactcctac	250
agaggagggg ttgaaggact cgaccagat gtcggccacc tattcccagg	300
gctttacggt atggctgggt cccatcatcc ccttcacgt tttatgccac	350
cctgacacca tccggtctat caccaatgcc tcagctgcca ttgcacccaa	400
ggataatctc ttcacaggt tcctgaagcc ctggctggga gaagggatac	450
tgctgagtgg cggtgacaag tggagccgc accgtcggat gctgacgccc	500
gccttccatt tcaacatcct gaagtcctat ataacgatct tcaacaagag	550
tgcaaacatc atgcttgaca agtggcagca cctggcctca gagggcagca	600
gtcgtctgga catgtttgag cacatcagcc tcatgacctt ggacagtcta	650
cagaaatgca tcttcagctt tgacagccat tgtcaggaga ggcccagtga	700
atatattgcc accatcttgg agctcagtgc ccttgtagag aaaagaagcc	750
agcatatcct ccagcacatg gactttctgt attacctctc ccatgacggg	800
cggcgcttcc acagggcctg ccgcctgtg catgacttca cagacgctgt	850
catccgggag cggcgctcga ccctcccccac tcagggtatt gatgattttt	900
tcaaagacaa agccaagtcc aagacttttg atttcattga tgtgcttctg	950
ctgagcaagg atgaagatgg gaaggcattg tcagatgagg atataagagc	1000
agaggctgac accttcatgt ttggaggcca tgacaccacg gccagtggcc	1050
tctcctgggt cctgtacaac cttgcgaggc acccagaata ccaggagcgc	1100
tgccgacagg aggtgcaaga gcttctgaag gaccgcgac ctaaagagat	1150
tgaatgggac gacctggccc agctgccctt cctgaccatg tgcgtgaagg	1200
agagcctgag gttacatccc ccagctccct tcacctccc atgctgcacc	1250
caggacattg ttctcccaga tggccgagtc atccccaag gcattacctg	1300
cctcatcgat attatagggg tccatcacia cccaactgtg tggccggatc	1350
ctgaggctca cgacccttc cgctttgacc cagagaacag caaggggagg	1400
tcacctctgg cttttattcc tttctccgca gggcccagga actgcacgg	1450
gcaggcgctc gccatggcgg agatgaaagt ggtcctggcg ttgatgctgc	1500
tgcaacttcg gttcctgcca gaccacactg agccccgag gaagctggaa	1550
ttgatcatgc gcgccgagg cgggcttttg ctgcgggtgg agcccctgaa	1600
tgtaggcttg cagtgacttt ctgaccatc cacctgtttt tttgcagatt	1650
gtcatgaata aaacggtgct gtcaaa	1676

<210> SEQ ID NO 54
<211> LENGTH: 524
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 54

Met Ser Leu Leu Ser Leu Pro Trp Leu Gly Leu Arg Pro Val Ala
1 5 10 15

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Met	Ser	Pro	Trp	Leu	Leu	Leu	Leu	Val	Val	Gly	Ser	Trp	Leu	20	25	30	
Leu	Ala	Arg	Ile	Leu	Ala	Trp	Thr	Tyr	Ala	Phe	Tyr	Asn	Asn	Cys	35	40	45
Arg	Arg	Leu	Gln	Cys	Phe	Pro	Gln	Pro	Pro	Lys	Arg	Asn	Trp	Phe	50	55	60
Trp	Gly	His	Leu	Gly	Leu	Ile	Thr	Pro	Thr	Glu	Glu	Gly	Leu	Lys	65	70	75
Asp	Ser	Thr	Gln	Met	Ser	Ala	Thr	Tyr	Ser	Gln	Gly	Phe	Thr	Val	80	85	90
Trp	Leu	Gly	Pro	Ile	Ile	Pro	Phe	Ile	Val	Leu	Cys	His	Pro	Asp	95	100	105
Thr	Ile	Arg	Ser	Ile	Thr	Asn	Ala	Ser	Ala	Ala	Ile	Ala	Pro	Lys	110	115	120
Asp	Asn	Leu	Phe	Ile	Arg	Phe	Leu	Lys	Pro	Trp	Leu	Gly	Glu	Gly	125	130	135
Ile	Leu	Leu	Ser	Gly	Gly	Asp	Lys	Trp	Ser	Arg	His	Arg	Arg	Met	140	145	150
Leu	Thr	Pro	Ala	Phe	His	Phe	Asn	Ile	Leu	Lys	Ser	Tyr	Ile	Thr	155	160	165
Ile	Phe	Asn	Lys	Ser	Ala	Asn	Ile	Met	Leu	Asp	Lys	Trp	Gln	His	170	175	180
Leu	Ala	Ser	Glu	Gly	Ser	Ser	Arg	Leu	Asp	Met	Phe	Glu	His	Ile	185	190	195
Ser	Leu	Met	Thr	Leu	Asp	Ser	Leu	Gln	Lys	Cys	Ile	Phe	Ser	Phe	200	205	210
Asp	Ser	His	Cys	Gln	Glu	Arg	Pro	Ser	Glu	Tyr	Ile	Ala	Thr	Ile	215	220	225
Leu	Glu	Leu	Ser	Ala	Leu	Val	Glu	Lys	Arg	Ser	Gln	His	Ile	Leu	230	235	240
Gln	His	Met	Asp	Phe	Leu	Tyr	Tyr	Leu	Ser	His	Asp	Gly	Arg	Arg	245	250	255
Phe	His	Arg	Ala	Cys	Arg	Leu	Val	His	Asp	Phe	Thr	Asp	Ala	Val	260	265	270
Ile	Arg	Glu	Arg	Arg	Arg	Thr	Leu	Pro	Thr	Gln	Gly	Ile	Asp	Asp	275	280	285
Phe	Phe	Lys	Asp	Lys	Ala	Lys	Ser	Lys	Thr	Leu	Asp	Phe	Ile	Asp	290	295	300
Val	Leu	Leu	Leu	Ser	Lys	Asp	Glu	Asp	Gly	Lys	Ala	Leu	Ser	Asp	305	310	315
Glu	Asp	Ile	Arg	Ala	Glu	Ala	Asp	Thr	Phe	Met	Phe	Gly	Gly	His	320	325	330
Asp	Thr	Thr	Ala	Ser	Gly	Leu	Ser	Trp	Val	Leu	Tyr	Asn	Leu	Ala	335	340	345
Arg	His	Pro	Glu	Tyr	Gln	Glu	Arg	Cys	Arg	Gln	Glu	Val	Gln	Glu	350	355	360
Leu	Leu	Lys	Asp	Arg	Asp	Pro	Lys	Glu	Ile	Glu	Trp	Asp	Asp	Leu	365	370	375
Ala	Gln	Leu	Pro	Phe	Leu	Thr	Met	Cys	Val	Lys	Glu	Ser	Leu	Arg	380	385	390

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Leu	His	Pro	Pro	Ala	Pro	Phe	Ile	Ser	Arg	Cys	Cys	Thr	Gln	Asp
				395					400					405
Ile	Val	Leu	Pro	Asp	Gly	Arg	Val	Ile	Pro	Lys	Gly	Ile	Thr	Cys
				410					415					420
Leu	Ile	Asp	Ile	Ile	Gly	Val	His	His	Asn	Pro	Thr	Val	Trp	Pro
				425					430					435
Asp	Pro	Glu	Val	Tyr	Asp	Pro	Phe	Arg	Phe	Asp	Pro	Glu	Asn	Ser
				440					445					450
Lys	Gly	Arg	Ser	Pro	Leu	Ala	Phe	Ile	Pro	Phe	Ser	Ala	Gly	Pro
				455					460					465
Arg	Asn	Cys	Ile	Gly	Gln	Ala	Phe	Ala	Met	Ala	Glu	Met	Lys	Val
				470					475					480
Val	Leu	Ala	Leu	Met	Leu	Leu	His	Phe	Arg	Phe	Leu	Pro	Asp	His
				485					490					495
Thr	Glu	Pro	Arg	Arg	Lys	Leu	Glu	Leu	Ile	Met	Arg	Ala	Glu	Gly
				500					505					510
Gly	Leu	Trp	Leu	Arg	Val	Glu	Pro	Leu	Asn	Val	Gly	Leu	Gln	
				515					520					

<210> SEQ ID NO 55
<211> LENGTH: 644
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 55

atcgcatcaa ttgggagtac catcttcctc atgggaccag tgaaacagct	50
gaagcgaatg tttagaccta ctggtttgat tgcaactatc atggtgctgt	100
tgtgttttgc acttaccctg tgttctgcct tttggtggca taacaaggga	150
cttgacactta tcttctgcat tttagcagtct ttggcattga cgtggtacag	200
cctttccttc ataccatttg caagggatgc tgtgaagaag tgttttgccg	250
tgtgtcttgc ataattcatg gccagtttta tgaagctttg gaaggcacta	300
tggacagaag ctggtggaca gttttgtaac tatcttcgaa acctctgtct	350
tacagacatg tgccttttat ctgcagcaa tgtgttgctt gtgattcgaa	400
catttgaggg ttacttttgg aagcaacaat acattctcga acctgaatgt	450
cagtagcaca ggatgagaag tgggttctgt atcttggtga gtggaatctt	500
cctcatgtac ctgtttcctc tctggatgtt gtccactga attcccatga	550
atacaaacct attcagcaac agcaaaaaaa aaaaaaaaaa aaaaaaaaaa	600
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa	644

<210> SEQ ID NO 56
<211> LENGTH: 77
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 56

Met	Gly	Pro	Val	Lys	Gln	Leu	Lys	Arg	Met	Phe	Glu	Pro	Thr	Arg
1				5					10					15
Leu	Ile	Ala	Thr	Ile	Met	Val	Leu	Leu	Cys	Phe	Ala	Leu	Thr	Leu
				20					25					30

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Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe
35 40 45
Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe
50 55 60
Ile Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val Cys
65 70 75
Leu Ala

<210> SEQ ID NO 57
<211> LENGTH: 3334
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 57

cggctcgagc	tcgagccgaa	tcggctcgag	gggcagtgga	gcaccagca	50
ggccgccaac	atgctctgtc	tgtgcctgta	cgtgccggtc	atcggggaag	100
cccagaccga	gttcagtagc	tttgagtcga	aggggctccc	tgccgagctg	150
aagtccattt	tcaagctcag	tgtcttcata	ccctcccagg	aattctccac	200
ctaccgccag	tggaagcaga	aaattgtaca	agctggagat	aaggaccttg	250
atgggcagct	agactttgaa	gaatttgtcc	attatctcca	agatcatgag	300
aagaagctga	ggctggtggt	taagattttg	gacaaaaaga	atgatggacg	350
cattgacgcg	caggagatca	tgcagtcctt	gcgggacttg	ggagtcaaga	400
tatctgaaca	gcaggcagaa	aaaattctca	agagcatgga	taaaaacggc	450
acgatgacca	tcgactggaa	cgagtggaga	gactaccacc	tcctccaccc	500
cgtggaaaaa	atccccgaga	tcatacctcta	ctggaagcat	tccacgatct	550
ttgatgtggg	tgagaatcta	acgggtcccg	atgagttcac	agtggaggag	600
aggcagacgg	ggatgtgggt	gagacacctg	gtggcaggag	gtggggcagg	650
ggccgtatcc	agaacctgca	cggccccctt	ggacaggctc	aaggtgctca	700
tgacggtcca	tgctctccgc	agcaacaaca	tgggcatact	tggtggcttc	750
actcagatga	ttcgagaagg	aggggccagg	tcactctggc	ggggcaatgg	800
catcaacgtc	ctcaaaattg	cccccgaaac	agccatcaaa	ttcatggcct	850
atgagcagat	caagcgccct	gttggtagtg	accaggagac	tctgaggatt	900
cacgagaggg	ttgtggcagg	gtccttggca	ggggccatcg	cccagagcag	950
catctaccca	atggaggtcc	tgaagacctg	gatggcgctg	cgaagacag	1000
gccagtactc	aggaatgctg	gactgcgcga	ggaggatcct	ggccagagag	1050
gggtgtggcg	ccttctacaa	aggctatgtc	cccaacatgc	tgggcatcat	1100
cccctatgcc	ggcatcgacc	ttgcagtcta	cgagacgctc	aagaatgcct	1150
ggctgcagca	ctatgcagtg	aacagcgctg	acccggcggt	gtttgtgctc	1200
ctggcctgtg	gcacatgtgc	cagtacctgt	ggccagctgg	ccagctaccc	1250
cctggcccta	gtcaggaccc	ggatgcaggc	gcaagcctct	attgagggcg	1300
ctccggaggt	gaccatgagc	agcctcttca	aacatatcct	gcggaccgag	1350
ggggccttcg	ggctgtacag	ggggctggcc	cccaacttca	tgaagggtcat	1400

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cccagctgtg agcatcagct acgtgggtcta cgagaacctg aagatcaccc	1450
tgggcgtgca gtcgcggtga cggggggagg gccgccggc agtggactcg	1500
ctgatccctg gccgcagcct ggggtgtgca gccatctcat tctgtgaatg	1550
tgccaacact aagctgtctc gagccaagct gtgaaaacct tagacgcacc	1600
cgcagggagg gtggggagag ctggcaggcc cagggttgt cctgctgacc	1650
ccagcagacc ctctgttgg ttccagcgaa gaccacaggc attccttagg	1700
gtccagggtc agcaggctcc gggtcacat gtgtaaggac aggacatttt	1750
ctgcagtgcc tgccaatagt gagcttggag cctggaggcc ggcttagttc	1800
ttccatttca cccttgacg cagctgttgg ccacggcccc tgccctctgg	1850
tctgccgtgc atctccctgt gccctcttgc tgcctgcctg tctgctgagg	1900
taaggtggga ggagggctac agcccacatc ccacccctc gtccaatccc	1950
ataatccatg atgaaagggt aggtcacgtg gcctcccagg cctgacttcc	2000
caacctacag cattgacgcc aacttggctg tgaaggaaga ggaaggatc	2050
tggccttgtg gtcactggca tctgagccct gctgatggct ggggctctcg	2100
ggcatgcttg ggagtgcagg gggctcgggc tgcctggcct ggctgcacag	2150
aaggcaagtg ctggggctca tgggtctctg agctggcctg gacctgtca	2200
ggatggggccc cacctcagaa ccaaactcac tgtccccact gtggcatgag	2250
ggcagtggag caccatgttt gagggcgaag ggcagagcgt ttgtgtgttc	2300
tggggagggga aggaaaagg gttggaggcc ttaattatgg actgttggga	2350
aaagggtttt gtccagaagg acaagccgga caaatgagcg acttctgtgc	2400
ttccagagga agacgagggg gcaggagctt ggctgactgc tcagagtctg	2450
ttctgacgcc ctgggggttc ctgtccaacc ccagcagggg cgcagcggga	2500
ccagcccac attccacttg tgtcactgct tggaacctat ttattttcta	2550
tttatttgaa cagagtatat tcctaactat ttttatagat ttgtttaatt	2600
aatagcttgt cattttcaag ttcatTTTT attcataatt atgttcatgg	2650
ttgattgtac cttcccaagc ccgccagtg ggatgggagg aggaggagaa	2700
ggggggcctt gggccgctgc agtcacatct gtccagagaa attccttttg	2750
ggactggagg cagaaaagcg gccagaaggc agcagccctg gctcctttcc	2800
tttggcaggt tggggaaggg cttgccccca gccttaggat ttcagggttt	2850
gactgggggc gtggagagag agggaggaac ctcaataacc ttgaagggtg	2900
aatccagtta tttctgcgc tgcgagggtt tctttatttc actcttttct	2950
gaatgtcaag gcagtgaggt gcctctcact gtgaatttgt ggtgggagg	3000
ggctggagga gaggtgggg ggctggctcc gtccctccca gccttctgct	3050
gcccttgctt aacaatgcc gccaactggc gacctcacgg ttgcaacttc	3100
attccaccag aatgacctga tgaggaaatc ttcaatagga tgcaaagatc	3150
aatgcaaaaa ttgttatata tgaacatata actggagtcg tcaaaaagca	3200
aattaagaaa gaattggacg ttagaagttg tcatttaaag cagccttcta	3250
ataaagttgt ttcaaagctg aaaaaaaaa aaaaaaaaa aaaaaaaaa	3300

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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa

3334

<210> SEQ ID NO 58

<211> LENGTH: 469

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 58

Met Leu Cys Leu Cys Leu Tyr Val Pro Val Ile Gly Glu Ala Gln
1 5 10 15

Thr Glu Phe Gln Tyr Phe Glu Ser Lys Gly Leu Pro Ala Glu Leu
20 25 30

Lys Ser Ile Phe Lys Leu Ser Val Phe Ile Pro Ser Gln Glu Phe
35 40 45

Ser Thr Tyr Arg Gln Trp Lys Gln Lys Ile Val Gln Ala Gly Asp
50 55 60

Lys Asp Leu Asp Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr
65 70 75

Leu Gln Asp His Glu Lys Lys Leu Arg Leu Val Phe Lys Ile Leu
80 85 90

Asp Lys Lys Asn Asp Gly Arg Ile Asp Ala Gln Glu Ile Met Gln
95 100 105

Ser Leu Arg Asp Leu Gly Val Lys Ile Ser Glu Gln Gln Ala Glu
110 115 120

Lys Ile Leu Lys Ser Met Asp Lys Asn Gly Thr Met Thr Ile Asp
125 130 135

Trp Asn Glu Trp Arg Asp Tyr His Leu Leu His Pro Val Glu Asn
140 145 150

Ile Pro Glu Ile Ile Leu Tyr Trp Lys His Ser Thr Ile Phe Asp
155 160 165

Val Gly Glu Asn Leu Thr Val Pro Asp Glu Phe Thr Val Glu Glu
170 175 180

Arg Gln Thr Gly Met Trp Trp Arg His Leu Val Ala Gly Gly Gly
185 190 195

Ala Gly Ala Val Ser Arg Thr Cys Thr Ala Pro Leu Asp Arg Leu
200 205 210

Lys Val Leu Met Gln Val His Ala Ser Arg Ser Asn Asn Met Gly
215 220 225

Ile Val Gly Gly Phe Thr Gln Met Ile Arg Glu Gly Gly Ala Arg
230 235 240

Ser Leu Trp Arg Gly Asn Gly Ile Asn Val Leu Lys Ile Ala Pro
245 250 255

Glu Ser Ala Ile Lys Phe Met Ala Tyr Glu Gln Ile Lys Arg Leu
260 265 270

Val Gly Ser Asp Gln Glu Thr Leu Arg Ile His Glu Arg Leu Val
275 280 285

Ala Gly Ser Leu Ala Gly Ala Ile Ala Gln Ser Ser Ile Tyr Pro
290 295 300

Met Glu Val Leu Lys Thr Arg Met Ala Leu Arg Lys Thr Gly Gln
305 310 315

Tyr Ser Gly Met Leu Asp Cys Ala Arg Arg Ile Leu Ala Arg Glu
320 325 330

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Gly	Val	Ala	Ala	Phe	Tyr	Lys	Gly	Tyr	Val	Pro	Asn	Met	Leu	Gly
				335					340					345
Ile	Ile	Pro	Tyr	Ala	Gly	Ile	Asp	Leu	Ala	Val	Tyr	Glu	Thr	Leu
				350					355					360
Lys	Asn	Ala	Trp	Leu	Gln	His	Tyr	Ala	Val	Asn	Ser	Ala	Asp	Pro
				365					370					375
Gly	Val	Phe	Val	Leu	Leu	Ala	Cys	Gly	Thr	Met	Ser	Ser	Thr	Cys
				380					385					390
Gly	Gln	Leu	Ala	Ser	Tyr	Pro	Leu	Ala	Leu	Val	Arg	Thr	Arg	Met
				395					400					405
Gln	Ala	Gln	Ala	Ser	Ile	Glu	Gly	Ala	Pro	Glu	Val	Thr	Met	Ser
				410					415					420
Ser	Leu	Phe	Lys	His	Ile	Leu	Arg	Thr	Glu	Gly	Ala	Phe	Gly	Leu
				425					430					435
Tyr	Arg	Gly	Leu	Ala	Pro	Asn	Phe	Met	Lys	Val	Ile	Pro	Ala	Val
				440					445					450
Ser	Ile	Ser	Tyr	Val	Val	Tyr	Glu	Asn	Leu	Lys	Ile	Thr	Leu	Gly
				455					460					465
Val	Gln	Ser	Arg											

<210> SEQ ID NO 59
<211> LENGTH: 1658
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 59

ggaaggcagc	ggcagctcca	ctcagccagt	accagatac	gctgggaacc	50
ttccccagcc	atggcttccc	tggggcagat	cctcttcttg	agcataatta	100
gcatcatcat	tattctggct	ggagcaattg	cactcatcat	tggctttggt	150
atttcaggga	gacactccat	cacagtcact	actgtcgcct	cagctgggaa	200
cattggggag	gatggaatcc	tgagctgcac	ttttgaacct	gacatcaaac	250
tttctgatat	cgtgatacaa	tggctgaagg	aagtggtttt	aggcttggtc	300
catgagttca	aagaaggcaa	agatgagctg	tcggagcagg	atgaaatgtt	350
cagaggccgg	acagcagtgt	ttgctgatca	agtgatagtt	ggcaatgcct	400
ctttgcggct	gaaaaacgtg	caactcacag	atgctggcac	ctacaaatgt	450
tatatcatca	cttctaaagg	caaggggaat	gctaaccttg	agtataaaac	500
tggagccttc	agcatgccgg	aagtgaatgt	ggactataat	gccagctcag	550
agaccttgcg	gtgtgaggct	ccccgatggt	tccccagcc	cacagtggtc	600
tgggcatccc	aagttgacca	gggagccaac	ttctcggaag	tctccaatac	650
cagcttttag	ctgaactctg	agaatgtgac	catgaaggtt	gtgtctgtgc	700
tctacaatgt	tacgatcaac	aacacatact	cctgtatgat	tgaaaatgac	750
attgccaaag	caacagggga	tatcaaagtg	acagaatcgg	agatcaaaag	800
gcggagtccac	ctacagctgc	taaactcaaa	ggcttctctg	tgtgtctctt	850
ctttctttgc	catcagctgg	gcacttctgc	ctctcagccc	ttacctgatg	900
ctaaaataat	gtgccttggc	cacaaaaaag	catgcaaagt	cattgttaca	950
acagggatct	acagaactat	ttcaccacca	gatatgacct	agttttatat	1000

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```
ttctgggagg aaatgaattc atatctagaa gtctggagtg agcaaacaag      1050
agcaagaaac aaaaagaagc caaaagcaga aggctccaat atgaacaaga      1100
taaatctatc ttcaaagaca tattagaagt tgggaaaata attcatgtga      1150
actagacaag tgtgttaaga gtgataagta aaatgcacgt ggagacaagt      1200
gcatccccag atctcaggga cctccccctg cctgtcacct ggggagtgag      1250
aggacaggat agtgcattgt ctttgtctct gaatttttag ttatatgtgc      1300
tgtaatgttg ctctgaggaa gcccctggaa agtctatccc aacatatcca      1350
catcttatat tccacaaatt aagctgtagt atgtacccta agacgtgtct      1400
aattgactgc cacttcgcaa ctacggggcg gctgcatttt agtaatgggt      1450
caaatgattc actttttatg atgcttccaa aggtgccttg gcttctcttc      1500
ccaactgaca aatgccaaag ttgagaaaaa tgatcataat tttagcataa      1550
acagagcagt cggggacacc gattttataa ataaactgag caccttcttt      1600
ttaaacaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1650
aaaaaaaaa                                     1658
```

<210> SEQ ID NO 60
<211> LENGTH: 282
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 60

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

<210> SEQ ID NO 61
<211> LENGTH: 1617
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 61

tgacgtcaga atcaccatgg ccagctatcc ttaccggcag ggctgcccag	50
gagctgcagg acaagcacca ggagcccctc cgggtagcta ctaccctgga	100
cccccaata gtggagggca gtatggtagt gggctacccc ctggtggtgg	150
ttatgggggt cctgcccctg gagggcctta tggaccacca gctggtggag	200
ggccctatgg acacccaat cctgggatgt tcccctctgg aactccagga	250
ggaccatatg gcggtgcagc tcccgggggc ccctatggtc agccacctcc	300
aagttcctac ggtgcccagc agcctgggct ttatggacag ggtggcgccc	350
ctcccaatgt ggatcctgag gcctactcct ggttcagtc ggtggactca	400
gatcacagtg gctatatctc catgaaggag ctaaagcagg ccctggtcaa	450
ctgcaattgg tcttcattca atgatgagac ctgcctcatg atgataaaca	500
tgtttgacaa gaccaagtca ggccgcacog atgtctacgg cttctcagcc	550
ctgtggaagt tcatccagca gtggaagaac ctcttcagc agtatgaccg	600
ggaccgctcg ggctccatta gctacacaga gctgcagcaa gctctgtccc	650
aaatgggcta caacctgagc ccccagttca ccagcttctt ggtctcccgc	700
tactgcccac gctctgcca tcttgccatg cagcttgacc gcttcatcca	750
ggtgtgcacc cagctgcagg tgctgacaga ggccttcggg gagaaggaca	800
cagctgtaca aggcaacatc cggtcagct tcgaggactt cgtcaccatg	850
acagcttctc ggatgctatg acccaacat ctgtggagag tggagtgcac	900
cagggacctt tcctggcttc ttagagttag agaagtatgt ggacatctct	950
tcttttctctg tccctctaga agaacattct cccttgcttg atgcaacact	1000
gttccaaaag aggggtggaga gtccctgcac atagccacca aatagtggag	1050
accggggctg aggccacaca gataggggcc tgatggagga gaggatagaa	1100
gttgaatgtc ctgatggcca tgagcagttg agtggcacag cctggcacca	1150
ggagcaggtc cttgtaatgg agttaagtgc cagtcagctg agctccaccc	1200
tgatgccagt ggtgagtgtt catcgccctg ttaccgtagg tacctgtgtt	1250

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ccctcaccag gccatcctgt caaacgagcc cttttctcc aaagtggaat	1300
ctgaccaagc atgagagaga tctgtctatg ggaccagtgg cttggattct	1350
gccacaccca taaatccttg tgtgttaact tctagctgcc tggggctggc	1400
cctgtctcaga caaatctgct ccctgggcat ctttgccag gcttctgcc	1450
cctgcagctg ggaccctca cttgcctgcc atgctctgct cggttcagt	1500
ctccaggaga cagtggcac ctctccctgc caatactttt ttaatttgc	1550
attttttttc atttggggcc aaaagtccag tgaaattgta agcttcaata	1600
aaaggatgaa actctga	1617

<210> SEQ ID NO 62

<211> LENGTH: 284

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 62

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

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Ala Phe Arg Glu Lys Asp Thr Ala Val Gln Gly Asn Ile Arg Leu
260 265 270
Ser Phe Glu Asp Phe Val Thr Met Thr Ala Ser Arg Met Leu
275 280

<210> SEQ ID NO 63
<211> LENGTH: 1234
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 63
caggatgcag ggcgcgtgg caggagctg cgctcctctg ggcctgctcc 50
tggtctgtct tcatctccca ggctctttg cccggagcat cgggtgtgtg 100
gaggagaaa tttccaaaa ctccgggacc aacttgctc agctcggaca 150
accttctctc actggccct ctaactctga acatccgcag cccgctctgg 200
accctaggtc taatgacttg gcaagggctt ctctgaagct cagcgtgcct 250
ccatcagatg gcttcccacc tgcaggaggt tctgcagtgc agaggtggcc 300
tccatcgttg gggctgcctg ccatggattc ctggcccctt gaggatcctt 350
ggcagatgat ggctgctgct gctgaggacc gcctggggga agcgtgcct 400
gaagaactct cttacctctc cagtgtctgc gccctcgtc cgggcagtgg 450
ccctttgcct ggggagtctt ctcccgatgc cacaggcctc tcacctgagg 500
cttactcct ccaccaggac tcggagtcca gacgactgcc ccgttcta 550
tcactgggag ccgggggaaa aatcctttcc caacgccctc cctggtctct 600
catccacagg gttctgcctg atcacccttg gggtagcctg aatccagt 650
tgtctgggg aggtggaggc cctgggactg gttggggaac gaggcccatg 700
ccacaccctg agggaatctg gggtagaat aatcaacccc caggtagacc 750
ctggggaaat attaatcgtt atccaggagg cagctgggga aatattaat 800
ggtagccagg aggcagctgg gggaatatta atcggtatcc aggaggcagc 850
tgggggaata ttcactata ccaggtatc aataacccat ttcctcctgg 900
agttctccgc cctcctggct ctctctggaa catccagct ggcttcctta 950
atcctccaag ccctagggtg cagtggggct agagcacgat agagggaac 1000
ccaacattgg gagttagagt cctgctcccg ccccttgctg tgtgggctca 1050
atccaggccc tgtaaacatg tttccagcac tatccccact ttcagtgcc 1100
tccctgctc atctccaata aaataaaagc acttatgaaa aaaaaaaaaa 1150
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1234

<210> SEQ ID NO 64
<211> LENGTH: 325
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 64
Met Gln Gly Arg Val Ala Gly Ser Cys Ala Pro Leu Gly Leu Leu
1 5 10 15

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Leu	Val	Cys	Leu	His	Leu	Pro	Gly	Leu	Phe	Ala	Arg	Ser	Ile	Gly	
				20					25					30	
Val	Val	Glu	Glu	Lys	Val	Ser	Gln	Asn	Phe	Gly	Thr	Asn	Leu	Pro	
				35					40					45	
Gln	Leu	Gly	Gln	Pro	Ser	Ser	Thr	Gly	Pro	Ser	Asn	Ser	Glu	His	
				50					55					60	
Pro	Gln	Pro	Ala	Leu	Asp	Pro	Arg	Ser	Asn	Asp	Leu	Ala	Arg	Val	
				65					70					75	
Pro	Leu	Lys	Leu	Ser	Val	Pro	Pro	Ser	Asp	Gly	Phe	Pro	Pro	Ala	
				80					85					90	
Gly	Gly	Ser	Ala	Val	Gln	Arg	Trp	Pro	Pro	Ser	Trp	Gly	Leu	Pro	
				95					100					105	
Ala	Met	Asp	Ser	Trp	Pro	Pro	Glu	Asp	Pro	Trp	Gln	Met	Met	Ala	
				110					115					120	
Ala	Ala	Ala	Glu	Asp	Arg	Leu	Gly	Glu	Ala	Leu	Pro	Glu	Glu	Leu	
				125					130					135	
Ser	Tyr	Leu	Ser	Ser	Ala	Ala	Ala	Leu	Ala	Pro	Gly	Ser	Gly	Pro	
				140					145					150	
Leu	Pro	Gly	Glu	Ser	Ser	Pro	Asp	Ala	Thr	Gly	Leu	Ser	Pro	Glu	
				155					160					165	
Ala	Ser	Leu	Leu	His	Gln	Asp	Ser	Glu	Ser	Arg	Arg	Leu	Pro	Arg	
				170					175					180	
Ser	Asn	Ser	Leu	Gly	Ala	Gly	Gly	Lys	Ile	Leu	Ser	Gln	Arg	Pro	
				185					190					195	
Pro	Trp	Ser	Leu	Ile	His	Arg	Val	Leu	Pro	Asp	His	Pro	Trp	Gly	
				200					205					210	
Thr	Leu	Asn	Pro	Ser	Val	Ser	Trp	Gly	Gly	Gly	Gly	Pro	Gly	Thr	
				215					220					225	
Gly	Trp	Gly	Thr	Arg	Pro	Met	Pro	His	Pro	Glu	Gly	Ile	Trp	Gly	
				230					235					240	
Ile	Asn	Asn	Gln	Pro	Pro	Gly	Thr	Ser	Trp	Gly	Asn	Ile	Asn	Arg	
				245					250					255	
Tyr	Pro	Gly	Gly	Ser	Trp	Gly	Asn	Ile	Asn	Arg	Tyr	Pro	Gly	Gly	
				260					265					270	
Ser	Trp	Gly	Asn	Ile	Asn	Arg	Tyr	Pro	Gly	Gly	Ser	Trp	Gly	Asn	
				275					280					285	
Ile	His	Leu	Tyr	Pro	Gly	Ile	Asn	Asn	Pro	Phe	Pro	Pro	Gly	Val	
				290					295					300	
Leu	Arg	Pro	Pro	Gly	Ser	Ser	Trp	Asn	Ile	Pro	Ala	Gly	Phe	Pro	
				305					310					315	
Asn	Pro	Pro	Ser	Pro	Arg	Leu	Gln	Trp	Gly						
				320					325						

<210> SEQ ID NO 65
<211> LENGTH: 422
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 65

aaggagaggc caccgggact tcagtgtctc ctccatccca ggagcgcagt	50
ggccactatg gggctctgggc tgccccttgt cctcctcttg accctccttg	100
gcagctcaca tggaacaggg ccgggtatga ctttgcaact gaagctgaag	150

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gagtccttttc tgacaaattc ctccctatgag tccagcttcc tggaattgct	200
tgaaaagctc tgcctcctcc tccatctccc ttcagggacc agcgtcacc	250
tccaccatgc aagatctcaa caccatgttg tctgcaacac atgacagcca	300
ttgaagcctg tgtccttctt ggcccgggct tttgggccgg ggatgcagga	350
ggcaggcccc gaccctgtct ttcagcaggc ccccccctc ctgagtggca	400
ataaataaaa ttcggtatgc tg	422

<210> SEQ ID NO 66
<211> LENGTH: 78
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 66

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

<210> SEQ ID NO 67
<211> LENGTH: 744
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 67

acggaccgag ggttcgaggg agggacacgg accaggaacc tgagctaggt	50
caaagacgcc cgggccaggt gccccgtcgc aggtgccctt ggccggagat	100
gcggtaggag gggcgagcgc gagaagcccc ttcctcgcg ctgccaaacc	150
gccaccacgc ccatggcgaa ccccgggctg gggctgcttc tggcgctggg	200
cctgccgttc ctgctggccc gctggggcgg agcctggggg caaatacaga	250
ccacttctgc aaatgagaat agcactgttt tgccttcac caccagctcc	300
agctccgatg gcaacctgcg tccggaagcc atcactgcta tcatcgtggt	350
cttctccctc ttggctgcct tgctcctggc tgtggggctg gcactgttgg	400
tgcggaagct tcgggagaag cggcagacgg agggcaccta ccggcccagt	450
agcgaggagc agttctccca tgcagccgag gcccgggccc ctgaggactc	500
caaggagacg gtgcagggct gcctgcccat ctaggctccc tctcctgcat	550
ctgtctccct tcattgtgtg gtgaccttgg ggaaaggcag tgccctctct	600
gggcagtcat atccaccacg tgcttaatag cagggaagaa ggtacttcaa	650
agactctgcc cctgaggta agagaggatg gggctattca cttttatata	700
tttatataaa attagtagtg agatgtaaaa aaaaaaaaa aaaa	744

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<210> SEQ ID NO 68
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 68

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

<210> SEQ ID NO 69
<211> LENGTH: 3265
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 69

gccaggaata actagagagg aacaatgggg ttattcagag gttttgtttt 50
cctcttagtt ctgtgcctgc tgcaccagtc aaatacttcc ttcattaagc 100
tgaataataa tggctttgaa gatattgtca ttgttataga tcctagtgtg 150
ccagaagatg aaaaaataat tgaacaaata gaggatatgg tgactacagc 200
ttctacgtac ctgtttgaag ccacagaaaa aagatttttt ttcaaaaatg 250
tatctatatt aattcctgag aattggaagg aaaatcctca gtacaaaagg 300
ccaaaacatg aaaaccataa acatgctgat gttatagttg caccacctac 350
actcccaggt agagatgaac catacaccaa gcagttcaca gaatgtggag 400
agaaaggcga atacattcac ttcaccctcg accttctact tggaaaaaaa 450
caaaatgaat atggaccacc aggcaaactg tttgtccatg agtgggctca 500
cctccggtgg ggagtgtttg atgagtacaa tgaagatcag cctttctacc 550
gtgctaagtc aaaaaaaatc gaagcaacaa ggtgttccgc aggtatctct 600
ggtagaaata gagtttataa gtgtcaagga ggcagctgtc ttagtagagc 650
atgcagaatt gattctacaa caaaactgta tggaaaagat tgtcaattct 700
ttcctgataa agtacaaaca gaaaaagcat ccataatgtt tatgcaaagt 750
attgattctg ttgttgaatt ttgtaacgaa aaaaccata atcaagaagc 800
tccaagccta caaaacataa agtgcaattt tagaagtaca tgggaggtga 850

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ttagcaattc tgaggatddd aaaaacacca taccatggt gacaccacct	900
cctccacctg tcttctcatt gctgaagatc agtcaaagaa ttgtgtgctt	950
agttcttgat aagtctggaa gcatggggg taaggaccgc ctaaatcgaa	1000
tgaatcaagc agcaaaacat ttcctgctgc agactgttga aaatggatcc	1050
tgggtgggga tggttcactt tgatagtact gccactattg taaataagct	1100
aatccaaata aaaagcagtg atgaagaaa cactcatg gcaggattac	1150
ctacatatcc tctgggagga acttccatct gctctggaat taaatatgca	1200
tttcaggdga ttggagagct acattcccaa ctcgatggat ccgaagtact	1250
gctgctgact gatggggagg ataactctgc aagttcttgt attgatgaag	1300
tgaacaaaag tggggccatt gttcatttta ttgctttggg aagagctgct	1350
gatgaagcag taatagagat gagcaagata acaggaggaa gtcattttta	1400
tgtttcagat gaagctcaga acaatggcct cattgatgct tttggggctc	1450
ttacatcagg aaatactgat ctctccaga agtccctca gctcgaaagt	1500
aagggattaa cactgaatag taatgcctgg atgaacgaca ctgtcataat	1550
tgatagtaca gtgggaaagg acacgttctt tctcatcaca tggaacagtc	1600
tgccctccag tatttctctc tgggatccca gtggaacaat aatggaaaat	1650
ttcacagtgg atgcaacttc caaaatggcc tatctcagta ttccaggaa	1700
tgcaagggtg ggcacttggg catacaatct tcaagccaaa gcgaaccag	1750
aaacattaac tattacagta acttctcgag cagcaaatc tctgtgcct	1800
ccaatcacag tgaatgctaa aatgaataag gacgtaaaca gtttcccag	1850
cccaatgatt gtttacgag aaattctaca aggatatgta cctgttcttg	1900
gagccaatgt gactgctttc attgaatcac agaatggaca tacagaagtt	1950
ttggaacttt tggataatgg tgcaggcgct gattctttca agaattgatg	2000
agttactacc aggtatttta cagcatatac agaaaatggc agatatagct	2050
taaaagtctg ggctcatgga ggagcaaa caagccaggct aaaattacgg	2100
cctccactga atagagccgc gtacatacca ggctgggtag tgaacgggga	2150
aattgaagca aaccgcca gacctgaaat tgatgaggat actcagacca	2200
ccttgaggga tttcagcca acagcatccg gaggtgcatt tgtggtatca	2250
caagtcccaa gccttccctt gcctgaccaa taccaccaa gtcaaatcac	2300
agaccttgat gccacagttc atgaggataa gattattctt acatggacag	2350
caccaggaga taattttgat gttgaaaag ttcaacgtta tatcataaga	2400
ataagtgcaa gtattcttga tctaagagac agttttgatg atgctcttca	2450
agtaataact actgatctgt caccaaagga ggccaactcc aaggaaagct	2500
ttgcatttaa accagaaaat atctcagaag aaaatgcaac ccacatattt	2550
attgccatta aaagtataga taaaagcaat ttgacatcaa aagtatocaa	2600
cattgcacaa gtaactttgt ttatccctca agcaaatcct gatgacattg	2650
atcctacacc tactcctact cctactccta ctctgataa aagtcataat	2700
tctggagtta atatttctac gctggtattg tctgtgattg ggtctgttgt	2750

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aattgttaac tttattttaa gtaccacccat ttgaacctta acgaagaaaa	2800
aaatcttcaa gtagacctag aagagagttt taaaaaacia aacaatgtaa	2850
gtaaaggata tttctgaatc ttaaaattca tcccatgtgt gatcataaac	2900
tcataaaaaa aattttaaga tgtcggaaaa ggatactttg attaaataaa	2950
aacactcatg gatatgtaaa aactgtcaag attaaaattt aatagtttca	3000
tttattttgt attttatttg taagaaatag tgatgaacaa agatcctttt	3050
tcatactgat acctggttgt atattatttg atgcaacagt tttctgaaat	3100
gatattttcaa attgcatcaa gaaattaaaa tcacttatct gagtagtcaa	3150
aatacaagta aaggagagca aataaacaac atttgaaaa aaaaaaaaaa	3200
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	3250
aaaaaaaaaa aaaaaa	3265

<210> SEQ ID NO 70

<211> LENGTH: 919

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 70

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

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Phe	Pro	Asp	Lys	Val	Gln	Thr	Glu	Lys	Ala	Ser	Ile	Met	Phe	Met
				230					235					240
Gln	Ser	Ile	Asp	Ser	Val	Val	Glu	Phe	Cys	Asn	Glu	Lys	Thr	His
				245					250					255
Asn	Gln	Glu	Ala	Pro	Ser	Leu	Gln	Asn	Ile	Lys	Cys	Asn	Phe	Arg
				260					265					270
Ser	Thr	Trp	Glu	Val	Ile	Ser	Asn	Ser	Glu	Asp	Phe	Lys	Asn	Thr
				275					280					285
Ile	Pro	Met	Val	Thr	Pro	Pro	Pro	Pro	Pro	Val	Phe	Ser	Leu	Leu
				290					295					300
Lys	Ile	Ser	Gln	Arg	Ile	Val	Cys	Leu	Val	Leu	Asp	Lys	Ser	Gly
				305					310					315
Ser	Met	Gly	Gly	Lys	Asp	Arg	Leu	Asn	Arg	Met	Asn	Gln	Ala	Ala
				320					325					330
Lys	His	Phe	Leu	Leu	Gln	Thr	Val	Glu	Asn	Gly	Ser	Trp	Val	Gly
				335					340					345
Met	Val	His	Phe	Asp	Ser	Thr	Ala	Thr	Ile	Val	Asn	Lys	Leu	Ile
				350					355					360
Gln	Ile	Lys	Ser	Ser	Asp	Glu	Arg	Asn	Thr	Leu	Met	Ala	Gly	Leu
				365					370					375
Pro	Thr	Tyr	Pro	Leu	Gly	Gly	Thr	Ser	Ile	Cys	Ser	Gly	Ile	Lys
				380					385					390
Tyr	Ala	Phe	Gln	Val	Ile	Gly	Glu	Leu	His	Ser	Gln	Leu	Asp	Gly
				395					400					405
Ser	Glu	Val	Leu	Leu	Leu	Thr	Asp	Gly	Glu	Asp	Asn	Thr	Ala	Ser
				410					415					420
Ser	Cys	Ile	Asp	Glu	Val	Lys	Gln	Ser	Gly	Ala	Ile	Val	His	Phe
				425					430					435
Ile	Ala	Leu	Gly	Arg	Ala	Ala	Asp	Glu	Ala	Val	Ile	Glu	Met	Ser
				440					445					450
Lys	Ile	Thr	Gly	Gly	Ser	His	Phe	Tyr	Val	Ser	Asp	Glu	Ala	Gln
				455					460					465
Asn	Asn	Gly	Leu	Ile	Asp	Ala	Phe	Gly	Ala	Leu	Thr	Ser	Gly	Asn
				470					475					480
Thr	Asp	Leu	Ser	Gln	Lys	Ser	Leu	Gln	Leu	Glu	Ser	Lys	Gly	Leu
				485					490					495
Thr	Leu	Asn	Ser	Asn	Ala	Trp	Met	Asn	Asp	Thr	Val	Ile	Ile	Asp
				500					505					510
Ser	Thr	Val	Gly	Lys	Asp	Thr	Phe	Phe	Leu	Ile	Thr	Trp	Asn	Ser
				515					520					525
Leu	Pro	Pro	Ser	Ile	Ser	Leu	Trp	Asp	Pro	Ser	Gly	Thr	Ile	Met
				530					535					540
Glu	Asn	Phe	Thr	Val	Asp	Ala	Thr	Ser	Lys	Met	Ala	Tyr	Leu	Ser
				545					550					555
Ile	Pro	Gly	Thr	Ala	Lys	Val	Gly	Thr	Trp	Ala	Tyr	Asn	Leu	Gln
				560					565					570
Ala	Lys	Ala	Asn	Pro	Glu	Thr	Leu	Thr	Ile	Thr	Val	Thr	Ser	Arg
				575					580					585
Ala	Ala	Asn	Ser	Ser	Val	Pro	Pro	Ile	Thr	Val	Asn	Ala	Lys	Met
				590					595					600

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Asn	Lys	Asp	Val	Asn	Ser	Phe	Pro	Ser	Pro	Met	Ile	Val	Tyr	Ala	
				605					610					615	
Glu	Ile	Leu	Gln	Gly	Tyr	Val	Pro	Val	Leu	Gly	Ala	Asn	Val	Thr	
				620					625					630	
Ala	Phe	Ile	Glu	Ser	Gln	Asn	Gly	His	Thr	Glu	Val	Leu	Glu	Leu	
				635					640					645	
Leu	Asp	Asn	Gly	Ala	Gly	Ala	Asp	Ser	Phe	Lys	Asn	Asp	Gly	Val	
				650					655					660	
Tyr	Ser	Arg	Tyr	Phe	Thr	Ala	Tyr	Thr	Glu	Asn	Gly	Arg	Tyr	Ser	
				665					670					675	
Leu	Lys	Val	Arg	Ala	His	Gly	Gly	Ala	Asn	Thr	Ala	Arg	Leu	Lys	
				680					685					690	
Leu	Arg	Pro	Pro	Leu	Asn	Arg	Ala	Ala	Tyr	Ile	Pro	Gly	Trp	Val	
				695					700					705	
Val	Asn	Gly	Glu	Ile	Glu	Ala	Asn	Pro	Pro	Arg	Pro	Glu	Ile	Asp	
				710					715					720	
Glu	Asp	Thr	Gln	Thr	Thr	Leu	Glu	Asp	Phe	Ser	Arg	Thr	Ala	Ser	
				725					730					735	
Gly	Gly	Ala	Phe	Val	Val	Ser	Gln	Val	Pro	Ser	Leu	Pro	Leu	Pro	
				740					745					750	
Asp	Gln	Tyr	Pro	Pro	Ser	Gln	Ile	Thr	Asp	Leu	Asp	Ala	Thr	Val	
				755					760					765	
His	Glu	Asp	Lys	Ile	Ile	Leu	Thr	Trp	Thr	Ala	Pro	Gly	Asp	Asn	
				770					775					780	
Phe	Asp	Val	Gly	Lys	Val	Gln	Arg	Tyr	Ile	Ile	Arg	Ile	Ser	Ala	
				785					790					795	
Ser	Ile	Leu	Asp	Leu	Arg	Asp	Ser	Phe	Asp	Asp	Ala	Leu	Gln	Val	
				800					805					810	
Asn	Thr	Thr	Asp	Leu	Ser	Pro	Lys	Glu	Ala	Asn	Ser	Lys	Glu	Ser	
				815					820					825	
Phe	Ala	Phe	Lys	Pro	Glu	Asn	Ile	Ser	Glu	Glu	Asn	Ala	Thr	His	
				830					835					840	
Ile	Phe	Ile	Ala	Ile	Lys	Ser	Ile	Asp	Lys	Ser	Asn	Leu	Thr	Ser	
				845					850					855	
Lys	Val	Ser	Asn	Ile	Ala	Gln	Val	Thr	Leu	Phe	Ile	Pro	Gln	Ala	
				860					865					870	
Asn	Pro	Asp	Asp	Ile	Asp	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Pro	
				875					880					885	
Thr	Pro	Asp	Lys	Ser	His	Asn	Ser	Gly	Val	Asn	Ile	Ser	Thr	Leu	
				890					895					900	
Val	Leu	Ser	Val	Ile	Gly	Ser	Val	Val	Ile	Val	Asn	Phe	Ile	Leu	
				905					910					915	
Ser	Thr	Thr	Ile												

<210> SEQ ID NO 71
<211> LENGTH: 3877
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 71

ctccttaggt ggaaccctg ggagtagagt actgacagca aagaccggga	50
aagaccatac gtccccgggc aggggtgaca acaggtgtca tctttttgat	100

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ctcgtgtgtg gctgccttcc tatttcaagg aaagacgcca aggtaatttt	150
gaccagagg agcaatgatg tagccacctc ctaaccttcc cttcttgaaac	200
ccccagttat gccaggattt actagagagt gtcaactcaa ccagcaagcg	250
gctccttcgg ctttaacttgt ggttgaggga gagaaccttt gtggggctgc	300
gttctcttag cagtgcctcag aagtgacttg cctgaggggtg gaccagaaga	350
aaggaaagggt cccctcttgc tgttggtctgc acatcaggaa ggctgtgatg	400
ggaatgaagg tgaaaacttg gagatttcac ttcagtcatt gcttctgcct	450
gcaagatcat cctttaaaag tagagaagct gctctgtgtg gtgggttaact	500
ccaagaggca gaactcgttc tagaaggaaa tggatgcaag cagctccggg	550
ggccccaac gcctgcttcc tgtggtctag cccagggaag cccttccgtg	600
ggggcccggt ctttgaggga tgccaccggt tctggacgca tggctgattc	650
ctgaatgatg atggttcgcc gggggctgct tgcgtggatt tcccggttg	700
tggttttgct ggtgctcctc tgctgtgcta tctctgtcct gtacatgttg	750
gcctgcacc caaaagggtga cgaggagcag ctggcactgc ccagggccaa	800
cagccccacg ggggaaggagg ggtaccagc cgctccttcag gagtgggagg	850
agcagcaccg caactacgtg agcagcctga agcggcagat cgcacagctc	900
aaggaggagc tgcaggagag gagtgagcag ctcaggaatg ggcagtacca	950
agccagcgat gctgctggcc tgggtctgga caggagcccc ccagagaaaa	1000
cccaggccga cctcctggcc ttcctgcact cgcagggtgga caaggcagag	1050
gtgaatgctg gcgtcaagct ggccacagag tatgcagcag tgcctttcga	1100
tagctttact ctacagaagg tgtaccagct ggagactggc cttaccgcc	1150
accccgagga gaagcctgtg aggaaggaca agcgggatga gttggtggaa	1200
gccattgaat cagccttgga gaccctgaac aatcctgcag agaacagccc	1250
caatcacctg ccttacacgg cctctgattt catagaaggg atctaccgaa	1300
cagaaaggga caaagggaca ttgtatgagc tcaccttcaa aggggaccac	1350
aaacacgaat tcaaacggct catcttattt cgaccattca gccccatcat	1400
gaaagtgaat aatgaaaagc tcaacatggc caacacgctt atcaatgtta	1450
tcgtgcctct agcaaaaagg gtggacaagt tccggcagtt catgcagaat	1500
ttcagggaga tgtgcattga gcaggatggg agagtccatc tcaactgtgt	1550
ttactttggg aaagaagaaa taaatgaagt caaaggaata cttgaaaaca	1600
cttccaaagc tgccaacttc aggaacttta ccttcatcca gctgaatgga	1650
gaatttttct ggggaaaggg acttgatgtt ggagcccgtc tctggaaggg	1700
aagcaacgtc cttctctttt tctgtgatgt ggacatctac ttcacatctg	1750
aattcctcaa tacgtgtagg ctgaatacac agccaggga gaaggatatt	1800
tatccagttc ttttcagtca gtacaatcct ggcataatat acggccacca	1850
tgatgcagtc cctcccttgg aacagcagct ggtcataaag aaggaaactg	1900
gattttggag agactttgga tttgggatga cgtgtcagta tcggtcagac	1950
ttcatcaata taggtgggtt tgatctggac atcaaaggct ggggcggaga	2000

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ggatgtgcac ctttatcgca agtatctcca cagcaacctc atagtggtag	2050
ggacgcctgt gcgaggactc ttccacctct ggcatgagaa gcgctgcatg	2100
gacgagctga ccccgagca gtacaagatg tgcatgcagt ccaaggccat	2150
gaacgaggca tcccacggcc agctgggcat gctggtgttc aggcacgaga	2200
tagaggctca ccttcgcaaa cagaaacaga agacaagtag caaaaaaaca	2250
tgaactccca gagaaggatt gtgggagaca ctttttcttt ccttttgcaa	2300
ttactgaaa tggtcgcaac agagaaaaga cttccataaa ggacgacaaa	2350
agaattggac tgatgggtca gagatgagaa agcctccgat ttctctctgt	2400
tgggcttttt acaacagaaa tcaaaatctc cgctttgcct gcaaaagtaa	2450
cccagttgca ccctgtgaag tgtctgacaa aggcagaatg cttgtgagat	2500
tataagccta atggtgtgga ggttttgatg gtgtttacaa taaactgaga	2550
cctgttgttt tgtgtgctca ttgaaatatt catgatttaa gagcagtttt	2600
gtaaaaaatt cattagcatg aaaggcaagc atatttctcc tcatatgaat	2650
gagcctatca gcagggctct agtttctagg aatgctaaaa tatcagaagg	2700
caggagagga gataggctta ttatgatact agtgagtaca ttaagtaaaa	2750
taaaatggac cagaaaagaa aagaaacat aaatatcgtg tcatattttc	2800
cccaagatta accaaaaata atctgcttat ctttttggtt gtccttttaa	2850
ctgtctccgt ttttttcttt tatttaaaaa tgcacttttt ttcccttggt	2900
agttatagtc tgcttattta attaccactt tgcaagcctt acaagagagc	2950
acaagtgggc ctacattttt atatttttta agaagatact ttgagatgca	3000
ttatgagaac tttcagttca aagcatcaaa ttgatgcat atccaaggac	3050
atgccaaatg ctgattctgt caggcactga atgtcaggca ttgagacata	3100
gggaaggaat ggtttgtact aatacagacg tacagatact ttctctgaag	3150
agtattttcg aagaggagca actgaacact ggaggaaaag aaaatgacac	3200
tttctgcttt acagaaaagg aaactcattc agactggtga tatcgtgatg	3250
tacctaanaa tcagaaacca ctttttctcc tcagaagtag ggaccgcttt	3300
cttacctgtt taaataaacc aaagtatacc gtgtgaacca aacaatctct	3350
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gagaaaaata tatatatata tatatatatt gtgaaagatc aatccatctg	3450
ccagaatcta gtgggatgga agtttttgct acatgttatc caccacaggc	3500
cagggtgaag taactgaatt attttttaaa ttaagcagtt ctactcaatc	3550
accaagatgc ttctgaaaat tgcattttat taccatttca aactattttt	3600
taaaaaataaa tacagttaac atagagtggg ttcttcattc atgtgaaaat	3650
tattagccag caccagatgc atgagctaata tatctctttg agtccttgct	3700
tctgtttgct cacagtaaac tcattgttta aaagcttcaa gaacattcaa	3750
gctgttggtg tgttaaaaaa tgcattgtat tgatttgtag tggtagttta	3800
tgaaatttaa ttaaaacaca ggccatgaat ggaagggtgt attgcacagc	3850
taataaaaata tgatttggtg atatgaa	3877

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<210> SEQ ID NO 72

<211> LENGTH: 532

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 72

Met	Met	Met	Val	Arg	Arg	Gly	Leu	Leu	Ala	Trp	Ile	Ser	Arg	Val
1				5					10					15
Val	Val	Leu	Leu	Val	Leu	Leu	Cys	Cys	Ala	Ile	Ser	Val	Leu	Tyr
				20					25					30
Met	Leu	Ala	Cys	Thr	Pro	Lys	Gly	Asp	Glu	Glu	Gln	Leu	Ala	Leu
				35					40					45
Pro	Arg	Ala	Asn	Ser	Pro	Thr	Gly	Lys	Glu	Gly	Tyr	Gln	Ala	Val
				50					55					60
Leu	Gln	Glu	Trp	Glu	Glu	Gln	His	Arg	Asn	Tyr	Val	Ser	Ser	Leu
				65					70					75
Lys	Arg	Gln	Ile	Ala	Gln	Leu	Lys	Glu	Glu	Leu	Gln	Glu	Arg	Ser
				80					85					90
Glu	Gln	Leu	Arg	Asn	Gly	Gln	Tyr	Gln	Ala	Ser	Asp	Ala	Ala	Gly
				95					100					105
Leu	Gly	Leu	Asp	Arg	Ser	Pro	Pro	Glu	Lys	Thr	Gln	Ala	Asp	Leu
				110					115					120
Leu	Ala	Phe	Leu	His	Ser	Gln	Val	Asp	Lys	Ala	Glu	Val	Asn	Ala
				125					130					135
Gly	Val	Lys	Leu	Ala	Thr	Glu	Tyr	Ala	Ala	Val	Pro	Phe	Asp	Ser
				140					145					150
Phe	Thr	Leu	Gln	Lys	Val	Tyr	Gln	Leu	Glu	Thr	Gly	Leu	Thr	Arg
				155					160					165
His	Pro	Glu	Glu	Lys	Pro	Val	Arg	Lys	Asp	Lys	Arg	Asp	Glu	Leu
				170					175					180
Val	Glu	Ala	Ile	Glu	Ser	Ala	Leu	Glu	Thr	Leu	Asn	Asn	Pro	Ala
				185					190					195
Glu	Asn	Ser	Pro	Asn	His	Arg	Pro	Tyr	Thr	Ala	Ser	Asp	Phe	Ile
				200					205					210
Glu	Gly	Ile	Tyr	Arg	Thr	Glu	Arg	Asp	Lys	Gly	Thr	Leu	Tyr	Glu
				215					220					225
Leu	Thr	Phe	Lys	Gly	Asp	His	Lys	His	Glu	Phe	Lys	Arg	Leu	Ile
				230					235					240
Leu	Phe	Arg	Pro	Phe	Ser	Pro	Ile	Met	Lys	Val	Lys	Asn	Glu	Lys
				245					250					255
Leu	Asn	Met	Ala	Asn	Thr	Leu	Ile	Asn	Val	Ile	Val	Pro	Leu	Ala
				260					265					270
Lys	Arg	Val	Asp	Lys	Phe	Arg	Gln	Phe	Met	Gln	Asn	Phe	Arg	Glu
				275					280					285
Met	Cys	Ile	Glu	Gln	Asp	Gly	Arg	Val	His	Leu	Thr	Val	Val	Tyr
				290					295					300
Phe	Gly	Lys	Glu	Glu	Ile	Asn	Glu	Val	Lys	Gly	Ile	Leu	Glu	Asn
				305					310					315
Thr	Ser	Lys	Ala	Ala	Asn	Phe	Arg	Asn	Phe	Thr	Phe	Ile	Gln	Leu
				320					325					330

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Asn Gly Glu Phe Ser Arg Gly Lys Gly Leu Asp Val Gly Ala Arg	335	340	345
Phe Trp Lys Gly Ser Asn Val Leu Leu Phe Phe Cys Asp Val Asp	350	355	360
Ile Tyr Phe Thr Ser Glu Phe Leu Asn Thr Cys Arg Leu Asn Thr	365	370	375
Gln Pro Gly Lys Lys Val Phe Tyr Pro Val Leu Phe Ser Gln Tyr	380	385	390
Asn Pro Gly Ile Ile Tyr Gly His His Asp Ala Val Pro Pro Leu	395	400	405
Glu Gln Gln Leu Val Ile Lys Lys Glu Thr Gly Phe Trp Arg Asp	410	415	420
Phe Gly Phe Gly Met Thr Cys Gln Tyr Arg Ser Asp Phe Ile Asn	425	430	435
Ile Gly Gly Phe Asp Leu Asp Ile Lys Gly Trp Gly Gly Glu Asp	440	445	450
Val His Leu Tyr Arg Lys Tyr Leu His Ser Asn Leu Ile Val Val	455	460	465
Arg Thr Pro Val Arg Gly Leu Phe His Leu Trp His Glu Lys Arg	470	475	480
Cys Met Asp Glu Leu Thr Pro Glu Gln Tyr Lys Met Cys Met Gln	485	490	495
Ser Lys Ala Met Asn Glu Ala Ser His Gly Gln Leu Gly Met Leu	500	505	510
Val Phe Arg His Glu Ile Glu Ala His Leu Arg Lys Gln Lys Gln	515	520	525
Lys Thr Ser Ser Lys Lys Thr	530		

<210> SEQ ID NO 73
<211> LENGTH: 1701
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien
<220> FEATURE:
<221> NAME/KEY: unsure
<222> LOCATION: 1528
<223> OTHER INFORMATION: unknown base

<400> SEQUENCE: 73	
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt	50
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc	100
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact	150
cacgccagga gtcgctcgc tctctctctc tctctctcac tcctccctcc	200
ctctctctct gcctgtccta gtccctctagt cctcaaattc ccagtcccct	250
gcaccccttc ctgggacact atgttgttct cgcacctcct gctggagggtg	300
atttgatcc tggctgcaga tgggggtcaa cactggacgt atgagggcc	350
acatggtcag gaccattggc cagcctctta cctgagtgt ggaacaatg	400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat	450
ttgcctgctc tgcagcccca cgatatgac cagcctggca ccgagccttt	500
ggacctgcac aacaatggcc acacagtgca actctctctg ccctctaccc	550

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tgtatctggg tggacttccc cgaaaatatg tagctgccca gctccacctg	600
cactgggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag	650
tgaagccaca ttgacagagc tccacattgt acattatgac tctgattcct	700
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg	750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat	800
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc	850
ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc	900
cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg	950
gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc	1000
ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta	1050
cagaactacc gagcccttca gcctctcaat cagcgcatgg tctttgcttc	1100
tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag	1150
gtgtaggaat cttggttggc tgtctctgcc ttctcctggc tgtttatttc	1200
attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt	1250
cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac	1300
catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg	1350
gggtgtagga tctggccaga aacctgtag gtagtagtaag cagatgtcct	1400
ccttccccctg gacatctctt agagaggaat ggaccaggc tgcattcca	1450
ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag	1500
gaaatcgctg tgttgттаат gcagaganca aactctgttt agttgcaggg	1550
gaagtttggg atatacccca aagtctctta cccctcact tttatggccc	1600
tttccttaga tatactgcgg gatctctcct taggataaag agttgctggt	1650
gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt	1700
t	1701

<210> SEQ ID NO 74
<211> LENGTH: 337
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 74

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

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Pro	Ser	Thr	Leu	Tyr	Leu	Gly	Gly	Leu	Pro	Arg	Lys	Tyr	Val	Ala	
			95						100					105	
Ala	Gln	Leu	His	Leu	His	Trp	Gly	Gln	Lys	Gly	Ser	Pro	Gly	Gly	
			110						115					120	
Ser	Glu	His	Gln	Ile	Asn	Ser	Glu	Ala	Thr	Phe	Ala	Glu	Leu	His	
			125						130					135	
Ile	Val	His	Tyr	Asp	Ser	Asp	Ser	Tyr	Asp	Ser	Leu	Ser	Glu	Ala	
			140						145					150	
Ala	Glu	Arg	Pro	Gln	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Ile	Glu	
			155						160					165	
Val	Gly	Glu	Thr	Lys	Asn	Ile	Ala	Tyr	Glu	His	Ile	Leu	Ser	His	
			170						175					180	
Leu	His	Glu	Val	Arg	His	Lys	Asp	Gln	Lys	Thr	Ser	Val	Pro	Pro	
			185						190					195	
Phe	Asn	Leu	Arg	Glu	Leu	Leu	Pro	Lys	Gln	Leu	Gly	Gln	Tyr	Phe	
			200						205					210	
Arg	Tyr	Asn	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Tyr	Gln	Ser	Val	
			215						220					225	
Leu	Trp	Thr	Val	Phe	Tyr	Arg	Arg	Ser	Gln	Ile	Ser	Met	Glu	Gln	
			230						235					240	
Leu	Glu	Lys	Leu	Gln	Gly	Thr	Leu	Phe	Ser	Thr	Glu	Glu	Glu	Pro	
			245						250					255	
Ser	Lys	Leu	Leu	Val	Gln	Asn	Tyr	Arg	Ala	Leu	Gln	Pro	Leu	Asn	
			260						265					270	
Gln	Arg	Met	Val	Phe	Ala	Ser	Phe	Ile	Gln	Ala	Gly	Ser	Ser	Tyr	
			275						280					285	
Thr	Thr	Gly	Glu	Met	Leu	Ser	Leu	Gly	Val	Gly	Ile	Leu	Val	Gly	
			290						295					300	
Cys	Leu	Cys	Leu	Leu	Leu	Ala	Val	Tyr	Phe	Ile	Ala	Arg	Lys	Ile	
			305						310					315	
Arg	Lys	Lys	Arg	Leu	Glu	Asn	Arg	Lys	Ser	Val	Val	Phe	Thr	Ser	
			320						325					330	
Ala	Gln	Ala	Thr	Thr	Glu	Ala									
			335												

<210> SEQ ID NO 75
<211> LENGTH: 1743
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 75

tgccgctgcc gccgctgctg ctgttgctcc tggcgggcgcc ttggggacgg	50
gcagttccct gtgtctctgg tggttgcct aaacctgcaa acatcacctt	100
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc	150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg	200
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgtcc	250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc	300
atgcaacaaa tatactcaa tctgaagtat aacgtgtctg tgttgaatac	350
taaatcaaac agaacgtggt cccagtgtgt gaccaaccac acgctggtgc	400

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tcacctgggt ggagccgaac actctttact gcgtacacgt ggagtccttc	450
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag	500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt	550
atgttttgcc catatctatt accgtgttcc ttttttctgt gatgggctat	600
tccatctacc gatatatcca cgttggaaca gagaaacacc cagcaaattt	650
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg	700
aaaaaatcgt gattaacttt atcacccctca atatctcgga tgattctaaa	750
atttctcatc aggatatgag ttactggga aaaagcagtg atgtatccag	800
ccttaatgat cctcagccca gcgggaacct gagccccct caggagggaag	850
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt	900
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtcctc	950
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg	1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg	1050
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcggt	1100
ggcagtcctg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc	1150
aagacttaga cccctggcg caggagcaca cagactcgga ggaggggccc	1200
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag	1250
gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg	1300
agccttctga gggggatggg ctgggagagg agggcttct atctagactc	1350
tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct	1400
catgcaattc atggaggaat gggggttata tgtgcagatg gaaaactgat	1450
gccaacactt ccttttgccct ttgttttcct gtgcaacaa gtgagtcacc	1500
cctttgatcc cagccataaa gtacctggga tgaaagaagt tttttccagt	1550
ttgtcagtg ctgtgagaat tacttatttc ttttctctat tctcatagca	1600
cgtgtgtgat tggttcatgc atgtaggctc cttacaatg atgggtgggc	1650
tctggagtcc aggggctggc cgttgttct atgcagagaa agcagtcaat	1700
aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt	1743

<210> SEQ ID NO 76

<211> LENGTH: 442

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 76

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

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Asn Thr Lys Ser	Asn Arg Thr Trp Ser	Gln Cys Val Thr	Asn His
80	85		90
Thr Leu Val Leu	Thr Trp Leu Glu Pro	Asn Thr Leu Tyr Cys	Val
95	100		105
His Val Glu Ser	Phe Val Pro Gly Pro	Pro Arg Arg Ala Gln	Pro
110	115		120
Ser Glu Lys Gln	Cys Ala Arg Thr Leu	Lys Asp Gln Ser Ser	Glu
125	130		135
Phe Lys Ala Lys	Ile Ile Phe Trp Tyr	Val Leu Pro Ile Ser	Ile
140	145		150
Thr Val Phe Leu	Phe Ser Val Met Gly	Tyr Ser Ile Tyr Arg	Tyr
155	160		165
Ile His Val Gly	Lys Glu Lys His Pro	Ala Asn Leu Ile Leu	Ile
170	175		180
Tyr Gly Asn Glu	Phe Asp Lys Arg Phe	Phe Val Pro Ala Glu	Lys
185	190		195
Ile Val Ile Asn	Phe Ile Thr Leu Asn	Ile Ser Asp Asp Ser	Lys
200	205		210
Ile Ser His Gln	Asp Met Ser Leu Leu	Gly Lys Ser Ser Asp	Val
215	220		225
Ser Ser Leu Asn	Asp Pro Gln Pro Ser	Gly Asn Leu Arg Pro	Pro
230	235		240
Gln Glu Glu Glu	Glu Val Lys His Leu	Gly Tyr Ala Ser His	Leu
245	250		255
Met Glu Ile Phe	Cys Asp Ser Glu Glu	Asn Thr Glu Gly Thr	Ser
260	265		270
Leu Thr Gln Gln	Glu Ser Leu Ser Arg	Thr Ile Pro Pro Asp	Lys
275	280		285
Thr Val Ile Glu	Tyr Glu Tyr Asp Val	Arg Thr Thr Asp Ile	Cys
290	295		300
Ala Gly Pro Glu	Glu Gln Glu Leu Ser	Leu Gln Glu Glu Val	Ser
305	310		315
Thr Gln Gly Thr	Leu Leu Glu Ser Gln	Ala Ala Leu Ala Val	Leu
320	325		330
Gly Pro Gln Thr	Leu Gln Tyr Ser Tyr	Thr Pro Gln Leu Gln	Asp
335	340		345
Leu Asp Pro Leu	Ala Gln Glu His Thr	Asp Ser Glu Glu Gly	Pro
350	355		360
Glu Glu Glu Pro	Ser Thr Thr Leu Val	Asp Trp Asp Pro Gln	Thr
365	370		375
Gly Arg Leu Cys	Ile Pro Ser Leu Ser	Ser Phe Asp Gln Asp	Ser
380	385		390
Glu Gly Cys Glu	Pro Ser Glu Gly Asp	Gly Leu Gly Glu Glu	Gly
395	400		405
Leu Leu Ser Arg	Leu Tyr Glu Glu Pro	Ala Pro Asp Arg Pro	Pro
410	415		420
Gly Glu Asn Glu	Thr Tyr Leu Met Gln	Phe Met Glu Glu Trp	Gly
425	430		435
Leu Tyr Val Gln	Met Glu Asn		
440			

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<210> SEQ ID NO 77

<211> LENGTH: 1636

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 77

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt	50
gctgccctct gacacctggg aagatggccg gcccgtagac cttcacccctt	100
ctctgtggtt tgctggcagc caccttgatc caagccacc tcagtcccac	150
tgcagtttct atcctcggcc caaaagtcac caaagaaaag ctgacacagg	200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc	250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct	300
ggtgaacacc gtcctgaagc acatcatctg gctgaaggtc atcacagcta	350
acatcctcca gctgcagggt aagccctcgg ccaatgacca ggagctgcta	400
gtcaagatcc ccctggacat ggtggctgga ttcaaacgcg ccctggtcaa	450
gaccatcgtg gagtccaca tgacgactga ggcccaagcc accatccgca	500
tggacaccag tgcaagtggc cccacccgcc tggctcctcag tgactgtgcc	550
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttcct	600
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagtg ccatccctgc	650
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttcttcaat	700
ggcatgtatg cagacctcct gcagctgggt aaggtgccc tttccctcag	750
cattgaccgt ctggagtttg accttctgta tcctgccatc aagggtgaca	800
ccattcagct ctacctgggg gccaaagtgt tggactcaca gggaaagggtg	850
accaagtggg tcaataactc tgcagcttcc ctgacaatgc ccacctgga	900
caacatcccg ttacgctca tcgtgagtca ggacgtgggt aaagctgcag	950
tggctgctgt gctctctcca gaagaattca tggctcgtgt ggactctgtg	1000
cttctgaga gtgcccacg gctgaagtca agcatcgggc tgatcaatga	1050
aaaggctgca gataagctgg gatctacca gatcgtgaag atcctaactc	1100
aggacactcc cgagtttttt atagaccaag gccatgcaa ggtggcccaa	1150
ctgatcgtgc tggaagtgtt tccctccagt gaagccctcc gccctttgtt	1200
caccttgggc atcgaagcca gctcggaagc tcagttttac accaaagggtg	1250
accaacttat actcaacttg aataacatca gctctgatcg gatccagctg	1300
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat	1350
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa	1400
gatctggggg ccagtgatca ttggtgaagg ccttgggatt cgaggcagct	1450
gagtcctcac tgaccaagga tgcccttggt cttactccag cctccttggtg	1500
gaaaccagc tctcctgtct ccagtgaaag acttggatgg cagccatcag	1550
ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc	1600
cctctctgca atcaataaac acttgccctg gaaaaa	1636

<210> SEQ ID NO 78

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<211> LENGTH: 484

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 78

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

Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile
 20           25           30

Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys
 35           40           45

Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
 50           55           60

Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
 65           70           75

Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
 80           85           90

Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
 95           100          105

Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
110           115          120

Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
125           130          135

Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
140           145          150

Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
155           160          165

Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu
170           175          180

Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu
185           190          195

Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly
200           205          210

Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu
215           220          225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys
230           235          240

Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser
245           250          255

Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu
260           265          270

Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser
275           280          285

Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu
290           295          300

Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His
305           310          315

Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp
320           325          330

Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr
335           340          345

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Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu
350 355 360

Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu
365 370 375

Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr
380 385 390

Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp
395 400 405

Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp
410 415 420

Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu
425 430 435

Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu
440 445 450

Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys
455 460 465

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
470 475 480

Pro Val Ser Gln

<210> SEQ ID NO 79
<211> LENGTH: 1475
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 79

gagagaagtc agcctggcag agagactctg aaatgagggg ttagagggtg 50

tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100

gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150

ctacatccta ggcttctctg ggcttttggg cacactggtt gccatgctgc 200

tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250

gttggtctct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300

catcaccagc tgtgacatct atagcaccct tctgggcctg cccgctgaca 350

tccaggctgc ccaggccatg atggtgacat ccagtgaat ctctccctg 400

gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atcccagacc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500

ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatc 550

ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600

tggagaggct ctttacttgg gcattatttc ttccctgttc tcctgatag 650

ctggaatcat cctctgcttt tcctgctcat ccagagagaa tcgctccaac 700

tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750

gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800

cagggtatgt gtgaagaacc aggggccaga gctggggggg gctgggtct 850

gtgaaaaaca gtggacagca ccccgagggc cacagggtgag ggacactacc 900

actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950

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ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga      1000
attgccaaagg atgctcgcca tgccagcctt tctgttttcc tcaccttgct      1050
gtccccctgc cctaagtccc caacctcaa cttgaaaccc cattccctta      1100
agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat      1150
ccccaacccc actaatcaca tcccactgac tgaccctctg tgatcaaaga      1200
ccctctctct ggctgaggtt ggctcttagc tcattgctgg ggatgggaag      1250
gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc      1300
cctccaaaga aactgattgg ccctggaacc tccatccac tcttgttatg      1350
actccacagt gtccagacta atttgatgat gaactgaaat aaaaccatcc      1400
tacggtatcc agggaacaga aagcaggatg caggatggga ggacaggaag      1450
gcagcctggg acatttaaaa aaata                                     1475

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<210> SEQ ID NO 80

<211> LENGTH: 230

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 80

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

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Leu Thr Gly Tyr Val
230

<210> SEQ ID NO 81
<211> LENGTH: 1732
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 81

cccacgcgtc cgcgcctctc ccttctgctg gaccttcctt cgtctctcca	50
ttcttccctc ctttccccgc gttctcttct cacctttctc ttcttccac	100
cttagacctc ccttcctgcc ctcttttctt gccaccgct gcttctctgg	150
ccttctccga ccccgctcta gcagcagacc tcctggggtc tgtgggttga	200
ttctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact	250
ccgctccccg accagcggcc tgacctggg gaaaggatgg ttcccagagg	300
gagggtcctc tcctccttgc tgggactcgc gctgctctgg ttccccctgg	350
actcccacgc tcgagccccg ccagacatgt tctgcctttt ccatgggaag	400
agatactccc ccggcgagag ctggcacccc tacttgaggc cacaaggcct	450
gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagtgtt	500
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca	550
cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg	600
ggccccacca aagtccctgcc agcacacagg gaccatgtac caaacggag	650
agatcttcag tgcccatgag ctgttcccct cccgcctgcc caaccaggt	700
gtcctctgca gctgcacaga gggccagatc tactgaggcc tcacaacctg	750
ccccgaacca ggctgcccag caccctccc actgcagac tcctgtgtgc	800
aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg	850
cagtcgctcc atggggtag acatcctcag gatccatgtt ccagtgatgc	900
tgggagaaag agaggcccg gcacccacgc cccactggc ctacagcgcc	950
ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca	1000
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg	1050
cgggaagacg tactcccacg gggagggtgt gcacccggcc ttccgtgcct	1100
tcggccccct gccctgcac ctatgcacct gtgaggatgg ccgccaggac	1150
tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa	1200
agtggtctgg aagtgtgca agatttgccc agaggacaaa gcagaccctg	1250
gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc	1300
ctcgccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc	1350
cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg	1400
taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg	1450
ccacacagcc agaactttcc acttgactca gatcaagaaa gtcaggaagc	1500
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac	1550
gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac	1600

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ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca	1650
gatatgagct gtataattgt tgttattata tattaataaa taagaagttg	1700
cattaccctc aaaaaaaaaa aaaaaaaaaa aa	1732

<210> SEQ ID NO 82
 <211> LENGTH: 451
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 82

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

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Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg
320 325 330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser
335 340 345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala
350 355 360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu
365 370 375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His
380 385 390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala
395 400 405
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro
410 415 420
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala
425 430 435
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys
440 445 450

Thr

<210> SEQ ID NO 83
<211> LENGTH: 2052
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 83

gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgcctt 50
ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100
gttctcctct tctctctaata ccatccgtca cctctcctgt catccgtttc 150
catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
ttggtttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250
gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300
gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350
aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
attctattgc ggaggggcgc atctctctga ggctggaaaa cattactgtg 500
ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600
tttccatcac gggatatggt gatagagaca tccagctact ctgtcagttc 650
tcgggctggt tcccccggcc cacagcgaag tggaaaggtc cacaaggaca 700
ggatttgttc acagactcca ggacaacag agacatgcat ggcctgtttg 750
atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800
tccatgcggc atgctcatct gagccgagag gtggaatcca ggtacagat 850
aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900
tggaataact ctgctgtggc ctattttttg gcattgttg actgaagatt 950

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ttcttctcca aattccagtg gaaaatccag gcggaactgg actggagaag	1000
aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg	1050
tgactctgga tccagagacg gctcaccgga agctctgcgt ttctgatctg	1100
aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa	1150
gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcagggg	1200
aacattactg ggaggtggac ggaggacaca ataaaagggtg gcgcgtggga	1250
gtgtgccggg atgatgtgga caggaggaag gactacgtga ctttgtctcc	1300
cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca	1350
cattaaatcc ccgttttacc agcgtcttcc ccaggacccc acctacaaaa	1400
ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat	1450
aatgaccag tcccttattt ataccctgac atgtcggttt gaaggcttat	1500
tgaggcccta cattgagtat ccgtccata atgagcaaaa tggaactccc	1550
atagtcatct gccagtcac ccaggaatca gagaaagggt cctcttgga	1600
aagggcctct gcaatcccag agacaagcaa cagtgaagtc tcctcacagg	1650
caaccacgcc cttcctcccc aggggtgaaa tgtaggatga atcacatccc	1700
acattcttct ttagggatat taaggtctct ctcccagatc caaagtcccg	1750
cagcagccgg ccaaggtggc ttccagatga agggggactg gcctgtccac	1800
atgggagtca ggtgtcatgg ctgccctgag ctgggaggga agaaggctga	1850
cattacattt agtttgtctt cactccatct ggctaagtga tcttgaata	1900
ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg	1950
tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg	2000
acagagtgtg tcctaattgt ttgttcatta tattacactt tcagtaaaaa	2050
aa	2052

<210> SEQ ID NO 84

<211> LENGTH: 500

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 84

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

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Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser		110	115	120
Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly		125	130	135
Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile		140	145	150
Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala		155	160	165
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg		170	175	180
Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu		185	190	195
Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His		200	205	210
Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp		215	220	225
Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu		230	235	240
Gly	Ile	Leu	Cys	Cys	Gly	Leu	Phe	Phe	Gly	Ile	Val	Gly	Leu	Lys		245	250	255
Ile	Phe	Phe	Ser	Lys	Phe	Gln	Trp	Lys	Ile	Gln	Ala	Glu	Leu	Asp		260	265	270
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys		275	280	285
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys		290	295	300
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro		305	310	315
Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val		320	325	330
Val	Ala	Ser	Gln	Ser	Phe	Gln	Ala	Gly	Lys	His	Tyr	Trp	Glu	Val		335	340	345
Asp	Gly	Gly	His	Asn	Lys	Arg	Trp	Arg	Val	Gly	Val	Cys	Arg	Asp		350	355	360
Asp	Val	Asp	Arg	Arg	Lys	Glu	Tyr	Val	Thr	Leu	Ser	Pro	Asp	His		365	370	375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Asn	Gly	Glu	His	Leu	Tyr	Phe	Thr		380	385	390
Leu	Asn	Pro	Arg	Phe	Ile	Ser	Val	Phe	Pro	Arg	Thr	Pro	Pro	Thr		395	400	405
Lys	Ile	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Cys	Gly	Thr	Ile	Ser	Phe		410	415	420
Phe	Asn	Ile	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Thr	Cys	Arg		425	430	435
Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Glu	Tyr	Pro	Ser	Tyr	Asn		440	445	450
Glu	Gln	Asn	Gly	Thr	Pro	Ile	Val	Ile	Cys	Pro	Val	Thr	Gln	Glu		455	460	465
Ser	Glu	Lys	Glu	Ala	Ser	Trp	Gln	Arg	Ala	Ser	Ala	Ile	Pro	Glu		470	475	480

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Thr Ser Asn Ser Glu Ser Ser Ser Gln Ala Thr Thr Pro Phe Leu
485 490 495

Pro Arg Gly Glu Met
500

<210> SEQ ID NO 85
<211> LENGTH: 1665
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 85

aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct	50
gctgctgctg cccctgctct gggggaggga gagggcgaa ggacagacaa	100
gtaaactgct gacgatgcag agttccgtga cggtcagga aggcctgtgt	150
gtccatgtgc cctgctcctt ctccaccctc tcgcatggct ggatttaccc	200
tggcccagta gttcatggct actggttcgg ggaaggggcc aatacagacc	250
aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag	300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac	350
cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc	400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct	450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac	500
cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct	550
gtgagcaggg gacacccct atgatctcct ggatagggac ctccgtgtcc	600
cccctggacc cctccaccac ccgctcctcg gtgctcacc tcaccccaca	650
gcccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg	700
ccagcgtgac caggaacaag accgtccatc tcaacgtgtc ctacccgcct	750
cagaacttga ccatgactgt ctccaagga gacggcacag tatccacagt	800
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc	850
tggctctgtg agttgatgca gttgacagca atccccctgc caggctgagc	900
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg	950
ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct	1000
gcagagctca gaacctctc ggctctcagc aggtctacct gaacgtctcc	1050
ctgcagagca aagccacatc aggagtgact cagggggtgg tcgggggagc	1100
tggagccaca gccctggtct tcctgtcctt ctgcgtcatc ttcgtttag	1150
tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat	1200
acgggcatag aggatgcaa cgctgtcagg ggttcagcct ctacggggcc	1250
cctgactgaa ccttgggcag aagacagtcc cccagaccag cctccccag	1300
cttctgcccc ctccctcagt ggggaaggag agtccagta tgcattccct	1350
agcttccaga tggtaagcc ttgggactcg cggggacagg aggccactga	1400
caccgagtac tcggagatca agatccacag atgagaaact gcagagactc	1450
accctgattg agggatcaca gcccctccag gcaagggaga agtcagaggc	1500
tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataacact	1550

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atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc	1600
tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag	1650
acagacaaat tccta	1665

<210> SEQ ID NO 86
<211> LENGTH: 463
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 86

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

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Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln
320 325 330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val
335 340 345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe
350 355 360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys
365 370 375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu
380 385 390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr
395 400 405
Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
410 415 420
Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser
425 430 435
Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
440 445 450
Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
455 460

<210> SEQ ID NO 87
<211> LENGTH: 1176
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 87

agaaagctgc actctgttga gctccagggc gcagtggagg gagggagtga 50
aggagctctc tgtacccaag gaaagtgcag ctgagactca gacaagatta 100
caatgaacca actcagcttc ctgctgtttc tcatagcgac caccagagga 150
tggaagtacag atgaggctaa tacttacttc aaggaatgga cctgtttctc 200
gtctccatct ctgcccagaa gctgcaagga aatcaaagac gaatgtccta 250
gtgcatttga tggcctgtat ttctcccgca ctgagaatgg tgttatctac 300
cagaccttct gtgacatgac ctctgggggt ggcggctgga ccctgtgtggc 350
cagcgtgcat gagaatgaca tgcgtgggaa gtgcacgttg ggcgatcgct 400
gggccagtca gcagggcagc aaagcagact acccagaggg ggacggcaac 450
tgggccaact acaacacctt tggatctgca gaggcggcca cgagcgatga 500
ctacaagaac cctggctact acgacatcca ggccaaggac ctgggcatct 550
ggcacgtgcc caataagtcc cccatgcagc actggagaaa cagctccctg 600
ctgaggtacc gcacggacac tggcttccto cagacactgg gacataatct 650
gtttggcatc taccagaaat atccagtga atatggagaa gaaaagtgtt 700
ggactgacaa cggcccgggtg atccctgttg tctatgattt tggcgacgcc 750
cagaaaacag catcttatta ctacacctat ggccagcggg aattcactgc 800
gggatttgtt cagttcaggg tatttaataa cgagagagca gccaacgcct 850
tgtgtgctgg aatgagggtc accggatgta aactgagca tcaactgcatt 900
ggtggaggag gatactttcc agaggccagt cccagcagt gtggagattt 950

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ttctggtttt gattggagtg gatatggaac tcatgttggt tacagcagca      1000
gccgtgagat aactgaggca gctgtgcttc tattctatcg ttgagagttt      1050
tgtgggaggg aaccagacc tctcctccca accatgagat cccaaggatg      1100
gagaacaact taccagtag ctagaatgtt aatggcagaa gagaaaacaa      1150
taaatacatat tgactcaaga aaaaaa                                1176

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<210> SEQ ID NO 88
<211> LENGTH: 313
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 88

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```

Met Asn Gln Leu Ser Phe Leu Leu Phe Leu Ile Ala Thr Thr Arg
 1              5              10              15

Gly Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr
              20              25              30

Cys Ser Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys
              35              40              45

Asp Glu Cys Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr
              50              55              60

Glu Asn Gly Val Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly
              65              70              75

Gly Gly Gly Trp Thr Leu Val Ala Ser Val His Glu Asn Asp Met
              80              85              90

Arg Gly Lys Cys Thr Val Gly Asp Arg Trp Ser Ser Gln Gln Gly
              95              100             105

Ser Lys Ala Asp Tyr Pro Glu Gly Asp Gly Asn Trp Ala Asn Tyr
              110             115             120

Asn Thr Phe Gly Ser Ala Glu Ala Ala Thr Ser Asp Asp Tyr Lys
              125             130             135

Asn Pro Gly Tyr Tyr Asp Ile Gln Ala Lys Asp Leu Gly Ile Trp
              140             145             150

His Val Pro Asn Lys Ser Pro Met Gln His Trp Arg Asn Ser Ser
              155             160             165

Leu Leu Arg Tyr Arg Thr Asp Thr Gly Phe Leu Gln Thr Leu Gly
              170             175             180

His Asn Leu Phe Gly Ile Tyr Gln Lys Tyr Pro Val Lys Tyr Gly
              185             190             195

Glu Gly Lys Cys Trp Thr Asp Asn Gly Pro Val Ile Pro Val Val
              200             205             210

Tyr Asp Phe Gly Asp Ala Gln Lys Thr Ala Ser Tyr Tyr Ser Pro
              215             220             225

Tyr Gly Gln Arg Glu Phe Thr Ala Gly Phe Val Gln Phe Arg Val
              230             235             240

Phe Asn Asn Glu Arg Ala Ala Asn Ala Leu Cys Ala Gly Met Arg
              245             250             255

Val Thr Gly Cys Asn Thr Glu His His Cys Ile Gly Gly Gly Gly
              260             265             270

Tyr Phe Pro Glu Ala Ser Pro Gln Gln Cys Gly Asp Phe Ser Gly
              275             280             285

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Phe Asp Trp Ser Gly Tyr Gly Thr His Val Gly Tyr Ser Ser Ser
290 295 300

Arg Glu Ile Thr Glu Ala Ala Val Leu Leu Phe Tyr Arg
305 310

<210> SEQ ID NO 89
<211> LENGTH: 759
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 89

```
ctagatttgt cggttgccg ggagacttca ggagtcgctg tctctgaact      50
tccagcctca gagaccgcc cccttgcccc cgagggccat gggccgggtc      100
tcagggtctg tgccctctcg cttcctgacg ctctggcgc atctggtggt      150
cgtcacacacc ttattctggt ccgggacag caacatacag gcctgcctgc      200
ctctcacgtt caccgccgag gagtatgaca agcaggacat tcagctggtg      250
gccgcgctct ctgtcacctt gggcctcttt gcagtggagc tggccgggtt      300
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg      350
gggctcactg tagtgcaccc gtggccctgt ccttcttcat attcgagcgt      400
tgggagtgca ctacgtattg gtacattttt gtcttctgca gtgcccttcc      450
agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga      500
aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg      550
ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggt      600
ttccctctcg aaactgcttc tgctggagga tatgtgttg aataattacg      650
tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata      700
tgttttgtag taacattaag acttatatac agttttaggg gacaattaaa      750
aaaaaaaaa                                                    759
```

<210> SEQ ID NO 90
<211> LENGTH: 140
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 90

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

<210> SEQ ID NO 91
<211> LENGTH: 1871
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 91

ctgggacccc gaaaagagaa ggggagagcg aggggacgag agcggaggag	50
gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc	100
tctatctggt catctgtggc caggatgatg gtcctcccgg ctcagaggac	150
cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcggaa	200
gcggggccac atctcaccta agtcccggcc catggccaat tccactctcc	250
tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc	300
cccaaccgoc cgaaccacag cccccacccc tcagccaagg tgaagaaaat	350
ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc	400
tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc	450
cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt	500
gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg	550
aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta	600
gaacgggggc gccggacctc gctttgcacc cacgacccag ccaagatctg	650
ctcccagagc cacgctcaga gctcagccac ctggagctgc tcccagccct	700
tcaaagtcgt ctgtgtctac atcgccctct acagcacgga ctatcggtg	750
gtccagaagg tgtgcccaga ttacaactac catagtgata cccctacta	800
cccactctgg tgacccgggg caggccacag aggccaggcc agggctggaa	850
ggacaggcct gcccatgcag gagaccatct ggacaccggg cagggaaggg	900
gttgggcctc aggcagggag gggggtggag acgaggagat gccaagtggg	950
gccagggcca agtctcaagt ggcagagaaa ggggtccaag tgctggctcc	1000
aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg	1050
ggctctctgt gcagcctcac agggctttgc cacggagcca cagagagatg	1100
ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc ccagatcaa	1150
gtcatgggag gaagctaagc ccttggttct tgccatcctg aggaaagata	1200
gcaacaggga gggggagatt tcatcagtggt ggacagcctg tcaacttagg	1250
atggatggct gagagggctt ctaggagacc agtcagcagg gtggggtggg	1300
gccagaggag ctctccagcc ctgcctagtg ggccgctga gcccttgtc	1350
gtgtgctgag catggcatga ggctgaagtg gcaaccctgg ggtctttgat	1400
gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa	1450

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ttccctcttc tgccagtact cccctgtac caccattgc tgatggcaca	1500
cccatcctta agctaagaca ggacgattgt ggtcctcca cactaaggcc	1550
acagcccac cgcgtgctgt gtgtccctct tccaccccaa cccctgctgg	1600
ctcctctggg agcatccatg tcccgagag ggtccctca acagtcagcc	1650
tcacctgtca gaccggggtt ctccggatc tggatggcgc cgccctctca	1700
gcagcgggca cgggtggggc ggggccgggc cgcagagcat gtgctggatc	1750
tgttctgtgt gtctgtctgt ggggtggggg aggggaggga agtcttgtga	1800
aaccgctgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga	1850
aataaagctt gccccggggc a	1871

<210> SEQ ID NO 92

<211> LENGTH: 252

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 92

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

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<210> SEQ ID NO 93
<211> LENGTH: 902
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 93

cggtggccat gactgcggcc gtgttcttcg gctgcgcctt cattgccttc	50
gggcctgcgc tcgcccttta tgtcttcacc atcgccatcg agccgttgcg	100
tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga	150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat	200
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta	250
tatccaagaa atgttcgat ttgcatatta taaactctta aaaaaagcca	300
gtgaaggttt gaagagtata aaccagggtg agacagcacc ctctatgcga	350
ctgctggcct atgtttctgg cttgggcttt ggaatcatga gtggagtatt	400
ttcctttgtg aataccctat ctgactcctt ggggccaggc acagtgggca	450
ttcatggaga ttctcctcaa ttcttccttt attcagcttt catgacgctg	500
gtcattatct tgctgcatgt attctggggc attgtatttt ttgatggctg	550
tgagaagaaa aagtggggca tcctccttat cgttctcctg acccacctgc	600
tggtgtcagc ccagaccttc ataagttctt attatggaat aaacctggcg	650
tcagcattta taatcctggt gctcatgggc acctgggcat tcttagctgc	700
gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga	750
actttctttt ttacaaccag cgtcccatg aacctcaggg aaccagcact	800
tcccaaaccg cagactacat ctttagagga agcacaactg tgcctttttc	850
tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga	900
ta	902

<210> SEQ ID NO 94
<211> LENGTH: 257
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 94

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

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Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser
				110					115					120
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn
				125					130					135
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly
				140					145					150
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val
				155					160					165
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly
				170					175					180
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr
				185					190					195
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly
				200					205					210
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr
				215					220					225
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu
				230					235					240
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg
				245					250					255
Ser	Arg													

<210> SEQ ID NO 95
<211> LENGTH: 1073
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 95

aatTTTTcAc	cagagtaaAc	ttgagaaacc	aactggacCt	tgagtattgt	50
acatTTTgCc	tcgtggacCc	aaagtagca	atctgaaaca	tgaggagtac	100
gattctactg	TTTTgtcttc	taggatcaac	tcggtcatta	ccacagctca	150
aacctgcttt	gggactccct	cccacaaaac	tggtcccgga	tcaggaaca	200
ctaccaaacc	aacagcagtc	aaatcaggtc	tttccttctt	taagtctgat	250
accattaaca	cagatgctca	cactggggcc	agatctgcat	ctgttaaatc	300
ctgctgcagg	aatgacacCt	ggtacccaga	cccaccCatt	gaccctggga	350
gggttgaatg	tacaacagca	actgcaccca	catgtgttac	caatTTTtgt	400
cacacaactt	ggagcccagg	gcactatcCt	aagctcagag	gaattgccac	450
aaatcttcac	gagcctcatc	atccattcCt	tgttcccggg	aggcatcctg	500
cccaccagtc	aggcaggggc	taatccagat	gtccaggatg	gaagccttcc	550
agcaggagga	gcaggtgtaa	atcctgccac	ccagggaacc	ccagcaggcc	600
gcctcccaac	tcccagtggc	acagatgacg	actttgcagt	gaccaccCct	650
gcaggcatcc	aaaggagcac	acatgccatc	gaggaagcca	ccacagaatc	700
agcaaatgga	attcagtaag	ctgtttcaaa	TTTTttcaac	taagctgcCt	750
cgaatttggt	gatacatgtg	aatctttatc	attgattata	ttatggaata	800
gattgagaca	cattggatag	tcttagaaga	aattaattct	taatttacCt	850
gaaaatattc	ttgaaatttc	agaaaatatg	ttctatgtag	agaatcccaa	900

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cttttaaaaa caataattca atggataaat ctgtctttga aatataacat	950
tatgctgcct ggatgatatg catattaaaa catatttgga aaactggaaa	1000
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1050
aaaaaaaaa aaaaaaaaaa aaa	1073

<210> SEQ ID NO 96
<211> LENGTH: 209
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 96

Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg	
1 5 10 15	
Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys	
20 25 30	
Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn	
35 40 45	
Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu	
50 55 60	
Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met	
65 70 75	
Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn	
80 85 90	
Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr	
95 100 105	
Gln Leu Gly Ala Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro	
110 115 120	
Gln Ile Phe Thr Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly	
125 130 135	
Ile Leu Pro Thr Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp	
140 145 150	
Gly Ser Leu Pro Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln	
155 160 165	
Gly Thr Pro Ala Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp	
170 175 180	
Asp Phe Ala Val Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His	
185 190 195	
Ala Ile Glu Glu Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln	
200 205	

<210> SEQ ID NO 97
<211> LENGTH: 2848
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 97

gctcaagtgc cctgccttgc cccacccagc ccagcctggc cagagccccc	50
tggagaagga gctctcttct tgcttggcag ctggaccaag ggagccagtc	100
ttgggcgctg gagggcctgt cctgaccatg gtccctgcct ggctgtggct	150
gctttgtgtc tccgtccccc aggctctccc caaggcccag cctgcagagc	200
tgtctgtgga agttccagaa aactatgggtg gaaatttccc tttatacctg	250

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accaagtgc	cgctgcccc	tgagggggct	gaaggccaga	tcgtgctgtc	300
aggggactca	ggcaaggcaa	ctgagggccc	atttgctatg	gatccagatt	350
ctggcttcc	gctggtgacc	agggccctgg	accgagagga	gcaggcagag	400
taccagctac	aggtcaccct	ggagatgcag	gatggacatg	tcttgtgggg	450
tccacagcct	gtgcttgtgc	acgtgaagga	tgagaatgac	caggtgcccc	500
atttctctca	agccatctac	agagctcggc	tgagccgggg	taccaggcct	550
ggcattccct	tcctcttcc	tgaggcttca	gaccgggatg	agccaggcac	600
agccaaactcg	gatcttcgat	tccacatcct	gagccaggct	ccagcccagc	650
cttccccaga	catgttccag	ctggagccctc	ggctgggggc	tctggccctc	700
agccccaag	ggagcaccag	ccttgaccac	gccctggaga	ggacctacca	750
gctgttgga	caggtcaagg	acatgggtga	ccaggcctca	ggccaccagg	800
ccactgccac	cgtggaagtc	tccatcatag	agagcacctg	ggtgtcccta	850
gagcctatcc	acctggcaga	gaatctcaaa	gtcctatacc	cgcaccacat	900
ggcccaggta	cactggagtg	gggtgatgt	gcactatcac	ctggagagcc	950
atcccccg	accctttgaa	gtgaatgcag	agggaaacct	ctacgtgacc	1000
agagagctgg	acagagaagc	ccaggctgag	tacctgctcc	aggtgcgggc	1050
tcagaattcc	catggcgagg	actatgcggc	ccctctggag	ctgcacgtgc	1100
tggtgatgga	tgagaatgac	aacgtgccta	tctgccctcc	ccgtgacccc	1150
acagtcagca	tccttgagct	cagtccacca	ggtactgaag	tgactagact	1200
gtcagcagag	gatgcagatg	cccccgctc	ccccattcc	cacgttgtgt	1250
atcagctcct	gagccctgag	cctgaggatg	gggtagaggg	gagagccttc	1300
caggtggacc	ccacttcagg	cagtgtgacg	ctgggggtgc	tcccactccg	1350
agcaggccag	aacatcctgc	ttctggtgct	ggccatggac	ctggcaggcg	1400
cagaggggtg	cttcagcagc	acgtgtgaag	tcgaagtcgc	agtcacagat	1450
atcaatgatc	acgcccctga	gttcatcact	tcccagattg	ggcctataag	1500
cctccctgag	gatgtggagc	ccgggactct	ggtggccatg	ctaacagcca	1550
ttgatgctga	cctcgagccc	gccttccgcc	tcatggattt	tgccattgag	1600
aggggagaca	cagaagggac	ttttggcctg	gattgggagc	cagactctgg	1650
gcatgttaga	ctcagactct	gcaagaacct	cagttatgag	gcagctccaa	1700
gtcatgaggt	ggtggtggtg	gtgcagagtg	tggcgaagct	ggtggggcca	1750
ggcccaggcc	ctggagccac	cgccacgggtg	actgtgctag	tgagagagtg	1800
gatgccaccc	cccaagttgg	accaggagag	ctacgaggcc	agtgtcccca	1850
tcagtgcctc	agccggctct	ttctgtctga	ccatccagcc	ctccgacccc	1900
atcagccgaa	ccctcagggtt	ctccctagtc	aatgactcag	agggtgggt	1950
ctgcattgag	aaattctccg	gggaggtgca	caccgccag	tcctgcag	2000
gcgcccagcc	tggggacacc	tacacggtgc	ttgtggaggc	ccaggataca	2050
gccctgactc	ttgcccctgt	gccctcccaa	tacctctgca	caccccgcca	2100
agaccatggc	ttgatcgtga	gtggaccag	caaggacccc	gatctggcca	2150

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gtgggcacgg tccctacagc ttcacccttg gtcccaaccc cacggtgcaa	2200
cgggattggc gcctccagac tctcaatggt tcccatgcct acctcacctt	2250
ggccctgcat tgggtggagc cacgtgaaca cataatcccc gtgggtggtca	2300
gccacaatgc ccagatgtgg cagctcctgg ttcgagtgat cgtgtgtcgc	2350
tgcaacgtgg aggggcagtg catgcgcaag gtgggccgca tgaagggcat	2400
gccacgaag ctgtcggcag tgggcatacct tgtaggcacc ctggtagcaa	2450
taggaatctt cctcatcctc attttcaccc actggaccat gtcaaggaag	2500
aaggaccogg atcaaccagc agacagcgtg cccctgaagg cgactgtctg	2550
aatggcccag gcagctctag ctgggagctt ggcctctggc tccatctgag	2600
ttccctggga gagagcccag caccgaagat ccagcagggg acaggacaga	2650
gtagaagccc ctccatctgc cctggggtgg aggcaccatc accatcacca	2700
ggcatgtctg cagagcctgg acaccaactt tatggactgc ccatgggagt	2750
gctccaaatg tcaggggtgtt tgcccaataa taaagcccca gagaactggg	2800
ctgggcccta tgggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaag	2848

<210> SEQ ID NO 98

<211> LENGTH: 807

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 98

Met Val Pro Ala Trp Leu Trp Leu Leu Cys Val Ser Val Pro Gln	
1 5 10 15	
Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro	
20 25 30	
Glu Asn Tyr Gly Gly Asn Phe Pro Leu Tyr Leu Thr Lys Leu Pro	
35 40 45	
Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile Val Leu Ser Gly Asp	
50 55 60	
Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala Met Asp Pro Asp Ser	
65 70 75	
Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala	
80 85 90	
Glu Tyr Gln Leu Gln Val Thr Leu Glu Met Gln Asp Gly His Val	
95 100 105	
Leu Trp Gly Pro Gln Pro Val Leu Val His Val Lys Asp Glu Asn	
110 115 120	
Asp Gln Val Pro His Phe Ser Gln Ala Ile Tyr Arg Ala Arg Leu	
125 130 135	
Ser Arg Gly Thr Arg Pro Gly Ile Pro Phe Leu Phe Leu Glu Ala	
140 145 150	
Ser Asp Arg Asp Glu Pro Gly Thr Ala Asn Ser Asp Leu Arg Phe	
155 160 165	
His Ile Leu Ser Gln Ala Pro Ala Gln Pro Ser Pro Asp Met Phe	
170 175 180	
Gln Leu Glu Pro Arg Leu Gly Ala Leu Ala Leu Ser Pro Lys Gly	
185 190 195	

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Ser Thr Ser Leu Asp His Ala Leu Glu Arg Thr Tyr Gln Leu Leu	200	205	210
Val Gln Val Lys Asp Met Gly Asp Gln Ala Ser Gly His Gln Ala	215	220	225
Thr Ala Thr Val Glu Val Ser Ile Ile Glu Ser Thr Trp Val Ser	230	235	240
Leu Glu Pro Ile His Leu Ala Glu Asn Leu Lys Val Leu Tyr Pro	245	250	255
His His Met Ala Gln Val His Trp Ser Gly Gly Asp Val His Tyr	260	265	270
His Leu Glu Ser His Pro Pro Gly Pro Phe Glu Val Asn Ala Glu	275	280	285
Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp Arg Glu Ala Gln Ala	290	295	300
Glu Tyr Leu Leu Gln Val Arg Ala Gln Asn Ser His Gly Glu Asp	305	310	315
Tyr Ala Ala Pro Leu Glu Leu His Val Leu Val Met Asp Glu Asn	320	325	330
Asp Asn Val Pro Ile Cys Pro Pro Arg Asp Pro Thr Val Ser Ile	335	340	345
Pro Glu Leu Ser Pro Pro Gly Thr Glu Val Thr Arg Leu Ser Ala	350	355	360
Glu Asp Ala Asp Ala Pro Gly Ser Pro Asn Ser His Val Val Tyr	365	370	375
Gln Leu Leu Ser Pro Glu Pro Glu Asp Gly Val Glu Gly Arg Ala	380	385	390
Phe Gln Val Asp Pro Thr Ser Gly Ser Val Thr Leu Gly Val Leu	395	400	405
Pro Leu Arg Ala Gly Gln Asn Ile Leu Leu Val Leu Ala Met	410	415	420
Asp Leu Ala Gly Ala Glu Gly Gly Phe Ser Ser Thr Cys Glu Val	425	430	435
Glu Val Ala Val Thr Asp Ile Asn Asp His Ala Pro Glu Phe Ile	440	445	450
Thr Ser Gln Ile Gly Pro Ile Ser Leu Pro Glu Asp Val Glu Pro	455	460	465
Gly Thr Leu Val Ala Met Leu Thr Ala Ile Asp Ala Asp Leu Glu	470	475	480
Pro Ala Phe Arg Leu Met Asp Phe Ala Ile Glu Arg Gly Asp Thr	485	490	495
Glu Gly Thr Phe Gly Leu Asp Trp Glu Pro Asp Ser Gly His Val	500	505	510
Arg Leu Arg Leu Cys Lys Asn Leu Ser Tyr Glu Ala Ala Pro Ser	515	520	525
His Glu Val Val Val Val Val Gln Ser Val Ala Lys Leu Val Gly	530	535	540
Pro Gly Pro Gly Pro Gly Ala Thr Ala Thr Val Thr Val Leu Val	545	550	555
Glu Arg Val Met Pro Pro Pro Lys Leu Asp Gln Glu Ser Tyr Glu	560	565	570

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Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr
				575					580					585
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu
				590					595					600
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly
				605					610					615
Glu	Val	His	Thr	Ala	Gln	Ser	Leu	Gln	Gly	Ala	Gln	Pro	Gly	Asp
				620					625					630
Thr	Tyr	Thr	Val	Leu	Val	Glu	Ala	Gln	Asp	Thr	Ala	Leu	Thr	Leu
				635					640					645
Ala	Pro	Val	Pro	Ser	Gln	Tyr	Leu	Cys	Thr	Pro	Arg	Gln	Asp	His
				650					655					660
Gly	Leu	Ile	Val	Ser	Gly	Pro	Ser	Lys	Asp	Pro	Asp	Leu	Ala	Ser
				665					670					675
Gly	His	Gly	Pro	Tyr	Ser	Phe	Thr	Leu	Gly	Pro	Asn	Pro	Thr	Val
				680					685					690
Gln	Arg	Asp	Trp	Arg	Leu	Gln	Thr	Leu	Asn	Gly	Ser	His	Ala	Tyr
				695					700					705
Leu	Thr	Leu	Ala	Leu	His	Trp	Val	Glu	Pro	Arg	Glu	His	Ile	Ile
				710					715					720
Pro	Val	Val	Val	Ser	His	Asn	Ala	Gln	Met	Trp	Gln	Leu	Leu	Val
				725					730					735
Arg	Val	Ile	Val	Cys	Arg	Cys	Asn	Val	Glu	Gly	Gln	Cys	Met	Arg
				740					745					750
Lys	Val	Gly	Arg	Met	Lys	Gly	Met	Pro	Thr	Lys	Leu	Ser	Ala	Val
				755					760					765
Gly	Ile	Leu	Val	Gly	Thr	Leu	Val	Ala	Ile	Gly	Ile	Phe	Leu	Ile
				770					775					780
Leu	Ile	Phe	Thr	His	Trp	Thr	Met	Ser	Arg	Lys	Lys	Asp	Pro	Asp
				785					790					795
Gln	Pro	Ala	Asp	Ser	Val	Pro	Leu	Lys	Ala	Thr	Val			
				800					805					

<210> SEQ ID NO 99
<211> LENGTH: 2436
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 99

ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc	50
agctgcccac gcctgagtcc aagattcttc ccaggaacac aaacgtagga	100
gaccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc	150
ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta	200
ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag	250
aaaggaaatg ttctccttat gtttggtcta ctattgcatt tagaagctgc	300
aacaaattcc aatgagacta gcacctctgc caacactgga tccagtgtga	350
tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc	400
agtggggtoa gcacagccac catctcaggg tccagcgtga cctccaatgg	450
ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca	500

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gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata	550
gccaccaact ctgagtccag cacaacctcc agtggggcca gcacagccac	600
caactctgag tccagcacac cctccagtgg ggccagcaca gtcaccaact	650
ctgggtccag tgtgacctcc agtggagcca gcaactgccac caactctgag	700
tccagcacag tgtccagtag ggccagcact gccaccaact ctgagtctag	750
cacactctcc agtggggcca gcacagccac caactctgac tccagcaca	800
cctccagtgg ggctagcaca gccaccaact ctgagtccag cacaacctcc	850
agtggggcca gcacagccac caactctgag tccagcacag tgtccagtag	900
ggccagcact gccaccaact ctgagtccag cacaacctcc agtggggcca	950
gcacagccac caactctgag tccagaacga cctccaatgg ggctggcaca	1000
gccaccaact ctgagtccag cagcactcc agtggggcca gcacagccac	1050
caactctgac tccagcacag tgtccagtgg ggccagcact gccaccaact	1100
ctgagtccag cagcactcc agtggggcca gcacagccac caactctgag	1150
tccagcacga cctccagtgg ggctagcaca gccaccaact ctgactccag	1200
cacaacctcc agtggggccg gcacagccac caactctgag tccagcacag	1250
tgtccagtgg gatcagcaca gtcaccaatt ctgagtccag cacaccctcc	1300
agtggggcca acacagccac caactctgag tccagtacga cctccagtgg	1350
ggccaacaca gccaccaact ctgagtccag cacagtgtcc agtggggcca	1400
gcaactgccac caactctgag tccagcaca cctccagtgg ggtcagcaca	1450
gccaccaact ctgagtccag cacaacctcc agtggggcta gcacagccac	1500
caactctgac tccagcaca cctccagtga ggccagcaca gccaccaact	1550
ctgagtctag cacagtgtcc agtgggatca gcacagtcac caattctgag	1600
tccagcaca cctccagtgg ggccaacaca gccaccaact ctgggtccag	1650
tgtgacctct gcaggctctg gaacagcagc tctgactgga atgcacaca	1700
cttcccatag tgcactact gcagtgagt agggcaagcc tggtggtcc	1750
ctgggtccgt gggaaatctt cctcatcacc ctggtctcgg ttgtggcggc	1800
cgtggggctc tttgctgggc tcttctcttg tgtgagaaac agcctgtccc	1850
tgagaaacac cttaacaca gctgtctacc accctcatgg cctcaaccat	1900
ggccttggtc caggccctgg agggaaatcat ggagccccc acaggccag	1950
gtggagtcct aactggttct ggaggagacc agtatcatcg atagccatgg	2000
agatgagcgg gaggaacagc gggccctgag cagccccgga agcaagtgc	2050
gcattcttca ggaaggaaga gacctgggca cccaagacct ggtttccttt	2100
cattcatccc aggagacccc tcccagcttt gtttgagatc ctgaaaatct	2150
tgaagaaggt attcctcacc tttctgcct ttaccagaca ctggaaagag	2200
aatactatat tgctcattta gctaagaaat aaatacatct catctaacac	2250
acacgacaaa gagaagctgt gcttgccccg gggtggtat ctagctctga	2300
gatgaactca gttataggag aaaacctcca tgtgggactc catctggcat	2350
tcaaaatctc cacagtaaaa tccaagacc tcaaaaaaaaa aaaaaaaaaa	2400

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa

2436

<210> SEQ ID NO 100

<211> LENGTH: 596

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 100

Met	Lys	Met	Gln	Lys	Gly	Asn	Val	Leu	Leu	Met	Phe	Gly	Leu	Leu
1				5					10					15

Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20					25					30

Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35					40					45

Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50					55					60

Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65					70					75

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala
				80					85					90

Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala
				95					100					105

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				110					115					120

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val
				125					130					135

Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				140					145					150

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala
				155					160					165

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				170					175					180

Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				185					190					195

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				200					205					210

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala
				215					220					225

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				230					235					240

Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala
				245					250					255

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				260					265					270

Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				275					280					285

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				290					295					300

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				305					310					315

Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala
				320					325					330

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

<210> SEQ ID NO 101
<211> LENGTH: 1728
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 101

ggccggacgc	ctccgcgtta	cgggatgaat	taacggcggg	ttccgcacgg	50
aggttgtgac	ccctacggag	ccccagcttg	cccacgcacc	ccactcggcg	100
tcgcgcggcg	tgccttgctt	gtcacagggtg	ggaggctgga	actatcaggc	150
tgaaaaacag	agtggttact	ctcttctggg	aagctggcaa	caaatggatg	200
atgtgatata	tgattccag	gggaagggaa	attgtgtg	ttctgaaccc	250
atggtaatt	aacgaggcag	tttctagcta	ctgcacgtac	ttcataaagc	300
aggactctaa	aagctttgga	atcatggtgt	catggaaagg	gatttacttt	350

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atactgactc	tgttttggg	aagcttttt	ggaagcattt	tcatgctgag	400
tcccttttta	cctttgatgt	ttgtaaacc	atcttggtat	cgctggatca	450
acaaccgcct	tgtaggaaca	tggtcaccc	tacctgtggc	attattggag	500
accatgtttg	gtgtaaaagt	gattataact	gggatgcat	ttgttcctgg	550
agaaagaagt	gtcattatca	tgaaccatcg	gacaagaatg	gactggatgt	600
tcctgtggaa	ttgcctgatg	cgatatagct	acctcagatt	ggagaaaatt	650
tgccctcaaag	cgagtctcaa	aggtgttcct	ggatttggtt	gggccatgca	700
ggctgctgcc	tatatcttca	ttcataggaa	atggaaggat	gacaagagcc	750
atctcgaaag	catgattgat	tacttttttg	atattcacga	accacttcaa	800
ctcctcatat	tcccagaagg	gactgatctc	acagaaaaca	gcaagtctcg	850
aagtaatgca	tttgctgaaa	aaaatggact	tcagaaatat	gaatatgttt	900
tacatccaag	aactacaggc	tttacttttg	tggtagaccg	tctaagagaa	950
ggtaagaacc	ttgatgctgt	ccatgatatc	actgtggcgt	atcctcacia	1000
cattcctcaa	tcagagaagc	acctcctcca	aggagacttt	cccagggaaa	1050
tccactttca	cgccaccggg	tatccaatag	acaccctccc	cacatccaag	1100
gaggaccttc	aactctgggt	ccacaacgg	tggaagaga	agaagagag	1150
gctgcgttcc	ttctatcaag	gggagaagaa	ttttattttt	accggacaga	1200
gtgtcattcc	accttgcaag	tctgaactca	gggtccttgt	ggtcaaattg	1250
ctctctatac	tgtattggac	cctgttcagc	cctgcaatgt	gcctactcat	1300
atatttgtac	agtcttggtt	agtgttattt	tataatcacc	attgtaattct	1350
ttgtgctgca	agagagaata	tttggtggac	tgagatcat	agaacttgca	1400
tgttaccgac	ttttacacia	acagccacat	ttaaattcaa	agaaaaatga	1450
gtaagattat	aaggtttgcc	atgtgaaaac	ctagagcata	ttttggaaat	1500
gttctaaaacc	tttctaagct	cagatgcatt	tttgcacgac	tatgtcgaat	1550
atttcttact	gccatcatta	tttgttaaag	atattttgca	cttaattttg	1600
tggaagaaat	attgctacia	ttttttttta	tctctgaatg	taatttcgat	1650
actgtgtaca	tagcaggggg	tgatcggggg	gaaataactt	gggccagaat	1700
attattaaac	aatcatcagg	ctttttaa			1728

<210> SEQ ID NO 102

<211> LENGTH: 414

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 102

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

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Phe	Met	Leu	Ser	Pro	Phe	Leu	Pro	Leu	Met	Phe	Val	Asn	Pro	Ser	65	70	75
Trp	Tyr	Arg	Trp	Ile	Asn	Asn	Arg	Leu	Val	Ala	Thr	Trp	Leu	Thr	80	85	90
Leu	Pro	Val	Ala	Leu	Leu	Glu	Thr	Met	Phe	Gly	Val	Lys	Val	Ile	95	100	105
Ile	Thr	Gly	Asp	Ala	Phe	Val	Pro	Gly	Glu	Arg	Ser	Val	Ile	Ile	110	115	120
Met	Asn	His	Arg	Thr	Arg	Met	Asp	Trp	Met	Phe	Leu	Trp	Asn	Cys	125	130	135
Leu	Met	Arg	Tyr	Ser	Tyr	Leu	Arg	Leu	Glu	Lys	Ile	Cys	Leu	Lys	140	145	150
Ala	Ser	Leu	Lys	Gly	Val	Pro	Gly	Phe	Gly	Trp	Ala	Met	Gln	Ala	155	160	165
Ala	Ala	Tyr	Ile	Phe	Ile	His	Arg	Lys	Trp	Lys	Asp	Asp	Lys	Ser	170	175	180
His	Phe	Glu	Asp	Met	Ile	Asp	Tyr	Phe	Cys	Asp	Ile	His	Glu	Pro	185	190	195
Leu	Gln	Leu	Leu	Ile	Phe	Pro	Glu	Gly	Thr	Asp	Leu	Thr	Glu	Asn	200	205	210
Ser	Lys	Ser	Arg	Ser	Asn	Ala	Phe	Ala	Glu	Lys	Asn	Gly	Leu	Gln	215	220	225
Lys	Tyr	Glu	Tyr	Val	Leu	His	Pro	Arg	Thr	Thr	Gly	Phe	Thr	Phe	230	235	240
Val	Val	Asp	Arg	Leu	Arg	Glu	Gly	Lys	Asn	Leu	Asp	Ala	Val	His	245	250	255
Asp	Ile	Thr	Val	Ala	Tyr	Pro	His	Asn	Ile	Pro	Gln	Ser	Glu	Lys	260	265	270
His	Leu	Leu	Gln	Gly	Asp	Phe	Pro	Arg	Glu	Ile	His	Phe	His	Val	275	280	285
His	Arg	Tyr	Pro	Ile	Asp	Thr	Leu	Pro	Thr	Ser	Lys	Glu	Asp	Leu	290	295	300
Gln	Leu	Trp	Cys	His	Lys	Arg	Trp	Glu	Glu	Lys	Glu	Glu	Arg	Leu	305	310	315
Arg	Ser	Phe	Tyr	Gln	Gly	Glu	Lys	Asn	Phe	Tyr	Phe	Thr	Gly	Gln	320	325	330
Ser	Val	Ile	Pro	Pro	Cys	Lys	Ser	Glu	Leu	Arg	Val	Leu	Val	Val	335	340	345
Lys	Leu	Leu	Ser	Ile	Leu	Tyr	Trp	Thr	Leu	Phe	Ser	Pro	Ala	Met	350	355	360
Cys	Leu	Leu	Ile	Tyr	Leu	Tyr	Ser	Leu	Val	Lys	Trp	Tyr	Phe	Ile	365	370	375
Ile	Thr	Ile	Val	Ile	Phe	Val	Leu	Gln	Glu	Arg	Ile	Phe	Gly	Gly	380	385	390
Leu	Glu	Ile	Ile	Glu	Leu	Ala	Cys	Tyr	Arg	Leu	Leu	His	Lys	Gln	395	400	405
Pro	His	Leu	Asn	Ser	Lys	Lys	Asn	Glu							410		

<210> SEQ ID NO 103

<211> LENGTH: 2403

<212> TYPE: DNA

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<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 103

cggtctcgagc ggctcgagtg aagagcctct ccacggctcc tgcgcctgag	50
acagctgggc tgacctccaa atcatccatc caccctgct gtcattctgtt	100
ttcatagtggt gagatcaacc cacaggaata tccatggctt ttgtgctcat	150
tttggttctc agtttctacg agctggtgtc aggacagtgg caagtcactg	200
gaccgggcaa gtttgtccag gccttggtgg gggaggacgc cgtgttctcc	250
tgctccctct ttcctgagac cagtgcagag gctatggaag tgcggttctt	300
caggaatcag ttccatgctg tggccacct ctacagagat ggggaagact	350
gggaatctaa gcagatgcc aagtatcgag ggagaactga gtttgtgaag	400
gactccattg caggggggag tgtctctcta aggctaaaa acatcactcc	450
ctcggacatc ggctgtatg ggtgctggtt cagttccag atttacgatg	500
aggaggccac ctgggagctg cgggtggcag cactgggctc acttcctctc	550
atttccatcg tgggatatgt tgacggaggt atccagttac tctgcctgtc	600
ctcaggctgg ttccccagc ccacagccaa gtggaaaggt ccacaaggac	650
aggattttgtc ttcagactcc agagcaaatg cagatgggta cagcctgtat	700
gatgtggaga tctccattat agtcaggaa aatgctggga gcatattgtg	750
ttccatccac cttgctgagc agagtcatga ggtggaatcc aaggtattga	800
taggagagac gtttttccag ccctcacctt ggcgcctggc ttctatttta	850
ctcgggttac tctgtgtgtc cctgtgtggt gttgtcatgg ggaatgataat	900
tgttttcttc aaatccaaag ggaaaatcca ggcggaactg gactggagaa	950
gaaagcacgg acaggcagaa ttgagagacg cccggaaaca cgcagtggag	1000
gtgactctgg atccagagac ggctcaccgg aagctctgag tttctgatct	1050
gaaaactgta acccatagaa aagctcccca ggaggtgcct cactctgaga	1100
agagatttac aaggaagagt gtggtggctt ctacgggttt ccaagcaggg	1150
agacattact gggaggtgga cgtgggacaa aatgtagggt ggtatgtggg	1200
agtgtgtcgg gatgacgtag acagggggaa gaacaatgtg actttgtctc	1250
ccaacaatgg gtattgggtc ctacagactga caacagaaca ttgtatttc	1300
acattcaatc ccatttttat cagcctcccc ccagcacc ctcctacacg	1350
agtaggggtc ttcctggact atgaggtggt gaccatctcc ttcttcaata	1400
caaatgacca gtcccttatt tatacctgtc tgacatgtca gtttgaaggc	1450
ttgttgagac cctatatcca gcatgcgatg tatgacgagg aaaaggggac	1500
tcccatattc atatgtccag tgcctgggg atgagacaga gaagaccctg	1550
cttaaagggc cccacaccac agaccagac acagccaagg gagagtgtc	1600
ccgacaggtg gccccagctt cctctccgga gcctgcgcac agagagtcac	1650
gcccccaact ctcccttagg gagctgaggt tcttctgccc tgagccctgc	1700
agcagcgcca gtcacagctt ccagatgagg ggggattggc ctgaccctgt	1750
gggagtcaga agccatggct gcctgaagt ggggacggaa tagactcaca	1800

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ttaggttttag tttgtgaaaa ctccatccag ctaagcgatc ttgaacaagt	1850
cacaacctcc caggctcctc atttgctagt cacggacagt gattcctgcc	1900
tcacagggtga agattaaaga gacaacgaat gtgaatcatg cttgcagggt	1950
tgagggcaca gtgtttgcta atgatgtgtt tttatattat acattttccc	2000
accataaaact ctgtttgctt attccacatt aatttacttt tctctatacc	2050
aaatcaccca tggaatagtt attgaacacc tgctttgtga ggctcaaaga	2100
ataaagagga ggtaggattt ttcactgatt ctataagccc agcattacct	2150
gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag	2200
gtccatatcc ctcattaaca cagacacaaa aattctaaat aaaattttaa	2250
caaattaaac taaacaatat atttaaagat gatataaac tactcagtgt	2300
ggtttgtccc acaaatgcag agttggttta atatttaaat atcaaccagt	2350
gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa	2400
aaa	2403

<210> SEQ ID NO 104

<211> LENGTH: 466

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 104

Met	Ala	Phe	Val	Leu	Ile	Leu	Val	Leu	Ser	Phe	Tyr	Glu	Leu	Val
1				5					10					15
Ser	Gly	Gln	Trp	Gln	Val	Thr	Gly	Pro	Gly	Lys	Phe	Val	Gln	Ala
				20					25					30
Leu	Val	Gly	Glu	Asp	Ala	Val	Phe	Ser	Cys	Ser	Leu	Phe	Pro	Glu
				35					40					45
Thr	Ser	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Asn	Gln	Phe
				50					55					60
His	Ala	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Glu	Asp	Trp	Glu	Ser
				65					70					75
Lys	Gln	Met	Pro	Gln	Tyr	Arg	Gly	Arg	Thr	Glu	Phe	Val	Lys	Asp
				80					85					90
Ser	Ile	Ala	Gly	Gly	Arg	Val	Ser	Leu	Arg	Leu	Lys	Asn	Ile	Thr
				95					100					105
Pro	Ser	Asp	Ile	Gly	Leu	Tyr	Gly	Cys	Trp	Phe	Ser	Ser	Gln	Ile
				110					115					120
Tyr	Asp	Glu	Glu	Ala	Thr	Trp	Glu	Leu	Arg	Val	Ala	Ala	Leu	Gly
				125					130					135
Ser	Leu	Pro	Leu	Ile	Ser	Ile	Val	Gly	Tyr	Val	Asp	Gly	Gly	Ile
				140					145					150
Gln	Leu	Leu	Cys	Leu	Ser	Ser	Gly	Trp	Phe	Pro	Gln	Pro	Thr	Ala
				155					160					165
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Ser	Asp	Ser	Arg
				170					175					180
Ala	Asn	Ala	Asp	Gly	Tyr	Ser	Leu	Tyr	Asp	Val	Glu	Ile	Ser	Ile
				185					190					195
Ile	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Leu	Cys	Ser	Ile	His	Leu
				200					205					210

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

Gly

<210> SEQ ID NO 105
<211> LENGTH: 2103
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 105

ccttcacagg actcttcatt gctggttggc aatgatgtat cggccagatg	50
tggtgagggc taggaaaaga gtttgttggg aacctgggt tatcggcctc	100
gtcatcttca tatccctgat tgtcctggca gtgtgcattg gactcactgt	150
tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat	200
tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct	250
aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc	300
attttataaa tctccattaa gggaagaatt tgtcaagtct caggttatca	350
agttcagtc aacagaagcat ggagtgttgg ctcatatgct gttgatttgt	400

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agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact	450
tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc	500
ctcactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat	550
ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct	600
caggatcggt ggtgggacag aagtagaaga gggatgaatgg ccctggcagg	650
ctagcctgca gtgggatggg agtcacgcgt gtggagcaac cttaattaat	700
gccacatggc ttgtgagtgc tgctcactgt tttacaacat ataagaaccc	750
tgccagatgg actgcttctt ttggagtaac aataaaacct tcgaaaatga	800
aacgggggtct ccggagaata attgtccatg aaaaatacaa acacccatca	850
catgactatg atattttctt tgcagagctt tctagccctg ttccctacac	900
aaatgcagta catagagttt gtctccctga tgcacacctat gagtttcaac	950
caggatgatg gatgtttgtg acaggatttg gagcactgaa aaatgatgg	1000
tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac	1050
aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt	1100
tatgtgctgg ctcccttaga ggaaaaacag atgcatgccg gggtgactct	1150
ggaggaccac tggtagttc agatgctaga gatatctggt accttgctgg	1200
aatagtgcag tggggagatg aatgtgcgaa acccaacaag cctggtgttt	1250
atactagagt tacggccttg cgggactgga ttacttcaaa aactggatatc	1300
taagagacaa aagcctcatg gaacagataa cttttttttt tgttttttgg	1350
gtgtggaggc cttttttaga gatacagaat tggagaagac ttgcacaaac	1400
gctagatttg actgatctca ataaactgtt tgcttgatgc atgtattttc	1450
ttcccagctc tgttccgcac gtaagcatcc tgcttctgcc agatcaactc	1500
tgctcatctg gagcaatagt tgaacttta tgtacataga gaaatagata	1550
atacaatatt acattacagc ctgtattcat ttgttctcta gaagttttgt	1600
cagaattttg acttggtgac ataaatttgt aatgcatata tacaatttga	1650
agcactcctt ttcttcagtt cctcagctcc tctcatttca gcaaatatcc	1700
attttcaagg tgcagaacaa ggagtgaag aaaatataag aagaaaaaaa	1750
tcccctacat tttattggca cagaaaagta ttaggtgttt ttcttagtgg	1800
aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag	1850
aataccaatc acttcatcat ttaggaagta tgggaactaa gttaagggaag	1900
tccagaaaga agccaagata tatccttatt ttcatttcca aacaactact	1950
atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata	2000
caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat	2050
ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac	2100
cca	2103

<210> SEQ ID NO 106

<211> LENGTH: 423

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

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<400> SEQUENCE: 106

Met	Met	Tyr	Arg	Pro	Asp	Val	Val	Arg	Ala	Arg	Lys	Arg	Val	Cys	1	5	10	15
Trp	Glu	Pro	Trp	Val	Ile	Gly	Leu	Val	Ile	Phe	Ile	Ser	Leu	Ile	20	25	30	
Val	Leu	Ala	Val	Cys	Ile	Gly	Leu	Thr	Val	His	Tyr	Val	Arg	Tyr	35	40	45	
Asn	Gln	Lys	Lys	Thr	Tyr	Asn	Tyr	Tyr	Ser	Thr	Leu	Ser	Phe	Thr	50	55	60	
Thr	Asp	Lys	Leu	Tyr	Ala	Glu	Phe	Gly	Arg	Glu	Ala	Ser	Asn	Asn	65	70	75	
Phe	Thr	Glu	Met	Ser	Gln	Arg	Leu	Glu	Ser	Met	Val	Lys	Asn	Ala	80	85	90	
Phe	Tyr	Lys	Ser	Pro	Leu	Arg	Glu	Glu	Phe	Val	Lys	Ser	Gln	Val	95	100	105	
Ile	Lys	Phe	Ser	Gln	Gln	Lys	His	Gly	Val	Leu	Ala	His	Met	Leu	110	115	120	
Leu	Ile	Cys	Arg	Phe	His	Ser	Thr	Glu	Asp	Pro	Glu	Thr	Val	Asp	125	130	135	
Lys	Ile	Val	Gln	Leu	Val	Leu	His	Glu	Lys	Leu	Gln	Asp	Ala	Val	140	145	150	
Gly	Pro	Pro	Lys	Val	Asp	Pro	His	Ser	Val	Lys	Ile	Lys	Lys	Ile	155	160	165	
Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys	Cys	Gly	Thr	170	175	180	
Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	Gly	Gly	185	190	195	
Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	200	205	210	
Trp	Asp	Gly	Ser	His	Arg	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr	215	220	225	
Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	230	235	240	
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	245	250	255	
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	260	265	270	
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	275	280	285	
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	290	295	300	
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	305	310	315	
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	320	325	330	
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	335	340	345	
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	350	355	360	

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Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly
365 370 375

Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly
380 385 390

Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro Asn Lys Pro Gly
395 400 405

Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr Ser Lys
410 415 420

Thr Gly Ile

<210> SEQ ID NO 107
<211> LENGTH: 2397
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 107

agagaaagaa gcgtctccag ctgaagccaa tgcagccctc cggctctccg50

cgaagaagtt ccctgcccc atgagcccc gccgtgcgtc cccgactatc100

cccaggcggg cgtggggcac cgggccacg gccgacgac gctgccgttt150

tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg200

gttcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct250

acgccctcaa tctgctcttt tggttaatgt ccacagtggt gttggcagtt300

tctgcttgga tgagggacta cctaaataat gttctcactt taactgcaga350

aacgagggta gaggaagcag tcattttgac ttactttcct gtggttcac400

cggcatgat tgctgtttgc tgtttcccta tcattgtggg gatgttagga450

tattgtgga cggtgaaaaa aaatctgttg cttcttgcat ggtactttgg500

aagtttgctt gtcattttct gtgtagaact ggcttgtggc gtttgacat550

atgaacagga acttatgggt ccagtacaat ggtcagatat ggtcactttg600

aaagccagga tgacaaatta tggattacct agatatcggg ggttactca650

tgcttggaat ttttttcaga gagagtttaa gtgctgtgga gtagtatatt700

tcactgactg gttggaaatg acagagatgg actggcccc agattcctgc750

tgtgttagag aattcccagg atgttccaaa caggcccacc aggaagatct800

cagtgacctt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga850

gaggaaccaa acaactgcag gtgctgaggt ttctgggaat ctccattggg900

gtgacacaaa tcctggccat gattctcacc attactctgc tctgggctct950

gtattatgat agaagggagc ctgggacaga ccaaatgatg tccttgaaga1000

atgacaactc tcagcacctg tcatgtccct cagtagaact gttgaaacca1050

agcctgtcaa gaatctttga acacacatcc atggcaaaca gctttaatac1100

acactttgag atggaggagt tataaaaaga aatgtcacag aagaaaacca1150

caaacttggt ttattggact tgtgaatttt tgagtacata ctatgtgttt1200

cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata1250

tactattcta tgctttaaaa tgaggatgga aaagtttcat gtcataagtc1300

accacctgga caataattga tgcccttaaa atgctgaaga cagatgtcat1350

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accactgtg tagcctgtgt atgactttta ctgaacacag ttatgttttg      1400
aggcagcatg gtttgattag catttccgca tccatgcaaa cgagtcacat      1450
atgggtgggac tggagccata gtaaagggtg atttacttct accaactagt      1500
atataaagta ctaattaaat gctaacatag gaagttagaa aatactaata      1550
acttttatta ctcagcgatc tattcttctg atgctaaata aattatatat      1600
cagaaaactt tcaatattgg tgactaccta aatgtgattt ttgctgggta      1650
ctaaaaatatt cttaccactt aaaagagcaa gctaacacat tgtcttaagc      1700
tgatcagggg ttttttgat ataagtctgt gttaaactcg tataattcag      1750
tcgatttcag ttctgataat gttaagaata accattatga aaaggaaaat      1800
ttgtcctgta tagcatcatt attttttagcc tttcctgtta ataaagcttt      1850
actattctgt cctgggctta tattacacat ataactgtta tttaaatact      1900
taaccactaa ttttgaaaat taccagtgtg atacatagga atcattattc      1950
agaatgtagt ctggtcttta ggaagtatta ataagaaaat ttgcacataa      2000
cttagttgat tcagaaagga ctgtgatgct gtttttctcc caaatgaaga      2050
ctctttttga cactaaacac tttttaaaaa gcttatcttt gccttctcca      2100
aacaagaagc aatagtctcc aagtcaatat aaattctaca gaaaatagtg      2150
ttctttttct ccagaaaaat gcttgtgaga atcattaaaa catgtgacaa      2200
tttagagatt ctttgtttta tttcactgat taatatactg tggcaaatta      2250
cacagattat taaatttttt tacaagagta tagtatatth atttgaaatg      2300
ggaaaagtgc attttactgt attttgtgta ttttgtttat ttctcagaat      2350
atggaagaaa aattaaaatg tgtcaataaa tattttctag agagtaa      2397

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<210> SEQ ID NO 108
<211> LENGTH: 305
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien
<400> SEQUENCE: 108

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

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Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met
			125						130					135
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp
			140						145					150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe
			155						160					165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser
			170						175					180
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln
			185						190					195
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met
			200						205					210
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe
			215						220					225
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu
			230						235					240
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro
			245						250					255
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His
			260						265					270
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg
			275						280					285
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe
			290						295					300
Glu	Met	Glu	Glu	Leu										
			305											

<210> SEQ ID NO 109
<211> LENGTH: 2339
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 109

ccaaggccag agctgtggac accttatccc actcatcctc atcctcttcc	50
tctgataaag cccctaccag tgctgataaa gtctttctcg tgagagccta	100
gaggccttaa aaaaaaaagt gcttgaaaga gaaggggaca aaggaacacc	150
agtattaaga ggattttcca gtgtttctgg cagttggtcc agaaggatgc	200
ctccattcct gcttctcacc tgccctcttca tcacaggcac ctccgtgtca	250
cccgtggccc tagatccttg ttctgcttac atcagcctga atgagccctg	300
gaggaacact gaccaccagt tggatgagtc tcaaggctct cctctatgtg	350
acaaccatgt gaatggggag tggtaggact tcacgggcat ggcgggagat	400
gccatgccta ccttctgcat accagaaaac cactgtggaa cccacgcacc	450
tgtctggctc aatggcagcc accccctaga aggcgacggc attgtgcaac	500
gccaggcttg tgccagcttc aatgggaact gctgtctctg gaacaccacg	550
gtggaagtca aggcttgccc tggaggctac tatgtgtatc gtctgaccaa	600
gccagcgctc tgcttccacg tctactgtgg tcatttttat gacatctgct	650
acgaggactg ccatggcagc tgctcagata ccagcgagtg cacatgcgct	700

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ccaggaactg tgctaggccc tgacaggcag acatgctttg atgaaaatga	750
atgtgagcaa aacaacggtg gctgcagtga gatctgtgtg aacctcaaaa	800
actcctaccg ctgtgagtgt ggggttggcc gtgtgctaag aagtgatggc	850
aagactttgt aagacgttga aggatgccac aataacaatg gtggctgcag	900
ccactcttgc cttggatctg agaaaggcta ccagtgtgaa tgtccccggg	950
gcctgggtgt gtctgaggat aaccacactt gccaaagtcg tgtgttgtgc	1000
aaatcaaatg ccattgaagt gaacatcccc agggagctgg ttgggtggcct	1050
ggagctcttc ctgaccaaca cctcctgccg aggagtgtcc aacggcaccc	1100
atgtcaacat cctcttctct ctcaagacat gtggtacagt ggtcgatgtg	1150
gtgaatgaca agatttgtgc cagcaacctc gtgacaggtc tacccaagca	1200
gaccccgggg agcagcgggg acttcatcat ccgaaccagc aagctgctga	1250
tccccgtgac ctgcgagtth ccacgcctgt acaccatttc tgaaggatac	1300
gttcccaacc ttcgaaactc cccactggaa atcatgagcc gaaatcatgg	1350
gatctttcca ttactcttg agatcttcaa ggacaatgag ttgaaagagc	1400
cttaccggga agctctgccc accctcaagc ttcgtgactc cctctacttt	1450
ggcattgagc ccgtggtgca cgtgagcggc ttgaaagct tggtgagag	1500
ctgctttgcc acccccacct ccaagatcga cgaggtcctg aaatactacc	1550
tcattccggga tggctgtgtt tcagatgact cggtaaagca gtacacatcc	1600
cgggatcacc tagcaaagca cttccaggtc cctgtcttca agtttgtggg	1650
caaagaccac aaggaagtgt ttctgcactg ccgggttctt gtctgtggag	1700
tgttgagaca gcgttccgc tgtgcccagg gttgccaccg gcgaatgcgt	1750
cgtggggcag gaggagagga ctcagccggt ctacagggcc agacgctaac	1800
aggcgggccc atccgcatcg actgggagga ctagtctgta gccatactc	1850
gagtcctgc attggacggc tctgctcttt ggagcttctc cccccaccgc	1900
cctctaagaa catctgcaa cagctgggtt cagacttcac actgtgagtt	1950
cagactccca gcaccaactc actctgattc tgggtccattc agtgggcaca	2000
ggtcacagca ctgctgaaca atgtggcctg ggtggggttt catctttcta	2050
gggttgaaaa ctaaaactgt caccagaaa gacactcacc ccatttcct	2100
catttctttc ctacacttaa atacctcgtg tatggtgcaa tcagaccaca	2150
aaatcagaag ctgggtataa tatttcaagt tacaaccctt agaaaaatta	2200
aacagttact gaaattatga cttaaatacc caatgactcc ttaaatatgt	2250
aaattatagt tataccttga aatttcaatt caaatgcaga ctaattatag	2300
ggaatttgga agtgtatcaa taaaacagta tataattht	2339

<210> SEQ ID NO 110
<211> LENGTH: 545
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 110

Met Pro Pro Phe Leu Leu Leu Thr Cys Leu Phe Ile Thr Gly Thr
1 5 10 15

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Ser	Val	Ser	Pro	Val	Ala	Leu	Asp	Pro	Cys	Ser	Ala	Tyr	Ile	Ser	20	25	30
Leu	Asn	Glu	Pro	Trp	Arg	Asn	Thr	Asp	His	Gln	Leu	Asp	Glu	Ser	35	40	45
Gln	Gly	Pro	Pro	Leu	Cys	Asp	Asn	His	Val	Asn	Gly	Glu	Trp	Tyr	50	55	60
His	Phe	Thr	Gly	Met	Ala	Gly	Asp	Ala	Met	Pro	Thr	Phe	Cys	Ile	65	70	75
Pro	Glu	Asn	His	Cys	Gly	Thr	His	Ala	Pro	Val	Trp	Leu	Asn	Gly	80	85	90
Ser	His	Pro	Leu	Glu	Gly	Asp	Gly	Ile	Val	Gln	Arg	Gln	Ala	Cys	95	100	105
Ala	Ser	Phe	Asn	Gly	Asn	Cys	Cys	Leu	Trp	Asn	Thr	Thr	Val	Glu	110	115	120
Val	Lys	Ala	Cys	Pro	Gly	Gly	Tyr	Tyr	Val	Tyr	Arg	Leu	Thr	Lys	125	130	135
Pro	Ser	Val	Cys	Phe	His	Val	Tyr	Cys	Gly	His	Phe	Tyr	Asp	Ile	140	145	150
Cys	Asp	Glu	Asp	Cys	His	Gly	Ser	Cys	Ser	Asp	Thr	Ser	Glu	Cys	155	160	165
Thr	Cys	Ala	Pro	Gly	Thr	Val	Leu	Gly	Pro	Asp	Arg	Gln	Thr	Cys	170	175	180
Phe	Asp	Glu	Asn	Glu	Cys	Glu	Gln	Asn	Asn	Gly	Gly	Cys	Ser	Glu	185	190	195
Ile	Cys	Val	Asn	Leu	Lys	Asn	Ser	Tyr	Arg	Cys	Glu	Cys	Gly	Val	200	205	210
Gly	Arg	Val	Leu	Arg	Ser	Asp	Gly	Lys	Thr	Cys	Glu	Asp	Val	Glu	215	220	225
Gly	Cys	His	Asn	Asn	Asn	Gly	Gly	Cys	Ser	His	Ser	Cys	Leu	Gly	230	235	240
Ser	Glu	Lys	Gly	Tyr	Gln	Cys	Glu	Cys	Pro	Arg	Gly	Leu	Val	Leu	245	250	255
Ser	Glu	Asp	Asn	His	Thr	Cys	Gln	Val	Pro	Val	Leu	Cys	Lys	Ser	260	265	270
Asn	Ala	Ile	Glu	Val	Asn	Ile	Pro	Arg	Glu	Leu	Val	Gly	Gly	Leu	275	280	285
Glu	Leu	Phe	Leu	Thr	Asn	Thr	Ser	Cys	Arg	Gly	Val	Ser	Asn	Gly	290	295	300
Thr	His	Val	Asn	Ile	Leu	Phe	Ser	Leu	Lys	Thr	Cys	Gly	Thr	Val	305	310	315
Val	Asp	Val	Val	Asn	Asp	Lys	Ile	Val	Ala	Ser	Asn	Leu	Val	Thr	320	325	330
Gly	Leu	Pro	Lys	Gln	Thr	Pro	Gly	Ser	Ser	Gly	Asp	Phe	Ile	Ile	335	340	345
Arg	Thr	Ser	Lys	Leu	Leu	Ile	Pro	Val	Thr	Cys	Glu	Phe	Pro	Arg	350	355	360
Leu	Tyr	Thr	Ile	Ser	Glu	Gly	Tyr	Val	Pro	Asn	Leu	Arg	Asn	Ser	365	370	375
Pro	Leu	Glu	Ile	Met	Ser	Arg	Asn	His	Gly	Ile	Phe	Pro	Phe	Thr	380	385	390

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Leu	Glu	Ile	Phe	Lys	Asp	Asn	Glu	Phe	Glu	Glu	Pro	Tyr	Arg	Glu	
				395					400					405	
Ala	Leu	Pro	Thr	Leu	Lys	Leu	Arg	Asp	Ser	Leu	Tyr	Phe	Gly	Ile	
				410					415					420	
Glu	Pro	Val	Val	His	Val	Ser	Gly	Leu	Glu	Ser	Leu	Val	Glu	Ser	
				425					430					435	
Cys	Phe	Ala	Thr	Pro	Thr	Ser	Lys	Ile	Asp	Glu	Val	Leu	Lys	Tyr	
				440					445					450	
Tyr	Leu	Ile	Arg	Asp	Gly	Cys	Val	Ser	Asp	Asp	Ser	Val	Lys	Gln	
				455					460					465	
Tyr	Thr	Ser	Arg	Asp	His	Leu	Ala	Lys	His	Phe	Gln	Val	Pro	Val	
				470					475					480	
Phe	Lys	Phe	Val	Gly	Lys	Asp	His	Lys	Glu	Val	Phe	Leu	His	Cys	
				485					490					495	
Arg	Val	Leu	Val	Cys	Gly	Val	Leu	Asp	Glu	Arg	Ser	Arg	Cys	Ala	
				500					505					510	
Gln	Gly	Cys	His	Arg	Arg	Met	Arg	Arg	Gly	Ala	Gly	Gly	Glu	Asp	
				515					520					525	
Ser	Ala	Gly	Leu	Gln	Gly	Gln	Thr	Leu	Thr	Gly	Gly	Pro	Ile	Arg	
				530					535					540	
Ile	Asp	Trp	Glu	Asp											
				545											

<210> SEQ ID NO 111
<211> LENGTH: 2063
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 111

gagagagacca	gcagcttgct	cagcggacaa	ggatgctggg	cgtgagggac	50
caaggcctgc	cctgcactcg	ggcctcctcc	agccagtgtc	gaccagggac	100
ttctgacctg	ctggccagcc	aggacctgtg	tggggaggcc	ctcctgctgc	150
cttgggggtg	caatctcagc	tccaggctac	agggagaccg	ggaggatcac	200
agagccagca	tggtacagga	tcctgacagt	gatcaacctc	tgaacagcct	250
cgatgtcaaa	ccccgcgca	aaccccgat	ccccatggag	accttcagaa	300
aggtggggat	ccccatcatc	atagcactac	tgagcctggc	gagtatcatc	350
attgtggttg	tcctcatcaa	ggtgattctg	gataaatact	acttcctctg	400
cgggcagcct	ctccacttca	tcccaggaa	gcagctgtgt	gacggagagc	450
tggactgtcc	cttgggggag	gacgaggagc	actgtgtcaa	gagcttcccc	500
gaagggcctg	cagtggcagt	ccgcctctcc	aaggaccgat	ccacactgca	550
ggtgtgtgac	tcggccacag	ggaactggtt	ctctgcctgt	ttcgacaact	600
tcacagaagc	tctcgctgag	acagcctgta	ggcagatggg	ctacagcaga	650
gctgtggaga	ttggcccaga	ccaggatctg	gatgttgttg	aaatcacaga	700
aaacagccag	gagcttcgca	tgcggaactc	aagtggggccc	tgtctctcag	750
gtcccttggt	ctccctgcac	tgtcttgctt	gtgggaagag	cctgaagacc	800
ccccgtgtgg	tgggtgggga	ggaggcctct	gtggattctt	ggccttgcca	850
ggtcagcatc	cagtagcaca	aacagcacgt	ctgtggaggg	agcatcctgg	900

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acccccactg ggtcctcacg gcagccact gttcaggaa acataccgat	950
gtgttcaact ggaaggtgcg ggcaggtca gacaaactgg gcagttccc	1000
atccctggct gtggccaaga tcatcatcat tgaattcaac cccatgtacc	1050
ccaaagacaa tgacatcgcc ctcatgaagc tgcagttccc actcactttc	1100
tcaggcacag tcaggcccat ctgtctgccc ttctttgatg aggagctcac	1150
tccagccacc ccaactctgga tcattggatg gggctttacg aagcagaatg	1200
gagggaagat gtctgacata ctgctgcagg cgtcagtcca ggtcattgac	1250
agcacacggt gcaatgcaga cgatgcgtac cagggggaag tcaccgagaa	1300
gatgatgtgt gcaggcatcc cggaaggggg tgtggacacc tgccagggtg	1350
acagtgggtg gccctgatg taccaatctg accagtggca tgtgggtggc	1400
atcgtagctg ggggctatgg ctgcgggggc cagagcacc caggagtata	1450
caccaaggtc tcagcctatc tcaactggat ctacaatgtc tggaaggctg	1500
agctgtaatg ctgctgcccc ttgcagtgc tgggagccgc ttcttctctg	1550
ccctgccac tcggggatcc cccaaagtca gacacagagc aagagtcccc	1600
ttgggtacac ccctctgccc acagcctcag catttcttgg agcagcaaa	1650
ggcctcaatt cctgtaagag accctcgag cccagaggcg cccagaggaa	1700
gtcagcagcc ctagctcggc cacacttggg gctccagca tcccaggag	1750
agacacagcc cactgaacaa ggtctcagg gtattgctaa gccagaagg	1800
aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga	1850
tcactgtggg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg	1900
tcttcaccca tcccgaagc tactagagca agaaaccagt tgtaataata	1950
aatgcactgc cctactgttg gtatgactac cgttacctac tgttgtcatt	2000
gttattacag ctatggccac tattattaaa gagctgtgta acatctctgg	2050
caaaaaaaaa aaa	2063

<210> SEQ ID NO 112
<211> LENGTH: 432
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 112

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

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His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg	95	100	105
Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr	110	115	120
Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu	125	130	135
Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu	140	145	150
Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn	155	160	165
Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser	170	175	180
Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu	185	190	195
Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser	200	205	210
Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys	215	220	225
Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His	230	235	240
Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala	245	250	255
Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala Val Ala Lys	260	265	270
Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp	275	280	285
Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr	290	295	300
Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro	305	310	315
Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn	320	325	330
Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val	335	340	345
Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu	350	355	360
Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val	365	370	375
Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser	380	385	390
Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys	395	400	405
Gly Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr	410	415	420
Leu Asn Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu	425	430	

<210> SEQ ID NO 113

<211> LENGTH: 1768

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

-continued

<400> SEQUENCE: 113

ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc	50
aaggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac	100
tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac	150
tatgtctgtg tggctagtgc tcctactcct acctacatta aaatctgttt	200
tttgtttctt tgtaactagc ctttaccttc ctaacacaga ggatctgtca	250
ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt	300
ttctacccac accgtccctt cgaagccggg gacagcctca ccttgctggc	350
ctctcgctgg agcagtgtcc tcaccaactg tctcacgtct ggaggcactg	400
actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg	450
tgggccttgc cctggccgta gaagggattg acaagccga agatttcata	500
ggcgatggct cccactgtcc aggcacagc cttgtgttag tcaatcactg	550
ccctggggcc aggcaggggc gtggacacct gctcagaagc agtgggtgag	600
acatcacgct gcccgcccat ctaacctttt catgtcctgc acatcacctg	650
atccatgggc taatctgaac tctgtcccaa ggaaccaga gcttgagtga	700
gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg	750
acaggacttg cattctcctg gaacatgagg gaacgccga ggaagcaaaa	800
gtggcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt	850
gttgggttat cacaaggcat cgagtctcct goattcagtg gacatgtggg	900
ggaagggtct ccgatggcgc atgacacact cgggactcac ctctggggcc	950
atcacagagc cgtttccgcc ccgatccacg taccagctgc tgaagggcaa	1000
ctgcaggcgc atgtctctcat cagccaggca gcagccaaaa tctgcgatca	1050
ccagccaggg gcagccgtct gggaaggagc aagcaaagt accatttctc	1100
ctccccctct tccctctgag aggcctcct atgtccctac taaagccacc	1150
agcaagacat agctgacagg ggctaattgg tcagtgttgg ccagagaggt	1200
cagcaaggcc tgagagctga tcagaaggcc ctgctgtgcg aacacggaaa	1250
tgctccagct aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg	1300
ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaaag	1350
agctagagct tggttcaaat gatctccaag ggcccttata cccaggaga	1400
ctttgatttg aatttgaaac cccaaatcca aacctaaaga ccagggtgat	1450
taagaatcag ttattgccg gtgtgtgtgg ctgtaatgcc aacattttgg	1500
gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg	1550
gccaaatagg tgaacccctt gtctctacta aaaatacaaa aaaactagcc	1600
agggatgggt gtgtgtgcct gtatcccagc tactcgggag gctgagacag	1650
gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac	1700
ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaaag	1750
aattatgggt atttgtaa	1768

<210> SEQ ID NO 114

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<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 114

Met Leu Trp Trp Leu Val Leu Leu Leu Pro Thr Leu Lys Ser
1 5 10 15

Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu
20 25 30

Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
35 40 45

Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
50 55 60

Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
65 70 75

Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
80 85 90

Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
95 100 105

Arg Arg Arg Asp

<210> SEQ ID NO 115
<211> LENGTH: 1197
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 115

cagcagtggt ctctcagtcc tctcaaagca aggaaagagt actgtgtgct 50
gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150
ttgtggactg gtgtttggta tcctggccct aactctaatt gtctgtttt 200
gggggagcaa gcacttctgg cgggaggtac ccaaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatattcag aagcggaaat ggcactgatg 350
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550
aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600
gaccatgtat tggatcaatc cactccta atcagtttct gagttacaag 650
actttgagga ggaggagaa gatcttcact ttcctgcaa cgaaaaaaa 700
gggattgaac aaaatgaaca gtgggtgtgc cctcaagtga aagtagagaa 750
gaccgcgtcac gccagacaag caagtgagga agaactcca ataaatgact 800
atactgaaaa tggaatagaa tttgatccca tgctggatga gagaggttat 850
tgttgtatatt actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900
acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950
tcactctgtg tgtcatcatg ccttgtaact ggtgggtggc ccgcatgtg 1000

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gggaggggtct aataggaggt ttgagctcaa atgcttaaac tgctggcaac      1050
atataataaa tgcatgctat tcaatgaatt tctgcctatg aggcacatctgg      1100
ccccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca      1150
tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa      1197

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<210> SEQ ID NO 116
<211> LENGTH: 317
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 116

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Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile Leu
 1              5              10              15

Asn Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys
      20              25              30

Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val
      35              40              45

Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys
      50              55              60

Ala Tyr Asp Met Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys
      65              70              75

Lys Ile Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe
      80              85              90

Arg Ser Gly Asn Gly Thr Asp Glu Thr Leu Glu Val His Asp Phe
      95              100             105

Lys Asn Gly Tyr Thr Gly Ile Tyr Phe Val Gly Leu Gln Lys Cys
     110              115             120

Phe Ile Lys Thr Gln Ile Lys Val Ile Pro Glu Phe Ser Glu Pro
     125              130             135

Glu Glu Glu Ile Asp Glu Asn Glu Glu Ile Thr Thr Thr Phe Phe
     140              145             150

Glu Gln Ser Val Ile Trp Val Pro Ala Glu Lys Pro Ile Glu Asn
     155              160             165

Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu Ile Cys Asp Asn
     170              175             180

Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser Val Ser Glu
     185              190             195

Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe Pro Ala
     200              205             210

Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val Pro
     215              220             225

Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu
     230              235             240

Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe
     245              250             255

Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg
     260              265             270

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
     275              280             285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
     290              295             300

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Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
305 310 315

Arg Val

<210> SEQ ID NO 117
<211> LENGTH: 2121
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 117

gagctcccct caggagcgcg ttagcttcac accttcggca gcaggagggc	50
ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac	100
cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct	150
gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac	200
aaccccgta cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt	250
gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg	300
gacttcagc catgctgcag gcagtgcgag ccctgatgat cgtaggcac	350
gtcctgggtg ccattggcct cctggtatcc atctttgccc tgaatgcat	400
ccgcatgggc agcatggagg actctgcaa agccaacatg aactgacct	450
ccgggatcat gttcattgtc tcaggctctt gtgaattgc tggagtgtct	500
gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat	550
gtacaccggc atgggtggga tgggtcagac tgttcagacc aggtacacat	600
ttgggtcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt	650
gggggtgtga tgatgtgcat cgctgccgg ggctggcac cagaagaaac	700
caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca	750
agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac	800
aagaagatat acgatggagg tgcccgacac gaggacgagg tacaatctta	850
tccttccaag cagcactatg tgtaatgtc taagacctct cagcacgggc	900
ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag	950
atctcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt	1000
catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata	1050
ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac	1100
atcttcaatc ctctatttct ttttttaaat ataactttct actctgatga	1150
gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact	1200
ccccctcttc ctctagtca ataaacccat tgatgatcta tttccagct	1250
tatccccaag aaaacttttg aaaggaaaga gtagaccaa agatgttatt	1300
ttctgctgtt tgaattttgt ctccccacco ccaacttggc tagtaataaa	1350
cacttactga agaagaagca ataagagaaa gatatttgta atctctccag	1400
cccatgatct cggttttctt aactgtgat cttaaaagt accaaaccaa	1450
agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct	1500
tcttattaca gcaacacat tctaggagtt tcctgagctc tccactggag	1550

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tcctctttct gtcgcggtc agaaattgtc cctagatgaa tgagaaaatt	1600
atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag	1650
taaaatgata cactatctct gtgaaatagc ctcaccccta catgtggata	1700
gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt	1750
aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct	1800
agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga	1850
gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag	1900
aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg	1950
gaggctgagg tgggaggatc acttgagccc agggaggttg gggctgcagt	2000
gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct	2050
gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt	2100
aggttaaac taattcttta a	2121

<210> SEQ ID NO 118

<211> LENGTH: 261

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 118

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

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Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
230 235 240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro
245 250 255
Ser Lys His Asp Tyr Val
260

<210> SEQ ID NO 119
<211> LENGTH: 2010
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 119

ggaaaaactg ttctcttctg tggcacagag aaccttgctt caaagcagaa	50
gtagcagttc cggagtccag ctggctaaaa ctcatcccag aggataatgg	100
caacccatgc cttagaaatc gctgggctgt ttcttggttg tgttggaatg	150
tggggcacag tggctgtcac tgtcatgcct cagtggagag tgcggcctt	200
cattgaaaaa aacatcgttg tttttgaaaa cttctgggaa ggactgtgga	250
tgaattgcgt gaggcaggct aacatcagga tgcagtcaa aatctatgat	300
tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg	350
tgctgcttcc gtgatgtcct tcttggtctt catgatggcc atccttgcca	400
tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt	450
ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat	500
ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa	550
tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga	600
tggaaccagg cactggtgct gattgttgga ggagctctgt tctgctgcgt	650
tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc	700
atcgcacaac ccaaaaaagt tatcacacgg gaaagaagtc accgagcgtc	750
tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta	800
taaagccatg caaatgacaa aaatctatat tactttctca aaatggaccc	850
caaagaaaact ttgatttact gttcttaact gcctaatctt aattacagga	900
actgtgcacg agctatttat gattctataa gctatttcag cagaatgaga	950
tattaaaccc aatgctttga ttgttctaga aagtatagta atttgttttc	1000
taagtggtgt caagcatcta ctctttttat catttacttc aaaatgacat	1050
tgctaaagac tgcattattt tactactgta atttctccac gacatagcat	1100
tatgtacata gatgagtgtg acatttatat ctcacataga gacatgctta	1150
tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga	1200
actcaactat tgcttttcag ggaaatcatg gataggggtg aagaaggtta	1250
ctattaattg tttaaaaaca gcttagggat taatgtcctc cattttataat	1300
gaagattaaa atgaaggcct taatcagcat tgtaaaggaa attgaatggc	1350
tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcottt	1400
atcctcttct cccagaggct ttttttttct tgtgtattaa attaacattt	1450

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ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc	1500
agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg	1550
gttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat	1600
gcattttgac aagaaatcat atatgtatgg atatatTTTA ataagtattt	1650
gagtacagac tttgagggtt catcaatata aataaaagag cagaaaaata	1700
tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt	1750
cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc	1800
atttttgttc tgtgaaaaat aaatttcctt cttgtacat ttctgtttag	1850
ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga	1900
tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta	1950
aatgaatgtg ttctatttgc ttatataatt tatattaata aattgtacat	2000
ttttctaatt	2010

<210> SEQ ID NO 120

<211> LENGTH: 225

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 120

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

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<210> SEQ ID NO 121
<211> LENGTH: 1257
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 121

ggagagagggc gcgcgggtga aaggcgctt gatgcagcct gcggcggcct	50
cggagcgcg cgagaccaga cgctgaccac gttcctctcc tcggtctcct	100
ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgacccacag	150
gccccgcgcg ctccccgcag cggtccgcg gcctcctgct gctcctgctg	200
ctgcagctgc ccgcgcgctc gagcgccctc gagatcccca aggggaagca	250
aaagcgcgag ctccggcaga gggaggtggt ggacctgtat aatggaatgt	300
gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc	350
aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg	400
agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacaccca	450
actacaagca gtgttcattg agttcattga attatggcat agatcttggg	500
aaaattgcgg agtgtacatt tacaagatg cgttcaaata gtgctctaag	550
agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc	600
agcgttggtt tttcacattc aatggagctg aatgttcagg acctcttccc	650
attgaagcta taattttatt ggaccaagga agccctgaaa tgaattcaac	700
aattaatat catcgacctt cttctgtgga aggactttgt gaaggaaattg	750
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac	800
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat	850
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt	900
ttattatgcc ttggaatggt tcacttaaat gacattttaa ataagtttat	950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagt	1000
tgatttcaca ctgtttttaa atctagcatt attcattttg cttcaatcaa	1050
aagtggtttc aatatttttt ttagttggtt agaatacttt cttcatagtc	1100
acattctctc aacctataat ttggaatatt gttgtgtct tttgtttttt	1150
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac	1200
aatgtgtaaa tgtaagaat tttttttata tctgttaaat aaaaattatt	1250
tccaaca	1257

<210> SEQ ID NO 122
<211> LENGTH: 243
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 122

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
1				5					10					15
Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	
				20				25					30	

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Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
35 40 45

Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60

Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75

Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90

Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105

Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120

Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
200 205 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
215 220 225

Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
230 235 240

Leu Pro Lys

<210> SEQ ID NO 123
<211> LENGTH: 2379
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 123

gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50

agctctgtgg ctgaactggg tgctcatcac gggaaactgct gggctatgga 100

atacagatgt ggcagctcag gtagcccaaa attgcctgga agaatacatc 150

atgtttttcg ataagaagaa attgtaggat ccagtttttt tttaaccgc 200

cccctcccca cccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250

atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300

tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350

atgttcctaaa atcgggtccat ctccaagggt gtccaatttt tcttctctggg 400

tgtcagcgag ccctgactca ctacagtgca gctgacaggg gctgtcatgc 450

aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500

acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550

cactgggttat agccccact gtcttactga caatgctttc ttctgccgaa 600

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cgaggatgcc ctaagggctg taggtgtgaa ggcaaaatgg tatattgtga	650
atctcagaaa ttacaggaga taccctcaag tataatctgct ggttgcttag	700
gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt	750
aaagggctca accagctcac ctggctatac cttgaccata accatatcag	800
caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga	850
ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct	900
gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct	950
gggatctgaa cagtttcggg gcttgccgaa gctgctgagt ttacatttac	1000
ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc	1050
aacctggaac ttttggaact ggatataaac cggatccgaa gtttagccag	1100
gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca	1150
atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagacct	1200
cagaaccttt acttgcatg gaataaaatc agtgtcatag gacagacct	1250
gtcctggacc tggagctcct tacaaggct tgatttatca ggcaatgaga	1300
tcgaagcttt cagtggacct agtgttttcc agtgtgtccc gaatctgcag	1350
cgctcaacc tggattccaa caagctcaca tttattggtc aagagatttt	1400
ggattcttgg atatccctca atgacatcag tottgctggg aatatatggg	1450
aatgcagcag aaatatgtgc tccctgttaa actggctgaa aagttttaaa	1500
ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg	1550
agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta	1600
ctacagagag gtttgatctg gccagggctc tcccaaagcc gacgtttaag	1650
cccaagctcc ccaggccgaa gcatgagagc aaacccccct tgcctccgac	1700
ggtgggagcc acagagcccg gccagagac cgatgctgac gccgagcaca	1750
tctctttcca taaaatcatc gcgggcagcg tggcgctttt cctgtccgtg	1800
ctcgtcatcc tgcgtgttat ctacgtgtca tggaagcggg accctgcgag	1850
catgaagcag ctgcagcagc gtcctcatc gcgaaggcac aggaaaaaga	1900
aaagacagtc cctaaagcaa atgactccca gcacccagga attttatgta	1950
gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac	2000
gggaccctgc acctataaca aatcgggctc caggagtggt gaggtatgaa	2050
ccattgtgat aaaaagagct cttaaagct gggaaataag tgggtcttta	2100
ttgaactctg gtgactatca agggaacgcy atgcccccc tccccctccc	2150
tctccctctc actttggtgg caagatcctt cctgtgccgt ttagtgcat	2200
tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt	2250
aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta	2300
ttgtataaga ccctttactg attccattaa tgcgcgcat tttttaagat	2350
aaaacttctt tcataggtaa aaaaaaaaa	2379

<210> SEQ ID NO 124

<211> LENGTH: 513

-continued

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 124

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala	1	5	10	15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala	20	25	30	
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val	35	40	45	
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser	50	55	60	
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys	65	70	75	
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu	80	85	90	
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe	95	100	105	
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg	110	115	120	
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu	125	130	135	
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser	140	145	150	
Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	155	160	165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	170	175	180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	185	190	195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu	200	205	210	
His	Leu	Glu	His	Asn	Gln	Phe	Ser	Lys	Leu	Asn	Leu	Ala	Leu	Phe	215	220	225	
Pro	Arg	Leu	Val	Ser	Leu	Gln	Asn	Leu	Tyr	Leu	Gln	Trp	Asn	Lys	230	235	240	
Ile	Ser	Val	Ile	Gly	Gln	Thr	Met	Ser	Trp	Thr	Trp	Ser	Ser	Leu	245	250	255	
Gln	Arg	Leu	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Ala	Phe	Ser	Gly	260	265	270	
Pro	Ser	Val	Phe	Gln	Cys	Val	Pro	Asn	Leu	Gln	Arg	Leu	Asn	Leu	275	280	285	
Asp	Ser	Asn	Lys	Leu	Thr	Phe	Ile	Gly	Gln	Glu	Ile	Leu	Asp	Ser	290	295	300	
Trp	Ile	Ser	Leu	Asn	Asp	Ile	Ser	Leu	Ala	Gly	Asn	Ile	Trp	Glu	305	310	315	
Cys	Ser	Arg	Asn	Ile	Cys	Ser	Leu	Val	Asn	Trp	Leu	Lys	Ser	Phe	320	325	330	
Lys	Gly	Leu	Arg	Glu	Asn	Thr	Ile	Ile	Cys	Ala	Ser	Pro	Lys	Glu	335	340	345	
Leu	Gln	Gly	Val	Asn	Val	Ile	Asp	Ala	Val	Lys	Asn	Tyr	Ser	Ile	350	355	360	

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Cys Gly Lys Ser Thr Thr Glu Arg Phe Asp Leu Ala Arg Ala Leu
365 370 375
Pro Lys Pro Thr Phe Lys Pro Lys Leu Pro Arg Pro Lys His Glu
380 385 390
Ser Lys Pro Pro Leu Pro Pro Thr Val Gly Ala Thr Glu Pro Gly
395 400 405
Pro Glu Thr Asp Ala Asp Ala Glu His Ile Ser Phe His Lys Ile
410 415 420
Ile Ala Gly Ser Val Ala Leu Phe Leu Ser Val Leu Val Ile Leu
425 430 435
Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys
440 445 450
Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys
455 460 465
Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr
470 475 480
Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr Ser Glu Met Leu Leu
485 490 495
Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510
Cys Glu Val

<210> SEQ ID NO 125
<211> LENGTH: 998
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 125

ccgttatcgt cttgcgctac tgctgaatgt ccgtcccgga ggaggaggag 50
aggcttttgc cgctgaccga gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggctaccg tggccgagct agcaaccttt ccctcggtac 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctaggggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
cacccgccat ttacagacac gtagtgattt ctggaggtcg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tccccttttg aaatcagtca ttggagggat gatggctggt gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
tgcatattga aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tggtaatat gggagattta 650
accacttatg atacagtga acactacttg gtattgaata caccacttga 700
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900

-continued

gctttttacc atcttggtg agaatagaccc cttgggtcaat ggtgttcttg 950

cttacttatg aaaaaatcag agagatgagt ggagtcagtc catttttaa 998

<210> SEQ ID NO 126

<211> LENGTH: 323

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 126

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

-continued

Glu Met Ser Gly Val Ser Pro Phe
320

<210> SEQ ID NO 127
<211> LENGTH: 1505
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 127

cgcggatcgg acccaagcag gtcggcggcg gcggcaggag agcggccggg	50
cgtcagctcc tcgacccccg tgtcgggcta gtccagcgag gcggacgggc	100
ggcgtgggcc catggccagg cccggcatgg agcggtgggc cgaccggctg	150
gcgctggtag cggggggcctc ggggggcata ggcgcggccg tggcccgggc	200
cctgtgccag cagggactga aggtggtggg ctgcgcccgc actgtgggca	250
acatcgagga gctggctgct gaatgtaaga gtgcaggcta ccccgggact	300
ttgatccccct acagatgtga cctatcaaat gaagaggaca tcctctccat	350
gttctcagct atccgttctc agcacagcgg tgtagacatc tgcataca	400
atgtcggctt ggcccgccct gacacctgc tctcaggcag caccagtgg	450
tggaaggaca tgttcaatgt gaacgtgctg gccctcagca tctgcacacg	500
ggaagcctac cagtccatga aggagcggaa tgtggacgat gggcacatca	550
ttaacatcaa tagcatgtct ggccaccgag tgttaccctc gtctgtgacc	600
cacttctata gtgccaccaa gtatgccgtc actgcgctga cagagggact	650
gaggcaagag cttcgggagg ccacagacca catccgagcc acgtgcatct	700
ctccagggtg ggtggagaca caattgcctt tcaaactcca cgacaaggac	750
cctgagaagg cagctgccac ctatgagcaa atgaagtgtc tcaaaccgga	800
ggatgtggcc gaggtgttta tctacgtcct cagcaccctc gcacacatcc	850
agattggaga catccagatg agggcccagg agcagggtgac ctagtgactg	900
tgggagctcc tccttccttc ccacaccttc atggcttgcc tcctgcctct	950
ggatttttagg tgttgatttc tggatcacgg gataccactt cctgtccaca	1000
ccccgaccag gggctagaaa atttgtttga gatttttata tcatctgtc	1050
aaattgcttc agttgtaaat gtgaaaaatg ggctggggaa aggagtggt	1100
gtccctaatt gttttacttg ttaacttgtt cttgtgcccc tgggcacttg	1150
gcctttgtct gctctcagtg tcttcctttt gacatgggaa aggagtgtg	1200
gccaaaatcc ccatcttctt gcacctcaac gtctgtggct cagggctggg	1250
gtggcagagg gaggccttca ccttatatct gtgttggtat ccagggctcc	1300
agacttcctc ctctgcctgc cccactgcac cctctcccc ttatctatct	1350
ccttctcggc tccccagccc agtcttggtc tctgtcccc tcctggggtc	1400
atccctccac tctgactctg actatggcag cagaacacca gggcctggcc	1450
cagtggattt catggtgac attaaaaag aaaaatcgca accaaaaaa	1500
aaaaa	1505

<210> SEQ ID NO 128
<211> LENGTH: 260

-continued

<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 128

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

<210> SEQ ID NO 129
<211> LENGTH: 1177
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 129

aactttctaca tgggcctcct gctgctggtg ctcttctctca gcctcctgcc	50
ggtggcctac accatcatgt ccctcccacc ctcctttgac tgcgggccgt	100
tcaggtgcag agtctcagtt gcccgggagc acctcccctc ccgaggcagt	150
ctgctcagag ggcctcggcc cagaattcca gttctggttt catgccagcc	200
tgtaaaaggc catggaactt tgggtgaatc accgatgccca tttaagaggg	250

-continued

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ttttctgcca ggatggaaat gttaggtcgt tctgtgtctg cgctgttcat      300
ttcagtagcc accagccacc tgtggccgtt gagtgcttga aatgaggaac      350
tgagaaaatt aatttctcat gtatttttct catttattta ttaattttta      400
actgatagtt gtacatatatt gggggtacat gtgatatttg gatacatgta      450
tacaatatat aatgatcaaa tcagggtaac tgggatatcc atcacatcaa      500
acatttatatt tttattcttt ttagacagag tctcactctg tcaccagggc      550
tggagtgcac tggtgccatc tcagcttact gcaacctctg cctgccaggt      600
tcaagcgatt ctcatgcctc cacctcccaa gtactgggga ctacaggcat      650
gcaccacaat gcccaactaa tttttgtatt tttagtagag acgggggttt      700
gccatgttgc ccaggctggc cttgaactcc tggcctcaaa caatccactt      750
gcctcggcct cccaaagtgt tatgattaca ggcgtgagcc accgtgcttg      800
gcctaaacat ttatcttttc tttgtgttgg gaactttgaa attatacaat      850
gaattattgt taactgtcat ctccctgctg tgctatggaa cactgggact      900
tcttccctct atctaactgt atattgttac cagttaacca accgtacttc      950
atccccactc ctctctatcc ttcccaacct ctgatcacct cattctactc     1000
tctacctcca tgagatccac ttttttagct cccacatgtg agtaagaaaa     1050
tgcaatatatt gtctttctgt gcctggccta ttccacttaa cataatgact     1100
tcctgtttcca tccatgttgc tgcaaatgac aggatttcgt tcttaatttc     1150
aattaaaata accacacatg gcaaaaaa                                1177
```

<210> SEQ ID NO 130
<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 130

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

<210> SEQ ID NO 131
<211> LENGTH: 2061
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

-continued

<400> SEQUENCE: 131

ttctgaagta acggaagcta ccttgtataa agacctcaac actgctgacc	50
atgatcagcg cagcctggag catcttcctc atcgggacta aaattgggct	100
gttccttcaa gtagcacctc tatcagttat ggctaaatcc tgtccatctg	150
tgtgtcgctg cgatgcgggt ttcatttact gtaatgatcg ctttctgaca	200
tccattccaa caggaatacc agaggatgct acaactctct accttcagaa	250
caaccaaata aataatgctg ggattccttc agatttgaag aacttgctga	300
aagtagaaag aatataccta taccacaaca gtttagatga atttcctacc	350
aacctcccaa agtatgtaaa agagttacat ttgcaagaaa ataacataag	400
gactatcact tatgattcac tttcaaaaat tccctatctg gaagaattac	450
atttagatga caactctgtc tctgcagtta gcatagaaga gggagcattc	500
cgagacagca actatctccg actgcttttc ctgtcccgta atcaccttag	550
cacaattccc tgggggtttgc ccaggactat agaagaacta cgcttggatg	600
ataatcgcat atccactatt tcatcaccat ctcttcaagg tctcactagt	650
ctaaaacgcc tggttctaga tggaaacctg ttgaacaatc atgggttagg	700
tgacaaagtt ttcttcaacc tagttaattt gacagagctg tccctgggtg	750
ggaattccct gactgctgca ccagtaaac ttccaggcac aaacctgagg	800
aagctttatc ttcaagataa ccacatcaat cgggtgcccc caaatgcttt	850
ttcttatcta aggcagctct atcgactgga tatgtccaat aataacctaa	900
gtaattttac tcagggatc tttgatgatt tggacaatat aacacaactg	950
attcttcgca acaatccctg gtattgcggg tgcaagatga aatgggtacg	1000
tgactgggta caatcactac ctgtgaaggt caacgtgcgt gggctcatgt	1050
gccaaagccc agaaaagggt cgtgggatgg ctattaagga tctcaatgca	1100
gaactgtttg attgtaagga cagtgggatt gtaagcacca ttcagataac	1150
cactgcaata cccaacacag tgtatccctg ccaaggacag tggccagctc	1200
cagtgaccaa acagccagat attaagaacc ccaagctcac taaggatcaa	1250
caaaccacag ggagtccctc aagaaaaaca attacaatta ctgtgaagtc	1300
tgtcacctct gataccattc atatctcttg gaaacttgct ctacctatga	1350
ctgcttttag actcagctgg cttaactgg gccatagccc ggcatttgga	1400
tctataacag aaacaattgt aacaggggaa cgcagtgagt acttggtcac	1450
agccctggag cctgattcac cctataaagt atgcatgggt cccatggaaa	1500
ccagcaacct ctacctatt gatgaaactc ctgtttgtat tgagactgaa	1550
actgcacccc ttcgaatgta caaccctaca accaccctca atcgagagca	1600
agagaaagaa ccttacaaaa accccaattt acctttgggt gccatcattg	1650
gtggggctgt ggcctgggt accattgccc ttcttgcttt agtgtgttg	1700
tatgttcata ggaatggatc gctcttctca aggaactgtg catatagcaa	1750
aggaggaga agaaaggatg actatgcaga agctggcact aagaaggaca	1800
actctatcct ggaaatcagg gaaacttctt ttcagatggt accaataagc	1850

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aatgaaccca tctcgaagga ggagtttgta atacacacca tatttcctcc      1900
taatggaatg aatctgtaca aaaacaatca cagtgaagc agtagtaacc      1950
gaagctacag agacagtggg attccagact cagatcactc acactcatga      2000
tgctgaagga ctcacagcag acttggtgtt tgggtttttt aaacctaagg      2050
gaggtgatgg t                                                  2061

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<210> SEQ ID NO 132
<211> LENGTH: 649
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 132

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Met Ile Ser Ala Ala Trp Ser Ile Phe Leu Ile Gly Thr Lys Ile
 1             5             10             15

Gly Leu Phe Leu Gln Val Ala Pro Leu Ser Val Met Ala Lys Ser
          20             25             30

Cys Pro Ser Val Cys Arg Cys Asp Ala Gly Phe Ile Tyr Cys Asn
          35             40             45

Asp Arg Phe Leu Thr Ser Ile Pro Thr Gly Ile Pro Glu Asp Ala
          50             55             60

Thr Thr Leu Tyr Leu Gln Asn Asn Gln Ile Asn Asn Ala Gly Ile
          65             70             75

Pro Ser Asp Leu Lys Asn Leu Leu Lys Val Glu Arg Ile Tyr Leu
          80             85             90

Tyr His Asn Ser Leu Asp Glu Phe Pro Thr Asn Leu Pro Lys Tyr
          95             100            105

Val Lys Glu Leu His Leu Gln Glu Asn Asn Ile Arg Thr Ile Thr
          110            115            120

Tyr Asp Ser Leu Ser Lys Ile Pro Tyr Leu Glu Glu Leu His Leu
          125            130            135

Asp Asp Asn Ser Val Ser Ala Val Ser Ile Glu Glu Gly Ala Phe
          140            145            150

Arg Asp Ser Asn Tyr Leu Arg Leu Leu Phe Leu Ser Arg Asn His
          155            160            165

Leu Ser Thr Ile Pro Trp Gly Leu Pro Arg Thr Ile Glu Glu Leu
          170            175            180

Arg Leu Asp Asp Asn Arg Ile Ser Thr Ile Ser Ser Pro Ser Leu
          185            190            195

Gln Gly Leu Thr Ser Leu Lys Arg Leu Val Leu Asp Gly Asn Leu
          200            205            210

Leu Asn Asn His Gly Leu Gly Asp Lys Val Phe Phe Asn Leu Val
          215            220            225

Asn Leu Thr Glu Leu Ser Leu Val Arg Asn Ser Leu Thr Ala Ala
          230            235            240

Pro Val Asn Leu Pro Gly Thr Asn Leu Arg Lys Leu Tyr Leu Gln
          245            250            255

Asp Asn His Ile Asn Arg Val Pro Pro Asn Ala Phe Ser Tyr Leu
          260            265            270

Arg Gln Leu Tyr Arg Leu Asp Met Ser Asn Asn Asn Leu Ser Asn
          275            280            285

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Leu	Pro	Gln	Gly	Ile	Phe	Asp	Asp	Leu	Asp	Asn	Ile	Thr	Gln	Leu		290	295	300
Ile	Leu	Arg	Asn	Asn	Pro	Trp	Tyr	Cys	Gly	Cys	Lys	Met	Lys	Trp		305	310	315
Val	Arg	Asp	Trp	Leu	Gln	Ser	Leu	Pro	Val	Lys	Val	Asn	Val	Arg		320	325	330
Gly	Leu	Met	Cys	Gln	Ala	Pro	Glu	Lys	Val	Arg	Gly	Met	Ala	Ile		335	340	345
Lys	Asp	Leu	Asn	Ala	Glu	Leu	Phe	Asp	Cys	Lys	Asp	Ser	Gly	Ile		350	355	360
Val	Ser	Thr	Ile	Gln	Ile	Thr	Thr	Ala	Ile	Pro	Asn	Thr	Val	Tyr		365	370	375
Pro	Ala	Gln	Gly	Gln	Trp	Pro	Ala	Pro	Val	Thr	Lys	Gln	Pro	Asp		380	385	390
Ile	Lys	Asn	Pro	Lys	Leu	Thr	Lys	Asp	Gln	Gln	Thr	Thr	Gly	Ser		395	400	405
Pro	Ser	Arg	Lys	Thr	Ile	Thr	Ile	Thr	Val	Lys	Ser	Val	Thr	Ser		410	415	420
Asp	Thr	Ile	His	Ile	Ser	Trp	Lys	Leu	Ala	Leu	Pro	Met	Thr	Ala		425	430	435
Leu	Arg	Leu	Ser	Trp	Leu	Lys	Leu	Gly	His	Ser	Pro	Ala	Phe	Gly		440	445	450
Ser	Ile	Thr	Glu	Thr	Ile	Val	Thr	Gly	Glu	Arg	Ser	Glu	Tyr	Leu		455	460	465
Val	Thr	Ala	Leu	Glu	Pro	Asp	Ser	Pro	Tyr	Lys	Val	Cys	Met	Val		470	475	480
Pro	Met	Glu	Thr	Ser	Asn	Leu	Tyr	Leu	Phe	Asp	Glu	Thr	Pro	Val		485	490	495
Cys	Ile	Glu	Thr	Glu	Thr	Ala	Pro	Leu	Arg	Met	Tyr	Asn	Pro	Thr		500	505	510
Thr	Thr	Leu	Asn	Arg	Glu	Gln	Glu	Lys	Glu	Pro	Tyr	Lys	Asn	Pro		515	520	525
Asn	Leu	Pro	Leu	Ala	Ala	Ile	Ile	Gly	Gly	Ala	Val	Ala	Leu	Val		530	535	540
Thr	Ile	Ala	Leu	Leu	Ala	Leu	Val	Cys	Trp	Tyr	Val	His	Arg	Asn		545	550	555
Gly	Ser	Leu	Phe	Ser	Arg	Asn	Cys	Ala	Tyr	Ser	Lys	Gly	Arg	Arg		560	565	570
Arg	Lys	Asp	Asp	Tyr	Ala	Glu	Ala	Gly	Thr	Lys	Lys	Asp	Asn	Ser		575	580	585
Ile	Leu	Glu	Ile	Arg	Glu	Thr	Ser	Phe	Gln	Met	Leu	Pro	Ile	Ser		590	595	600
Asn	Glu	Pro	Ile	Ser	Lys	Glu	Glu	Phe	Val	Ile	His	Thr	Ile	Phe		605	610	615
Pro	Pro	Asn	Gly	Met	Asn	Leu	Tyr	Lys	Asn	Asn	His	Ser	Glu	Ser		620	625	630
Ser	Ser	Asn	Arg	Ser	Tyr	Arg	Asp	Ser	Gly	Ile	Pro	Asp	Ser	Asp		635	640	645
His	Ser	His	Ser															

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<211> LENGTH: 1882

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 133

ccgtcatccc cctgcagcca cccttcccag agtcctttgc ccaggccacc	50
ccaggcttct tggcagccct gccgggccac ttgtcttcat gtctgccagg	100
gggagggtgg aaggaggtag gaggaggcgg tgcagaggca gtctgggctt	150
ggccagagct cagggtgctg agcgtgtgac cagcagttag cagaggccgg	200
ccatggccag cctggggctg ctgctcctgc tcttactgac agcactgcca	250
ccgctgtggt cctcctcact gcctgggctg gacactgctg aaagtaaagc	300
caccattgca gacctgatcc tgtctgctgct ggagagagcc accgtcttcc	350
tagaacagag gctgcctgaa atcaacctgg atggcatggt gggggtcoga	400
gtgctggaag agcagctaaa aagtgtccgg gagaagtggg cccaggagcc	450
cctgctgtag ccgctgagcc tgcgcgtggg gatgctgggg gagaagtggg	500
aggctgccat ccagagatcc ctccactacc tcaagctgag tgatcccaag	550
tacctaagag agttccagct gacctccag cccgggtttt ggaagctccc	600
acatgcctgg atccacactg atgcctcctt ggtgtacccc acgttcgggc	650
cccaggactc attctcagag gagagaagtg acgtgtgcct ggtgcagctg	700
ctgggaaccg ggacggacag cagcgagccc tgcggcctct cagacctctg	750
caggagcctc atgaccaagc ccggctgctc aggtactgct ctgtcccacc	800
aactgctctt cttcctctgg gccagaatga ggggatgcac acagggacca	850
ctccaacaga gccaggacta tatcaacctc ttctgcgcca acatgatgga	900
cttgaaccgc agagctgagg ccacgagata cgcctaccct acccgggaca	950
tcttcatgga aaacatcatg ttctgtggaa tgggcggctt ctccgacttc	1000
tacaagctcc ggtggctgga ggccattctc agctggcaga aacagcagga	1050
aggatgcttc ggggagcctg atgctgaaga tgaagaatta tctaaagcta	1100
ttcaatatca gcagcatttt tcgaggagag tgaagaggcg agaaaaacaa	1150
tttccagatt ctgctctgtg tgctcaggct ggagtacagt ggcgcaatct	1200
cggctcactg caacctttgc ctctggggtt caagcaattc tcttgctca	1250
tcctcccgag tagctgggac tacaggagcg tgccaccata cctggcta	1300
ttttatattt ttttagtaga gacagggttt catcatgttg ctcatgctgg	1350
tctcgaactc ctgatctcaa gagatccgcc cacctcaggc tcccaaagtg	1400
tgggattata ggtgtgagcc accgtgtctg gctgaaaagc actttcaaag	1450
agactgtgtt gaataaaggg ccaaggttct tgccaccag cactcatggg	1500
ggctctctcc cctagatggc tgctctctcc acaacacagc cacagcagt	1550
gcagccctgg gtggcttcct atacatcctg gcagaatacc cccagcaaa	1600
cagagagcca ccccatcca caccgccacc accaagcagc cgctgagacg	1650
gacgggtcca tgccagctgc ctggaggagg aacagacccc tttagtctc	1700
atcccttaga tcctggaggg caccgatcac atcctgggaa gaaggcatct	1750

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ggaggataag caaagccacc ccgacaccca atcttggaag ccctgagtag	1800
gcagggccag ggtaggtggg ggccgggagg gacccaggtg tgaacggatg	1850
aataaagttc aactgcaact gaaaaaaaaa aa	1882

<210> SEQ ID NO 134
<211> LENGTH: 440
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 134

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

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Trp Gln Lys Gln Gln Glu Gly Cys Phe Gly Glu Pro Asp Ala Glu
320 325 330
Asp Glu Glu Leu Ser Lys Ala Ile Gln Tyr Gln Gln His Phe Ser
335 340 345
Arg Arg Val Lys Arg Arg Glu Lys Gln Phe Pro Asp Ser Arg Ser
350 355 360
Val Ala Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln
365 370 375
Pro Leu Pro Pro Gly Phe Lys Gln Phe Ser Cys Leu Ile Leu Pro
380 385 390
Ser Ser Trp Asp Tyr Arg Ser Val Pro Pro Tyr Leu Ala Asn Phe
395 400 405
Tyr Ile Phe Leu Val Glu Thr Gly Phe His His Val Ala His Ala
410 415 420
Gly Leu Glu Leu Leu Ile Ser Arg Asp Pro Pro Thr Ser Gly Ser
425 430 435
Gln Ser Val Gly Leu
440

<210> SEQ ID NO 135
<211> LENGTH: 884
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 135

ggctctgagtg cagagctgct gtcattggcgg ccgctctgtg gggcttcttt 50
cccgtcctgc tgctgctgct gctatcgggg gatgtccaga gctcggaggt 100
gcccggggct gctgctgagg gatcgggagg gaggggggtc ggcataggag 150
atcgcttcaa gattgagggg cgtgcagttg ttccaggggt gaagcctcag 200
gactggatct cggcggcccc agtgctggta gacggagaag agcacgtcgg 250
tttccttaag acagatggga gttttgtggt tcatgatata ctttctggat 300
cttatgtagt ggaagttgta tctccagctt acagatttga tcccgttcga 350
gtggatatca cttcgaaagg aaaaatgaga gcaagatatg tgaattacat 400
caaaacatca gaggttgta gactgcccta tcctctccaa atgaaatctt 450
caggtcacc ttcttacttt attaaaagg aatcgtgggg ctggacagac 500
tttctaatag acccaatggt tatgatgatg gttcttcctt tattgatatt 550
tgtgcttctg cctaaagtgg tcaacacaag tgatcctgac atgagacggg 600
aaatggagca gtcaatgaat atgctgaatt ccaaccatga gttgcctgat 650
gtttctgagt tcatgacaag actcttctct tcaaaatcat ctggcaaatc 700
tagcagcggc agcagtaaaa caggcaaaa tggggctggc aaaaggaggt 750
agtcaggcgg tccagagctg gcatttgac aaacacggca aactgggtg 800
gcatccaagt cttggaaaac cgtgtgaagc aactactata aacttgagtc 850
atcccgaagt tgatctctta caactgtgta tggt 884

<210> SEQ ID NO 136
<211> LENGTH: 242
<212> TYPE: PRT

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<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 136

Met Ala Ala Ala Leu Trp Gly Phe Phe Pro Val Leu Leu Leu Leu
1 5 10 15

Leu Leu Ser Gly Asp Val Gln Ser Ser Glu Val Pro Gly Ala Ala
20 25 30

Ala Glu Gly Ser Gly Gly Ser Gly Val Gly Ile Gly Asp Arg Phe
35 40 45

Lys Ile Glu Gly Arg Ala Val Val Pro Gly Val Lys Pro Gln Asp
50 55 60

Trp Ile Ser Ala Ala Arg Val Leu Val Asp Gly Glu Glu His Val
65 70 75

Gly Phe Leu Lys Thr Asp Gly Ser Phe Val Val His Asp Ile Pro
80 85 90

Ser Gly Ser Tyr Val Val Glu Val Val Ser Pro Ala Tyr Arg Phe
95 100 105

Asp Pro Val Arg Val Asp Ile Thr Ser Lys Gly Lys Met Arg Ala
110 115 120

Arg Tyr Val Asn Tyr Ile Lys Thr Ser Glu Val Val Arg Leu Pro
125 130 135

Tyr Pro Leu Gln Met Lys Ser Ser Gly Pro Pro Ser Tyr Phe Ile
140 145 150

Lys Arg Glu Ser Trp Gly Trp Thr Asp Phe Leu Met Asn Pro Met
155 160 165

Val Met Met Met Val Leu Pro Leu Leu Ile Phe Val Leu Leu Pro
170 175 180

Lys Val Val Asn Thr Ser Asp Pro Asp Met Arg Arg Glu Met Glu
185 190 195

Gln Ser Met Asn Met Leu Asn Ser Asn His Glu Leu Pro Asp Val
200 205 210

Ser Glu Phe Met Thr Arg Leu Phe Ser Ser Lys Ser Ser Gly Lys
215 220 225

Ser Ser Ser Gly Ser Ser Lys Thr Gly Lys Ser Gly Ala Gly Lys
230 235 240

Arg Arg

<210> SEQ ID NO 137
<211> LENGTH: 1571
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 137

gatggcgag ccacagcttc tgtgagattc gatttctccc cagttcccct 50

gtgggtctga ggggaccaga agggtagact acgttggtt tctggaaggg 100

gaggctatat gcgtaattc cccaaacaa gttttgacat ttcccctgaa 150

atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

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<210> SEQ ID NO 138
<211> LENGTH: 261
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 138

Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met
  1             5             10             15

Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu
             20             25             30

Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys
             35             40             45

Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu
             50             55             60

Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu
             65             70             75

Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser
             80             85             90

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Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr
			95						100					105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile
			110						115					120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg
			125						130					135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu
			140						145					150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys
			155						160					165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe
			170						175					180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser
			185						190					195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu
			200						205					210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys
			215						220					225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln
			230						235					240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln
			245						250					255
Trp	Met	Glu	Glu	Thr	Glu									
			260											

<210> SEQ ID NO 139
<211> LENGTH: 2395
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 139

cctggagccg gaagcgcggc tgcagcaggg cgaggctcca ggtgggggtcg	50
gttcgcgcatc cagcctagcg tgtccacgat gcggctgggc tccgggactt	100
tcgtaccttg ttgcgtagcg atcgaggtgc tagggatcgc ggtcttctct	150
cggggattct tcccggtcc cgttcgttcc tctgccagag cggaacacgg	200
agcggagccc ccagcgccc aacctcggc tggagccagt tctaactgga	250
ccacgctgcc accacctctc ttcagtaaag ttgttattgt tctgatagat	300
gccttgagag atgattttgt gtttgggtca aaggtgtga aatttatgcc	350
ctacacaact taccttgtgg aaaaaggagc atctcacagt tttgtggctg	400
aagcaaagcc acctacagtt actatgcctc gaatcaaggc attgatgacg	450
gggagccttc ctggctttgt cgacgtcatc aggaacctca attctcctgc	500
actgctggaa gacagtgtga taagacaagc aaaagcagct gaaaaaagaa	550
tagtctttta tggagatgaa acctgggtta aattattccc aaagcathtt	600
gtggaatatg atggaacaac ctcatctttc gtgtcagatt acacagaggt	650
ggataataat gtcacgaggc atttgataaa agtattaaaa agaggagatt	700
gggacatatt aatcctccac tacctggggc tggaccacat tggccacatt	750
tcaggggcca acagccccct gattgggcag aagctgagcg agatggacag	800

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cggtgctgatg aagatccaca cctcactgca gtcgaaggag agagagacgc	850
ctttacccaa tttgctggtt ctttgtggtg accatggcat gtctgaaaca	900
ggaagtccacg gggcctcctc caccgaggag gtgaatacac ctctgatttt	950
aatcagttct gcgtttgaaa ggaaaccggt tgatatccga catccaaagc	1000
acgtccaata gacggatgtg gctgcgacac tggcgatagc acttggtta	1050
ccgattccaa aagacagtgt agggagcctc ctattcccag ttgtggaag	1100
aagaccaatg agagagcagt tgagattttt acatttgaat acagtgcagc	1150
ttagtaaaact gttgcaagag aatgtgccgt catatgaaaa agatcctggg	1200
tttgagcagt ttaaaatgtc agaaagattg catgggaact ggatcagact	1250
gtacttgagg gaaaagcatt cagaagtcct attcaacctg ggctccaagg	1300
ttctcaggca gtacctggat gctctgaaga cgctgagctt gtccctgagt	1350
gcacaagtgg ccagttctc accctgctcc tgctcagcgt ccacacaggca	1400
ctgcacagaa aggctgagct ggaagtccca ctgtcatctc ctgggttttc	1450
tctgtctctt tatttggtga tcctggttct ttcggccgtt cacgtcattg	1500
tggtgcacctc agctgaaagt tcgtgtact tctgtggcct ctcgtggctg	1550
gcggcagggt gcctttcgtt taccagactc tgggtgaaca cctggtgtgt	1600
gccaaagtgt ggcagtgcc tggacagggg gcctcagga aggacgtgga	1650
gcagccttat ccaggcctc tgggtgtccc gacacaggtg ttcacatctg	1700
tgctgtcagg tcagatgcct cagttccttg aaagctaggt tcctgcgact	1750
gttaccaagg tgattgtaaa gagctggcgg tcacagagga acaagcccc	1800
cagctgaggg ggtgtgtgaa tcggacagcc tcccagcaga ggtgtgggag	1850
ctgcagctga ggaagaaga gacaatcggc ctggacactc aggagggta	1900
aaaggagact tggtcgcacc actcatcctg ccacccccag aatgcacct	1950
gcctcatcag gtccagattt ctttccaagg cgacgcttt ctgttggaat	2000
tcttagtcct tggcctcgga caccttcatt cgtagctgg ggagtgggtg	2050
tgaggcagtg aagaagaggc ggatgggtcac actcagatcc acagagccca	2100
ggatcaaggg acccactgca gtggcagcag gactgttggg cccccacccc	2150
aacctgcac agccctcatc ccctcttggc ttgagccgtc agaggccctg	2200
tgctgagtgt ctgaccgaga cactcacagc tttgtcatca gggcacaggc	2250
ttcctcggag ccaggatgat ctgtgccag cttgcacctc gggcccatct	2300
gggctcatgc tctctctcct gctattgaat tagtacctag ctgcacacag	2350
tatgtagtta ccaaaagaat aaacggcaat aattgagaaa aaaaa	2395

<210> SEQ ID NO 140
<211> LENGTH: 310
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 140

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

-continued

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

<210> SEQ ID NO 141
<211> LENGTH: 754
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 141

ggcacgaggg aagccttcca ggttatcgtg acgcaccttg aaagtctgag 50
agctactgcc ctacagaaag ttactagtgc cctaaagctg gcgctggcac 100
tgatgttact gctgctgttg gagtacaact tccctataga aaacaactgc 150
cagcacctta agaccactca caccttcaga gtgaagaact taaaccgaa 200

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gaaattcagc attcatgacc aggatcacaa agtactggtc ctggactctg 250
ggaatctcat agcagttcca gataaaaact acatacgccc agagatcttc 300
tttgcattag cctcatcctt gagctcagcc tctgcggaga aaggaagtcc 350
gattctcctg ggggtctcta aaggggagtt ttgtctctac tgtgacaagg 400
ataaaggaca aagtcattcca tcccttcagc tgaagaagga gaaactgatg 450
aagctggctg ccctaaaagga atcagcacgc cggcccttca tcttttatag 500
ggctcagggt ggctcctgga acatgctgga gtcggcggct caccctggat 550
ggttcatctg cacctcctgc aattgtaatg agcctgttgg ggtgacagat 600
aaatttgaga acaggaaaca cattgaattt tcatttcaac cagtttgcaa 650
agctgaaatg agccccagtg aggtcagcga ttaggaaact gccccattga 700
acgccttcct cgctaatttg aactaattgt ataaaaacac caaacctgct 750
cact 754

<210> SEQ ID NO 142

<211> LENGTH: 193

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 142

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

<210> SEQ ID NO 143

<211> LENGTH: 961

<212> TYPE: DNA

-continued

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 143

```

ctagagagta tagggcagaa ggatggcaga tgagtgactc cacatccaga      50
gctgccctccc tttaatccag gatcctgtcc ttctgtcctt gtaggagtgc      100
ctgttgccag tgtggggtga gacaagtttg tcccacaggg ctgtctgagc      150
agataagatt aagggctggg tctgtgctca attaactcct gtgggcacgg      200
gggctgggaa gagcaaagtc agcgggtgcct acagtcagca ccatgctggg      250
cctgccgtgg aagggaggtc tgtcctgggc gctgctgctg cttctcttag      300
gctcccagat cctgctgata tatgcctggc atttcacga gcaaaggac      350
tgtgatgaac acaatgtcat ggctcgttac ctccctgcca cagtggagt      400
tgctgtccac acattcaacc aacagagcaa ggactactat gcctacagac      450
tggggcacat cttgaattcc tggaaggagc aggtggagtc caagactgta      500
ttctcaatgg agctactgct ggggagaact aggtgtggga aatttgaaga      550
cgacattgac aactgccatt tccaagaaag cacagagctg aacaatactt      600
tcacctgctt cttcaccatc agcaccaggc cctggatgac tcagttcagc      650
ctcctgaaca agacctgctt ggagggattc cactgagtga aaccactca      700
caggcttgtc catgtgtctg tcccacattc cgtggacatc agcactactc      750
tcctgaggac tcttcagtgg ctgagcagct ttggacttgt ttgttatcct      800
attttgcatg tgtttgagat ctcatgacag tgttttagaa aatccacaca      850
tcttgagcct aatcatgtag ttagatcat taaacatcag cattttaaga      900
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      950
aaaaaaaaa a                                     961

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<210> SEQ ID NO 144

<211> LENGTH: 147

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 144

```

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

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Thr Cys Phe Phe Thr Ile Ser Thr Arg Pro Trp Met Thr Gln Phe
125 130 135

Ser Leu Leu Asn Lys Thr Cys Leu Glu Gly Phe His
140 145

<210> SEQ ID NO 145
<211> LENGTH: 1157
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 145

ctgtgcagct cgaggctcca gaggcacact ccagagagag ccaaggttct 50
gacgcgatga ggaagcacct gagctggtgg tggctggcca ctgtctgcat 100
gctgctcttc agccacctct ctgcggtcca gacgaggggc atcaagcaca 150
gaatcaagtg gaaccggaag gccctgcccc gcaactgccc gatcactgag 200
gcccagggtg ctgagaaccg cccgggagcc ttcataaagc aagggccgaa 250
gctcgacatt gacttcggag ccgagggcaa caggtactac gaggccaaact 300
actggcagtt ccccgatggc atccactaca acggctgctc tgaggctaata 350
gtgaccaagg aggcatttgt caccggctgc atcaatgcca cccaggcggc 400
gaaccagggg gagtccaga agccagacaa caagctccac cagcagggtg 450
tctggcggct ggtccaggag ctctgctccc tcaagcattg cgagttttgg 500
ttggagaggg gcgcaggact tcgggtcacc atgcaccagc cagtgtctct 550
ctgccttctg gctttgatct ggctcatggt gaaataagct tgccaggagg 600
ctggcagtag agagcgagc agcgagcaaa tcctggcaag tgaccagct 650
cttctccccc aaaccacgc gtgttctgaa ggtgccagg agcggcgatg 700
cactcgcact gcaaatgccg ctcccacgta tgcgccctgg tatgtgctg 750
cgttctgata gatgggggac tgtggcttct ccgtcactcc attctcagcc 800
cctagcagag cgtctggcac actagattag tagtaaatgc ttgatgagaa 850
gaacacatca ggcactgcgc cacctgcttc acagtacttc ccaacaactc 900
ttagaggtag gtgtattccc gttttacaga taaggaaact gagggccaga 950
gagctgaagt actgcaccca gcatcaccag ctagaaagtg gcagagccag 1000
gattcaaccc tggcttgtct aaccccaggt tttctgctct gtccaattcc 1050
agagctgtct ggtgatcact ttatgtctca cagggaccca catccaaaca 1100
tgtatctcta atgaaattgt gaaagctcca tgtttagaaa taaatgaaaa 1150
cacctga 1157

<210> SEQ ID NO 146
<211> LENGTH: 176
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 146

Met Arg Lys His Leu Ser Trp Trp Trp Leu Ala Thr Val Cys Met
1 5 10 15

Leu Leu Phe Ser His Leu Ser Ala Val Gln Thr Arg Gly Ile Lys
20 25 30

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

<210> SEQ ID NO 147
<211> LENGTH: 333
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 147

gccttggcct cccaaagggc tgggattata ggcgtgacca ccatgtctgg	50
tccagagtct catttcctga tgatttatag actcaaagaa aactcatgtt	100
cagaagctct cttctcttct ggctcctct ctgtcttctt tccctctttc	150
ttcttatttt aattagtagc atctactcag agtcatgcaa gctggaaatc	200
tttcattttg cttgtcagtg gggtaggtca ctgagtctta gtttttattt	250
tttgaaattt caactttcag attcaggggg tacatgtgaa ggtttgtttt	300
atgagtatat tgcgatgatc tgaggtttgg ggt	333

<210> SEQ ID NO 148
<211> LENGTH: 73
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 148

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

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<210> SEQ ID NO 149

<211> LENGTH: 1893

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 149

gtctccgcgt cacaggaact tcagcaccca cagggcggac agcgcctccc	50
tctacctgga gacttgactc ccgcgcgccc caaccctgct tatcccttga	100
ccgtcgagtg tcagagatcc tgcagccgcc cagtcccggc ccctctcccg	150
ccccacaccc accctcctgg ctcttcctgt ttttactcct ccttttcatt	200
cataacaaaa gctacagctc caggagccca gcgcgggct gtgacccaag	250
ccgagcgtgg aagaatgggg ttctcggga ccggcacttg gattctggtg	300
ttagtgtccc cgattcaagc ttccccaaa cctggaggaa gccaaagaaa	350
atctctacat aatagagaat taagtgcaga aagaccttg aatgaacaga	400
ttgctgaagc agaagaagac aagattaaaa aaacatatcc tccagaaaac	450
aagccaggtc agagcaacta ttcttttgtt gataacttga acctgctaaa	500
ggcaataaca gaaaaggaaa aaattgagaa agaaagacaa tctataagaa	550
gtccccact tgataataag ttgaatgttg aagatgttga ttcaaccaag	600
aatcgaaaac tgatcgatga ttatgactct actaagagtg gattggatca	650
taaatattcaa gatgatccag atggtcttca tcaactagac gggactcctt	700
taaccgctga agacattgtc cataaaatcg ctgccaggat ttatgaagaa	750
aatgacagag ccgtgtttga caagattgtt tctaaactac ttaatctcgg	800
ccttatcaca gaaagccaag cacatacact ggaagatgaa gtagcagagg	850
ttttacaaaa attaatctca aaggaagcca acaattatga ggaggatccc	900
aataagccca caagctggac tgagaatcag gctggaaaaa taccagagaa	950
agtactcca atggcagcaa ttcaagatgg tottgctaag ggagaaaacg	1000
atgaaacagt atctaacaca ttaaccttga caaatggctt ggaaaggaga	1050
actaaaacct acagtgaaga caactttgag gaactccaat atttccaaa	1100
tttctatgcg ctactgaaaa gtattgattc agaaaaagaa gcaaaagaga	1150
aagaaacact gattactatc atgaaaacac tgattgactt tgtgaagatg	1200
atggtgaaat atggaacaat atctccagaa gaaggtgttt cctaccttga	1250
aaacttggat gaaatgattg ctcttcagac caaaaacaag ctagaaaaaa	1300
atgctactga caatataagc aagcttttcc cagcaccatc agagaagagt	1350
catgaagaaa cagacagtac caaggaagaa gcagctaaga tggaaaagga	1400
atatggaagc ttgaaggatt ccacaaaaga tgataactcc aaccaggag	1450
gaaagacaga tgaacccaaa ggaaaaacag aagcctatctt ggaagccatc	1500
agaaaaata ttgaatggtt gaagaacat gacaaaaagg gaaataaaga	1550
agattatgac ctttcaaaga tgagagactt catcaataaa caagctgatg	1600
cttatgtgga gaaaggcatc cttgacaagg aagaagccga ggccatcaag	1650
cgcatttata gcagcctgta aaaatggcaa aagatccagg agtctttcaa	1700
ctgttttcga aaacataata tagcttaaaa cacttctaata tctgtgatta	1750

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aaattttttg acccaagggt tattagaaag tgctgaattt acagtagtta 1800
acctttttaca agtgggttaaa acatagcttt cttcccgtaa aaactatctg 1850
aaagtaaagt tgtatgtaag ctgaaaaaaa aaaaaaaaaa aaa 1893

<210> SEQ ID NO 150

<211> LENGTH: 468

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 150

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

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Thr Ile Met Lys Thr Leu Ile Asp Phe Val Lys Met Met Val Lys
305 310 315

Tyr Gly Thr Ile Ser Pro Glu Glu Gly Val Ser Tyr Leu Glu Asn
320 325 330

Leu Asp Glu Met Ile Ala Leu Gln Thr Lys Asn Lys Leu Glu Lys
335 340 345

Asn Ala Thr Asp Asn Ile Ser Lys Leu Phe Pro Ala Pro Ser Glu
350 355 360

Lys Ser His Glu Glu Thr Asp Ser Thr Lys Glu Glu Ala Ala Lys
365 370 375

Met Glu Lys Glu Tyr Gly Ser Leu Lys Asp Ser Thr Lys Asp Asp
380 385 390

Asn Ser Asn Pro Gly Gly Lys Thr Asp Glu Pro Lys Gly Lys Thr
395 400 405

Glu Ala Tyr Leu Glu Ala Ile Arg Lys Asn Ile Glu Trp Leu Lys
410 415 420

Lys His Asp Lys Lys Gly Asn Lys Glu Asp Tyr Asp Leu Ser Lys
425 430 435

Met Arg Asp Phe Ile Asn Lys Gln Ala Asp Ala Tyr Val Glu Lys
440 445 450

Gly Ile Leu Asp Lys Glu Glu Ala Glu Ala Ile Lys Arg Ile Tyr
455 460 465

Ser Ser Leu

<210> SEQ ID NO 151
<211> LENGTH: 2598
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 151

cggctcgagg ctcccgccag gagaaggaa cattctgagg ggagtctaca 50

ccctgtggag ctcaagatgg tcctgagtg ggcgctgtgc ttccgaatga 100

aggactcgcc attgaagggtg ctttatctgc ataataacca gcttctagct 150

ggagggctgc atgcagggaa ggtcattaaa ggtgaagaga tcagcgtggt 200

ccccaatcgg tggctggatg ccagcctgtc ccccgtcac tcgggtgtcc 250

agggtggaag ccagtcctg tcatgtgggg tggggcagga gccgactcta 300

acactagagc cagtgaacat catggagctc tatcttggtg ccaaggaatc 350

caagagcttc accttctacc ggcgggacat ggggctcacc tccagcttcg 400

agtcggctgc ctaccgggc tggttcctgt gcacgggtgcc tgaagccgat 450

cagcctgtca gactcaccca gcttcccag aatggtggct ggaatgcccc 500

catcacagac ttctacttcc agcagtgta ctagggcaac gtgcccccca 550

gaactccctg ggcagagcca gtcgggtga ggggtgagtg gaggagacc 600

atggcggaac atcactctct ctgctctcag gacccccacg tctgacttag 650

tgggcacctg accactttgt cttctggttc ccagtttgga taaattctga 700

gatttgagc tcagtccacg gtctccccc actggatggt gctactgctg 750

tggaaccttg taaaaacat gtggggtaaa ctgggaataa catgaaaaga 800

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tttctgtggg ggtgggggtgg gggagtggtg ggaatcattc ctgcttaatg	850
gtaactgaca agtgttaccc tgagccccgc aggccaaccc atccccagtt	900
gagccttata gggtcagtag ctctccacat gaagtcctgt cactcaccac	950
tgtgcaggag agggaggtgg tcatagagtc agggatctat ggcccttggc	1000
ccagccccac ccccttcctt ttaatcctgc cactgtcata tgctaccttt	1050
cctatctctt ccctcatcat ctgttggtgg gcatgaggag gtggtgatgt	1100
cagaagaaat ggctcgagct cagaagataa aagataagta gggtatgtgt	1150
atcctctttt aaaaacccaa gatacaatca aaatcccaga tgctgggtctc	1200
tattcccatg aaaaagtgtc catgacatat tgagaagacc tacttacaaa	1250
gtggcatata ttgcaattta ttttaattaa aagataccta tttatatatt	1300
tctttataga aaaaagtctg gaagagttaa cttcaattgt agcaatgtca	1350
gggtggtggc agtatagggt atttttcttt taattctgtt aatttatctg	1400
tatttcctaa tttttctaca atgaagatga attccttgta taaaaataag	1450
aaaagaaatt aatcttgagg taagcagagc agacatcatc tctgattgtc	1500
ctcagcctcc acttccccag agtaaattca aattgaatcg agctctgctg	1550
ctctggttgg ttgtagtagt gatcaggaaa cagatctcag caaagccact	1600
gaggaggagg ctgtgctgag ttgtgtggc tggaatctct gggttaaggaa	1650
cttaagaagc aaaaatcatc tggtaattct ttcctagaag gatcacagcc	1700
cctgggattc caaggcattg gatccagtct ctaagaaggc tgctgtactg	1750
gttgaattgt gtccccctca aattcacatc cttcttgga tctcagtctg	1800
tgagtttatt tggagataag gtctctgcag atgtagttag ttaagacaa	1850
gtcatgctgg atgaaggtag acctaaattc aatatgactg gtttccttgt	1900
atgaaaagga gaggacacag agacagagga gacgcgggga agactatgta	1950
aagatgaagg cagagatcgg agttttgcag ccacaagcta agaaacacca	2000
aggattgtgg caaccatcag aagcttgga gaggcaaaga agaattcttc	2050
cctagaggct ttagagggat aacggctctg ctgaaacctt aatctcagac	2100
ttccagcctc ctgaacgaag aaagaataaa tttcggctgt ttttaagccac	2150
caaggataat tggttacagc agctctagga aactaatata gctgctaaaa	2200
tgatccctgt ctctctgtgt ttacattctg tgtgtgtccc ctcccacaat	2250
gtaccaaagt tgtctttgtg accaatagaa tatggcagaa gtgatggcat	2300
gccacttcca agattaggtt ataaaagaca ctgcagcttc tacttgagcc	2350
ctctctctct gccaccacc gcccacaatc tatcttggt cactcgctct	2400
gggggaagct agctgccatg ctatgagcag gcctataaag agacttacgt	2450
ggtaaaaaat gaagtctcct gccacagcc acattagtga acctagaagc	2500
agagactctg tgagataatc gatgtttgtt gttttaagtt gctcagtttt	2550
ggtctaactt gttatgcagc aatagataaa taatatgcag agaaagag	2598

<210> SEQ ID NO 152

<211> LENGTH: 155

<212> TYPE: PRT

-continued

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 152

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

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

Leu His Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val
35 40 45

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

Val Gln Gly Gly Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu
65 70 75

Pro Thr Leu Thr Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu
80 85 90

Gly Ala Lys Glu Ser Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met
95 100 105

Gly Leu Thr Ser Ser Phe Glu Ser Ala Ala Tyr Pro Gly Trp Phe
110 115 120

Leu Cys Thr Val Pro Glu Ala Asp Gln Pro Val Arg Leu Thr Gln
125 130 135

Leu Pro Glu Asn Gly Gly Trp Asn Ala Pro Ile Thr Asp Phe Tyr
140 145 150

Phe Gln Gln Cys Asp
155

<210> SEQ ID NO 153
<211> LENGTH: 1152
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 153

cttcagaaca ggttctcctt cccagctcac cagttgctcg agttagaatt 50

gtctgcaatg gccgccctgc agaaatctgt gagctctttc cttatgggga 100

ccctggccac cagctgcctc cttctcttgg ccctcttggt acagggagga 150

gcagctgcmc ccatcagctc cactgcagg cttgacaagt ccaacttcca 200

gcagccctat atcaccaacc gcaccttcat gctggctaag gaggctagct 250

tggtgataa caacacagac gttcgtctca ttggggagaa actgttccac 300

ggagtcagta tgagtgagcg ctgctatctg atgaagcagg tgctgaactt 350

caccttgaa gaagtgtgt tccctcaatc tgataggttc cagccttata 400

tgaggagggt ggtgcccttc ctggccaggc tcagcaacag gctaagcaca 450

tgtcatattg aaggtgatga cctgcatatc cagaggaatg tgcaaaagct 500

gaagacaca gtgaaaaagc ttggagagag tggagagatc aaagcaattg 550

gagaactgga tttgctgttt atgtctctga gaaatgcctg catttgacca 600

gagcaaaagt gaaaaatgaa taactaaccc ctttccctg ctagaaataa 650

caattagatg ccccaaagcg atttttttta accaaaagga agatgggaag 700

ccaaactcca tcatgatggg tggattccaa atgaaccctt gcgttagtta 750

caaaggaaac caatgccact tttgtttata agaccagaag gtagactttc 800

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```
taagcataga tatttattga taacatttca ttgtaactgg tgttctatac      850
acagaaaaca atttattttt taaataattg tctttttcca taaaaaagat      900
tactttccat tcctttaggg gaaaaaaccc ctaaatagct tcatgtttcc      950
ataatcagta ctttatattt ataaatgtat ttattattat tataagactg     1000
cattttattt atatcatttt attaatatgg atttatttat agaaacatca     1050
ttcgatattg ctacttgagt gtaaggctaa tattgatatt tatgacaata     1100
attatagagc tataacatgt ttatttgacc tcaataaaca cttggatatc     1150
cc                                                           1152
```

<210> SEQ ID NO 154
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 154

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

<210> SEQ ID NO 155
<211> LENGTH: 1320
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 155

```
ggcttgctga aaataaaatc aggactccta acctgctcca gtcagcctgc      50
ttccacgagg cctgtcagtc agtgcccagc ttgtgactga gtgtgcagtg     100
cccagcatgt accaggtcag tgcagagggc tgcctgaggg ctgtgctgag     150
agggagagga gcagagatgc tgctgagggg ggagggaggg caagctgccca     200
```

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ggtttggggc tgggggccaa gtggagtgaag aaactgggat ccaggggga 250
gggtgcagat gaggagcga ccagattag gtgaggacag ttctctcatt 300
agccttttcc tacaggtggt tgcattcttg gcaatggta tgggaacca 350
cacctacagc cactggccca gctgctgccc cagcaaaggg caggacacct 400
ctgaggagct gctgaggtgg agcactgtgc ctgtgcctcc cctagagcct 450
gctaggccca accgccccc agagtccctg agggccagtg aagatggacc 500
cctcaacagc agggccatct ccccctggag atatgagttg gacagagact 550
tgaaccggct ccccaggac ctgtaccacg ccggttcct gtgccgcac 600
tgctgcagcc tacagacagg ctccacatg gacccccggg gcaactcgga 650
gctgctctac cacaaccaga ctgtcttcta caggcggcca tgccatggcg 700
agaagggcac ccacaaggc tactgcctgg agcgcaggct gtaccgtgtt 750
tccttagctt gtgtgtgtgt gcggccccgt gtgatgggct agccggacct 800
gctggaggct ggtccctttt tgggaaacct ggagccaggt gtacaaccac 850
ttgccatgaa gggccaggat gccagatgc ttggcccctg tgaagtgtg 900
tctggagcag caggatcccg ggacaggatg gggggctttg gggaaaacct 950
gcactttctg acattttgaa aagagcagct gctgcttagg gccgccggaa 1000
gctggtgtcc tgtcattttc tctcaggaaa ggttttcaa gttctgccca 1050
tttctggagg ccaccactcc tgtctcttcc tcttttccca tcccctgcta 1100
ccctggccca gcacaggcac tttctagata tttccccctt gctggagaag 1150
aaagagcccc tggttttatt tgtttgttta ctcactcctc agtgagcctc 1200
tactttgggt gcattctagt gtagttacta gtcttttgac atggatgatt 1250
ctgaggagga agctgttatt gaatgtatag agatttatcc aaataaatat 1300
ctttatttaa aatgaaaaa 1320

<210> SEQ ID NO 156
<211> LENGTH: 177
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 156

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

-continued

Tyr	His	Ala	Arg	Cys	Leu	Cys	Pro	His	Cys	Val	Ser	Leu	Gln	Thr
				110					115					120
Gly	Ser	His	Met	Asp	Pro	Arg	Gly	Asn	Ser	Glu	Leu	Leu	Tyr	His
				125					130					135
Asn	Gln	Thr	Val	Phe	Tyr	Arg	Arg	Pro	Cys	His	Gly	Glu	Lys	Gly
				140					145					150
Thr	His	Lys	Gly	Tyr	Cys	Leu	Glu	Arg	Arg	Leu	Tyr	Arg	Val	Ser
				155					160					165
Leu	Ala	Cys	Val	Cys	Val	Arg	Pro	Arg	Val	Met	Gly			
				170					175					

<210> SEQ ID NO 157
<211> LENGTH: 1515
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 157

ccggcgatgt cgctcgtgct gctaagcctg gccgcgctgt gcaggagcgc	50
cgtaccccga gagccgaccg ttcaatgtgg ctctgaaact gggccatctc	100
cagagtggat gctacaacat gatctaattcc ccggagactt gagggacctc	150
cgagtagaac ctgttacaac tagtgttgca acaggggact attcaatttt	200
gatgaatgta agctgggtac tccgggcaga tgccagcatc cgcttggtga	250
aggccaccaa gatttgtgtg acgggcaaaa gcaacttcca gtcctacagc	300
tgtgtgaggt gcaattacac agaggccttc cagactcaga ccagaccctc	350
tggtggtaaa tggacatttt cctacatcgg ctccctgta gagctgaaca	400
cagtctattt cattggggcc cataatatcc ctaatgcaa tatgaatgaa	450
gatggccctt ccatgtctgt gaatttcacc tcaccaggct gcctagacca	500
cataatgaaa tataaaaaaa agtgtgtcaa ggccggaagc ctgtgggatc	550
cgaacatcac tgcttgtaag aagaatgagg agacagtaga agtgaacttc	600
acaaccactc ccctgggaaa cagatacatg gctcttatcc aacacagcac	650
tatcatcggg ttttctcagg tgtttgagcc acaccagaag aaacaaacgc	700
gagcttcagt ggtgattcca gtgactgggg atagtgaagg tgctacggtg	750
cagctgactc catattttcc tacttggtgc agcgactgca tccgacataa	800
aggaacagtt gtgctctgcc cacaaacagg cgtccctttc cctctggata	850
acaacaaaaa caagccggga ggctggctgc ctctcctcct gctgtctctg	900
ctggtggcca catgggtgct ggtggcagg atctatctaa tgtggaggca	950
cgaaaggatc aagaagactt ccttttctac caccacacta ctgccccca	1000
taaaggttct tgtggtttac ccatctgaaa tatgtttcca tcacacaatt	1050
tgttacttca ctgaatttct tcaaaaccat tgcagaagtg aggtcatcct	1100
tgaaaagtgg cagaaaaaga aaatagcaga gatgggtcca gtgcagtggc	1150
ttgccactca aaagaaggca gcagacaaag tcgtcttcct tctttccaat	1200
gacgtcaaca gtgtgtgcga tggtagctgt ggcaagagcg agggcagtcc	1250
cagtgagaac tctcaagacc tcttccccct tgcctttaac cttttctgca	1300
gtgatctaa aagccagatt catctgcaca aatacgtggt ggtctacttt	1350

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agagagattg atacaaaaga cgattacaat gctctcagtg tctgccccaa 1400
gtaccacctc atgaaggatg ccactgcttt ctgtgcagaa cttctccatg 1450
tcaagcagca ggtgtcagca ggaaaaagat cacaagcctg ccacgatggc 1500
tgctgctcct tgtag 1515

<210> SEQ ID NO 158
<211> LENGTH: 502
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 158

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

-continued

Ala Thr Trp Val Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His
305 310 315

Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro
320 325 330

Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile Cys Phe His
335 340 345

His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His Cys Arg
350 355 360

Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala Glu
365 370 375

Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp
380 385 390

Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp
395 400 405

Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln
410 415 420

Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg
425 430 435

Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu
440 445 450

Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys
455 460 465

Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
470 475 480

His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys
485 490 495

His Asp Gly Cys Cys Ser Leu
500

<210> SEQ ID NO 159
<211> LENGTH: 535
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 159

agccaccagc gcaacatgac agtgaagacc ctgcatggcc cagccatggt	50
caagtacttg ctgctgtcga tattggggct tgcctttctg agtgaggcgg	100
cagctcggaa aatccccaaa gtaggacata cttttttcca aaagcctgag	150
agttgcccg cgtgtgccagg aggtagtatg aagcttgaca ttggcatcat	200
caatgaaaac cagcgcgttt ccatgtcacg taacatcgag agccgctcca	250
cctccccctg gaattacact gtcacttggg accccaaccg gtaccctctg	300
gaagttgtac aggcccagtg taggaacttg ggctgcatca atgctcaagg	350
aaaggaagac atctccatga attccgttcc catccagcaa gagaccctgg	400
tcgtccggag gaagcaccaa ggctgctctg tttctttcca gttggagaag	450
gtgctgtgta ctgttggtg cactgcgtc acccctgtca tccaccatgt	500
gcagtaagag gtgcatatcc actcagctga agaag	535

<210> SEQ ID NO 160
<211> LENGTH: 163

-continued

<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 160

Met Thr Val Lys Thr Leu His Gly Pro Ala Met Val Lys Tyr Leu
1 5 10 15

Leu Leu Ser Ile Leu Gly Leu Ala Phe Leu Ser Glu Ala Ala Ala
20 25 30

Arg Lys Ile Pro Lys Val Gly His Thr Phe Phe Gln Lys Pro Glu
35 40 45

Ser Cys Pro Pro Val Pro Gly Gly Ser Met Lys Leu Asp Ile Gly
50 55 60

Ile Ile Asn Glu Asn Gln Arg Val Ser Met Ser Arg Asn Ile Glu
65 70 75

Ser Arg Ser Thr Ser Pro Trp Asn Tyr Thr Val Thr Trp Asp Pro
80 85 90

Asn Arg Tyr Pro Ser Glu Val Val Gln Ala Gln Cys Arg Asn Leu
95 100 105

Gly Cys Ile Asn Ala Gln Gly Lys Glu Asp Ile Ser Met Asn Ser
110 115 120

Val Pro Ile Gln Gln Glu Thr Leu Val Val Arg Arg Lys His Gln
125 130 135

Gly Cys Ser Val Ser Phe Gln Leu Glu Lys Val Leu Val Thr Val
140 145 150

Gly Cys Thr Cys Val Thr Pro Val Ile His His Val Gln
155 160

<210> SEQ ID NO 161
<211> LENGTH: 2380
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 161

acactggcca acaaaaaacg aaagcactcc gtgctggaag taggaggaga 50

gtcaggactc ccaggacaga gagtgcacaa actaccacgc acagccccct 100

ccgccccctc tggaggctga agagggatcc cagccccctgc caccacaga 150

cacgggctga ctgggggtgtc tgccccctt gggggggggc agcacagggc 200

ctcaggcctg ggtgccacct ggcacctaga agatgcctgt gccctggttc 250

ttgctgtcct tggcactggg ccgaagccca gtggtccttt ctctggagag 300

gcttgtgggg cctcaggacg ctaccactg ctctccgggc ctctcctgcc 350

gcctctggga cagtgcata ctctgcctgc ctggggacat cgtgcctgct 400

ccgggccccg tgctggcgcc tacgcacctg cagacagagc tgggtctgag 450

gtgccagaag gagaccgact gtgacctctg tctgcgtgtg gctgtccact 500

tgcccggtga tgggcactgg gaagagcctg aagatgagga aaagtttgga 550

ggagcagctg actcaggggt ggaggagcct aggaatgcct ctctccaggc 600

ccaagtcgtg ctctccttcc aggcctaccc tactgcccgc tgcgtcctgc 650

tggaagtgtg agtgcctgct gcccttgtgc agtttggtca gtctgtgggc 700

tctgtggtat atgactgctt cgaggctgcc ctagggagtg aggtacgaat 750

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ctggtcctat actcagccca ggtacgagaa ggaactcaac cacacacagc	800
agctgcctgc cctgccctgg ctcaacgtgt cagcagatgg tgacaacgtg	850
catctggttc tgaatgtctc tgaggagcag cacttcggcc tctccctgta	900
ctggaatcag gtccaggggc ccccaaaacc ccggtggcac aaaaacctga	950
ctggaccgca gatcattacc ttgaaccaca cagacctggt tccctgcctc	1000
tgtattcagg tgtggcctct ggaacctgac tccgttagga cgaacatctg	1050
ccccttcagg gaggacccc gcgcacacca gaacctctgg caagccgccc	1100
gactgcgact gctgacctg cagagctggc tgctggacgc accgtgctcg	1150
ctgcccgcag aagcggcact gtgctggcgg gctccgggtg gggacctctg	1200
ccagccactg gtcccacgc tttcctggga gaacgtcact gtggacaagg	1250
ttctcgagtt ccattgctg aaaggccacc ctaacctctg tgttcagggtg	1300
aacagctcgg agaagctgca gctgcaggag tgcttggtgg ctgactccct	1350
ggggcctctc aaagacgatg tgctactgtt ggagacacga ggccccagg	1400
acaacagatc cctctgtgcc ttggaaccca gtggtgtac ttactaccc	1450
agcaaagcct ccacgagggc agctcgcctt ggagagtact tactacaaga	1500
cctgcagtcg ggccagtgtc tcgagctatg ggacgatgac ttgggagcgc	1550
tatgggcctg ccccatggac aaatacatcc acaagcgtg ggccctcgtg	1600
tggtgggcct gcctactctt tgccgctcgg ctttccctca tcctccttct	1650
caaaaaggat cacgcgaaag ggtggctgag gctcttgaaa caggacgtcc	1700
gtcgcggggc ggccgccagg ggccgcgcgg ctctgctcct ctactcagcc	1750
gatgactcgg gtttcgagcg cctgggtggc gccctggcgt cggccctgtg	1800
ccagctgcog ctgcgcgtgg ccgtagacct gtggagccgt cgtgaactga	1850
gcgcgcaggg gcccggtggt tggtttcacg cgcagcggcg ccagacctg	1900
caggaggggc gcgtggtggt cttgctcttc tctcccggtg cggtggcgct	1950
gtgcagcgag tggctacagg atggggtgtc cgggcccggg gcgcacggcc	2000
cgcacgacgc cttccgcgcc tcgctcagct gcgtgctgcc cgacttcttg	2050
caggggccgg cgcccggcag ctacgtgggg gcctgcttcg acaggctgct	2100
ccacccggag gccgtacccg cccttttccg caccgtgccc gtcttcacac	2150
tgccctccca actgccagac ttcctggggg ccctgcagca gcctcgcgcc	2200
ccgcgttccg ggcggtcca agagagagcg gagcaagtgt cccgggccct	2250
tcagccagcc ctggatagct acttccatcc cccggggact cccgcgccgg	2300
gacgcggggg gggaccaggg gcgggacctg gggcggggga cgggacttaa	2350
ataaaggcag acgctgtttt tctaaaaaaa	2380

<210> SEQ ID NO 162

<211> LENGTH: 705

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 162

Met	Pro	Val	Pro	Trp	Phe	Leu	Leu	Ser	Leu	Ala	Leu	Gly	Arg	Ser
1						5				10				15

-continued

Pro	Val	Val	Leu	Ser	Leu	Glu	Arg	Leu	Val	Gly	Pro	Gln	Asp	Ala	20	25	30
Thr	His	Cys	Ser	Pro	Gly	Leu	Ser	Cys	Arg	Leu	Trp	Asp	Ser	Asp	35	40	45
Ile	Leu	Cys	Leu	Pro	Gly	Asp	Ile	Val	Pro	Ala	Pro	Gly	Pro	Val	50	55	60
Leu	Ala	Pro	Thr	His	Leu	Gln	Thr	Glu	Leu	Val	Leu	Arg	Cys	Gln	65	70	75
Lys	Glu	Thr	Asp	Cys	Asp	Leu	Cys	Leu	Arg	Val	Ala	Val	His	Leu	80	85	90
Ala	Val	His	Gly	His	Trp	Glu	Glu	Pro	Glu	Asp	Glu	Glu	Lys	Phe	95	100	105
Gly	Gly	Ala	Ala	Asp	Ser	Gly	Val	Glu	Glu	Pro	Arg	Asn	Ala	Ser	110	115	120
Leu	Gln	Ala	Gln	Val	Val	Leu	Ser	Phe	Gln	Ala	Tyr	Pro	Thr	Ala	125	130	135
Arg	Cys	Val	Leu	Leu	Glu	Val	Gln	Val	Pro	Ala	Ala	Leu	Val	Gln	140	145	150
Phe	Gly	Gln	Ser	Val	Gly	Ser	Val	Val	Tyr	Asp	Cys	Phe	Glu	Ala	155	160	165
Ala	Leu	Gly	Ser	Glu	Val	Arg	Ile	Trp	Ser	Tyr	Thr	Gln	Pro	Arg	170	175	180
Tyr	Glu	Lys	Glu	Leu	Asn	His	Thr	Gln	Gln	Leu	Pro	Ala	Leu	Pro	185	190	195
Trp	Leu	Asn	Val	Ser	Ala	Asp	Gly	Asp	Asn	Val	His	Leu	Val	Leu	200	205	210
Asn	Val	Ser	Glu	Glu	Gln	His	Phe	Gly	Leu	Ser	Leu	Tyr	Trp	Asn	215	220	225
Gln	Val	Gln	Gly	Pro	Pro	Lys	Pro	Arg	Trp	His	Lys	Asn	Leu	Thr	230	235	240
Gly	Pro	Gln	Ile	Ile	Thr	Leu	Asn	His	Thr	Asp	Leu	Val	Pro	Cys	245	250	255
Leu	Cys	Ile	Gln	Val	Trp	Pro	Leu	Glu	Pro	Asp	Ser	Val	Arg	Thr	260	265	270
Asn	Ile	Cys	Pro	Phe	Arg	Glu	Asp	Pro	Arg	Ala	His	Gln	Asn	Leu	275	280	285
Trp	Gln	Ala	Ala	Arg	Leu	Arg	Leu	Leu	Thr	Leu	Gln	Ser	Trp	Leu	290	295	300
Leu	Asp	Ala	Pro	Cys	Ser	Leu	Pro	Ala	Glu	Ala	Ala	Leu	Cys	Trp	305	310	315
Arg	Ala	Pro	Gly	Gly	Asp	Pro	Cys	Gln	Pro	Leu	Val	Pro	Pro	Leu	320	325	330
Ser	Trp	Glu	Asn	Val	Thr	Val	Asp	Lys	Val	Leu	Glu	Phe	Pro	Leu	335	340	345
Leu	Lys	Gly	His	Pro	Asn	Leu	Cys	Val	Gln	Val	Asn	Ser	Ser	Glu	350	355	360
Lys	Leu	Gln	Leu	Gln	Glu	Cys	Leu	Trp	Ala	Asp	Ser	Leu	Gly	Pro	365	370	375
Leu	Lys	Asp	Asp	Val	Leu	Leu	Leu	Glu	Thr	Arg	Gly	Pro	Gln	Asp	380	385	390

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Asn	Arg	Ser	Leu	Cys	Ala	Leu	Glu	Pro	Ser	Gly	Cys	Thr	Ser	Leu	
			395						400					405	
Pro	Ser	Lys	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	Gly	Glu	Tyr	Leu	
			410						415					420	
Leu	Gln	Asp	Leu	Gln	Ser	Gly	Gln	Cys	Leu	Gln	Leu	Trp	Asp	Asp	
			425						430					435	
Asp	Leu	Gly	Ala	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	Tyr	Ile	His	
			440						445					450	
Lys	Arg	Trp	Ala	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Phe	Ala	Ala	
			455						460					465	
Ala	Leu	Ser	Leu	Ile	Leu	Leu	Leu	Lys	Lys	Asp	His	Ala	Lys	Gly	
			470						475					480	
Trp	Leu	Arg	Leu	Leu	Lys	Gln	Asp	Val	Arg	Ser	Gly	Ala	Ala	Ala	
			485						490					495	
Arg	Gly	Arg	Ala	Ala	Leu	Leu	Leu	Tyr	Ser	Ala	Asp	Asp	Ser	Gly	
			500						505					510	
Phe	Glu	Arg	Leu	Val	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Cys	Gln	Leu	
			515						520					525	
Pro	Leu	Arg	Val	Ala	Val	Asp	Leu	Trp	Ser	Arg	Arg	Glu	Leu	Ser	
			530						535					540	
Ala	Gln	Gly	Pro	Val	Ala	Trp	Phe	His	Ala	Gln	Arg	Arg	Gln	Thr	
			545						550					555	
Leu	Gln	Glu	Gly	Gly	Val	Val	Val	Leu	Leu	Phe	Ser	Pro	Gly	Ala	
			560						565					570	
Val	Ala	Leu	Cys	Ser	Glu	Trp	Leu	Gln	Asp	Gly	Val	Ser	Gly	Pro	
			575						580					585	
Gly	Ala	His	Gly	Pro	His	Asp	Ala	Phe	Arg	Ala	Ser	Leu	Ser	Cys	
			590						595					600	
Val	Leu	Pro	Asp	Phe	Leu	Gln	Gly	Arg	Ala	Pro	Gly	Ser	Tyr	Val	
			605						610					615	
Gly	Ala	Cys	Phe	Asp	Arg	Leu	Leu	His	Pro	Asp	Ala	Val	Pro	Ala	
			620						625					630	
Leu	Phe	Arg	Thr	Val	Pro	Val	Phe	Thr	Leu	Pro	Ser	Gln	Leu	Pro	
			635						640					645	
Asp	Phe	Leu	Gly	Ala	Leu	Gln	Gln	Pro	Arg	Ala	Pro	Arg	Ser	Gly	
			650						655					660	
Arg	Leu	Gln	Glu	Arg	Ala	Glu	Gln	Val	Ser	Arg	Ala	Leu	Gln	Pro	
			665						670					675	
Ala	Leu	Asp	Ser	Tyr	Phe	His	Pro	Pro	Gly	Thr	Pro	Ala	Pro	Gly	
			680						685					690	
Arg	Gly	Val	Gly	Pro	Gly	Ala	Gly	Pro	Gly	Ala	Gly	Asp	Gly	Thr	
			695						700					705	

<210> SEQ ID NO 163
<211> LENGTH: 2478
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 163

gtcagtgcgg	gaggccggtc	agccaccaag	atgactgaca	ggttcagctc	50
tctgcagcac	actaccctca	agccacctga	tgtgacctgt	atctccaaag	100
tgagatcgat	tcagatgatt	gttcaccta	ccccacgcc	aatccgtgca	150

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ggcgaaggcc accggctaac cctggaagac atcttccatg acctgttcta	200
ccacttagag ctccagggtca accgcaccta ccaaatagcac cttggaggga	250
agcagagaga atatgagttc ttcggcctga cccctgacac agagtctcct	300
ggcaccatca tgatttgcgt tcccacctgg gccaaaggaga gtgcccccta	350
catgtgccga gtgaagacac tgccagaccg gacatggacc tactccttct	400
cggagcctt cctgttctcc atgggcttcc tcgtcgcagt actctgctac	450
ctgagctaca gatatgtcac caagccgcct gcacctccca actccctgaa	500
cgtccacgca gtcttgactt tccagccgct gcgttctatc caggagcacg	550
tctgatccc tgtctttgac ctccagcgcc ccagcagtct ggcccagcct	600
gtccagtact ccagatcag ggtgtctgga cccagggagc ccgcaggagc	650
tccacagcgg catagcctgt ccgagatcac ctacttaggg cagccagaca	700
tctccatcct ccagccctcc aacgtgccac ctcccagat cctctcccca	750
ctgtcctatg ccccaaagc tgcccctgag gtcgggcccc catcctatgc	800
acctcaggtg acccccgaag ctcaattccc attctacgcc ccacaggcca	850
tctctaaggt ccagccttcc tcctatgccc ctcaagccac tccggacagc	900
tggcctccct cctatggggt atgcatggaa ggttctggca aagactcccc	950
cactgggaca ctttctagtc ctaaacacct taggcctaaa ggtcagcttc	1000
agaaagagcc accagctgga agctgcatgt taggtggcct ttctctgcag	1050
gaggtagcct ccttggtat ggaggaatcc caagaagcaa aatcattgca	1100
ccagcccctg gggatttgca cagacagaac atctgaccca aatgtgctac	1150
acagtgggga ggaagggaca ccacagtacc taaagggccca gctccccctc	1200
ctctcctcag tccagatcga gggccacccc atgtccctcc ctttgcaacc	1250
tccttcctgt ccatgttccc cctcggacca aggtccaagt ccctggggcc	1300
tgctggagtc ccttgtgtgt cccaaggatg aagccaagag cccagcccct	1350
gagacctcag acctggagca gccacagaaa ctggattctc ttttcagagg	1400
cctggccctg actgtgcagt gggagtcctg aggggaatgg gaaaggcttg	1450
gtgcttcctc cctgtcccta cccagtgtca catccttggc tgtcaatccc	1500
atgcctgccc atgccacaca ctctgcgac tgccctcaga cgggtgccct	1550
tgagagaagc agagggagtg gcatgcaggg cccctgccat ggggtgcgctc	1600
ctcaccggaa caaagcagca tgataaggac tgcagcgggg gagctctggg	1650
gagcagcttg tgtagacaag cgcgtgctcg ctgagccctg caaggcagaa	1700
atgacagtgc aaggaggaaa tgcagggaaa ctcccagggt ccagagcccc	1750
acctcctaac accatggatt caaagtgtc agggaatttg cctctccttg	1800
ccccattcct ggccagtttc acaatctagc tcgacagagc atgaggcccc	1850
tgccctctct gtcattgttc aaagtggtga agagagcctg gaaaagaacc	1900
aggcctggaa aagaaccaga aggaggtctg gcagaaccag aacaacctgc	1950
acttctgcca aggccagggc cagcaggacg gcaggactct agggaggggt	2000
gtggcctgca gctcattccc agccagggca actgcctgac gttgcacgat	2050

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ttcagcttca ttctctgat agaacaaagc gaaatgcagg tccaccaggg      2100
agggagacac acaagccttt tctgcaggca ggagtttcag accctatcct      2150
gagaatgggg tttgaaagga aggtgagggc tgtggcccct ggacgggtac      2200
aataacacac tgtactgatg tcacaacttt gcaagctctg ccttgggttc      2250
agcccatctg ggctcaaatt ccagcctcac cactcacaag ctgtgtgact      2300
tcaaacaaat gaaatcagtg ccagaaacct cggtttcctc atctgtaatg      2350
tggggatcat aacacctacc tcatggagtt gtggtgaaga tgaatgaag      2400
tcatgtcttt aaagtgccta atagtgcctg gtacatgggc agtgcccaat      2450
aaacggtagc tatttaaaaa aaaaaaaaa      2478

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<210> SEQ ID NO 164

<211> LENGTH: 574

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 164

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

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Phe	Leu	Val	Ala	Val	Leu	Cys	Tyr	Leu	Ser	Tyr	Arg	Tyr	Val	Thr	245	250	255
Lys	Pro	Pro	Ala	Pro	Pro	Asn	Ser	Leu	Asn	Val	Gln	Arg	Val	Leu	260	265	270
Thr	Phe	Gln	Pro	Leu	Arg	Phe	Ile	Gln	Glu	His	Val	Leu	Ile	Pro	275	280	285
Val	Phe	Asp	Leu	Ser	Gly	Pro	Ser	Ser	Leu	Ala	Gln	Pro	Val	Gln	290	295	300
Tyr	Ser	Gln	Ile	Arg	Val	Ser	Gly	Pro	Arg	Glu	Pro	Ala	Gly	Ala	305	310	315
Pro	Gln	Arg	His	Ser	Leu	Ser	Glu	Ile	Thr	Tyr	Leu	Gly	Gln	Pro	320	325	330
Asp	Ile	Ser	Ile	Leu	Gln	Pro	Ser	Asn	Val	Pro	Pro	Pro	Gln	Ile	335	340	345
Leu	Ser	Pro	Leu	Ser	Tyr	Ala	Pro	Asn	Ala	Ala	Pro	Glu	Val	Gly	350	355	360
Pro	Pro	Ser	Tyr	Ala	Pro	Gln	Val	Thr	Pro	Glu	Ala	Gln	Phe	Pro	365	370	375
Phe	Tyr	Ala	Pro	Gln	Ala	Ile	Ser	Lys	Val	Gln	Pro	Ser	Ser	Tyr	380	385	390
Ala	Pro	Gln	Ala	Thr	Pro	Asp	Ser	Trp	Pro	Pro	Ser	Tyr	Gly	Val	395	400	405
Cys	Met	Glu	Gly	Ser	Gly	Lys	Asp	Ser	Pro	Thr	Gly	Thr	Leu	Ser	410	415	420
Ser	Pro	Lys	His	Leu	Arg	Pro	Lys	Gly	Gln	Leu	Gln	Lys	Glu	Pro	425	430	435
Pro	Ala	Gly	Ser	Cys	Met	Leu	Gly	Gly	Leu	Ser	Leu	Gln	Glu	Val	440	445	450
Thr	Ser	Leu	Ala	Met	Glu	Glu	Ser	Gln	Glu	Ala	Lys	Ser	Leu	His	455	460	465
Gln	Pro	Leu	Gly	Ile	Cys	Thr	Asp	Arg	Thr	Ser	Asp	Pro	Asn	Val	470	475	480
Leu	His	Ser	Gly	Glu	Glu	Gly	Thr	Pro	Gln	Tyr	Leu	Lys	Gly	Gln	485	490	495
Leu	Pro	Leu	Leu	Ser	Ser	Val	Gln	Ile	Glu	Gly	His	Pro	Met	Ser	500	505	510
Leu	Pro	Leu	Gln	Pro	Pro	Ser	Gly	Pro	Cys	Ser	Pro	Ser	Asp	Gln	515	520	525
Gly	Pro	Ser	Pro	Trp	Gly	Leu	Leu	Glu	Ser	Leu	Val	Cys	Pro	Lys	530	535	540
Asp	Glu	Ala	Lys	Ser	Pro	Ala	Pro	Glu	Thr	Ser	Asp	Leu	Glu	Gln	545	550	555
Pro	Thr	Glu	Leu	Asp	Ser	Leu	Phe	Arg	Gly	Leu	Ala	Leu	Thr	Val	560	565	570
Gln	Trp	Glu	Ser														

<210> SEQ ID NO 165

<211> LENGTH: 1060

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 165

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tggcctactg gaaaaaaaaa aaaaaaaaaa aaaagtcacc cgggcccgcg	50
gtggccacaa catggctgcg gcgccggggc tgctcttctg gctgttcgtg	100
ctggggggcg tctggtgggt cccgggccag tcggatctca gccacggacg	150
gcgttttctg gacctcaaag tgtgcgggga cgaagagtgc agcatgttaa	200
tgtaccgtgg gaaagctctt gaagacttca cgggccctga ttgtcgtttt	250
gtgaatttta aaaaaggtga cgatgtatat gtctactaca aactggcagg	300
gggatccctt gaactttggg ctggaagtgt tgaacacagt tttggatatt	350
ttccaaaaga tttgatcaag gtacttcata aatacacgga agaagagcta	400
catattccag cagatgagac agactttgtc tgctttgaag gaggaagaga	450
tgattttaat agttataatg tagaagagct tttaggatct ttggaactgg	500
aggactctgt acctgaagag tcgaagaaa cgaagaagt ttctcagcac	550
agagagaaat ctctgagga gtctcggggg cgtgaacttg accctgtgcc	600
tgagcccag gcattcagag ctgattcaga ggatggagaa ggtgctttct	650
cagagagcac cgaggggctg cagggacagc cctcagctca ggagagccac	700
cctcacacca gcggtcctgc ggctaacgct cagggagtgc agtcttcgtt	750
ggacactttt gaagaaattc tgcacgataa attgaaagtg ccgggaagcg	800
aaagcagaac tggcaatagt tctcctgcct cggtggagcg ggagaagaca	850
gatgcctaca aagtcctgaa aacagaaatg agtcagagag gaagtggaca	900
gtgcgttatt cattacagca aaggatttcg ttggcatcaa aatctaagtt	950
tgttttacaa agattgtttt tagtactaag ctgccttggc agtttgcat	1000
tttgagccaa acaaaaatat attattttcc cttctaagta aaaaaaaaaa	1050
aaaaaaaaaa	1060

<210> SEQ ID NO 166
<211> LENGTH: 303
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 166

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

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Asp	Phe	Val	Cys	Phe	Glu	Gly	Gly	Arg	Asp	Asp	Phe	Asn	Ser	Tyr
125									130					135
Asn	Val	Glu	Glu	Leu	Leu	Gly	Ser	Leu	Glu	Leu	Glu	Asp	Ser	Val
140									145					150
Pro	Glu	Glu	Ser	Lys	Lys	Ala	Glu	Glu	Val	Ser	Gln	His	Arg	Glu
155									160					165
Lys	Ser	Pro	Glu	Glu	Ser	Arg	Gly	Arg	Glu	Leu	Asp	Pro	Val	Pro
170									175					180
Glu	Pro	Glu	Ala	Phe	Arg	Ala	Asp	Ser	Glu	Asp	Gly	Glu	Gly	Ala
185									190					195
Phe	Ser	Glu	Ser	Thr	Glu	Gly	Leu	Gln	Gly	Gln	Pro	Ser	Ala	Gln
200									205					210
Glu	Ser	His	Pro	His	Thr	Ser	Gly	Pro	Ala	Ala	Asn	Ala	Gln	Gly
215									220					225
Val	Gln	Ser	Ser	Leu	Asp	Thr	Phe	Glu	Glu	Ile	Leu	His	Asp	Lys
230									235					240
Leu	Lys	Val	Pro	Gly	Ser	Glu	Ser	Arg	Thr	Gly	Asn	Ser	Ser	Pro
245									250					255
Ala	Ser	Val	Glu	Arg	Glu	Lys	Thr	Asp	Ala	Tyr	Lys	Val	Leu	Lys
260									265					270
Thr	Glu	Met	Ser	Gln	Arg	Gly	Ser	Gly	Gln	Cys	Val	Ile	His	Tyr
275									280					285
Ser	Lys	Gly	Phe	Arg	Trp	His	Gln	Asn	Leu	Ser	Leu	Phe	Tyr	Lys
290									295					300

Asp Cys Phe

<210> SEQ ID NO 167
<211> LENGTH: 2570
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 167

ccaggaccag ggcgcaccgg ctcagcctct cacttgtcag aggccgggga	50
agagaagcaa agcgcaacgg tgtggtccaa gccggggcct ctgcttcgcc	100
tctaggacat acacgggacc ccctaacttc agtcccccaa acgcgcaccc	150
tcgaagtctt gaactccagc cccgcacatc cagcgcgggc acaggcgcg	200
caggcgggcag gtcccggccg aaggcgatgc gcgcaggggg tcgggcagct	250
gggctcgggc ggcgggagta gggcccggca gggaggcagg gaggctgcat	300
attcagagtc gcgggctgcg ccctgggcag aggcgcacct cgctccacgc	350
aacacctgct gctgccaccg cgccgcgatg agccgcgtgg tctcgctgct	400
gctgggggcc gcgctgctct ggggccaccg agccttctgc cgccgcgtgg	450
tcagcgggca aaaggtgtgt ttgtgtgact tcaagcatcc ctgctacaaa	500
atggcctact tccatgaact gtccagccga gtgagctttc aggaggcacg	550
cctggcttgt gagagtgagg gaggagtctt cctcagcctt gagaatgaag	600
cagaacagaa gttaatatag agcatgttgc aaaacctgac aaaacccggg	650
acagggattt ctgatggtga tttctggata gggctttgga ggaatggaga	700
tgggcaaaac tctggtgcct gccagatct ctaccagtgg tctgatggaa	750

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gcaattccca gtaccgaaac tggtagacag atgaaccttc ctgcggaagt	800
gaaaagtgtg ttgtgatgta tcaccaacca actgccaatc ctggccttgg	850
gggtccctac ctttaccagt ggaatgatga cagggtgaac atgaagcaca	900
attatatttg caagtatgaa ccagagatta atccaacagc ccctgtagaa	950
aagccttatac ttacaaatca accaggagac acccatcaga atgtggttgt	1000
tactgaagca ggtataattc ccaatctaata ttatgttgtt ataccaacaa	1050
tacccttgct cttactgata ctggttgctt ttggaacctg ttgtttccag	1100
atgtgctata aaagtaaagg aagaacaaaa actagtccaa accagtctac	1150
actgtggatt tcaaagagta ccagaaaaga aagtggcatg gaagtataat	1200
aactcattga cttggttcca gaattttgta attctggatc tgtataagga	1250
atggcatcag aacaatagct tggaatggct tgaaatcaca aaggatctgc	1300
aagatgaact gtaagctccc ccttgaggca aatattaag taatttttat	1350
atgtctatta ttctatttaa agaatatgct gtgctaataa tggagtgaga	1400
catgcttatt ttgctaaagg atgcaccaa acttcaaact tcaagcaaat	1450
gaaatggaca atgcagataa agttgttatac aacacgtcgg gagtatgtgt	1500
gttagaagca attcctttta ttcttttcac ctttcataag ttgttatcta	1550
gtcaatgtaa tgtatatgtt attgaaattt acagtgtgca aaagtatttt	1600
acctttgcat aagtgtttga taaaatgaa ctgttctaata atttattttt	1650
atggcatctc atttttcaat acatgctctt ttgattaaag aaacttatta	1700
ctgttgtcaa ctgaattcac acacacacaa atatagtacc atagaaaaag	1750
tttgtttctc cgaaataatt catctttcag cttctctgct ttgggtcaat	1800
gtctaggaaa tctcttcaga aataagaagc tatttcatta agtgtgatat	1850
aaacctcctc aaacatttta cttagaggca aggattgtct aatttcaatt	1900
gtgcaagaca tgtgccttat aattattttt agcttaaaat taaacagatt	1950
ttgtaataat gtaactttgt taataggtgc ataaacacta atgcagtcaa	2000
tttgaacaaa agaagtgaca tacacaatat aaatcatatg tcttcacacg	2050
ttgcctatat aatgagaagc agctctctga gggttctgaa atcaatgtgg	2100
tccctctctt gccactaaa caaagatggg tggtcggggg ttgggattga	2150
cactggaggc agatagtgtc aaagttagtc taaggtttcc ctactgtat	2200
ttagcctctg actatattag tatacaaaga ggtcatgtgg ttgagaccag	2250
gtgaatagtc actatcagtg tggagacaag cacagcacac agacatttta	2300
ggaaggaaa gaactacgaa atcgtgtgaa aatgggttgg aacctcatcag	2350
tgatcgcata ttcatgtatg agggtttgct tgagatagaa aatgggtggc	2400
cctttctgtc ttatctccta gtttcttcaa tgcttacgcc ttgttcttct	2450
caagagaaa ttgtaactct ctggtcttca tatgtccctg tgctcctttt	2500
aaccaaataa agagtctctg tttctggggg aaaaaaaaaa aaaaaaaaaa	2550
aaaaaaaaa aaaaaaaaaa	2570

-continued

<210> SEQ ID NO 168
<211> LENGTH: 273
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 168

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

Gly His Gly Ala Phe Cys Arg Arg Val Val Ser Gly Gln Lys Val
20 25 30

Cys Phe Ala Asp Phe Lys His Pro Cys Tyr Lys Met Ala Tyr Phe
35 40 45

His Glu Leu Ser Ser Arg Val Ser Phe Gln Glu Ala Arg Leu Ala
50 55 60

Cys Glu Ser Glu Gly Gly Val Leu Leu Ser Leu Glu Asn Glu Ala
65 70 75

Glu Gln Lys Leu Ile Glu Ser Met Leu Gln Asn Leu Thr Lys Pro
80 85 90

Gly Thr Gly Ile Ser Asp Gly Asp Phe Trp Ile Gly Leu Trp Arg
95 100 105

Asn Gly Asp Gly Gln Thr Ser Gly Ala Cys Pro Asp Leu Tyr Gln
110 115 120

Trp Ser Asp Gly Ser Asn Ser Gln Tyr Arg Asn Trp Tyr Thr Asp
125 130 135

Glu Pro Ser Cys Gly Ser Glu Lys Cys Val Val Met Tyr His Gln
140 145 150

Pro Thr Ala Asn Pro Gly Leu Gly Gly Pro Tyr Leu Tyr Gln Trp
155 160 165

Asn Asp Asp Arg Cys Asn Met Lys His Asn Tyr Ile Cys Lys Tyr
170 175 180

Glu Pro Glu Ile Asn Pro Thr Ala Pro Val Glu Lys Pro Tyr Leu
185 190 195

Thr Asn Gln Pro Gly Asp Thr His Gln Asn Val Val Val Thr Glu
200 205 210

Ala Gly Ile Ile Pro Asn Leu Ile Tyr Val Val Ile Pro Thr Ile
215 220 225

Pro Leu Leu Leu Leu Ile Leu Val Ala Phe Gly Thr Cys Cys Phe
230 235 240

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

Gln Ser Thr Leu Trp Ile Ser Lys Ser Thr Arg Lys Glu Ser Gly
260 265 270

Met Glu Val

<210> SEQ ID NO 169
<211> LENGTH: 43
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide probe

<400> SEQUENCE: 169

tgtaaaacga cggccagtta aatagacctg caattattaa tct

-continued

<210> SEQ ID NO 170
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide probe

<400> SEQUENCE: 170

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41

1. An isolated nucleic acid having at least 80% nucleic acid sequence identity to:

- (a) a nucleic acid sequence encoding the polypeptide shown in **FIG. 92** (SEQ ID NO:92);
- (b) a nucleic acid sequence encoding the polypeptide shown in **FIG. 92** (SEQ ID NO:92), lacking its associated signal peptide;
- (c) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 92** (SEQ ID NO:92);
- (d) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 92** (SEQ ID NO:92), lacking its associated signal peptide;
- (e) the nucleic acid sequence shown in **FIG. 91** (SEQ ID NO:91);
- (f) the full-length coding sequence of the nucleic acid sequence shown in **FIG. 91** (SEQ ID NO:91); or
- (g) the full-length coding sequence of the cDNA deposited under ATCC accession number 203225.

2. The isolated nucleic acid of claim 1 having at least 85% nucleic acid sequence identity to:

- (a) a nucleic acid sequence encoding the polypeptide shown in **FIG. 92** (SEQ ID NO:92);
- (b) a nucleic acid sequence encoding the polypeptide shown in **FIG. 92** (SEQ ID NO:92), lacking its associated signal peptide;
- (c) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 92** (SEQ ID NO:92);
- (d) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 92** (SEQ ID NO:92), lacking its associated signal peptide;
- (e) the nucleic acid sequence shown in **FIG. 91** (SEQ ID NO:91);
- (f) the full-length coding sequence of the nucleic acid sequence shown in **FIG. 91** (SEQ ID NO:91); or
- (g) the full-length coding sequence of the cDNA deposited under ATCC accession number 203225.

3. The isolated nucleic acid of claim 1 having at least 90% nucleic acid sequence identity to:

- (a) a nucleic acid sequence encoding the polypeptide shown in **FIG. 92** (SEQ ID NO:92);

(b) a nucleic acid sequence encoding the polypeptide shown in **FIG. 92** (SEQ ID NO:92), lacking its associated signal peptide;

(c) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 92** (SEQ ID NO:92);

(d) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 92** (SEQ ID NO:92), lacking its associated signal peptide;

(e) the nucleic acid sequence shown in **FIG. 91** (SEQ ID NO:91);

(f) the full-length coding sequence of the nucleic acid sequence shown in **FIG. 91** (SEQ ID NO:91); or

(g) the full-length coding sequence of the cDNA deposited under ATCC accession number 203225.

4. The isolated nucleic acid of claim 1 having at least 95% nucleic acid sequence identity to:

(a) a nucleic acid sequence encoding the polypeptide shown in **FIG. 92** (SEQ ID NO:92);

(b) a nucleic acid sequence encoding the polypeptide shown in **FIG. 92** (SEQ ID NO:92), lacking its associated signal peptide;

(c) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 92** (SEQ ID NO:92);

(d) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 92** (SEQ ID NO:92), lacking its associated signal peptide;

(e) the nucleic acid sequence shown in **FIG. 91** (SEQ ID NO:91);

(f) the full-length coding sequence of the nucleic acid sequence shown in **FIG. 91** (SEQ ID NO:91); or

(g) the full-length coding sequence of the cDNA deposited under ATCC accession number 203225.

5. The isolated nucleic acid of claim 1 having at least 99% nucleic acid sequence identity to:

(a) a nucleic acid sequence encoding the polypeptide shown in **FIG. 92** (SEQ ID NO:92);

(b) a nucleic acid sequence encoding the polypeptide shown in **FIG. 92** (SEQ ID NO:92), lacking its associated signal peptide;

(c) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 92** (SEQ ID NO:92);

- (d) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 92** (SEQ ID NO:92), lacking its associated signal peptide;
- (e) the nucleic acid sequence shown in **FIG. 91** (SEQ ID NO:91);
- (f) the full-length coding sequence of the nucleic acid sequence shown in **FIG. 91** (SEQ ID NO:91); or
- (g) the full-length coding sequence of the cDNA deposited under ATCC accession number 203225.
- 6. An isolated nucleic acid comprising:
 - (a) a nucleic acid sequence encoding the polypeptide shown in **FIG. 92** (SEQ ID NO:92);
 - (b) a nucleic acid sequence encoding the polypeptide shown in **FIG. 92** (SEQ ID NO:92), lacking its associated signal peptide;
 - (c) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 92** (SEQ ID NO:92);
 - (d) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 92** (SEQ ID NO:92), lacking its associated signal peptide;
 - (e) the nucleic acid sequence shown in **FIG. 91** (SEQ ID NO:91);
 - (f) the full-length coding sequence of the nucleic acid sequence shown in **FIG. 91** (SEQ ID NO:91); or
 - (g) the full-length coding sequence of the cDNA deposited under ATCC accession number 203225.
- 7. The isolated nucleic acid of claim 6 comprising a nucleic acid sequence encoding the polypeptide shown in **FIG. 92** (SEQ ID NO:92).
- 8. The isolated nucleic acid of claim 6 comprising a nucleic acid sequence encoding the polypeptide shown in **FIG. 92** (SEQ ID NO:92), lacking its associated signal peptide.
- 9. The isolated nucleic acid of claim 6 comprising a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 92** (SEQ ID NO:92).
- 10. The isolated nucleic acid of claim 6 comprising a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 92** (SEQ ID NO:92), lacking its associated signal peptide.
- 11. The isolated nucleic acid of claim 6 comprising the nucleic acid sequence shown in **FIG. 91** (SEQ ID NO:91).
- 12. The isolated nucleic acid of claim 6 comprising the full-length coding sequence of the nucleic acid sequence shown in **FIG. 91** (SEQ ID NO:91).
- 13. The isolated nucleic acid of claim 6 comprising the full-length coding sequence of the cDNA deposited under ATCC accession number 203225.
- 14. An isolated nucleic acid that hybridizes to:
 - (a) a nucleic acid sequence encoding the polypeptide shown in **FIG. 92** (SEQ ID NO:92);
 - (b) a nucleic acid sequence encoding the polypeptide shown in **FIG. 92** (SEQ ID NO:92), lacking its associated signal peptide;
 - (c) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 92** (SEQ ID NO:92);
 - (d) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 92** (SEQ ID NO:92), lacking its associated signal peptide;
 - (e) the nucleic acid sequence shown in **FIG. 91** (SEQ ID NO:91);
 - (f) the full-length coding sequence of the nucleic acid sequence shown in **FIG. 91** (SEQ ID NO:91); or
 - (g) the full-length coding sequence of the cDNA deposited under ATCC accession number 203225.
- 15. The isolated nucleic acid of claim 14, wherein said hybridization occurs under stringent conditions.
- 16. The isolated nucleic acid of claim 14 which is at least 10 nucleotides in length.
- 17. A vector comprising the nucleic acid of claim 1.
- 18. The vector of claim 17, wherein said nucleic acid is operably linked to control sequences recognized by a host cell transformed with the vector.
- 19. A host cell comprising the vector of claim 17.
- 20. The host cell of claim 19, wherein said cell is a CHO cell, an *E. coli* or a yeast cell.

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