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(54) SECRETED AND TRANSMEMBRANE
POLYPEPTIDES AND NUCLEIC ACIDS
ENCODING THE SAME

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(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.

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGTGCAGGTATG
AGCAGGCTCGAAGACTAARCTTTTGTGAAGTTGTAAACAGAAACCTGTTAGAAATGTGGTGGT
TTCAGCAGGGCTCAGTTTCCTTCCTTCAGCCCTGTAAITGGACATCTGCTGCTTTCATATTT
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG
TACAGTAGCTOCAGAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTATGCAATG
CTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCTCGAAGAGACGTTATCATCAAA
TTAAACAGGGCTGGCCTTGACTTGAATACAGTGTGTTTAGGACTTTCTATTTGGGCAACCT
CCAGAAACCAACCTTTTGTGTCACATGTAAGTGGAGCTGTCTTACCTTTGGTATGGGCTCAT
TATATATGTTTGTTCAGACCATCTTTCCTAACCAATGCAGCCCAAAATCCATGGCAACAGTC
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACITTAGCATGCTGACTTGCTC
ATCAGTTTTGCACAGTGGCAATTTTGGGACTGATTAGAACAGAACTCCATTGGAACCCCGAGG
ACAAAGGTTATGCTTCACATGATCACTACTGCAGCAGAAATGGTCTATGTCATTTTCCTTCITT
GGTTTTTTCCTGACTTACATTCGTGATTTTCAGAAATTTCTTTACGGGTGGAAGCCAATTTACA
TGGATTAAACCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACCGGCTACTTTCCA
GAGATATTTGATGAAGGATAAAATATTTCTGTAAATGATTATGATTCCTCAGGATTTGGGGAAGG
TTCACAGAGTTGCTTATTTCTCTGAAATTTTCACCCACTTAATCAAGGCTGACAGTAACACT
GATGAATGCTGATAATCAGGAACATGAAGAAGCCATTTGATAGATTATTTCTAAGGATATCAT
CAGAAGACTATTAAACACCTATGCCTATATCTTTTATCTCAGAAAATAAAGTCAAAAGACT
ATG

Related U.S. Application Data

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 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 continu-

ation 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.

FIGURE 1

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTACAAAAGGTGCAGGTATG
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGT
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTT
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTTATGCATTG
CTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAAA
TTAAACAAGGCTGGCCTTGTAAGTGGTACTGAGTTGTTTAGGACTTTCTATTGTGGCAAACCT
CCAGAAAACAACCTTTTTTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT
TATATATGTTTGTTCAGACCATCCTTTCCTACCAAATGCAGCCCAAATCCATGGCAAACAAGTC
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACTTAGCATGCTGACTTGCTC
ATCAGTTTTGCACAGTGGCAATTTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG
ACAAAGGTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCAATTTTCCTTCTTT
GGTTTTTTCCTGACTTACATTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA
TGGATTAACCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA
GAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG
TTCACAGAAGTTGCTTATTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACT
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCAT
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACT
ATG

FIGURE 2

<subunit 1 of 1, 266 aa, 1 stop

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

MWWFQQGLSFLPSALVIWTSAAFIIFS YITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV
LCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG
MGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW
NPEDKGYVLHMITTAAEWSMSFSFFGFFLT YIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR
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

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC
 GTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTC
 CTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG
 GATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAG
 GTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG
 AGTATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGG
 TTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGA
 CTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCC
 CATTCTCAGCCCCAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTGGTGTGATTGGAG
 TGACTCTCATGGCTCTTCTTTCTGGATTTGGTGTGTCAACTGCCCATACACTTACATGTCTTACTTC
 CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT
 CATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA
 AACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGGAAGTGAATACTTACT
 CTTATTCAACAGGAAGTGGATGCTTTTGAAGAATTAAGCAGGCAGCTTTTTCTGGAAACAGCTGATCT
 ATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTCAAGGGGAAATATTTAATTTCTTGGTT
 ACTTTTTCTCTATTTACTGTGTTTGGAAAATTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTT
 GGGAAAACGGATCCTGTCAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT
 GAAGTTTTGGTCCCAACACATTTCTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGAT
 TGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCCTCCAATGTCATTGTCTCTG
 CTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTT
 AGAATACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCCTTGGTTTG
 ATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCA
 GAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAAATTTA
 GATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAACAAACAAAATGCTATGGTAGC
 ATTTTTACCTTCATAGCATACTCCTTCCCCGTCAGGTGATACTATGACCATGAGTAGCATCAGCCAG
 AACATGAGAGGGGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG
 TGTAGAGGCGGAGAGGAGCCAAGAACTAAAGGTGAAAAATACACTGGAACTCTGGGGCAAGACATGT
 CTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTTG
 CCTTGAGATTGACTCATTAATAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAGGGCGGCCGCG
 ACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATG

FIGURE 4

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGV
LNSSSRYPFWKMNLCVILLILVFMVPPYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFFWKLGBP
FPILSPKHGILSIEQLISRVGIVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERRLLQ
TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQQEVDALAEELSRQ
LFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVVGKTDVPVTRGIEI
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLLAQIMGMY
FVSSVLLIRMSMPLEYRTIITEVLGELQNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

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
 GTTTCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT
 TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGT
 GTCATGCAGAATTATGGGGATCACCCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAG
 AAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCC
 TTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAG
 GATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAGGTTCAGTGA
 GCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATTCCAGAA
 ATTATCACCACCAAAGATCCCATATTCAACACTCAAACGCAACACAAACAACAGAATTTATTGT
 CAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTTACTACTCTCTC
 CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAGTTTTTATG
 GAACTAGCACCATGTCTACAGAACTGAACATTTGTTGAAAATAAAGCAGCATTCAAGAATGA
 AGCTGCTGGGTTTGGAGGTGTCCACGGCTCTGCTAGTGTCTGCTCTCTCTCTTTGGTGCTG
 CAGCTGGTCTTGGATTTTGTCTATGTCAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAT
 CAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAA
 TGAGGAATCAAAGAAAAGTATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAAAGTACCGTGC
 GATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTTCTTT
 CATGCTCCTTACCCTGCCCGAGCTGGGGAAATCAAAGGGCCAAAGAACCAAAGAAGAAAGTCCA
 CCCTTGGTTTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAAT
 GCCCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCT
 TTCTAGCCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTGCAAAGTGCAAGGAC
 CTAACCATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTTG
 AAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGACCCTTTCTTCA
 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAAAGAAT
 GGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAA
 GCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTGAGCAGGGACTGTAAAC
 ACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACA
 CTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACA
 AAAATAAAAAGTCTTATAAATTTCTATTTTCTGAGTTACAGAAATGATTACTAAGGAAGATT
 ACTCAGTAATTTGTTTAAAAAGTAATAAAATTCAACAAACATTTGCTGAATAGCTACTATATGTC
 AAGTGCTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCTCAAAAAATTGCACATAGTAG
 AACGCTATCTGGGAAGCTATTTTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAAACTAAT
 TTTTATTTTTGCTGAGACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATT
 TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAAGCACATTTTAAAAGTGCC
 ATTAACAAATGTATCACTAGCCCTCCTTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATT
 TGTGACAAAAAATTAAAGCATTTAGAAAAGT

FIGURE 6

MARCFSLVLLLTISIWTTRLIVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG
LSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYN
SSDTWTNSCIPEIIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR
RKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPTALLVLALLFFGAAAGLGFCYVK
RYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVRCLEAEV

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

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCAGCCCGGCGGCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCGGGGCGGCGGCTGCGGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCCTGCTGTGCCTGCTGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCGGCCCCGCTCTCAGCTACCCGCAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGAGGTTGAGGAACTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTATCACAATGAGACCAACACAGACACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAATTACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTGCTGTGGAGACCACTGTGTGTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGGCTGTGTGTGTGCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGACACCCCTGCCCCGTGGAGGGCGAGCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCCGCTGCACTGCTGGGAGGGGAAGAGATTTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCTCATCTTCTTCCAGTAAGTTTCCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCAGCTCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAACTGCAAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCCTTACCAGTTGGCAGACAGCCGTTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAAACAATGTGGAGTCTCCCTCTGATTGGTTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAACCTGGCAAAAATGCAACAAATGAATTTTCCACGCAGTTCCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGAGATGAAATGTTCTGTTTACCCTGCATTACATGTGTTTATTCATCCAGCAGTGTTGCTCAGCTCTTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCTCTCTCAGCACAGCCTGGGGAGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAACCTAATCTCACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTTCTCACAGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACTTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTTCAGGTGTATGAGTGTGTTGCCACCATGTATTTCATCCAGAGTTCTTAAAGTTTAAAGTTGCAATGATTGTATAAGCATGCTTTCTTTGAGTTTTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL
RSAVEEMEAEAAAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTGQMVFSE
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRLCTRDSECCGDQLCVWGHC
TKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRLDLITWELEPDG
ALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSGFMEEVRQLELDLE
RSLTEEMALGEPAAAAAALLGEEI

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
CCACAAGCCCCAGGACATCCCTACCTTCCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC
ACACTGGGTCAATTGGCATTTGGAGCCCTCATCCTGACCCTTGTGCAGATAGCCCGGGTCATCTTG
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGCCCGCTGCATCATGTGCTGTTT
CAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCCTAAACCGCAATGCATACATCATGA
TCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTCATGCTACTCATGCGAAAC
ATTGTCAGGGTGGTCGTCCTGGACAAAGTCAAGACCTGCTGCTGTTCTTTGGGAAGCTGCTGGT
GGTCGGAGGCGTGGGGGTCCTGTCTTCTTTTTTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAG
ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCCATCATGACCTCCATCCTGGGGGCTAT
GTCATCGCCAGCGGCTTCTTCAGCGTTTTTCGGCATGTGTGTGGACACGCTCTTCCTCTGCTTCCT
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA
AGATTCTGGGCAAGAAGAACGAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGACCAGCTCCGG
CCCTGATCCAGGACTGCACCCCCACCCGTCAGCCATCCAACCTCACTTCGCCTTACAGGT
CTCCATTTTGTGGTAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACT
TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG
AAACCTCCGTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCA
GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGA
GATCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAACAAA
AAGATTTTATTAAAGATATTTTGTAACTC

FIGURE 10

RTRGRTRGGCEKVPINTSCNPHTAHLVNSSCPGLMCVFQGYSSKGLIQRSVENLQIYGVLGLEFWTL
NWVLALGQCVLGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAFMLLMRN
IVRVVVLDDKVTDLLLFFGKLLVVGGVGVLSTFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYSKSLKILGKKNEAPPDNKKRKK

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

GCCCCGCGCCCGGCCGCCGGGCGCCCGAAGCCGGGAGCCACCGCCCATGGGGGCCTGCCTGGGAGCCTGC
 TCCCTGCTCAGCTGCGCGTCTGCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCTGCTGCCCCGC
 CAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCTCTTCTCTGGGGGTGCTGGTGTCCA
 TCATTATGCTGAGCCCCGGGCGTGGAGAGTCAGCTCTACAAGCTGCCCTGGGTGTGTGAGGAGGGGGCC
 GGGATCCCCACCGTCTCTGCAGGGCCACATCGACTGTGGCTCCCTGCTTGGCTACCGCGCTGTCTACCG
 CATGTGCTTCGCCACGGCGGCCTTCTTCTTCTTCTTTTTTACCCTGCTCATGCTCTGCGTGAGCAGCA
 GCCGGGACCCCCGGGTGCCATCCAGAATGGGTTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTC
 ACCGTGGGTGCCCTTCTACATCCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGCTCGTGGG
 CTCCTTCTCTTTCATCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGT
 GGCTGGGCAAGGCCGAGGAGTGCATTCCCGTGCCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTC
 TTCTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTTATGTACTACACTGAGCCAGCGGTGCCA
 CGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCTGCTGTCTCTGC
 CCAAGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTATCACCTCTACACCATG
 TTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTTGCCAACCAGCT
 GGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATGCCCCGAGCATTG
 TGGGCCTCATCATCTTCTCCTGTGCACCTCTTTCATCAGTCTGCGCTCCTCAGACCACCGGCAGGTG
 AACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGTT
 GGCAGCCTGTGAGGGCCGGGCCTTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCC
 ACTTCTGCCTGGTGTGCGCTCACTGCACGTTCATGATGACGCTCACCAACTGGTACAAGCCCCGGTGAG
 ACCCGGAAGATGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCT
 CCTCTACCTGTGGACCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTTGAGGCAGCCTCA
 CAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTC
 CCCACACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTGCCCCGTAGCCGGGC
 CTTCTAGTCGTAGTGCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCAC
 ACCCACACGGTGGAGCTGCCTCTTCTTCCCTCCTCCCTGTTGCCATACTCAGCATCTCGGATGAA
 AGGGCTCCCTTGTCCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACCTCCCACCACAG
 TGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTTCACGTCCCCCAGGGGACCCTGCCCCCTTCTCTG
 GACTTCGTGCCTTACTGAGTCTCTAAGACTTTTTTCTAATAAACAAGCCAGTGCCTGTAAAAAAA

FIGURE 12

MGACLGACSLLSASCCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGLVLSIIMLSPGVESQL
YKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFFTLLMLCVSSSRDPRAAIQ
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSWNQRWLKAE
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVSIAAVLPKV
QDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVAACEGRAFDNEQDGVITYSY
SFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVVKICASWAGLLLYLWTLVAPLLLRNRD
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

CGGGCCAGCCTGGGGCGGGCCGGCCAGGAACCAACCCGTTAAGGTGTCTTCTCTTTAGGGATGGTGA
GGTTGGAAAAAGACTCCTGTAAACCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAGAACG
CTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCACACAA
CTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC
TTTCTGTTTGTGTCACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATAGAGTTAAATG
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT
TTTGATATATTTCTTCTGGCAGTTTTTCGATTTAAAGTGTTAATACTTGCATATGCTGTGTGCAG
ACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTTTACTAGCAAAAG
TGATCCTTTTGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTGCCCATCATTTTCATTTCATC
CTTGCTGGATTGAGACGTGGTTCCTGGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA
CAGACTCCTGATAGTTCAGGATGCTTCAGAGAGGGCAGCACTTATACCTGGTGGTCTTTCTGATG
GTCAGTTTTTATTTCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT
GAGAAACCACTTTTAGAACTATTGAGTACTACTTTTTGTTAAATGTGAAAAACCCTCACAGAAAGTC
ATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTGTGACAGTAAAGTTGAAATGGTGACGTC
CACTGCTGGCTTTATTGAACAGCTAATAAAGATTTATTTATTGTAATACCTCACAAACGTTGTAC
CATATCCATGCACATTTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCATCCTCTCT
TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAGAAAGTCTTGTGCTGTATTCCTAATC
AAAAGACTTAATATATTGAAGTAACACTTTTTTAGTAAGCAAGATACCTTTTTTATTTCAATTAC
AGAATGGAATTTTTTGTTCATGTCTCAGATTTATTTGTATTTCTTTTTTAACACTCTACATT
TCCCTTGTTTTTTAACTCATGCACATGTGCTCTTTGTACAGTTTTTAAAAGTGAATAAAATCTG
ACATGTCAATGTGGCTAGTTTTATTTTCTTGTTTTGCATTATGTGTATGGCCTGAAGTGTGGA
CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGIAAAATGTCACCAGACATTTGTATTATTT
TTATCATGAAATCATGTTTTTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGC
ACAAAATGACTTAAACCATTTCATATCATGTTTCCTTTGCGTTTCAGCCAATTTCAATTAAAATGAA
CTAAATTAAAAA

FIGURE 14

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF
VTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT
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

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTGAGG
 CCGCGGCCCTGCCCCGCGCGGCTCCCTGCGCCGCGCGCCCTCCCGGGACAGAAGATGTGCTCCAG
 GGTCCCTCTGCTGCTGCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGGGCTGCCCAT
 CCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCCGCCAGGGGACCACGGTGCCC
 CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC
 AGGCAGCTTTGCCGGCCTGCCGGGCTGCAGCTCCTGGACCTGTACAGAACAGATCGCCAGCC
 TGCCAGCGGGGTCTTCCAGCCACTCGCCAACTCAGCAACCTGGACCTGACGGCCAACAGGCTG
 CATGAAATCACCAATGAGACCTTCCGTGGCTGCGGCGCCTCGAGCGCCTCTACCTGGGCAAGAA
 CCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGCTCGACCGCCTCCTGGAGCTCAAGCTGC
 AGGACAACGAGCTGCGGGCACTGCCCCGCTGCGCCTGCCCCGCTGCTGCTGCTGGACCTCAGC
 CACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACCTGGAGGCGCTGCGGCT
 GGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTTTCAGCCCTTGCGCAACCTCCACGACC
 TGGATGTGTCCGACAACAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACG
 CGCCTGCGGCTGGCCGGCAACACCCGCATTGCCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGC
 TGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCC
 TCTTCCCCCGCTGCGGCTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCCCTGAGC
 TGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTCACTTGCCAGCCCTGAGGAGACGCGCTGCCA
 CTTCCCCGCCAAGAAGCTGGCCGGCTGCTCCTGGAGCTGACTACGCCGACTTTGGCTGCCCAG
 CCACCACCACCACAGCCACAGTGCCACCACGAGGCCCGTGGTGCGGGAGCCCCACAGCCTTGTCT
 TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCCAGCCCGCCCTC
 CACTGCCCCACCGACTGTAGGGCCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCA
 ATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTGCCCCGAAGGCTTCACG
 GGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCGAG
 GCCACCACGGTCCCTGACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGC
 AGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTACCTATCGCAACCTATCG
 GGCCCTGATAAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCA
 GCTGCGGCCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGGCCCGGGCGGGTGCCGGAGG
 GCGAGGAGGCTGCGGGGAGGCCATACACCCCGAGCCGTCCACTCCAACCACGCCCCAGTCACC
 CAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGC
 GCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGCGGGCCATGGCAGCAGCGGCTCAGG
 ACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAACTGGAGGGAGTGAAGGTCCCCTTGGAG
 CCAGGCCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCC
 ACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCAACCCCTCCACGCAAAAGCCCTACATCTTAAGCCA
 GAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCC
 ACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCT
 GGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCC
 CTAACGTCCCCAGAACCGAGTGCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTC
 CCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCCAC
 TCCAGGCGGACCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGC
 GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGC
 TTTAGGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATTCT
 GGGAAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATATGAA
 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 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 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 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

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLDSEESSEL
ESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEPPKKVRKPALTAIEGTAHGEPCHFPFLFLDK
EYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAAKRRQMGEAEMMYQTGMKILNGSNKKSQKR
EAYRYLQKAASMNHTKALERSYALLFGDYLPQNIQAAREMFELTEEGSPKGTALGFLYASGLGVN
SSQAKALVYYTFGALGGNLIHMLVLSRL

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

AATTCAGATTTTAAAGCCATTCTGCAGTGGAATTCATGAACTAGCAAGAGGACACCATCTTCTT
GTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGG
CCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACCTAAAGATTGAAGACATCACTG
ATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAACCTTTTGAT
AAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA
AACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG
CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTGGTGT
CCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA
CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG
TTATTAATGTCTCCAGTGTGGAGGTGCGCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA
TATGCAGTGGAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC
ATGCATTGAACCAGGATTGTTCAAAACAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC
TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATGGAGAAGGTTACATTGAAAA
AGTCTAGACAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG
CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAA
GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGA
AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACT
CATTTAGATCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT
CCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCT
GTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAATGA
TCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTTAAGT
ATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 20

MLFWVLGLLILCGFLWTRKGKLIKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESG
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDWLTLEDY
REPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDSLRRDMK
AFGVHVSCIEPGLFKTNLADPVKVIKKLAIWEQLSPDIKQQYGEGYIEKSLDKLKGNKSYVNMD
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
 CATTGAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAGGCGAAGTAAATG
 AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATTCGGT
 CGTCATTGAGATCAGATCATGACGTTTAGAGAGAGGGCTGCTTCACAAAACTTGCAGGAGCATTT
 TTCAAACCAAGACCTTGTTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTCTACTC
 ATCGACTGGAACATTCCCTTATATAAACCTCAAAAAGGACTTTTTTCACAGGGTACCTTTAGTGGTT
 GCCAATCTGGGCATGTCTGAACAACTGGGTTATAAACTGTATCAGGTTCCCTGTATGTCCACTGG
 TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTTGAAGAAGATGGATCCTTAAAGGAGG
 TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAAGTG
 GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTAAAACGAGAAATTGA
 GAAAAGGAGAGGAGCACAGATTGAGGAGCAAGAGAGAAGAACATCCAAAAAGACCTCAGGAGA
 ACATTTTTCTTTGTCAGGCATTACGGACCTTTTTTCCAAATCTGAATTTCTTCATTGATGTT
 ATGTCTTTAAAAAATAGACATGTTTCTAAAAGTAGCTGTAACCTACAACCACCATCTCGATGTAGT
 AGACAATCTGACCTTAATGGTAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCAC
 AAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTA
 GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAT
 GAGCAGCCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC
 CTACATTTTGATCCTTTTAACTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAAC
 ATTTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTACC
 TGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAACATCA
 GATGCTTTTATTTCCAAACCTTTTTTTCACCTTCACTAAGTTGTTGAGGGGAAGGCTTACACAG
 ACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT
 TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT
 GAGACCATGTCTATTAAAAAATAAAATGAAAAGCAAGAATAGCCTTATTTTCAAATATGGAAA
 GAAATTTATATGAAAATTTATCTGAGTCATTAAATTTCTCCTTAAGTGATACTTTTTTTAGAAGTA
 CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT
 AAAATTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGGEVKGEAKNSITDSQMDDVEVVYTIDIQKYI
PCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL
VFLLLTPSIIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSSRAV
QTHSSKFFFEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLDVVDNLT
MVEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLDQDKRSKANTGSSNQDKASKMSSPET
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
GCGTCCCCGCTCGCCGCGCAGTCAGCTTGCCGGGTTGCTGCCCCGCGAAACCCGAGGTACCAGCCCGCGCCTCT
GCTTCCCTGGGCGCGCGCCGCTCCACGCCCTCCTTCTCCCCGGCGCGCCTGGCACCGGGGACCGTTGCCTGA
CGCGAGGCCCAGCTCTACTTTTCGCCCCGCGTCTCCTCGCCTGCTCGCCTCTTCCACCAACTCCAACCTCTCTCCC
TCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCCGCTGCCGTAGCGCCGCTTCCCGTCCGGTCCCAAA
GGTGGGAACGCGTCCGCCCGCGCCCGCACCATGGCACGGTTCGGCTTGCCCGCGCTTCTCTGCACCCTGGCAGTGCTC
AGCGCCGCGTCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCAGCGTCTTTACGTGTCCAAAGGCTTC
AACAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTGAAGATCTGTCCCCAGGGTTCTACCTGTGCTCT
CAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGATGATTTCAAAGTGTGGTCAGCGAACAGTGCAATCATTTG
CAAGCTGTCTTTGCTTACGTTACAAGAAGTTTGATGAATTCTTCAAAGAACTACTTGAAATGCAGAGAAATCCCTG
AATGATATGTTTGTGAAGACATATGGCCATTTATACATGCAAATTTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTG
AAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCTGGAGCGGATG
TTCCGCTGGTGAACCTCCAGTACCCTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAG
CCCTTCGGAGATGTCCCTCGCAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGTACTTTTCGTCAAGGC
TTAGCGGTTGCGGGAGATGCTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAG
ATGATCTACTGCTCCACTGCCGGGTCTCGTGAAGTGTGAAGCCATGTTACAATACTGCTCAAACATCATGAGAGGC
TGTTTGGCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTA
GAGGGTCTTTTCAACATTGAATCGGTCAATGGAATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGAT
AATAGTGTTCAAGTGTCTCAGAAGGTTTTCCAGGGATGTGGACCCCCCAAGCCCTCCCAGCTGGACGAATTTCTCGT
TCCATCTCTGAAAGTGCCTTCAGTGCTCGCTTCAGACCACATCACCCGAGGAACGCCCAACCACAGCAGCTGGCACT
AGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATCTGGTCTCCCTTCCGAGCAAC
GTTTGCAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTAC
CTGTTTGCAAGTACAGGAAATGGATTAGCCAACAGGGCAACAACCAGAGGTCCAGGTTGACACCAGCAAACCAGAC
ATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG
GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCAGAG
TTTGACTACAATGCCACTGACCATGTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGCTCTGGGGCA
CAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTCCTGGTTATGCAGAGAGAGTGGAGATTAATTCTCAAACCTCTGAG
AAAAAGTGTTTCATCAAAAAGTTAAAGGCACCAAGTTATCACTTTTCTACCATCCTAGTGACTTTGCTTTTAAATGAA
TGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGTGACTTTGTTTTCTCATTAGTTTTGGG
AGGAAAAGGACTGTGCATTGAGTTGGTTCCTGCTCCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAA
CTATAGTTAGTTGTGATTTGTGATTTTATCACTCTATTATTTGTTTGTATGTTTTTTCTCATTTCGTTTGTGGGTT
TTTTTTTCCAACGTGTGATCTCGCCTGTTTCTTACAAGCAAACAGGGTCCCTTCTTGGCACGTAACATGTACGTATT
TCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTATTTATCATGTTATCTTATTAAGAAAAAGCCCAAAAGC

FIGURE 24

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGST
CCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGH
LYMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFLVNSQYHFTDEYLECVSKYTE
QLKPFQGDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRL
VTVKPCYNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN
MQDNSVQVSQKVFQGCQPPKPLPAGRISRSISESAFSARFRPHHPEERPTTAAGTSLDRLVTDVK
EKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNNPEVQVDT
KPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG
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
TACAGCTGCACCGACAGTTGCGAATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGC
CAGGCTTCTAGGAGATGGCTCCAGGAAGCGGCCAAGAATGTGAGTGCAAAGATTGGTTCTGAG
AGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCCCTGTGATCATT
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA
GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG
AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC
TTCTTCTCCACCTCACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA
TGTTTTTCAAGATCATTTTGTTTGTTGCTCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCT
GTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAACTGTAGCTTCCT
AGCTAGTGTCAATTTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTT
AAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 26

MKVLISLLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM
TVSGLPKKQCPCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

Important features:

Signal peptide:

amino acids 1-22

N-myristoylation sites.

amino acids 27-33, 46-52

FIGURE 27

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG
AGCTGGTCTGCCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTACCCTGCC
CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCTGTGCAAAGCTACTTCCCCTACCTGA
TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG
ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCGGAACCGGAGC
CAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATCCCCACTTTGAGA
AGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGGCTCCT
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGCTGTG
CTCTGTGCAGAGCCCAAGGAAGGTCTTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGC
TCTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTC
GAGCCCACCTGGAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA
GAACGCCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG
GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCC
TTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTTA
GCAGAATGAGAGAAGACATTGATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG
AAACACTAGGACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTGCTC
CCAATGTTGTCCCTTTCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCTCCTGAGGCTACAC
CCATGCGTCTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGAC
CCTCTCTCCCCACTACCACCTTCTTCCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGG
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGAA
ACCACG

FIGURE 28

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSSQIKGL
TGASGKVALLELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM
RQLADGSMDVVVCTLVLCVQSQRKVLQEVRRVLRPGGVLEFFWEHVAEPYGSWAFMWQQVFPTW
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLVPVGPVHMGKAVKQSFPSKALICSFPSL
QLEQATHQPIYLPLRGT

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

CAATGTTTGCCTATCCACCTCCCCAAGCCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTGCT
GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCAGAAAGTCTCTTCTG
CCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCAT
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTA
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAA
GTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTCAATTAAGAAATT
GTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAC
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

MLLLTLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFPPSFLCLLPHRPAMTCSQAQPRG
EGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 31

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTT
 CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT
 ATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAATCATGTCGG
 GAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCCATGATGTTTACC
 TTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTATTTTGGGATTGTTGTT
 TGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA
 CAGAAAGGGAAAATATGAAGTGCGTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGGCAGTG
 CTGCTCGTCTTGATTTTTGTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCAC
 AAATAAAGCCATCAGCAGTGCTCCCTTCTGCTGTTCCAGCCACTGTGGACATTGCCCATCCTCA
 TTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAAGTGCAGGAGCTGCCAGGTT
 ATGGAAGGCGGCCAAGTGAATATAAGCCCCTTTCGGGCATTTCGGTACATGTGGTTCGTACCATTT
 AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAG
 TGGTTACTTGTATTTCAACAGAAGTAAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTC
 TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTAAATCTCTGTGGTGAG
 GATTCCGAGAATCATTGTCTGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT
 CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC
 AACCAGAATGCATATACTACAAGTCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGC
 ATTCAAAATCTTGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAA
 TTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTAC
 AATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGC
 CCATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACCTTTCCTGTGTTTTGCTGTTGATC
 TGGAACAAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA
 AAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGAATGAGGA
 GGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATT
 TCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTT
 TTAAAGACCTAATAAACCTATTCTTCTCAAAA

FIGURE 32

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYTDLSIE
LDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLEQPLWTFA
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQOMTIA
GAVVTCYFNRSKNDDPPDHPILSSLSILFFYHQGTVVKGSEFLISVVRIPRIIVMYMQNALKEQQHG
ALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD
FIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLVAFFAYLVAHSFSLSVFETVLDALFLCFA
VDLETNDGSSEKPYFMDQEFSLFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

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

GTTCGATTAGCTCCTCTGAGAGAAGAGAGAAAGGTTCTTGGACCTCTCCCTGTTTCTTCCTTAGA
ATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAATATTCATTCTGTGTGGT
GAAAATTTTTTGAAAAAAAATTGCCTTCTTCAACAAGGGTGTCAATTCTGATATTTATGAGGAC
TGTTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCCCTGTTTTGCTGGTGAAGTAC
ATTCAAAACAAAGAAACGGCAAAGAAGATTAAGGCCCCAAGTTCAGTGTGCCTCAGATCAACTGC
GATGTCAAAGCCGGAAGAATCATCGATCTGAGTTCATTGTGAAATGTCCAGCAGGATGCCAAGA
CCCCAAATACCATTGTTTATGGCACTGACGTGTATGCATCCTACTCCAGTGTGTGTGGCGTCCGC
TCCACAGTGGTGTGCTTGATAATTAGGAGGGAAAAATACTTGTTCGGAAGGTTGCTGGACAGTCT
GGTTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTTATCCCTACCACGATGGAGAGAATCCTT
TATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTAACTACCCATCAGCTCTTACATACTCATCAT
CGAAAAGTCCAGCTGCCCAAGCAGGTGAGACCACAAAAGCCTATCAGAGGCCACCTATTCCAGGG
ACAACTGCACAGCCGGTCACTCTGATGCAGCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCCAC
CACCTTGCCAAGGCCATCCCTTCTGCTGCTTCTACCACCAGCATCCCCAGACCACAATCAGTGG
GCCACAGGAGCCAGGAGATGGATCTCTGGTCCACTGCCACCTACACAAGCAGCCAAAACAGGCC
AGAGCTGATCCAGGTATCCAAAGGCCAAGTACTCTCAGGAGCTGCCTCCGAGAACTGTTGGAG
GGATGTGACCTGGGACTTGTTCAAAAGAGAATTTAGCACACAGTCTTTGGAGCCAGTATCCC
TGGGAGATCCAAACTGCAAAATTGACTTGTGCTTTTTTAATTGATGGGAGCACCAGCATTTGGCAA
CGGCGATTCCGAATCCAGAAGCAGCTCCTGGCTGATGTTGCCCAAGCTCTTGACATTGGCCCTGC
CGGTCCACTGATGGGTGTTGTCCAGTATGGAGACAACCTTGCTACTCACTTTAACCTCAAGACAC
ACACGAATTTCTGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAAT
GTAGGTGGGCCATCTCCTTTGTGACCAAGAATCTTTTTCAAAGCCAATGGAACAGAAGCGG
GGCTCCCAATGTGGTGGTGGTGTGGTGGATGGCTGGCCACGGACAAAGTGGAGGAGGCTTCAA
GACTTGCAGAGAGAGTCAGGAATCAACATTTTCTTCACTCACCATTGCAAGGTGCTGCTGAAATGAG
AAGCATATGTGGTGGAGCCCACTTTGCAACAAGCCGTGTGAGAGCAAAACGGCTTCTACTC
GCTCCAGTGTGAGAGCTGGTTTGGCCTCCACAAGACCTGTCAGCCTCTGGTGAAGCGGGTCTGCG
ACACTGACCGCCTGGCCTGCAGCAAGACCTGCTTGAAGTTCGGCTGACATTGGCTTCGTATCGAC
GGCTCCAGCAGTGTGGGGACGGGCAACTTCCGCACCGTCTCCAGTTTGTGACCAACCTCACCAA
AGAGTTTGAGATTTCCGACACGGACACGCGCATCGGGGCCGTGAGTACACCTACGAACAGCGGC
TGGAGTTTGGGTTCGACAAGTACAGCAGCAAGCCTGACATCCTCAACGCCATCAAGAGGGTGGGC
TACTGGAGTGGTGGCACCAGCACGGGGGCTGCCATCAACTTCGCCCTGGAGCAGCTCTTCAAGAA
GTCCAAGCCCCAACAGAGGAAGTTAATGATCTTCATCACCAGCGGAGGTTCTACGACAGCTCC
GGATCCCCAGGATGGCTGCCATCTGAAGGAGTGATCACTTTCGATAGCGCTTGCTGGCTGGCT
GCCCAAGAGGAGCTAGAAGTCATTGCCACTCACCCGCCAGAGACCTCCTTCTTTGTGGACGA
GTTTGACAACCTCCATCAGTATGTCCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCAC
AGCCTCGGAACTGAATTCAAGAGCAGGCAGAGCACCAGCAAGTGCTGCTTTACTAACTGACGTGTT
GGACCACCCACCGCTTAATGGGGCACGCACGGTGCATCAAGTCTTGGGCAGGGCATGGAGAAAC
AAATGTCTTGTTATTATTCTTTGCCATCATGCTTTTTTCATATCCAAAACCTTGGAGTTACAAAGA
TGATCACAAACGTATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACAT
TTTGACAATTGTTTTCAAAATAAATGTTTCGGAATACAGTGCAGCCCTTACGACAGGCTTACGTAG
AGCTTTTGTGAGATTTTTAAGTTGTTATTTCTGATTTGAAGTCTGTAAACCTCAGCAAGTTTCAAT
TTTTGTCATGACAATGTAGGAATTTGCTGAATTAATGTTTAGAAGGATGAAAAATAAAAAA
AAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAA
AAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAAT

FIGURE 34

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINC DVKAGKIIDPEFIVKCPAG
CQDPKYHVGTDVYASYSSVCGA AVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWR
ESFIVLESKPKKGVITYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPV TLMQLLAVTVAVA
TPTTLPRPSPSAASTT SIPRQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQ RQDPSGAAFOKP
VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI
GPAGPLMGVVQYGDNPAT HFNLKTHTN SRDLKTAIEKITQRGGLSNVGR AISFVTKNFFSKANGN
RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG
FYSLHVQSWFGLHKT LQPLVKRVCDTDR LACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN
LTKEFEISD TDTRIGAVQYTYEQRL EFGFDKYSSKPDILNAIKRVGYWSSGGTSTGAAINFAL EQL
FKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG VITYAIGVAWAAQEELEVIATHPARDHSFF
VDEFDNLHQYVPR IIQNICTEFNSQPRN

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
CAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGTTTTAATTAAGCATGGAAT
ACAGAAAACAACAAAAAACTTAAGCTTTAATTTTCATCTGGAATTCCACAGTTTTCTTAGCTCCCTGGACCC
GGTTGACCTGTGGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGTCTCCGACTACTCACCCCGAGTGTA
AAGAACCTTCGGCTCGCGTGCTTCTGAGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCCTTCCGAGTA
GGATGTCACTGAGATCCCTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTAC
CTCAGCCTTCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTTA
CAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAACCTGCTCTCATCAAAATCCATTTCTGGTCATTCT
TGGTGACCTCCCACCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCT
TGGTGGGGATATGAGGTTCTTACATTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGGC
ATTGTCCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGACAAGATTTTTTAGACACATATAATA
ACCTGACCTTGAAAACCATATGGCATTGAGGTGGGTAAGTGAAGTATCTTTTAAACCTAAACCACTCAGA
AAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGA
GAAGTTTTTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATATTT
CTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTTATATAATGTCCAGAGAT
TTGGTGCCAAGGATCTATGAAATGATGGGTACGTAACCCATCAAGTTTGAAGATGTTTATGTCCGGAT
CTGTTTGAATTTATTAAAAGTGAACATTCATATCCAGAAGACACAAATCTTTTCTTTCTATATAGAATCC
ATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTT
TGCGAGGTGCTAAGGAACACCACATGCCATTATTAACTTCACATTCTACAAAAGCCTAGAAGGACAG
GATACCTTGTGGAAAGTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTGAGTGTGCTGGCTT
ACACTGAACTGAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGG
CCCTTCAAAGATGATATGTGGAGGAATTAAATATAAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGG
ACCAAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAAGGGTGTTACTGAGTTATAAGCTCA
CTAGGCTGTAAAAACAAAACAATGTAGAGTTTTATTTATTGAACAATGTAGTCACTTGAAGGTTTTGTGTA
TATCTTATGTGATTACCAATTTAAAAATATATGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATA
CTGAACAAAATTTTACCTGTTTTTGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATT
ATTATTTAAATTAAGTCACTTCACTTTGTGTTTTTAAATGTTTTGACGATTTCATAACAAGATAAAAAAGGATAG
TGAATCATTCCTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCACTCCA
TTAATGTAAAGTCATAGGTGATTATTGTCATATCAGTAATCTCTTGGACTTTGTTAAATATTTTACTGTGGT
AATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

FIGURE 36

MASALWTVLPSPRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDFHF
TLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEAEKEDKMLA
LSLEDEHLLYGDIIRQDFLDTYNNLTILKTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYL
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQYEPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHV
KPIKFEDVYVGICLNLKVNIIHIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR
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 38

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDDFYVKGFYCAECRAGWYGGDCMRGQ
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGQII
KRVCGNERPAPIQSIGSSSLHVLFSHSDGSKNFDGFAHYEEITACSSSPCFHDGTCVLDKAGSYKC
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSGNE
KRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLHQLYSAAFSKQKLSAPTK
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP
KTQGLRWPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADL
KVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR
DLSTSFAQESHITVAGWNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWI
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

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCGTGATTTATTAACGTGGCTTAATC
TGAAGGTTCTCAGTCAAATTCCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTTGGCTGG
TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGGCGCTTCTGTTGC
TGGTCTTGCCCTTGGCTCAGTCTGCTAACTACATTGACAATGTGGGCAACCTGCACCTTCCTGTATTAGAACTCTGTA
AAGGTGCCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAGACGGCTGTGCGAGCC
TCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCTTAATGACAGACGAGCCTGGCCTAGACA
ACCCTGCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCAGTGGACTCTGGCCGGAGCAACCGAACTA
GGGCACGGCCCTTTGAGAGATCCACTATAGAAAGCAGATCATTTAAAAAATAAATCGAGCTTTGAGTGTCTTCGAA
GGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGGGCAGGAAAATTCTGAAAACACCACTGCCCTGAAG
TCTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAAATTACAGCATCAAGATCAATCGAGTAGATCCAGTGAAA
GCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGG
TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTC
ACAACTACGCTGTGCGTCTCCTGCGGCAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCCA
GCAGGAACAATGGACAGGCCCGGATGCCTACAGACCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCC
CCGAGGAGCAGCTTGAATAAACTGGTGCGCAAGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCG
GTGTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCA
GCCCAGAAAGTGCGGCTCATCTGATTACAGCCAGTGAAAGACGTGTTACCTCGTCGTGTCCCGCCAGGTTCCGGCAGC
GGAGCCCTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCAGGGCCAGGGGAGAGGAGCAACA
CTCCAAGCCCTCCATCTACAATTACTTGTCTATGAGAAGGTGGTAAATATCCAAAAGACCCCGGTGAATCTCTCG
GCATGACCGTCGCAGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCATCAGTGTGAGCCCGGAGGAG
TCATAAGCAGAGATGGAAGAATAAAAAACAGGTGACATTTTGTGTAATGTGGATGGGGTCGAACTGACAGAGGTGAGCC
GGAGTGAGGCAGTGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGC
CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCT
GGGTCTATGTGGCTGGAATTACCACGGTGCTTGTATACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTC
TGGGCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAAACAAACCTTTTTTTCATCAATCCATTGTTGAAGGAA
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATCTTCTTGCTGTCAATGGTAGAAGTACATCAGGAATGA
TACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTGGCACTT
TTTTATAGAAATCAATGATGGGTGAGGAAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACTATATTTATC
TTGTCAGTTTTTATATTTAAAGAAAGAATACATTGTAAAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTT
ACACCTCAGAAAATATGATTCCAAAAAATTAATACTAGTTTTTTTTCAGTGTGGAGGATTTCTCATTACTCTAC
AACATTGTTTATATTTTTCTATTCAATAAAAGCCCTAAACAACATAAATGATTGATTGTATACCCCACTGAATT
CAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTATGGCCATTTTAAATTTACAGCT
AAAAATTTTTTAAATGCATTGCTGAGAAACGTGCTTTCATCAACAAGAATAAATATTTTTTCAGAAGTTAAA

FIGURE 40

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPS
PEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSEFKKINR
ALSVLRRTKSGSAVANHADQGRENSENTTAPEVFFPRLYHLIPDGEITSIKINRVDPSESLSIRLV
GGSETPLVHIIIQHIYRDGVIARDGRLLPGDIIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM
REQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVFIFNVLDGGVAYRHG
QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRQSPDIFQEAGWNSNGSWSPG
PGERSNTPKPLHPTITCHEKVVNIIQKDPGESLGMTVAGGASHREWDLPIYVISVEPPGGVISRDGR
IKTGDILLNVDPVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPP
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

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT
 CTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACT
 TTCCACCTTTCCACAAATCCGATTACTGTTGCTGTTGACTTTTGTGCCTGACAGTGGTTGGGTGGGC
 CACCAGTAACCTACTTCGTGGGTGCCATTCAAGAGATTCCATAAGCAAAGGAGTTCATGGCTAATTTCC
 ATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTT
 GACAACTGTCCTTCTGTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC
 TTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG
 CTTTACAGAGGGTCGCCATCCTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAA
 CATCTGCATCCCTTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGG
 TAAAAAGTTTAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG
 ACTGCTTTATATCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG
 CATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGG
 GGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACCTACTGGGGAT
 GGGGAGGCCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTG
 CCTGAAGTGGGTAAATATAACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG
 GATGAAGCTCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGGTGAGTAGTTGTTCTTATAAAT
 TAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGATTCTGGTTTGGTGCATGACCC
 TGGATCTTTTGGTGATGTTTGGGAAGAACTGATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAA
 ATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTCCTTTTTGTATTTTCT
 TAGCAGAGCTCCTGGTGATGTAGAGTATAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGAT
 CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA
 AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGAT
 AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA
 AGGTACGAAGATACAATACTGTTATTCAATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTCAGGT
 GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTTGGGAATGAAGA
 GGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC
 CTTCAGGGGAGGACCTGCCAGGTATGCCTTCCAGTGATGCCACCAGAGAATACATTCTCTATTAGT
 TTTTAAAGAGTTTTTGTAAAATGATTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT
 ATTAACATAATAAATATGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAAGCAAAA

FIGURE 42

MGFNLTFLHSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKTLTN
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH
RNREKHLMYLLEHLHPFLQRQQLDYGIIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFI FHDV
DLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTTALSREQFFKVNGFSNNYWGWGGED
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

MALSSQIWAACLLLLLLLLASLTSGSVFPQQTGQLAELOPQDRAGARASWMPMFQRRRRRDTHFPI
CIFCCGCCCHRSKCGMCCKT

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
GACCTTCAACACAACCCCTCTTGTCAACATACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAAGTGAAG
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAAGAGGATGTGATT
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC
CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGAGCAGAACT
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATG
GTCCTCCTGTGTCTCCTGTGGTGCCCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTG
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCTGGG
AAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT
GGAAATCCCCACTCACTGCTCAGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA
TCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCA

FIGURE 46

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP
EGGTIIIVTQNRNRERVDFFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK
PKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC
VARNPVS RNFS SPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE
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

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCAATGACCTGCTGCGAAGGATGGACATCCTGCAATGG
ATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCT
TAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCCAGGAATT
ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG
CTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCACAGTCATTGGTGCTC
TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATGTGTAATTCTCCAAGC
AACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTCATCCAGAATCCTTCAA
CTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTTCAATAAACCCACCAGTAACG
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG
CTTATCCACTTCTCAGTATTTTtaggtctattgcttggttggaattctggaggctcctgtttgggct
CAGTCAGATAGTCATCGGTTTCCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG
TGAGTTTAAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAA

FIGURE 48

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA
TTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCM 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
CATGGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGAAGCCAATGACC
CATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC
TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG
CAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTCTGCCA
CTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC
TCCTCCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCCCT
TTCTGATCAGGAGGCTTCTTTATGAATTAAACTCGCCCCACCACCCCTCA

FIGURE 50

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAITAGIAAVLSGKCKYKS
SQKQHSPVPEKAIP LITPGSATTC

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

MKFQGPLACLLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVS
EALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGV
GHSGAWETSGGGHGFSGSQGGLGGQGNPGGLGTPVWHGYPGNSAGSFGMNPQGAPWGQGGNGGPPNF
GTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGSSNSGGGSGSQSGSSGSGSNGDNNGSSSGGS
SSGSSSSGSSSGGSSGGSSGGSSGNSGGSRGDSGSESSWGSSTGSSSGNHGGSGGGNGHKPGCEKPGNE
ARGSGESGIQGFRGQGVSSNMREISKEGNRLLGGSGDNYRGQGSWSGGGDAVGGVNTVNSETSPGM
FNEDTFWKNEFKSKLGFINWDAINKDQRSSRIP

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

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG
CTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT
ACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACGCGCCGGCTCCAGTGTTTCC
CACAGCCCCCAAACGGAACCTGGTTTTGGGGTCACCTGGGCCTGATCACTCCTACAGAGGAGGGC
TTGAAGGACTCGACCCAGATGTGCGCCACCTATTCCCAGGGCTTTACGGTATGGCTGGGTCCCAT
CATCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCAATGCCTCAGCTGCCA
TTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATACTGCTG
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCCTTCCATTTCAACATCCT
GAAGTCCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG
CCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTA
CAGAAATGCATCTTCAGCTTTGACAGCCATTGTGAGGAGAGGCCAGTGAATATATTGCCACCAT
CTTGAGCTCAGTGCCCTTGTAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT
ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGAC
GCTGTCTATCCGGGAGCGGCGTCGACCCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAA
AGCCAAGTCCAAGACTTTGGATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACG
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCG
ACAGGAGGTGCAAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCC
AGCTGCCCTTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATC
TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTG
CCTCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGACC
CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCCCTTTCTCCGCA
GGGCCCAGGAACATGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCTGGCGTTGAT
GCTGCTGCACTTCCGGTTCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAATTGATCATGC
GCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCCTGAATGTAGGCTTGCATGACTTTCTGAC
CCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGCTGTCAA

FIGURE 54

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWGHLG
LITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP
WLGEGILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI
SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC
RLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLDLDFIDVLLLSKDEDGKALSDEDIRAEADTF
MFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR
LHPPAPFTISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENSKGRSP
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

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCIQLSLALTWYSLSFIPFAR
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

MLCLCLYVPVIGEAEQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDLDG
QLDFEEFVHYLQDHEKKRLRVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKILKSMDKNG
TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMWWRHLVAGGG
AGAVSRTCTAPLDRLKVLMOVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIAK
FMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQAQSSIYPMEVLKTRMALRKTGQYSGMLDCARR
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNSADPGVFVLLACGTMSSTC
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
 CACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTGCCTCAGCT
 GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAAACCTTCTGATAT
 CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG
 AGCTGTGCGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTGCTGATCAAGTGATAGTT
 GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT
 CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG
 AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCC
 CAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACTTCTCGGAAGTCTCCAATAC
 CAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGA
 TCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG
 ACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGT
 CTCTTCTTTCTTTGCCATCAGCTGGGCACCTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAAT
 GTGCCTTGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC
 CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG
 AGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAAT
 CTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAACTAGACAAGTGTGTTAAGA
 GTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT
 CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGC
 TGTAATGTTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCAC
 AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG
 GCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTC
 TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGT
 CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 60

MASLGQILFWSIIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKC
YIITSKKGKNANLEYKTGAFSMPEVNVNDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVS
NTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTESI KRRSHLQLLNSKASL
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

TGACGTCAGAATCACCATGGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG
CACCAGGAGCCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGT
GGGCTACCCCCCTGGTGGTGGTTATGGGGGTCTGCCCTGGAGGGCCTTATGGACCACCAGCTGG
TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCTCTGGAAGTCCAGGAGGACCATATG
GCGGTGCAGCTCCCGGGGGCCCCATATGGTCAGCCACCTCCAAGTTCCTACGGTGCCAGCAGCCT
GGGCTTTATGGACAGGGTGGCGCCCCCTCCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA
ATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA
GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGAAGAACCCTCTT
CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC
AAATGGGCTACAACCTGAGCCCCAGTTCACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCT
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA
CCATGACAGCTTCTCGGATGCTATGACCCCAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTCTGTCCCTCTAGAAGAAC
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCA
AATAGTGAGGACCGGGGCTGAGGCCACACAGATAGGGGCCTGATGGAGGAGAGGATAGAAGTTGA
ATGTCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCTTGTAATGG
AGTTAGTGTCCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAAGTGTTCATCGGCCTGTTACC
GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAACGAGCCCATTTCTCCAAAGTGGAAT
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCTGCCACACCCATAAAT
CCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT
CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCCTGCCATGCTCTGCTCGGCT
TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTTAATTGCATTTTTTTTC
ATTTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

FIGURE 62

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG
HPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDSH
SGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDR
DRSGSISYTELQQALSOMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREK
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

MQGRVAGSCAPLGLLLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSSTGPSNSEHPQPAL
DPRSNDLARVPLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPPEDPWQMMAAAEDRLGEA
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRLLPRSNSLGAGGKILSQRP
PWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRMPHPGEGIWGINNQPPGTSWGNINRYPGGS
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
TGGGCTGCCCCCTTGTCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA
CTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA
TTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCCTCCACCATGC
AAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTGTGTCCTTCTTGGCCC
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAGCAGGCCCCCACCCCTC
CTGAGTGGCAATAAATAAAATTCGGTATGCTG

FIGURE 66

MSGGLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSGTSVTL
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
CAGGTGCCCCGTGCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCC
TTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCG
CTGGGCCTGCCGTTCCCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC
AAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG
GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCCAGTAGCGA
GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT
GCCTGCCCATCTAGGTCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA
GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA
AGACTCTGCCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACCTTTTATATATTTATATAAAATTAG
TAGTGAGATGTAAAAAAAAAAAAAAAAAAAAA

FIGURE 68

MANPGLGLLLALGLPFLRLRWGRAWGQIQTTSANENSTVLPSTSSSSSDGNLRPEAITAIIVVFS
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

GCCAGGAATAACTAGAGAGGAACAATGGGGTTATTGAGAGGTTTTGTTTTCTTCTAGTTCTGTGCCTGCTGCACGAG
TCAAATACTTCCCTTCATTAAGCTGAATAATAATGGCTTTGAAGATATTGTCATTGTTATAGATCCTAGTGTGCCAGAA
GATGAAAAAATAATTGAACAAATAGAGGATATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGA
TTTTTTTTTCAAAAATGTATCTATATTAATTCTTGAGAATTGGAAGGAAATCCTCAGTACAAAAGGCCAAAACATGAA
AACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCCAGGTAGAGATGAACCATACACCAAGCAGTTTACA
GAATGTGGAGAGAAAGGCGAATACATTCACTTCACCCCGTGACCTTCTACTTGGAAAAAACAAAATGAATATGGACCA
CCAGGCCAACTGTTTGTCCATGAGTGGGCTCACCTCCGGTGGGGAGTGTTTGATGAGTACAATGAAGATCAGCCTTTC
TACCGTGCTAAGTCAAAAAAATCGAAGCAACAGGTGTTCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAAGTGT
CAAGGAGGCAGCTGCTTAGTAGAGCATGCAGAAATTGATTCTACAACAAAACCTGTATGGAAAAGATTGTCAATTCTTT
CCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATGCAAAGTATTGATTCTGTTGTTGAATTTTGTAAACGAA
AAAAACCATAATCAAGAAGCTCCAAGCCTACAAAACATAAAGTGCAATTTTAGAAGTACATGGGAGGTGATTAGCAAT
TCTGAGGATTTTAAAAACACCATACCCATGGTGACACCACTCTCCACCTGTCTTCTCATTGCTGAAGATCAGTCAA
AGAATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGGTAAGGACCGCCTAAATCGAATGAATCAAGCAGCA
AAACATTTCCCTGCTGCAGACTGTTGAAAATGGATCCTGGGTGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTA
AATAAGTAATCCAATAAAAAAGCAGTGATGAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGA
ACTTCCATCTGCTCTGGAATTAATATGCATTTTCAGGTGATTGGAGAGCTACATTCCTCACTCGATGGATCCGAAGTA
CTGCTGCTGACTGATGGGAGGATAACACTGCAAGTTCTTGATTGATGAAGTGAACAAAAGTGGGGCCATTGTTTCAT
TTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTTATGTT
TCAGATGAAGCTCAGAACAATGGCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAAAG
TCCCTTCAGCTCGAAAGTAAGGGATTAACACTGAATAGTAATGCCTGGATGAACGACACTGTCATAATTGATAGTACA
GTGGGAAAGGACACGTTCTTTCTCATCACATGGAACAGTCTGCCTCCAGTATTTCTCTGGGATCCAGTGGGAACA
ATAATGGAAAATTTACAGTGGATGCAACTTCCAAAATGGCCTATCTCAGTATTCAGGAAGTGCAGAGGTGGGCACT
TGGGCATACAATCTTCAAGCCAAAGCGAACCAGAAACATTAACATATTACAGTAACCTTCTCGAGCAGCAAATCTTCT
GTGCTCCAATCACAGTGAATGCTAAAATGAATAAGGACGTAAACAGTTTCCCCAGCCCAATGATTGTTTACGCAGAA
ATTCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTCATTGAATCACAGAATGGACATACAGAAGTT
TTGGAATTTTGGATAATGGTGCAGGCGCTGATTCTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATAT
ACAGAAAATGGCAGATATAGCTTAAAGTTTCGGGCTCATGGAGGAGCAACACTGCCAGGCTAAAATTACGGCCTCCA
CTGAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGGAAATTGAAGCAAACCCGCCAAGACCTGAAATTGAT
GAGGATACTCAGACCACCTTGGAGGATTTGAGCCGAACAGCATCCGGAGGTGCATTTGTGGTATCACAGTCCCAAGC
CTTCCCTTGCTGACCAATACCCACCAAGTCAAATCACAGACCTTGATGCCACAGTTCATGAGGATAAGATTATCTT
ACATGGACAGCACCAGGAGATAATTTTGATGTTGGAAAAGTTCAACGTTATATCATAGAATAAGTGCAAGTATTCTT
GATCTAAGAGACAGTTTGTATGATGCTCTTCAAGTAAATACTACTGATCTGTCCACCAAGGAGGCCAACTCCAAGGAA
AGCTTTGCATTTAAACCAGAAAATATCTCAGAAGAAAATGCAACCCACATATTTATGCCATTAAAAGTATAGATAAA
AGCAATTTGACATCAAAAGTATCCAACATTGCACAAGTAACTTTGTTTATCCCTCAAGCAAACTCCTGATGACATTGAT
CCTACACCTACTCCTACTCCTACTCCTACTCCTGATAAAAGTCATAATTCTGGAGTTAATATTCTACGCTGGTATTG
TCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAAGTACCACCATTGGAACCTTAACGAGAAAAAATCTTC
AAGTAGACCTAGAAGAGAGTTTTAAAAAACAAAACATGTAAGTAAAGGATATTTCTGAATCTTAAAATTCATCCCAT
GTGTGATCATAAATCATAAAAATAATTTTAAAGATGTCGGAAAAGGATACTTTGATTAAATAAAAAACACTCATGGATA
TGTA AAAAATGTCAAGATTAAAAATTAATAGTTTCAATTATTGTTATTTTATTTGTAAGAAATAGTGATGAACAAAG
ATCCTTTTTTACATACTGATACCTGGTTGTATATTATTTGATGCAACAGTTTCTGAAATGATATTTCAAATTCATCAA
GAAATTAATAATCATCTATCTGAGTAGTCAAAATACAAGTAAAGGAGAGCAAATAAACACATTTGGAAAAAATAAAAA
AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 70

MGLFRGFVFLVLCLLHQSNSTFIKLNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTYLFE
ATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY
IHFTPDLLLGGKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISAGISGRN
RVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDQVQTEKASIMFMQSIDSVVEFCNEKTHNQEAP
SLQNIKCENFRSTWEVISNSEDFKNTIPMVTTPPPPPVFSLLKISQIRIVCLVLDKSGSMGGKDRNLN
MNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTSICSGIK
YAFQVIGELHSQLDQSEVLLLLTDGEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG
SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFL
ITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR
AANSSVPPITVNAKMNDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA
GADSFKNQGVYSRYFTAYTENGRYSLKVRAGHGANTARLKLRPPLNRAAYIPGWVNGEIEANPP
RPEIDEDTQTTLEDFSRASGGAFVVSQVPSLPLPDQYPPSQITDLDTVHEDKIILTWTPAGDN
FDVGKVQRYIIRISASILDRLDSFDDALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAI
KSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPTPTPTPTPTPTDKSHNSGVNISTLVLSVIGSVVI
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

CTCCTTAGGTGGAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAGACCATACGTCCCCGGGCGAGGGTGA
CAACAGGTGTCTCTTTTTGATCTCGTGTGTGGCTGCCTTCTTATTTCAAGGAAAGACGCCAAGGTAATTTTGACCCA
GAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCAAGTTATGCCAGGATTTACTAGAGAGTGTCA
ACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTGTGGTTGGAGGAGAGAACCCTTTGTGGGGCTGCGTTCTCTTAGCA
GTGCTCAGAAGTGACTTGCCTGAGGGTGGACCAGAAGAAAGGAAAGGTCCCCTCTGTGCTTGGCTGCACATCAGGAA
GGCTGTGATGGGAATGAAGGTGAAACTTGGAGATTTCACTTCAGTCATTGCTTCTGCTGCAAGATCATCCTTTAAA
AGTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGCTC
CGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCAGGGAAGCCCTTCCGTGGGGGGCCCCGGCTTTGAGGGATGCC
ACCGGTTCTGGACGCATGGCTGATTCTGAATGATGATGTTTCCGCGGGGGCTGCTTGCCTGGATTTCCTGGGTGGT
GTTTTGCTGGTGTCTCTGTGTGTCTATCTCTGCTGTACATGTTGGCCTGCACCCCAAAAGGTGACGAGGAGCAG
CTGGCACTGCCCAGGGCCAACAGCCCCACGGGGAAGGAGGGGTACCAGGCCGTCTTCAGGAGTGGGAGGAGCAGCAG
CGCAACTACGTGAGCAGCCTGAAGCGGCAGATCGCACAGCTCAAGGAGGAGCTCAGGAGAGGAGTGTGAGCAGCTCAGG
AATGGGCAGTACCAAGCCAGCGATGCTGCTGGCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTC
CTGGCCTTCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGCAGCAGTG
CCTTTTCGATAGCTTTACTCTACAGAAGGTGTACCAAGCTGGAGACTGGCCTTACCCGCCACCCCGAGGAGAAGCCTGTG
AGGAAGGACAAGCGGGATGAGTTGGTGGAGCCATTGAATCAGCCTTGGAGACCCTGAACAATCTGCAGAGAACAGC
CCCAATCACCGTCTTACACGGCCTCTGATTTTCATAGAAGGGATCTACCGAACAGAAAGGGACAAAGGCACATTGTAT
GAGCTCACCTTCAAAGGGGACCACAAACAGGAATCAAACGGCTCATCTTATTTCGACCATTTCAGCCCCATCATGAAA
GTGAAAAATGAAAAGCTCAACATGGCCAAACAGCTTATCAATGTTATCGTGCCTTAGCAAAAAGGGTGGACAGTTT
CGGCAGTTTCATGCAGAAATTCAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGG
AAAGAAGAAATAATGAAGTCAAAGGAATACTTGAAAACACTTCCAAAGCTGCCAACTTCAGGAACCTTACCTTCATC
CAGCTGAATGGAGAATTTCTCGGGGAAAGGGACTTGATGTTGGAGCCCGCTTCTGGAAGGGAAGCAACGCTCCTTCTC
TTTTCTGTGATGTGGACATCTACTTCAACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAAG
GTATTTTATCCAGTTCTTTTTCAGTCAGTACAATCCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAA
CAGCAGCTGGTCATAAAGAAGGAACTGGATTTTGGAGAGACTTTGGATTTGGGATGACGTGTCACTATCGGTGAGAC
TTCATCAATATAGGTGGGTTTGTCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTC
CACAGCAACCTCATAGTGGTACGGACGCCTGTGCGAGGACTTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAG
CTGACCCCGGAGCAGTACAAGATGTGCATGCAGTCCAAGGCCATGAACGAGGCATCCACGGCCAGCTGGGCATGCTG
GTGTTTCAGGCACGAGATAGAGGCTCACCTTCGCAACAGAAACAGAGACAAGTAGCAAAAAACATGAACTCCGAGA
GAAGGATTGTGGGAGACACTTTTTCTTTCTTTTTCGAATTACTGAAAGTGGCTGCAACAGAGAAAAGACTTCCATAAA
GGACGACAAAAGAAATGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTCTGTTGGGCTTTTTTACAACAGA
AATCAAAATCTCCGCTTTCCTGCAAAAGTAACCCAGTTGACCCCTGTGAAGTGTCTGACAAAAGGCAGAAATGCTTGTG
AGATTATAAGCCTAATGGTGTGGAGGTTTTGATGGTGTTTACAATACTGAGACCTGTTGTTTTGTGTGCTCATTGA
AATATTCATGATTTAAGAGCAGTTTTGTAAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGA
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAAATATCAGAAGGCAGGAGAGGAGATAGGCTTATTATGATACT
AGTGAGTACATTAAGTAAATAAATGGACCAGAAAAGAAAAGAACATAAATATCGTGTCAATTTTCCCCAAGAT
TAACCAAAAATAATCTGCTTATCTTTTTGGTTGCTCTTTTAACTGTCTCCGTTTTTTTTCTTTTATTTAAAAATGCACT
TTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCACCTTGCAAGCCTTACAAGAGAGCACAAGTTGGCCTAC
ATTTTTATATTTTTTAAGAAGATACTTTGAGATGCATTATGAGAACTTTCAGTTCAAAGCATCAAATTTGATGCCATAT
CCAAGGACATGCCAAATGCTGATTCTGTGAGGCACTGAATGTGAGGCATTGAGACATAGGGAAGGAATGGTTGTACT
AATACAGACGTACAGATACTTTCTCTGAAGAGTATTTTGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATGAC
ACTTTCTGCTTTACAGAAAAGGAACTCATTGAGACTGGTGATATCGTGATGACCTAAAAGTCAGAAACCACTTTT
CTCCTCAGAAGTAGGGACCGCTTTCTTACCTGTTTAAATAAACCAAGTATACCGTGTGAACCAACAATCTCTTTTC
AAAACAGGGTGTCTCTCTGGCTTCTGGCTTCCATAAGAAGAAATGGAGAAAATATATATATATATATATATATTGT
GAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTTTGCTACATGTTATCCACCCAGGCCAGGTGGAAG
TAACTGAATATTTTTTAAATTAAGCAGTTCTACTCAATCACCAGATGCTTCTGAAAATTCATTTTATTACCATT
CAAATATTTTTTAAAAATAAATACAGTTAACATAGAGTGGTTTTCTTCATTGATGAAAATTTATTAGCCAGCACCAG
ATGCATGAGCTAATATCTCTTTGAGTCTTGTCTTCTGTTTGTCTCAGAGTAACTCATGTTTAAAGCTTCAAGAAC
ATTCAAGCTGTTGGTGTGTAAAAAATGCATTGTATTGATTGTACTGGTAGTTTATGAAATTTAATTAACACAGG
CCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

FIGURE 72

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALPRANSPTGKEGYQAVLQEW
EQHRNYVSSILKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETNNPA
ENSPNHRPYTASDFIEGIYRTERDKGTLTYELTFKGDHKHEFKRLILFRPFSPIMKVKNEKLNMAN
TLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNF
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSQY
NPGIIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYR
KYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPQYKCMQSKAMNEASHGQLGMLVFRHEIEAHL
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 73.

[illegible]

FIGURE 74

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPA SYPECGNNAQSPIDIQTDSVTFDLPALQ
PHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGSEHQINSEAT
FAELHIVHYDSYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHLHLHEVRHKDQKTSVPP
ENLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLV
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS
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
ATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCTTGACAGCTCC
AGAGAAGTGGAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAATATACTCCAATCTGA
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC
ACGCTGGTGTCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCCTCGTCCC
AGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT
CAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGTGTTCCTTTTT
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATTT
GATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGAAAAAATCGTGATTA
ACTTTATCACCCCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA
AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA
GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGAAAATTTTTGTGACTCTGAAG
AAAACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCCGGATAAA
ACAGTCATTGAATATGAATATGATGTCAGAACCACTGACATTTGTGCGGGGCTGAAGAGCAGGA
GCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG
TCTTGGGCCCCGAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTTGGCG
CAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGA
TCCCCAAACTGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCG
AGCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT
CCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGTTATA
TGTGCAGATGGAAAACTGATGCCAACACTTCCTTTTGCCTTTGTTCCTGTGCAAACAAGTGAG
TCACCCCTTTGATCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTGAGTGT
CTGTGAGAATTACTTATTTCTTTCTCTATTCTCATAGCACGTGTGTGATTGGTTCATGCATGTA
GGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGTTGTTCTATGCAGAGAA
AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGGTGGGTGT

FIGURE 76

MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQOIY
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLK
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNFDRFFVPAEK
IVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC
DSEENTEGTSLTQQESLSRTIPDKTVIEYEYDVRTTDICAGPEEQELSLQEEVSTQGTLLSQA
ALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLVDWDPQTGRLCIPSLSSFDQDS
EGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYILMQFMEEWGLYVQMEN

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

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCGAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC
 CTGGGAAGATGGCCGGCCCGTGGACCTTCACCCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATC
 CAAGCCACCCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCCAAAGTCATCAAAGAAAAGCTGAC
 ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC
 GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCCTGAAGCACATC
 ATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA
 GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCCCTGGTCAAGACCA
 TCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGC
 CCCACCCGCCTGGTCCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTGTGTA
 TAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGCAGGTGATGAACCTCCTAGTGCCATCCCTGC
 CCAATCTAGTGAAAAACCAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGAC
 CTCCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTA
 TCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAA
 AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCCTGGACAACATCCCG
 TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
 ATTCATGGTCCTGTTGGACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC
 TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC
 ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTT
 TCCCTCCAGTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT
 TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG
 ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA
 CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTGATGGTGAAGG
 CCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCC
 TTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGATGGCAGCCATCAGGGAAGGCTGG
 GTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTG
 CCTGTGAAAAA

FIGURE 78

MAGPWTFITLLCGLLAATLIQATLSPTAVLILGPKVIEKLTQELKDHNATSIQQLPILLSAMREK
PAGGIPVLGSLVNTVLKHIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYLGAKLLDSQGKVT
KWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPEEFMVLLDSVLPESAHLKSSIGLIN
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPLFTLGIEASSEAQFYT
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSLVKALG
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
CTTGGCCTCCAACCTTGTTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCAT
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCTGGTGCCAGCATTGTGACAGCAGTTGGCTTCT
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC
ACCCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCCAGGCCATGATGGTGACATCCAGTGCAAT
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTCATCCTTGGAGGCCTCCTGGGATTC
ATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTCACCCTGGTGCCTGACAG
CATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAG
CTGGAATCATCCTCTGCTTTTTCTGCTCATCCCAGAGAAATCGCTCCAACCTACTACGATGCCTAC
CAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA
GTTCAATTCTTACAGCCTGACAGGGTATGTGTGAAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTG
GGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCCTGGATCGT
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG
GCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCC
TCACCTTGCTGCTCCCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCA
GGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACA
TCCCACTGACTGACCCTCTGTGATCAAAGACCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATT
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTC
CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCCA
GACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 8o

MASLGLQLVGYILGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD
IYSTLLGLPADIQAAQAMMTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL
LGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQRNRSNYY
DAYQAQPLATRSSPRPGQPPKVKSEFNSSYSLTGYV

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
 CCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCCCT
 GCCCACCGCTGCTTCCTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG
 GTTGATCTGTGGCCCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCCTCCCGACTCCGCTCCCGG
 ACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCTCTCCTCCTTGCTGGGA
 CTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGACATGTTCTGCCTTTT
 CCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGT
 ACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCT
 GTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC
 TCCCTCTGGACTCCGGGCCCCACCAAGTCTGCCAGCACAACGGGACCATGTACCAACACGGAG
 AGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCCTGCCCAACCAGTGTGTCTCTGCAGCTGC
 ACAGAGGGCCAGATCTACTGCGGCCTCACAACTGCCCCGAACCAGGCTGCCAGCACCCCTCCC
 ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACA
 GTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAG
 AGAGGCCCGGGCACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT
 CAGACCCAAGGGAGCAGGCAGCACAACCTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCT
 GTGTGCATGGCGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC
 CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC
 CACCGAGTACCCCTGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCAGAGG
 ACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTC
 CTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGC
 CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAGAGAG
 GTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAG
 GAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAGGAAGGTCCT
 GGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAG
 ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTAATAAA
 TAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 82

MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHEL F
PSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR
HPQDPCSSDAGRKRGP GTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTYS
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPK VAGKCCKICPEDKADPGHSE
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH
SQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSPDPGAEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

FIGURE 83

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAGAGCCTCTCC
 GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCATCCGTCACCTCTCCTGTCA
 TCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGGTTCTGAGTC
 TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAG
 GACGCAGCATTCTCCTGTTTCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGGGTTCTTCAGGGG
 CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATC
 AAGGCAGGACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGGCGCATCTCTCTGAGGCTGGAAAACATTACT
 GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTPTCCAGTCTTACTACCAGAAGGCCATCTGGGAGCT
 ACAGGTGTGAGCACTGGGCTCAGTTCTCTCATTTCCATCACGGGATATGTTGATAGAGACATCCAGCTAC
 TCTGTCACTCCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTGGAAAGGTCCACAAGGACAGGATTGTGTC
 ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAA
 CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG
 GAGATACCTTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA
 TTTTTTGGCATTGTTGGACTGAAGATTTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGGAACCTGGACTG
 GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAG
 AGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACCTGTAACCCATAGAAAAGCTCCCCAGGAGGTG
 CCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAAACATTA
 CTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGA
 AGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTTC
 ACATTAAATCCCGTTTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTA
 TGAGTGTGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCTGACATGTGGTTTG
 AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTCTATAATGAGCAAAATGGAACCTCCCATAGTCATCTGC
 CCAGTCAACCAGGAATCAGAGAAAGAGGCCCTTTGGCAAAGGGCCTCTGCAATCCCAGAGACAAGCAACAG
 TGAGTCTCTCTCACAGGCAACCACGCCCTTCTCTCCCAGGGGTGAAATGTAGGATGAATCACATCCCACAT
 TCTTCTTTAGGGATATTAAGGTCTCTCTCCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCA
 GATGAAGGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGG
 CTGACATTACATTTAGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAG
 AACCGTCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAG
 ATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTTCATTATATTACACTTTCAGTAAAAAAA

FIGURE 84

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSSVVH
LYRDGKDQPFMQMPQYQGR TKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQKAIWELQ
VSALGSVPLISITGYVDRDIQLLCQSSGWFFRPTAKWKGPQGQDLSTDSRTNRDMHGLFDVEISL
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK
FQWKIQAE LDWRRKHGQAE LR DARK HAVE VTLD PET AHPKLCVSDLKTVTHR KAPQEVPHSEKRF
TRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVC RDDVD RRKEYVTLS PDHGYWVLR L NGEHLYFT
LNPRFISVFPRT PPTKIGVFLDYECGTISFFNINDQSLIYTLCRFEGLLRPYIEYPSYNEQNGT
PIVICPVTQESEKEASWQRASAIPETSNSSESSSQATT PFLPRGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 85

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCCCCCT
 GCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTTCCGTGA
 CGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATT
 TACCCTGGCCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGACCAGGATGCTCC
 AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACCGATTCCACCTCCTTG
 GGGACCCACATACCAAGAATTGCACCTGAGCATCAGAGATGCCAGAAGAAGTGATGCGGGGAGA
 TACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCTGTGAA
 TGTGACAGCCTTGACCCACAGGCCCCAACATCCTCATCCCAGGCACCCTGGAGTCCGGCTGCCCCC
 AGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATA
 GGGACCTCCGTGTCCCCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCTCATCCCACA
 GCCCCAGGACCATGGCACCAGCCTCACCTGTCAGGTGACCTTCCCTGGGGCCAGCGTGACCACGA
 ACAAGACCGTCCATCTCAACGTGTCTACCCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGA
 GACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCT
 GCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGA
 GAGGCCTGACCCTGTGCCCCCTCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCAC
 CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCT
 GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTGACTCAGGGGTGGTTCGGGGGAGCTGGAG
 CCACAGCCCTGGTCTTCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAA
 TCGGCAAGGCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTC
 AGCCTCTCAGGGGCCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCAG
 CTTCTGCCCCCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGTG
 AAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG
ATGAGAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCCTCCAGGCAAGGGAGAAGTCA
 GAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATG
 TGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCC
 TCCCTTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 86

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFYPSHGWIIYPGPVVHGYWFREG
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY
KHHRLSVNVTALTHRPNILIPGTLES GCPQNLTCSVPWACEQGTPPMISWIGTSVSP LDPSTTRS
SVLTLIPQPQDHGTS LTCQVTFPGASVTTNKT VHLNVSYPPQNLTMTVFQGDGT VSTVLGNGSSL
SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP
LGSQQVYLNVS LQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDTGIE
DANAVRGSASQGPLTEPWAEDSPPDQPPPASARSSVGE GELQYASLSFQMVKPWDSRGQEATDTE
YSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT
TCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTTGA
TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGACATGACCTCTG
GGGGTGGCGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC
CAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACT
ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCCAATAAGTCCCCCATGCAGCACTGG
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT
GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC
CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCCAGAAAACAGCATCTTATTACTCACCTAT
GGCCAGCGGGAATTCAGTGCAGGATTTGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAA
CGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG
GATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT
GGAACATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG
TGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAA
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA
AAAAAA

FIGURE 88

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAAT
SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYG
EGKCWTDNGPVIPIPVYDFGDAQKTASYYSYPYQREFTAGFVQFRVFNNERAANALCAGMRVTGCN
TEHHICIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSSSREITEAAVLLFYR

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
CGCCGCCCTTGTCCTCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACG
CTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTG
CCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGGTGGCCGCGCTCT
CTGTCAACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGAGTCTCCATGTTCAAC
AGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCTTCTTCAT
ATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCTTCTGCAGTGGCCCTCCAGCTG
TCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAAAAGAAACCCTTCTTGATTACCTTCA
TGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCCTGGAAGAAGGAAG
GCATAGGCTTCGGTTTTCCCTCGGAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG
TCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAATAAAATATGTTTTGTAGTAACA
TTAAGACTTATATACAGTTTTAGGGGACAATTAATAAAAAAAAAA

FIGURE 90

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPFTFTPEEYDKQDIQLVAALSVTLGLFA
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVTEMALFV
TVFGLKKKPF

Transmembrane domain:

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

FIGURE 91

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC
TCGCTGCTGCTTCGTGTTCCCTGGTGCAAGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG
GTCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT
CGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCT
GGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCCGAACCACAGCCCCC
CACCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG
GCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT
CCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAG
AGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG
GAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTG
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTG
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCCAGATTACAACACTAC
CATAGTGATACCCCCTACTACCCATCTGGGTGAACCGGGGCAGGCCACAGAGGCCAGGCCAGGGC
TGGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCTC
AGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG
AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG
TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC
CCTTGGTTCTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACA
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGG
GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTGTGCTGTGCTGAGCATGG
CATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC
CAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG
GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCACACTAAGGCCACAGCCCATC
CGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCG
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGTCTCCCGGATCTGGATGGCGC
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGCCGAGAGCATGTGCTGGATCTGTTC
TGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGTGAAACCGCTGATTGCTGACTTT
TGTGTGAAGAATCGTGTTCTTGAGCAGGAAATAAAGCTTGCCCCGGGGCA

FIGURE 92

MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDP
AKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHS DTPYYP SG

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

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCC
CTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTTTCTT
CTGGTTGGTGTCTCTACTGATTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACA
AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAA
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAAACC
AGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGGGCTTTGGAATCATGA
GTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTTCAT
GGAGATTCTCCTCAATTCTTCCTTTATTTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGT
ATTCTGGGGCATTGTATTTTTTTGATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTC
TCCTGACCCACCTGCTGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG
TCAGCATTTATAATCCTGGTGTCTATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG
AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGAT
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT
TTTTCTGAAAATCCCTTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 94

MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV
FSFVNTLSDSLPGTGVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVLLT
HLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCLLCQDKNFLLYNQSR

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

AATTTTTCACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTCGTG
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTTGTCTTCTAGGATCAAC
TCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACCTGGCTCCGGATCAGG
GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCCTTCTTTAAGTCTGATACCATTAACA
CAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACACCTGGTAC
CCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC
CAATTTTTGTACACAACCTGGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC
TTCACGAGCCTCATCATCCATTCCCTTGTTCCCGGGAGGCATCCTGCCCACCAGTCAGGCAGGGGC
TAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAGGAGCAGGTGTAAATCCTGCCACCCAGG
GAACCCAGCAGGCCGCTCCCAACTCCCACTGGCACAGATGACGACTTTGCAGTGACCACCCCT
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA
GTAAGCTGTTTCAAATTTTTTCAACTAAGCTGCCTCGAATTTGGTGATACATGTGAATCTTTATC
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATT
TACCTGAAAATATTCTTGAAATTTAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAA
CAATAATTCAATGGATAAATCTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATAT
TAAAACATATTTGAAAACCTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 96

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 97

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT
 CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTTGACCATG
 GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGCCAGCCTGC
 AGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAAATTTCCCTTTATACCTGACCAAGTTGC
 CGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGTGTGAGGGGACTCAGGCAAGGCAACTGAG
 GGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGTGCTGGTGACCAGGGGCCCTGGACCCAGAGGA
 GCAGGCAGAGTACCAGCTACAGGTCAACCTGGAGATGCAGGATGGACATGTCTTGTGGGGTCCAC
 AGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCCATTTCTCTCAAGCCATCTAC
 AGAGCTCGGCTGAGCCGGGGTACCAGGCCCTGGCATCCCCCTTCTCTTCTTGGAGGCTTCAGACCG
 GGATGAGCCAGGCACAGCCAACTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCCAGC
 CTTCCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC
 ACCAGCCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA
 CCAGGCCTCAGGCCACCAGGCCACTGCCACCGTGGAAAGTCTCCATCATAGAGAGCACCTGGGTGT
 CCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCTTATACCCGCACCACATGGCCCCAGGTA
 CACTGGAGTGGGGGTGATGTGCACATACCTGGAGAGCCATCCCCGGGACCCCTTTGAAGTGAA
 TGCAGAGGGAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCC
 AGGTGCGGGCTCAGAAATCCCATGGCGAGGACTATGCGGCCCTCTGAGCTGCACGTGCTGGTG
 ATGGATGAGAATGACAACGTGCCATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCT
 CAGTCCACCAGGTACTGAAGTGACTAGACTGTGACGAGAGGATGCAGATGCCCCCGGCTCCCCCA
 ATTTCCACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTC
 CAGGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAT
 CCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGTGAAG
 TCGAAGTCGCAGTCACAGATATCAATGATCACGCCCCTGAGTTCATCACTTCCAGATTGGGCCCT
 ATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA
 CCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACAGAGAAGGGACTTTTG
 GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG
 GCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCCC
 AGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGTGATGCCACCCCCCAAGTTGG
 ACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCCAGCCGGCTCTTTCTGTGCTGACCATC
 CAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT
 CTGCATTGAGAAATCTCCGGGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGG
 ACACCTACACGGTGCTTGTGGAGGGCCAGGATACAGCCCTGACTCTTGCCCTGTGCCCTCCCAA
 TACCTCTGCACACCCCGCCAAGACCATGGCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCT
 GGCCAGTGGGCACGGTCCCTACAGCTTCACCCCTGGTCCCAACCCACGGTGCAACGGGATTGGC
 GCCTCCAGACTCTCAATGGTTCCCATGCCTACCTCACCTTGCCCTGCATTGGGTGGAGCCACGT
 GAACACATAATCCCCGTGGTGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTTCGAGTGAT
 CGTGTGTGCTGCAACGTGGAGGGGCAGTGCATGCGCAAGGTGGGCCGCATGAAGGGCATGCCCCA
 CGAAGCTGTGCGCAGTGGGCATCCTTGTAGGCACCCCTGGTAGCAATAGGAATCTTCTCATCCTC
 ATTTTCACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCT
 GAAGGCGACTGTC**TGA**ATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAG
 TCCCCTGGGAGAGAGCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCTCCA
 TCTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAACTT
 TATGGACTGCCCATGGGAGTGCTCCAAATGTGAGGGTGTTTGCCCAATAATAAAGCCCCAGAGAA
 CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 98

MVPAWLWLLCVSVPOALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT
EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVPHFSQAI
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRLGALALSPKG
STSLDHALERTYQLLVQVKMDQASGHQATATVEVSIESTWVSLEPIHLAENLKVLYPHHMAQ
VHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDIAAPLELHVL
VMDENDNVPICPPRDPVTSIPELSPPGTEVTRLAEDADAPGSPNSHVYQLLSPEPEDGVEGRA
FQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCEVEVAVTDINDHAPEFITSQIG
PISLPEDVEPGTLVAMLTAIDADLEPAFRLMDFAIERGDTEGTFGLDWEPPDSGHVRLRLCKNLSY
EAAPSHEVVVVQSVAKLVGPGPGGATATVTVLVERVMPPPKLDQESYEASVPISAPAGSFLIT
IQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALT LAPVPS
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEP
REHIIPVVVSHNAQMWQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLI
LIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 99

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCACGCCTG
 AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA
 TCTCTTCACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTAC
 ATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG
 TTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAAGCTGCAACAAATTCCAATGAGACTAGCACC
 TCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG
 TGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA
 GCATAGTCACCAACTCTGAGTTCCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG
 TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCTCAGTGG
 GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTACCAACT
 CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC
 AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC
 CAACTCTGACTCCAGCACAACTCTCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA
 CCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT
 GCCACCAACTCTGAGTCCAGCACAACTCTCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG
 AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCA
 GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG
 TCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG
 GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACTCTCAGTGGGGCCGGCACAGCCACCAACT
 CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCTCC
 AGTGGGGCCAAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAAACACAGCCAC
 CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA
 CCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCTCAGTGGGGCTAGCACA
 GCCACCAACTCTGACTCCAGCACAACTCTCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAG
 CACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAACTCTCAGTGGGGCCA
 ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA
 ATGCACACAACTTCCCATAGTGCATCTACTGCAGTGAAGTGAAGGCAAAGCCTGGTGGGTCCCTGGT
 GCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGCCGTGGGGCTCTTTGCTGGGC
 TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCT
 CATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCACAGGCCAG
 GTGGAGTCCTAACTGGTTCTGGAGGAGACCAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA
 ACAGCGGGCCCTGAGCAGCCCCGGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCA
 CCCAAGACCTGGTTTCTTTTCATTTCATCCCAGGAGACCCCTCCCAGCTTTGTTTGAGATCCTGAA
 AATCTTGAAGAAGGTATTCCTCACCTTTCTTGCCTTTACCAGACACTGGAAAGAGAATACTATAT
 TGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACACACACGACAAAGAGAAGCTGTGCTTG
 CCCCAGGGTGGGTATCTAGCTCTGAGATGAAGTCAAGTTATAGGAGAAAACCTCCATGCTGGACTC
 CATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 100

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS
SVTSNGVSIIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS
GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTA
TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSES
STTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNSDSSTTSS
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA
TNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESSTVSSGISTVTNSES
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA
AVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFWRPVSII
AMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 101

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCCTA
CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTCACAGGTG
GGAGGCTGGAACATATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCAACAAAT
GGATGATGTGATATATGCATTCCAGGGGAAGGGAAATTGTGGTGCTTCTGAACCCATGGTCAATT
AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTTGGAATCAT
GGTGTGATGGAAAGGGATTTACTTTTATACTGACTCTGTTTTGGGGAAGCTTTTTTGGGAAGCATTT
TCATGCTGAGTCCCTTTTTACCTTTGATGTTTGTAACCCATCTTGGTATCGCTGGATCAACAAC
CGCCTTGTTGGCAACATGGCTCACCCCTACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAAGT
GATTATAACTGGGGATGCATTTGTTTCTGGAGAAAGAAGTGTCAATTATCATGAACCATCGGACAA
GAATGGACTGGATGTTCTGTGGAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT
TGCCTCAAAGCGAGTCTCAAAGGTGTTCTTGGATTTGGTTGGGCCATGCAGGCTGCTGCCTATAT
CTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTGGAAGACATGATTGATTACTTTTGTG
ATATTCACGAACCACTTCAACTCCTCATATTCCCAGAAGGGACTGATCTCACAGAAAACAGCAAG
TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTTACATCCAAG
AACTACAGGCTTTACTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCTTGATGCTGTCCATG
ATATCACTGTGGCGTATCCTCACAACATTCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT
CCCAGGGAAATCCACTTTCACGTCCACCGGTATCCAATAGACACCCTCCCCACATCCAAGGAGGA
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAAGAGAGGCTGCGTTCCTTCTATCAAG
GGGAGAAGAATTTTTATTTTACCGGACAGAGTGTCAATCCACCTTGCAAGTCTGAACTCAGGGTC
CTTGTGGTCAAATTGCTCTTATACTGTATTGGACCCTGTTTACGCCCTGCAATGTGCCTACTCAT
ATATTTGTACAGTCTTGTTAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA
GAATATTTGGTGGACTGGAGATCATAGAACTTGCAATGTTACCGACTTTTACACAAACAGCCACAT
TTAAATTCAAAGAAAAATGAGTTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTG
GAAATGTTCTAAACCTTTCTAAGCTCAGATGCATTTTTGTCATGACTATGTGGAATATTTCTTACT
GCCATCATTATTTGTTAAAGATATTTGCACTTAATTTTGTGGGAAAAATATTGCTACAATTTTT
TTAATCTCTGAATGTAATTTGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT
GGGCCAGAATATTATTAAACAATCATCAGGCTTTTAAA

FIGURE 102

MHSRGREIVLLNPWSINEAVSSYCTYFIKQDSKSFSGIMVSWKGIYFILTLFWGSFFGSI FMLS P
FLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDADFVPGERSVIIMNHRTRMDWM
FLWNCLMRYSYLRLEKICLKASLKGVPFGFGWAMQAAAYIFIHRKWKDDKSHFEDMIDYFCDIHEP
LQLLIFPEGTDLTENSKSRSNFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA
YPHNIPQSEKHLLOGDFPREIHFEHVHRYPIDTLPTSKE DLQLWCHKRWEEKEERLRSFYQGEKNF
YFTGQSVIPPCKSELRVLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG
LEIIELACYRLLHKQPHLNSKKNE

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
TCC**ATG**GCTTTTTGTGCTCATTGTTGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT
CACTGGACCGGGCAAGTTTGTCCAGGCCCTGGTGGGGGAGGACGCCGTGTTCTCCTGCTCCCTCT
TTCCTGAGACCAGTGCAGAGGCTATGGAAGTGGGTTCTTCAGGAATCAGTTCCATGCTGTGGTC
CACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAACTGA
GTTTGTGAAGGACTCCATTGCAGGGGGCGTGCTCTCTAAGGCTAAAAACATCACTCCCTCGG
ACATCGGCCTGTATGGGTGCTGGTTCAGTTCCAGATTTACGATGAGGAGGCCACCTGGGAGCTG
CGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCATCGTGGGATATGTTGACGGAGGTATCCA
GTTACTCTGCCTGTCTCAGGCTGGTTCCCCAGCCACAGCCAAGTGGAAAGGTCCACAAGGAC
AGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCATCCACCTTGCTGAGCAGATCTGA
GGTGAATCCCAAGGTATTGATAGGAGAGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTCTA
TTTTACTCGGGTTACTCTGTGGTGCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTC
AAATCCAAAGGGAAAATCCAGGCGGAACCTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAG
AGACGCCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCG
TTTCTGATCTGAAAACCTGTAACCCATAGAAAAGCTCCCAGGAGGTGCCTCACTCTGAGAAGAGA
TTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA
CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTGGGATGACGTAGACAGGGGGGAAGAACA
ATGTGACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTT
ACATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCCT
GGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCTGTC
TGACATGTCAGTTTGAAGGCTTGTGAGACCTATATCCAGCATGCGATGTATGACGAGGAAAAAG
GGGACTCCCATATTCATATGTCCAGTGTCTGGGGAT**TC**GAGACAGAGAAGACCCTGCTTAAAGGGC
CCACACCCACAGACCCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTTCCTCT
CCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCC
TGAGCCCTGCAGCAGCGGCAGTCCAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAG
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAA
CTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCCAGGCTCCTCATTTGCTAGTCACGG
ACAGTGATTCTGCCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGAGGTT
TGAGGGCACAGTGTGCTAATGATGTGTTTTTATATTATACATTTTCCACCATAAACTCTGTT
TGCTTATTCCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACACC
TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCACTGATTCTATAAGCCCAGCAT
TACCTGATACCAAAACAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCC
CTCATTAACACAGACACAAAAATTCTAAATAAAATTTTAAACAAATTAACTAAACAATATATTTA
AAGATGATATATAACTACTCAGTGTGTTTTGTCCACAAATGCAGAGTTGGTTTAAATATTTAAAT
ATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAAAAAAAAAA

FIGURE 104

MAFVLILVLVSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH
LYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLYDVEISI
IVQENAGSILCSIHAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALCGVVMGMIIVFFK
SKGKIQAELDWRRKHGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF
TRKSVVASQGFQAGRHYWEVDVGQNVGWYVGCRDDVDRGKNNVTLSNNNGYWVLRLTTEHLYFT
FNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLCQFEGLLRPYIQHAMYDEEKG
TPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 105

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG
 TTTGTTGGGAACCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCTGGCAGTGTGCATTGGA
 CTCACTGTTTCATTATGTGAGATATAATCAAAAGAAGACCTACAATTACTATAGCACATTGTCAATTACAAC
 TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAATTTTACAGAAATGAGCCAGAGACTTGAAT
 CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTC
 AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGA
 AACTGTAGATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCCTAAAGTAG
 ATCCTCACTCAGTTAAAATTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGGA
 ACACGAAGAAGTAAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGAGGGTGAATG
 GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTAATGCCACATGGC
 TTGTGAGTGCTGCTCACTGTTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACA
 ATAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAATAATTGTCCATGAAAAATACAAACCCCCATCACA
 TGACTATGATATTCTCTTGACAGAGCTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTC
 TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAAT
 GATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACC
 TCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT
 GCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAAGATGCTAGAGATATCTGGTACCTTGCTGGAATAGTG
 AGCTGGGGAGATGAATGTGCGAAACCAACAAGCCTGGTGTGTTATACTAGAGTTACGGCCTTGCGGGACTG
 GATTACTTCAAAAATGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTTG
 GGTGTGGAGGCCATTTTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCA
 ATAAACTGTTTGCTTGATGCATGTATTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA
 GATCAACTCTGTCTGTGAGCAATAGTTGAACTTTATGTACATAGAGAAATAGATAATACAATATTAC
 ATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTTGTGAGAATTTTGACTTGTTGACATAAATTTGTAAT
 GCATATATACAATTTGAAGCACTCCTTTCTTCAGTTCCCTCAGCTCCTCTCATTTCAAGCAATATCCATTT
 TCAAGGTGCAGAACAAAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCCACATTTTATTGGCACAGAA
 AAGTATTAGGTGTTTTCTTAGTGGAATATTAGAAATGATCATATTATTATGAAAGGTCAAGCAAAGACA
 GCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAACTAAGTTAAGGAAGTCCAGAAAGAAGCCAAG
 ATATATCCTTATTTTCATTTCCAAACAATACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTGACCT
 ATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATATTTATTTAACATTG
 TTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 106

MMYRPDVVRARKRVCWEPWVIGLVI FISLIVLAVCIGLTVHYVRYNQKKTYNYSTLSFTTDKLY
AEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFHSTED
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL
RRIIVHEKYKHPSHDYDISLAELSSVPYPYTNVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS
QNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSGGPLVSSDARDIWYLAG
IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 107

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCCTG
 CCCCAGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCAGGGCCAGC
 GCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTT
 ACGGGGCTCACAAATGGCCAGAGAAGATTCGGTGAAGTGTCTGCGCTGCCTGCTCTACGCCCTCAA
 TCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAA
 ATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTTCCCT
 GTGGTTCATCCGGTCATGATTGCTGTTTGTCTGTTTCCCTTATCATTGTGGGGATGTTAGGATATTG
 TGGAACGGTGAAAAGAAATCTGTGCTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCAATTTCT
 GTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTATGGTTCCAGTACAATGGTCA
 GATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA
 TGCTTGGAATTTTTTTCAGAGAGAGTTTAAGTGTGTGGAGTAGTATATTTCACTGACTGGTTGG
 AAATGACAGAGATGGACTGGCCCCCAGATTCCCTGCTGTGTGTTAGAGAATTCACAGGATGTTCCAAA
 CAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCCTT
 TTTGAGAGGAACCAAACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAA
 TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGG
 ACAGACCAAAATGATGTCTTGAAGAATGACAACCTCTCAGCACCTGTCTCATGTCCCTCAGTAGAACT
 GTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACT
 TTGAGATGGAGGAGTTATAAAAGAAATGTCAAGAGAAAACCAAACTTGTTTTATTGGACT
 TGTGAATTTTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAA
 TAACACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCTAAGTC
 ACCACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC
 TGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCA
 TCCATGCAAAGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAA
 CTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA
 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACCTTTCAATATTGGTGACT
 ACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCCTTAAAAGAGCAAGCTAACACAT
 TGTCTTAAGCTGATCAGGGATTTTTGTATATAAGTCTGTGTAAATCTGTATAATTCAGTCGAT
 TTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATT
 ATTTTtagccttttctgtttaataaagcttttactattctgtcctgggcttatattacacatatatac
 TGTATTTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTC
 AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGA
 AAGGACTTGATGCTGTTTTTCTCCCAAATGAAGACTCTTTTGGACACTAAACACTTTTTAAAAA
 GCTTATCTTTGCCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAAATCTACAGAAAA
 TAGTGTCTTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAACCATGTGACAATTTAGAGATT
 CTTTGTTTTTATTTCACTGATTAAATACTGTGGCAAATTACACAGATTATTAAATTTTTTTACAA
 GAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTATTAT
 TTCTCAGAATATGGAAGAAAATTTAAATGTGTCAATAAATATTTTCTAGAGAGTAA

FIGURE 108

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVVHP
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREPQTDQM
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

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

FIGURE 109

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCCTCTGATAAAGCCCCCTACCAGTGCT
GATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCTTAAAAAAAAAAGTGCTTGAAAGAGAAGGGGACAAAGGAACA
CCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTCCAGAAGGATGCTCCATTCTGCTTCTCACCTG
CCTCTTCATCACAGGCACCTCCGTGTCACCCGTGGCCCTAGATCCTTGTTCTGCTTACATCAGCCTGAATGAGC
CCTGGAGGAACACTGACCACCAGTTGGATGAGTCTCAAGGTCCTCCTCTATGTGACAACCATGTGAATGGGGAG
TGGTACCACTTCACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAACCCA
CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCGACGGCATTGTGCAACGCCAGGCTTGTGCCAGCT
TCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGGAAGTCAAGGCTTGCCCTGGAGGCTACTATGTGTATCGT
CTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGGTCATTTTTATGACATCTGCGACGAGGACTGCCATGG
CAGCTGCTCAGATACCAGCGAGTGCACATGCGCTCCAGGAACCTGTGCTAGGCCCTGACAGGCAGACATGCTTTG
ATGAAAATGAATGTGAGCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCTACCGCTGT
GAGTGTGGGGTTGGCCGTGTGCTAAGAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA
TGGTGGCTGCAGCCACTCTTGCCTTGGATCTGAGAAAGGCTACCAGTGTAATGTCCCCGGGGCTGGTGTCTGT
CTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG
CTGGTTGGTGGCCTGGAGCTCTTCCTGACCAACACCTCCTGCCGAGGAGTGTCACCGGCACCCATGTCAACAT
CCTCTCTCTCTCAAGACATGTGGTACAGTGGTCCATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA
CAGGTCTACCCAAGCAGACCCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTG
ACCTGCGAGTTTCCACGCCTGTACACCATTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCCACTGGAAAT
CATGAGCCGAAATCATGGGATCTTCCCATCACTCTGGAGATCTTCAAGGACAATGAGTTTGAAGAGCCTTACC
GGGAAGCTCTGCCACCTCAAGCTTCGTGACTCCCTCTACTTTGGCATTGAGCCCGTGGTGCACGTGAGCGGC
TTGGAAAGCTTGGTGGAGAGCTGCTTTGCCACCCCCACCTCCAAGATCGACGAGGTCTGAAATACTACCTCAT
CCGGGATGGCTGTGTTTCAGATGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGG
TCCCTGTCTTCAAGTTTGTGGGCAAAGACCACAAGGAAGTGTTCCTGCACTGCCGGGTCTTGTCTGTGGAGTG
TTGGACGAGCGTTCCCGCTGTGCCAGGGTTGCCACCGGCGAATGCGTCGTGGGGCAGGAGGAGAGGACTCAGC
CGGTCTACAGGGCCAGACGCTAACAGGCGGCCGATCCGCATCGACTGGGAGGACTAGTTTCGTAGCCATACCTC
GAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTCCCCCACCGCCCTCTAAGAACATCTGCCAACAGC
TGGGTTACAGACTTCACACTGTGAGTTCAGACTCCCAGCACCAACTCACTCTGATTCTGGTCCATTCACTGGGCA
CAGGTACAGCACTGCTGAACAATGTGGCCTGGGTGGGGTTTCATCTTTCTAGGGTTGAAAATAAAGTGTCCA
CCCAGAAAGACACTCACCCATTTCCCTCATTTCTTCTACACTTAAATACCTCGTGTATGGTGAATCAGAC
CACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCCTAGAAAAATTAAACAGTTACTGAAATTATGA
CTTAAATACCCAATGACTCCTTAAATATGTAATATATAGTTATACCTTGAAATTTCAATTCAAATGCAGACTAA
TTATAGGGAATTTGGAAGTGTATCAATAAAACAGTATATAATTTT

FIGURE 110

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFTGMAGDAMP
TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYVYRLTKPSVCFHV
YCGHFYDIEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV
LRSDGKTCEDEVEGCHNNNGGCSHSLGSEKGYQCECPRGLVLSEDNHTCQVPVLCKSNAIEVNI PRELVGG
LELFLTNTSCRGVSNNGTHVNILFSLKTCGTVDVNDKIVASNLTGLPKQTPGSSGDFIIRTSKLLIPVT
CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEOPYREALPTLKLRLDSLYFGIEPVVHV
SGLESLVESCFATPTSKIDEVLKYILIRDGCVSDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV
LVCGVLDERSRCAQGGCHRRMRGAGGEDSAGLQGQTLTGGP IRI DWED

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
 CCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCCATGT
 TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCC
 ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGT
 GGTGTCTCATCAAGGTGATTCTGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCCGA
 GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC
 CCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC
 AGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG
 GCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAATCACAGAAAACAGCCAG
 GAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTG
 TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGG
 TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCAGGGCA
 GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAG
 CTTCCCATCCCTGGCTGTGGCCAAGATCATCATTTGAATTCAACCCCATGTACCCCAAAGACAATGACA
 TCGCCCTCATGAAGCTGCAGTTCCTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT
 GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTTGGATGGGGCTTTACGAAGCAGAATGGAGGGAA
 GATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGT
 ACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGT
 GACAGTGGTGGGCCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG
 CTGCGGGGGCCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT
 GGAAGGCTGAGCTGTAATGCTGCTGCCCTTTGCAGTGTGGGAGCCGCTTCCTTCCTGCCCTGCCACCT
 GGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCAT
 TTCTTGGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGACCCTCGCAGCCCAGAGGCGCCAGAGGAAGTCA
 GCAGCCCTAGCTCGGCCACACTTGGTGCTCCAGCATCCAGGGAGAGACACAGCCCACTGAACAAGGTCT
 CAGGGGTATTGCTAAGCCAAGAAGGAACCTTTCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCC
 CAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAA
 GCCTACTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT
 ACTGTTGTCATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAA
 AAAA

FIGURE 112

MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFLCG
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN
FTEALAEACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPCLSGSLVSLHCLACGKSL
KTFRVVGEEASVDSWPWQVSIQYDKQHVCSSILDPHWLTAHCFRKHTDVFNWKVRAGSDKL
GSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIIGWG
FTKQNGGKMSDILLQASVQVIDSTRCNADDAVQGEVTEKMMCAGIPEGGVDTCCQDSSGGPLMYQS
DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 113

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGATTA
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCACAGGAGT
TGAAGTGTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAAATC
TGTTTTTTGTTCTCTTGTAAGTACCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT
GGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCCTCGAAG
CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAACTGTCTCACGTCT
GGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGTAGCTGCGGCTTTCAAGGTGGGC
CTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCCGAAGATTTCATAGGCGATGGCTCCCCTGCCCC
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCCGTGGACACCTGCTCA
GAAGCAGTGGGTGAGACATCACGCTGCCCCGCCATCTAACCTTTTTCATGTCTGACATCACCTG
ATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC
CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCAATTCTCCTGGAACATGAGG
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACCTGTGCCAAATTATGGGTGAGAAAAGATG
GAGGTGTTGGGTATCACAAAGGCATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTG
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGCAT
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA
TCTGCGATCACCAGCCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCC
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG
GGCTAATGGCTCAGTGTTGGCCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCT
GTGCGAACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGG
CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGTT
CAAATGATCTCCAAGGGCCCTTATACCCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCA
AACCTAAGAACCAGGTGCATTAAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACAT
TTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGG
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAGAATTA
TGGTTATTTGTAA

FIGURE 114

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:

amino acids 1-15

FIGURE 115

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA
AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA
ATATGTAAATCACTTAAGATTTGTGGACTGGTGTGGTATCCTGGCCCTAACTCTAATTGTCCT
GTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT
TCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAACTGAAATA
TTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGG
CATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAAACTCAGATTAAAGTGATTCTGAATTTT
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTTTCTTTGAACAGTCAGTG
ATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGA
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAG
ACTTTGAGGAGGAGGGGAGAAGATCTTCACTTTCTTGCCAACGAAAAAAAGGGATTGAACAAAAT
GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGA
AGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAG
GTTATTGTTGTATTTACTGCCGTGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTA
GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTGTCATCATGCCTTG
TAACTGGTGGGTGGCCCGCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAAC
TGCTGGCAACATATAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCT
GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACA
TTATCACCAAAAAAAAAAAAAAAAAAAAA

FIGURE 116

MAKNPPENCEDCHILNAAFAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPPKKAYDME
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKTQIKVIP
EFSEPEEEIDENEEITTTFFEQSVIWWPAEKPIENRDFLKNKILEICDNVTMYWINPTLISVSE
LQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLD
ERGYCCIIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWWVARMLGRV

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
GGGCGGGCGGCCAGGATCATGTCCACCACCACATGCCAAGTGGTGGCGTTCTCTCTGTCCATCCTGGGGCT
GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGGACCTGTACGACAACCCCGTCACCT
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCC
TATTTACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCGAGCCCTGATGATCGTAGGCATCGTCTT
GGGTGCCATTGGCCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG
CCAAAGCCAAATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGCTCTTGTGCAATTGCTGGAGTG
TCTGTGTTTGCCAAATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG
GATGGTGCAGACTGTTTACAGACCAGGTACACATTTGGTGGCGCTCTGTTCTGGGGCTGGGTGCTGGAGGCC
TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAGAAGAAACCAACTACAAA
GCCGTTTCTTATCATGCCTCAGGCCACAGTGTTCCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT
TGGGTCCAACACCAAAAACAAGAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC
CTTCCAAGCAGCACTATGTGTAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCA
CCCAAAAACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCT
CGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCACCATAAAACA
GCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTAAATATAACT
TTCTACTCTGATGAGAGAATGTGGTTTAAATCTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC
TTCTCTCTAGTCAATAAACCCATTGATGATCTATTTCCAGCTTATCCCCAAGAAACTTTTGAAAGGAAA
GAGTAGACCCAAAGATGTTATTTTCTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAA
ACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTT
ACACTGTGATCTTAAAAGTTACCAAACCAAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTGCTG
TTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCCTGAGCTCTCCACTGGAGTCCTCTTTCTGT
CGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAATTTAAGTCCTAAATATAGTTAA
AATAAATAATGTTTTAGTAAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG
GAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCC
ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGT
TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCA
TGGTGGCATAACCTGTAGTCCCAGCATTCGGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGT
TGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA
AATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCTTTAA

FIGURE 118

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTECRP
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGL
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDY
V

Signal peptide:

amino acids 1-23

Transmembrane domains:

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

FIGURE 119

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGGAGTCC
 AGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTG
 GTGGTGTGGAATGGTGGGCACAGTGGCTGTCAGTGTGCCTCAGTGGAGAGTGTGGGCCCTTCATT
 GAAAACAACATCGTGGTTTTTGAAAACCTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA
 CATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTTCTCCGGACCTACAGGCAGCCAGAG
 GACTGATGTGTGCTGCTTCCGTGATGTCCTTCTGGCTTTTCATGATGGCCATCCTTGGCATGAAATGC
 ACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT
 CATCACGGGCATGGTGGTGTCTATCCCTGTGAGCTGGGTGCCAATGCCATCATCAGAGATTTCTATA
 ACTCAATAGTGAATGTTGCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCA
 CTGGTGTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTA
 CAGATACTCGATACCTTCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCG
 TCTACTCCAGAAGTCAGTATGTGTAGTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAAATG
 AAAAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAACTTTGATTTACTGTTCTTAACTGCCT
 AATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTCAGCAGAATGAGATA
 TTAAACCCAAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA
 CTCTTTTTATCATTTACTTCAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAATTTCTCC
 ACGACATAGCATTATGTACATAGATGAGTGTAAACATTTATATCTCACATAGAGACATGCTTATATGGT
 TTTATTTAAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA
 ATCATGGATAGGGTTGAAGAAGGTTACTATTAATTGTTTTAAAAACAGCTTAGGGATTAATGTCCTCCA
 TTTATAATGAAGATTAAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATAT
 GCTGTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCCAGAGGCTTTTTTTTT
 CTTGTGTATTAATTAACATTTTTTAAACGCAGATAFTTTGTCAAGGGGCTTTGCATTCAAACCTGCTT
 TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTG
 AAAATATTTTTGTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGAT
 ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATA
 TGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTCACCT
 GCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTTTTGTTCTGTGAAAAATAAATTTCTTCTTGTA
 CCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAA
 ACTGACAATCCAATTTGAAAGTTTGTGTGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTT
 TATACATTTATATTAATAAATTGTACATTTTTCTAATT

FIGURE 120

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFW EGLWMNCVRQANIRMOCK
IYDSSLALSPDLQAARGLMCAASVMSFLAEMMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG
MVLVLPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

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

FIGURE 121

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG
CCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCGGCAGCC
GGGAGCCATGCGACCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCC
TGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAG
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC
TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTCGGGATG
GATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTAC
AAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGACATT
TACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTTCAGTGGCTCACTTCGGCTAAAAATGCA
GAAATGCATGCTGTCAGCGTTGGTATTTACATTCAATGGAGCTGAATGTTTCAGGACCTCTTCCC
ATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCG
CACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG
TTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC
ATTATTGAAGAATAACCAAAATTAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCC
TTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG
CTAAATATGTTTACAGACCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTG
CTTCAATCAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATT
CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTCTTTTCTCTTAGTATAGCATTTTTTA
AAAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGT
TAAATAAAAATTATTTCCAACA

FIGURE 122

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGR
DGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMNSTINIHRTS
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTGAA
 CTGGGTGCTCATCACGGGAAGTCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA
 ATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTTTTTTTA
 ACCGCCCCCTCCCCACCCCCCAAAAAACTGTAAAGATGCAAAAACGTAATATCCATGAAGATCC
 TATTACCTAGGAAGATTTTGTATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTTGTTCTTGGAG
 TGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAGGGGTCCAATTTT
 TCTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGGTGTCATGCAACTG
 GCCCCTAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTCAATG
 TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCACTGTCTTACTGACAATG
 CTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCAAAAATGGTATATTGTGA
 ATCTCAGAAATTACAGGAGATACCCTCAAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT
 ATAACAGCCTTCAAAAACCTTAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC
 CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTTAATGGAATACGCAGACTCAAAGA
 GCTGATTCTTAGTTCCAATAGAATCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATT
 TACGGAACCTGGATCTGTCTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTG
 CGGAAGCTGCTGAGTTTACATTTACGGTCTAATCCCTGAGAACCATCCCTGTGCGAATATTCCA
 AGACTGCCGCAACCTGGAACCTTTTGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG
 TCTTTGCTGGCATGATCAGACTCAAAGAACCTTCACCTGGAGCACAATCAATTTTCCAAGCTCAAC
 CTGGCCCTTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAATAAAATCAGTGT
 CATAGGACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGA
 TCGAAGCTTTCAGTGGACCCAGTGTTCAGTGTGTCCGAATCTGCAGCGCCTCAACCTGGAT
 TCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGATTCTTGGATATCCCTCAATGACATCAG
 TCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAACCTGGCTGAAAAGTT
 TTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTG
 ATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAGTACTACAGAGAGGTTTGATCTGGCCAG
 GGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAACCCCTT
 TGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCT
 TTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCCTGCTGGTTAT
 CTACGTGTATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA
 GGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCCAGCACCCAGGAATTTTATGTA
 GATTATAAACCCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCCTGCACCTA
 TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTTGTGATAAAAAGAGCTCTTAAAAGCT
 GGGAAATAAGTGGTGCTTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCC
 TTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCCTTGTCGTTTTAGTGCATTTCATAACT
 GGTCAATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTT
 GAACTCCGGTTTAATATAATACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTGCGATTT
 GTTTTAAGATAAACTTCTTTTCATAGGTAAAAA

FIGURE 124

MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCCEGKMVYCESQKLQEIPSSISAGCLG
LSLRYNQLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR
PVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRRTIPVRIFQDCRNLELLDLGYNRIRS
LARNVFAGMIRLKEHLEHNQFSKLNLALEPRLVSLQNLQWKNKISVIGQTMSWTWSSLQRLDL
SGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLAGNIWECSRNICSLVN
WLKSFKGLRENTIICASPKELOQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE
SKPPLPPTVGATEPGPETDADAHEHISFHKIIAGSVALFLSVLVILLVIYVSWKRYPASMKQLQQR
SLMRRHRKKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLNGTGPCTYNKSGSRECEV

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

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCGCTG
ACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGCCGAGCT
AGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTC
GGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC
ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT
GTATTCTGGAGGTGGAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAAG
ATGAGCATTATCCCCCTTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTTATTGGCCAGTTT
TTAGCCAATCCAACCTGACCTAGTGAAGGTTTCAGATGCAAATGGAAGGAAAAAGGAACTGGAAGG
AAAACCATTTGCGATTTTCGTGGTGACATCATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATAC
GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTA
ACCACTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC
TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA
TCAAAGCAGAATAATGAATCAACCACGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCG
ACTGACTGCTTGATTGAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACC
ATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAAATCAGAGAGA
TGAGTGAGTCAGTCCATTTTAA

FIGURE 126

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGARES
APYRGMVRTALGIIEEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEHYPLWKS
VIGGMMAGVIGQFLANPTDLVKVQMMEGKRRKLEGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCGLVASILGTPADVIKSRIMNQP
RDKQGRGLLYKSSTDCLIQAVQEGEFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

Transmembrane domains:

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

FIGURE 127

CGCGGATCGGACCCAAGCAGGTCGGCGGGCGGCGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCGAC
CCCCGTGTGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCATGGCCAGGCCCGGCATGG
AGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCGCTCGGGGGGCATCGGCGCGGCCGTGGCC
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCGAGGA
GCTGGCTGCTGAATGTAAGAGTGACAGGCTACCCCGGGACTTTGATCCCCTACAGATGTGACCTAT
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCCTCAGCACAGCGGTGTAGACATC
TGCATCAACAATGCTGGCTTGGCCCGGCGTGACACCCTGCTCTCAGGCAGCACCAAGTGGTTGGAA
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGA
AGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTTA
CCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGGACT
GAGGCAAGAGCTTCGGGAGGCCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTGGTGG
AGACACAATTGCGCTTCAAACCTCCACGACAAGGACCCTGAGAAGGCAGCTGCCACCTATGAGCAA
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCTCAGCACCCCCGCACA
CATCCAGATTGGAGACATCCAGATGAGGCCCACGGAGCAGGTGACCTAGTGACTGTGGGAGCTCC
TCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTGCCTCTGGATTTTAGGTGTTGATTTCTGGAT
CACGGGATACCACTTCCTGTCCACACCCCGACCAGGGGCTAGAAAATTTGTTTGAGATTTTATA
TCATCTTGTCAAATTGCTTCAGTTGTAAATGTGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCC
TAATTGTTTTACTTGTTAACTTGTTCTTGCGCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTG
TCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCCATCTTCTTGACCTCAACGTCTG
TGGCTCAGGGCTGGGGTGGCAGAGGGAGGCCTTCACCTTATATCTGTGTTGTTATCCAGGGCTCC
AGACTTCCTCCTCTGCCTGCCCCACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCC
AGCCCAGTCTTGGCTTCTTGTCCTCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG
CAGAACACCAGGGCCTGGCCAGTGGATTTCATGGTGATCATTAAAAAAGAAAAATCGCAACCAA
AAAAAAAAA

FIGURE 128

MARPGMERWRDRLALVTGASGGIGAAVARALVQQGLKVVGCA RTVG NIEELAAECKSAGYPGTLI
PYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPD TLLSGSTSGWKDMFNVNVLALSICTR
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
CATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTCAGGTGCAGAGTCTCAGTTGCCCGGGAGC
ACCTCCCCTCCCAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCCAGTTCTGGTTTCATGC
CAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAGGGTTTTCTGCCA
GGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTCAATTCAGTAGCCACCAGCCACCTGTGG
CCGTTGAGTGCTTGAAATGAGGAACTGAGAAAATTAATTTCTCATGTATTTTTCTCATTTATTTA
TTAATTTTTTAAGTATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA
TATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACATTTATTTTTTATTCCTT
TTAGACAGAGTCTCACTCTGTACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT
GCACCACAATGCCCAACTAATTTTTGTATTTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCGAGG
CTGGCCTTGAACCTCCTGGCCTCAAACAATCCACTTGCCCTCGGCCTCCCAAAGTGTTATGATTACA
GGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTCTTTGTGTTGGGAACCTTTGAAATTAT
ACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT
ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC
AACCTCTGATCACCTCATTCTACTCTCTACCTCCATGAGATCCACTTTTTTTAGCTCCCACATGTG
AGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTG
TTCCATCCATGTTGCTGCAAATGACAGGATTCGTTCTTAATTTCAATTAAATAACACACATG
GCAAAAA

FIGURE 130

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV
KGHGTLGESPMPPFKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

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
 ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCTTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG
 TCCATCTGTGTGTCGCTGCGATGCGGGTTTCATTTACTGTAATGATCGCTTCTGACATCCATTCCAACAG
 GAATACCAGAGGATGCTACAACCTCTCTACCTTCAGAACAACCAAATAAATAATGCTGGGATTCCCTCAGAT
 TTGAAAACTTGCTGAAAGTAGAAAGAATATACCTATACCACAACAGTTTAGATGAATTTCTACCAACCT
 CCCAAAGTATGTAAAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAA
 AAATTCCTATCTGGAAGAATTACATTTAGATGACAACTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA
 TTCCGAGACAGCAACTATCTCCGACTGCTTTTCTGTCCCGTAATCACCTTAGCACAATTCCTGGGGTTT
 GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTCATCACCATCTCTTCAAG
 GTCTCACTAGTCTAAACGCCTGGTTCTAGATGGAAACCTGTTGAACAATCATGGTTTAGGTGACAAAGTT
 TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATTCCTGACTGCTGCACCAGTAAACCT
 TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGCCCCCAAATGCTTTTT
 CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTT
 GATGATTTGGACAATATAACACAACCTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATG
 GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAA
 AGGTTCTGTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAAGC
 ACCATTCAAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCCAAGGACAGTGGCCAGCTCCAGTGAC
 CAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAGGGAGTCCCTCAAGAAAAA
 CAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTATATCTCTTGGAAGTCTGCTCTACCTATG
 ACTGCTTTGAGACTCAGCTGGCTTAACTGGGCCATAGCCCGGCATTTGGATCTATAACAGAAACAATTGT
 AACAGGGGAACGCAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTACCCCTATAAAGTATGCATGGTTC
 CCATGGAAACCAGCAACCTCTACCTATTTGATGAAACTCCTGTTTGTATTGAGACTGAAACTGCACCCCTT
 CGAATGTACAACCCTACAACCACCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACC
 TTTGGCTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTTGGTATG
 TTCATAGGAATGGATCGCTCTTCTCAAGGAAGTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT
 GCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAAACTTCTTTTCAGATGTTACCAAT
 AAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAATACACACCATATTTCTCCTAATGGAATGAATCTGT
 AAAAAACAATCACAGTGAAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC
 TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATG
 GT

FIGURE 132

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRELTSTIPTGIPEDATTLYL
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKIPYL
EELHLDNDSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQDNHIN
RVPPNAFSYLRLQLYRLDMSNNNLSNLPQGIFDDLNDITQLILRNNPWYCGCKMKWVRDWLQSLPV
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQGQWPAPVTKQPD
IKNPKLTKDQQTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWLKLGHSPAFGSITET
IVTGERSEYLVTALEPDSPYKVCMPMETSNLYLFEDETPVCJETETAPLRMYNPTTTLNREQEKE
PYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS
ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLKNNHSESSNRSYRDSGIPDSHSHS

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
 GCCCTGCCGGGCCACTTGTCTTCATGTCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG
 TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG
 GCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACCGCTGTGGT
 CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT
 GCGCTGGAGAGAGCCACCGTCTTCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT
 GGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGCCCAGGAGCCCCCTGC
 TGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC
 CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCAGCTGACCCTCCAGCCCCG
 GTTTTGGAAGCTCCACATGCCTGGATCCACACTGATGCCTCCTTGGTGTACCCACGTTCCGGG
 CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGGACG
 GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCCGGCTGCTC
 AGGCTACTGCCTGTCCCACTGCTCTTCTTCTCTGCGCCAGAATGAGGGGATGCACACAGG
 GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC
 AGAGCTGAGGCCATCGGATACGCCTACCCTACCCGGGACATCTTCATGGAAAACATCATGTTCTG
 TGGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA
 AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA
 TATCAGCAGCATTTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGT
 TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGC
 AATTCTCTTGCTCATCTCTCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAAT
 TTTTATATTTTTTTAGTAGAGACAGGGTTTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT
 CTCAAGAGATCCGCCCACCTCAGGCTCCCAAAGTGTGGGATTATTAGGTGTGAGCCACCGTGTCTG
 GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC
 ATGGGGGCTCTCTCCCCTAGATGGCTGCTCCTCCCACAACACAGCCACAGCAGTGGCAGCCCTGG
 GTGGCTTCTATACATCCTGGCAGAATACCCCCCAGCAAACAGAGAGCCACACCCATCCACACCG
 CCACCACCAAGCAGCCGCTGAGACGGACGGTTCATGCCAGCTGCCTGGAGGAGGAACAGACCCC
 TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG
 ATAAGCAAAGCCACCCGACACCCAATCTTGGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG
 GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAAAAA

FIGURE 134

MSARGRWEGGRRACRGSGLARAQGAERVTSSEQRPAMASLGLLLLLLLLTALPPLWSSSLPGLD
TAESKATIADLIISALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPLSLRV
GMLGEKLEAAIQRSLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE
RSDVCLVQLLGTGTDSSSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQQSQD
YINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILSQKQEGCFG
EPDAEDEELSKAIQYQQHFSSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQFSLILP
SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPTSGSQSVGL

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

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTG
CTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCCGGGGCTGCTGCTGAGGGATCGGGAGG
GAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGC
CTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCCGTTTTCCTTAAG
ACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAAGTTGTATCTCC
AGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCAAGATATG
TGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT
CCACCTTCTTACTTTATTAAAGGGGAATCGTGGGGCTGGACAGACTTTCTAATGAACCCAATGGT
TATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATTCCAACCATGAGTTGCCTGAT
GTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTGGCAAATCTAGCAGCGGCAGCAG
TAAACAGGCAAAAGTGGGGCTGGCAAAAGGAGGTTAGTCAGGCCGTCCAGAGCTGGCATTGAC
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAAACCGTGTGAAGCAACTACTATAAACTT
GAGTCATCCCGACGTTGATCTCTTACAACCTGTGTATGTT
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGTAT
GAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAATTAT
ATGAACTACTATACATTATGTATATTAATTAAACATCTTAATCCAGAAATCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAA

FIGURE 136

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGSGVGIGDRFKIEGRAVVPGVKPDWISAA
RVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDVPRVDITSKGKMRARYVNYIKTSE
VVRLPYPLOMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLI FVLLPKVVNTSDPDMRREME
QSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

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

GATGGCGCAGCCACAGCTTCTGTGAGATTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGA
CCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAAACAA
GTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC
CTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGC
CACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTCACGGGAGGCTTGGCAGT
TTTTCTTACTCCTGTGGTCTCCAGATTTCAAGCCTAAGATGAAAGCCTCTAGTCTTGCCTTCAGC
CTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACACTCAATTTGGG
AAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGTG
TGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACA
AAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGACAGGGTATTTAA
AAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCCTTTCTTA
CCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACATGCCATTGTGGGGAGGAAGCAATG
AAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC
TTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTG
CTGCTAAGAATATTGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAA
ACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTG
CTTCCTTGCATGATTGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTT
TGTAATATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTA
ATGTATTTATTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTG
ACTAGAGCAGGTGATGTATTTTTATACAGTAAAAAATAACCTTGTAATTTCTAGAAGAGTGG
CTAGGGGGGTATTCAATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGAT
ATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATTGCAC
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAG
CCAGGAATCCTACAGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAA
AAAAAAAAAA

FIGURE 138

MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNGATT CATNSHSDSELRPEIF
SSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG
FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS
SLANSFLT IKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET
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
TAGCGTGTCCACGATGCGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCGAGGTGC
TAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCTCTGCCAGAGCGGAA
CACGGAGCGGAGCCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGTTCTAACTGGACCACGCTGCC
ACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAGATGATTTTGTGTTTG
GGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTACCTTGTGGAAAAAGGAGCATCTCACAGT
TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCATTGATGACGGGGAG
CCTTCCTGGCTTTGTGCGACGTCAATCAGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGA
TAAGACAAGCAAAAGCAGCTGGAAAAAGAATAGTCTTTTATGGAGATGAAACCTGGGTTAAATTA
TTCCCAAAGCATTTTGTGGAATATGATGGAACAACCTCATTTTTTCGTGTGAGATTACACAGAGGT
GGATAATAATGTCACGAGGCATTTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAATCC
TCCACTACCTGGGGCTGGACCACATTGGCCACATTTAGGGCCCCAACAGCCCCCTGATTGGGCAG
AAGCTGAGCGAGATGGACAGCGTGCTGATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGA
GACGCCTTTACCCAATTTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACG
GGGCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAAGGAAA
CCCGGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTGGCTGCGACACTGGCGATAGC
ACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCCAGTTGTGGAAGGAAGAC
CAATGAGAGAGCAGTTGAGATTTTTACATTTGAATACAGTGCAGCTTAGTAACTGTTGCAAGAG
AATGTGCCGTGATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAATGTGAGAAAGATTGCATGG
GAACTGGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCCTATTCAACCTGGGCTCCAAGG
TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCAG
TTCTCACCCCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCA
CTGTCATCTCCTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTTCGGCCGTTACCGT
CATTGTGTGCACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGCAGGCT
GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGGCAGTGCCCTGGAC
AGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGGTGTCCCGACACAGGTG
TTCACATCTGTGCTGTGAGGTGAGATGCCTCAGTTCTTGAAAGCTAGGTTTCTGCGACTGTTAC
CAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAA
TCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAAGAGACAATCGGCCTGGA
CACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCACTCATCCTGCCACCCCCAGAATGCATCCT
GCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGACGTTTTCTGTTGGAATTCTTAGTCCTTGGCC
TCGGACACCTTCATTGCTTAGCTGGGGAGTGGTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCAC
ACTCAGATCCACAGAGCCCAGGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCC
ACCCCAACCTGCACAGCCCTCATCCCTCTTGGCTTGAGCCGTGAGAGCCCTGTGCTGAGTGT
CTGACCGAGACACTCACAGCTTTGTGATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTG
CCACGCTTGCACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCCTGCTATTGAATTAGTACCTAG
CTGCACACAGTATGTAGTTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA

FIGURE 140

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPPEPSAGASSNWTTLPPPLF
SKVVIVLIDALRDDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF
VDVIRNLNSPALLED SVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTSFFVSDYTEVDNNV
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
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGGATGTTACTGCTGCTGTTGGAGTACAAC
TCCCTATAGAAAACAAC TGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC
CCGAAGAAATTCAGCATTTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT
AGCAGTTCCAGATAAAAACTACATACGCCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTAAAGGGGAGTTTTGTCTCTAC
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCT
GGCTGCCCCAAAAGGAATCAGCACGCCGGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCCTGGA
ACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTTCAACCAGTTTGCAA
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTA
ATTTGAACTAATTGTATAAAAACACCAAACCTGCTCACT

FIGURE 142

MLLLLLLEYNFPIENNCQHLKTTHTFRVKNLNPKKFSIHDQDHKVLVLD SGNLI AVPDKNYIRPEI
FFALASSLSSASAEKGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFI
FYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

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
GACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCCAGCACTGCCCAGATCA
CTGAGGCCCAGGTGGCTGAGAACC GCCGGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCAACGGCTGCATCAATGCCA
CCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGGAGAGGGGCGCAGGACT
TCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAATAA
AGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT
CTTCTCCCCCAAACCCACGCGTGTCTGAAGGTGCCCAGGAGCGGCGATGCACTCGCACTGCAAA
TGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT
CCGTCACTCCATTCTCAGCCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT
GAGAAGAACACATCAGGCACTGCGCCACCTGCTTCACAGTACTTCCCAACAACCTCTTAGAGGTAG
GTGTATTCCCGTTTTACAGATAAGGAACTGAGGCCCAGAGAGCTGAAGTACTGCACCCAGCATC
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCTGGCTTGTCTAACCCAGGTTTTCTGCTCT
GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAAACATGTAT
CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

FIGURE 146

MRKHLSSWWLATVCMLLFSHLSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNKLHQQ
VLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWLMMVK

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
CCTGATGATTTATAGACTCAAAGAAAACTATGTTCAGAAGCTCTCTTCTCTTCTGGCCTCCTCT
CTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG
AAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCAGTCTTAGTTTTTATTTTTTGAAATTT
CAACTTTCAGATTCAGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCATTGATGTCTGAGG
TTTGGGGT

FIGURE 148

MFRSSLLFWPPLCLLSLFLLLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE
GLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

FIGURE 149

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGACTTGAC
TCCCGCGCGCCCCAACCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGCCGCCCAGTCC
CGGCCCCCTCTCCCGCCCCACACCCACCTCCTGGCTCTTCCTGTTTTTACTCCTCCTTTTCATTCTATA
ACAAAAGCTACAGCTCCAGGAGCCCAGCGCGGGCTGTGACCCAAGCCGAGCGTGGAAGAATGGGGTT
CCTCGGGACCGGCACTTGGATTCTGGTGTAGTGCTCCCGATTCAAGCTTTCCCCAACCTGGAGGAA
GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA
GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAAACAAGCCAGGTGAGAGCAACTATTCTTT
TGTTGATAACTTGAACCTGCTAAAGGCAATAACAGAAAAAGGAAAAAATTGAGAAAGAAAGACAATCTA
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACGT
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA
TCAACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAG
AAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGC
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCCAACAA
TTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG
TGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA
TTAACCTTGACAAATGGCTTGAAAGGAGAACTAAAACCTACAGTGAAGACAACCTTTGAGGAACTCCA
ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTTCAGAAAAAGAAGCAAAAGAGAAAGAAA
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCT
CCAGAAGAAGGTGTTTCCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCT
AGAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAA
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAA
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC
CATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGGAAATAAAGAAGATTATGACCTTT
CAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA
GAAGCCGAGGCCATCAAGCGCATTATAGCAGCCTGTAAAAATGGCAAAAGATCCAGGAGTCTTTCAA
CTGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATTCGTGATTAAAAATTTTTTGACCCAAGG
GTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCC
GTAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 150

MGFLGTGTWILVLVLPIQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE
VLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTMAAIQDGLAGENDETVSNTLTLTNGLE
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV
SYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHKDKGNKEDYDLSKMRDFINKQADAYVEKGILDK
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
GATGGTCCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC
ATAATAACCAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGC
GTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGGAAAG
CCAGTGCCTGTCTATGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG
AGCTCTATCTTTGGTGCCAAGGAATCCAAGAGCTTACCTTCTACCGGCGGGACATGGGGCTCACC
TCCAGCTTCGAGTCGGCTGCCTACCCGGGCTGGTTCTGTGCACGGTGCCTGAAGCCGATCAGCC
TGTCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTCTACTTCC
AGCAGTGTGACT**TAGG**GCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGT
GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTCTGCTCTCAGGACCCCCACGTCTGACTTAG
TGGGCACCTGACCACTTTGTCTTCTGGTTCCAGTTTGGATAAATTCTGAGATTTGGAGCTCAGT
CCACGGTCTCTCCCCACTGGATGGTGTCTACTGCTGTGGAACCTTGTA AAAACCATGTGGGGTAAA
CTGGGAATAACATGAAAAGATTTCTGTGGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCCTGTCT
TAATGGTAACCTGACAAGTGTTACCCTGAGCCCCGCAGGCCAACCATCCCAGTTGAGCCTTATA
GGGTCACTAGCTCTCCACATGAAGTCCTGTCACTCACCCTGTGCAGGAGAGGGAGGTGGTCATA
GAGTCAGGGATCTATGGCCCTTGGCCCCAGCCCCACCCCTTCCCTTTAATCCTGCCACTGTCTATA
TGCTACCTTTTCTATCTCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGATGTCAGAA
GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAA
GATACAATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGCTCATGACATATTGAGA
AGACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAATTAAAAGATAACCTATTTATATATT
TCTTTATAGAAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTCAAGGTGGTGGCAGTAT
AGGTGATTTTCTTTTAAATCTGTTAATTTATCTGTATTTTCTAATTTTTCTACAATGAAGATGA
ATTCCCTTGATATAAAAAATAAGAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA
TTGTCCTCAGCCTCCACTTCCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG
TTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT
GTGGCTGGAATCTCTGGGTAAGGAACCTAAAGAACA AAAAATCATCTGGTAATTCTTTCTAGAAAG
GATCACAGCCCCTGGGATTC AAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA
ATTGTGTCCCCCTCAAATTCACATCCTTCTTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAG
GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCTGCTGGATGAAGGTAGACCTAAATTC AATAT
GACTGGTTTCCTTGATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA
AAGATGAAGGCAGAGATCGGAGTTTTGTCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC
ATCAGAAGCTTGGAAGAGGCAAGAAGAAATCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG
CTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGAATAAATTTCGGCTGTTTTAA
GCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAAACTAATACAGCTGCTAAAATGATCCCTGT
CTCCTCGTGTTTACATTCTGTGTGTGTCCCCCTCCACAATGTACCAAAGTTGTCTTTGTGACCAA
TAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTC
TACTTGAGCCCTCTCTCTGCCCACCCACCGCCCCCAATCTATCTTGGCTCACTCGCTCTGGGGG
AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAAATGAAGTCTCCT
GCCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT
AAGTTGCTCAGTTTTGGTCTAACTTGTTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG

FIGURE 152

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESISVVPNRWLDASLSPVILGVQGGG
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP
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

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC
CCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTCTCTTGG
CCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAAC
TTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA
CAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT
ATCTGATGAAGCAGGTGCTGAACTTCACCCTTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTTT
CAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTTGCTGTTTATGTCTCTGAGAAAT
GCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCCCTGCTAGAAATAA
CAATTAGATGCCCCAAAGCGATTTTTTTTAAACAAAAGGAAGATGGGAAGCCAAACTCCATCATG
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTTTATA
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTTT
TATACACAGAAAACAATTTATTTTTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCAT
TCCTTTAGGGGAAAAAACCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAA
TGTATTTATTATTATTATAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTAT
AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT
AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGGATATCCC

FIGURE 154

MAALQKSVSSFLMGTLATSCLLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL
ADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLPQSDRFQPYMQEVVPFLARLSNRLS
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
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCTACAGGTGGTTGCAT
TCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGG
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCCTAGAGCCTGCTAG
GCCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCT
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCAGGACCTGTACCACGCCCCGT
TGCCTGTGCCCCGCACTGCGTCAGCCTACAGACAGGCTCCCACATGGACCCCCGGGGCAACTCGGA
GCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCAGCCACA
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTTCCCTTAGCTTGTGTGTGTGTGCGGCCCCGT
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTTGGGAAACCTGGAGCCAGGTGTACA
ACCACTTGCCATGAAGGGCCAGGATGCCCAGATGCTTGGCCCCTGTGAAGTGCTGTCTGGAGCAG
CAGGATCCCGGGACAGGATGGGGGGCTTTGGGGAAAACCTGCACTTCTGCACATTTTGAAAAGAG
CAGCTGCTGCTTAGGGCCGCCGAAGCTGGTGTCTCTGTCATTTTCTCTCAGGAAAGGTTTTCAAA
GTTCTGCCCATTTCTGGAGGCCACCACTCCTGTCTCTTCTCTTTTCCCATCCCCTGCTACCCTG
GCCCAGCACAGGCACTTTCTAGATATTTCCCCCTTGCTGGAGAAGAAAGAGCCCCTGGTTTTATT
TGTTTGTTTACTCATCACTCAGTGAGCATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTT
TTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTTATCCAAATAAATAT
CTTTATTTAAAAATGAAAAA

FIGURE 156

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHTYSHWPSCCPSKGQDTSEELLRWSTVPVPPLEPA
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS
ELLYHNQTVFYRRPCHGEKGTKGYCLERRLYRVSLACVCVRPRVMG

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
GACCGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAAC TAGTGTTGCAACAGGGGACTATTCA
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAGGCCACCAA
GATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGTGAGGTGCAATTACACAGAGG
CCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCCTACATCGGCTTCCCTGTA
GAGCTGAACACAGTCTATTTTCATTGGGGCCATAATATTCCTAATGCAAATATGAATGAAGATGG
CCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAA
AGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACA
GTAGAAGTGAAC TTCACAACCACTCCCCGAAACAGATACATGGCTCTTATCCAACACAGCAC
TATCATCGGGTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA
TTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGC
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCT
GGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCA
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT
TCTACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCA
TCACACAATTTGTTACTTCACTGAATTTCTTCAAACCATTCAGAGTGCAGGTCATCCTTGAAA
AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCA
GCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA
GAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCTTTAACCTTTTCTGCA
GTGATCTAAGAAAGCCAGATTCATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA
AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACG
ATGGCTGCTGCTCCTTGTAG

FIGURE 158

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRDLRVEPVTTTSVATGDYSILMNVSWV
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP
NANMNEDGPSMSVNFTSPGCLDHIMYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQH
STIIGFSQVFEPHQKKQTRASVVIPTVGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVPFPLDNNK
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL
QNHCRSEVILEKWQKKIAEMGPVQWLATQKKAADKVVFLSNDVNSVCDGTGKSEGSPSENSQDLFPLA
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVKKQVSAGKRSQACHD
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
CTTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC
ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG
GAATTACACTGTCACCTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAGTGTAGGA
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAA
GAGACCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCT
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTAAGAGGTGCATATCC
ACTCAGCTGAAGAAG

FIGURE 16o

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN
QRVMSRNIERSRSTSPWNYTVTWDPNRYPSEVVQAQCRNLGCINAQGKEDISMNSVPIQQETLVV
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 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 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 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 C C A G G C C A A G T C G T G C T 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 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 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 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 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 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 C 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 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 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 A C G C C G T A C C C G C C C T 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 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 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 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

MPVPWFLLSLALGRSPVVLSELERLVGPQDATHCSPGLSCRLWDSILCLPGDIVPAPGPVLAPTHLQTELV
LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSFQAYPTARCVLLEV
QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTPRYEKELNHTQQLPALPWLNVNSADGDNVHLVLNV
EEQHFGLSLYWNQVQGPPKPRWHKNLTGPPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQ
LWQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPEGDPQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ
VNSSEKLQQLQECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYLLQDLQS
GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLKQDVRSGAAARG
RAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVWFHAQRRQTLQEGGVVLLFSP
GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLHPDAVPALFRTVPVFT
LPSQLPDFLQALQPPRPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

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
 GCTCAGCCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCCAGTCCAGCAACTTTGA
 AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA
 AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTCAGCGGATCACCCGGAAGTCCTGC
 AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT
 GTCAGTGCAGGGAGGCGGTGAGCCACCAAGATGACTGACAGGTTGAGTCTCTGCAGCACACTAC
 CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTGAGATGATTGTTTCATCCTA
 CCCCCACGCCAATCCGTGCAGGCGATGGCCACCGGCTAACCCCTGGAAGACATCTTCCATGACCTG
 TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAGCAGAGAGA
 ATATGAGTTCTTCGGCCTGACCCCTGACACAGAGTTCTTGGCACCATCATGATTGCGTTCCCA
 CCTGGGCCAAGGAGAGTGCCCCCTACATGTGCCGAGTGAAGACACTGCCAGACCGGACATGGACC
 TACTCCTTCTCCGGAGCCTTCTGTCTCCATGGGCTTCTCGTCGAGTACTCTGCTACCTGAG
 CTACAGATATGTACCAAGCCGCTGCACCTCCCAACTCCCTGAACGTCCAGCGAGTCTGACTT
 TCCAGCCGCTGCGCTTCATCCAGGAGCACGTCTGATCCCTGTCTTTGACCTCAGCGGCCCCAGC
 AGTCTGGCCAGCCTGTCCAGTACTCCAGATCAGGGTGTCTGGACCCAGGGAGCCCGCAGGAGC
 TCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCCTCCAGC
 CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCTATGCCCCAAACGCTGCCCCCTGAG
 GTCGGGCCCCCATCTATGCACCTCAGGTGACCCCGAAGCTCAATTCCCATTCTACGCCCCACA
 GGCCATCTCTAAGGTCCAGCCTTCTCCTATGCCCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT
 CCTATGGGGTATGCATGGAAGGTTCTGGCAAAGACTCCCCACTGGGACACTTTCTAGTCTAAA
 CACCTTAGGCCTAAAGGTGAGCTTCAGAAAGAGCCACCAGCTGGAAGCTGCATGTTAGGTGGCCT
 TTCTCTGCAGGAGGTGACCTCCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATTGCACCAGC
 CCCTGGGGATTGTCACAGACAGAACATCTGACCCAAATGTGCTACACAGTGGGGAGGAAGGGACA
 CCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCTCCTCAGTCCAGATCGAGGGCCACCCCATGTC
 CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC
 TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCAGCCCCCTGAGACCTCAGACCTG
 GAGCAGCCACAGAACTGGATTCTCTTTTCAGAGGCCTGGCCCTGACTGTGCAGTGGGAGTCTG
 AGGGGAATGGGAAAGGCTTGGTGCTTCTCCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCA
 ATCCCATGCCTGCCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC
 AGAGGGAGTGGCATGCAGGGCCCCCTGCCATGGGTGCGCTCCTCACCGGAACAAAGCAGCATGATA
 AGGACTGCAGCGGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGCGTGCTCGCTGAGCCCTG
 CAAGGCAGAAATGACAGTGCAAGGAGGAAATGCAGGGAAACTCCCGAGGTCCAGAGCCCCACCTC
 CTAACACCATGGATTCAAAGTGCTCAGGGAATTTGCCTCTCCTTGCCCCATTCTTGCCAGTTTC
 ACAATCTAGCTCGACAGAGCATGAGGCCCTGCCTCTTCTGTATTGTTCAAAGGTGGGAAGAGA
 GCCTGGAAAAGAACCAGGCCTGGAAAAGAACCAGAAGGAGGCTGGGCAGAACCAGAACAACCTGC
 ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCCTGCAGCTCA
 TTCCCAGCCAGGGCAACTGCCTGACGTTGCACGATTTAGCTTCATTCTCTGATAGAACAAAGC
 GAAATGCAGGTCCACCAGGGAGGGAGACACACAAGCCTTTTCTGCAGGCAGGAGTTTCAGACCCT
 ATCCTGAGAAATGGGGTTTGAAAGGAAGGTGAGGGCTGTGGCCCTGGACGGGTACAATAACACAC
 TGTACTGATGTCACAACTTTGCAAGCTCTGCCTTGGGTTTCAGCCCATCTGGGCTCAAATTCCAGC
 CTCACCACTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCCAAGAACCTCGGTTTCCTC
 ATCTGTAATGTGGGGATCATAACACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG
 TCTTTAAAGTGCTTAATAGTGCTGGTACATGGGCAGTGCCCAATAAACGGTAGCTATTTAAAAA
 AAAAAAAA

FIGURE 164

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW
VAKKGCQRITRKSCNLTVETGNLTELYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVTCIS
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRITYQMHLGGKQREYEFFGLTPDT
EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFSGAFLFSMGFLVAVLCYLSYRYVTKPPAP
PNSLNVQRVLTTFQPLRFIQEHVLIPVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFPFYAPQAISKVQPSSY
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLQKEPPAGSCMLGGLSLQEVTSLAM
EESQEAKSLHQPLGICTDRTSDPNVLHSGEEGTPQYLKGQLPLLSSVQIEGHPMSLPLQPPSGPC
SPSDQGPPSPWGLLESVLCPKDEAKSPAPETSDLEQPTELDSLFRGLALTVQWES

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
TCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT
GTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGTGAATTTTA
AAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAACCTTGGGCTGGA
AGTGTTGAACACAGTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCATAAATACACGGA
AGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGGAGGAAGAGATGATT
TTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAACTGGAGGACTCTGTACCTGAAGAG
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA
ACTTGACCCTGTGCCTGAGCCCGAGGCATTTCAGAGCTGATTTCAGAGGATGGAGAAGGTGCTTTCT
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCTCACACCAGCGGT
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATTCTGCACGATAA
ATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGC GTTATT
CATTACAGCAAAGGATTTGTTGGCATCAAAATCTAAGTTTGTTTTACAAAGATTGTTTTTAGTA
CTAAGCTGCCTTGGCAGTTTGCATTTTTGAGCCAAACAAAAATATATTATTTTCCCTTCTAAGTA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 166

MAAAPGLLFWLFWLGALWWVPGQSDLSHGRRFSDLKVCGDEECSMIMYRGKALEDFTGPDCRFVN
FKKGDDVYVYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADETDFVCFEGGRD
DFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELDPVPEPEAFRADSEGEA
FSESTEGLOQGPSAQESHPTSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYKDCF

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

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCTCAGAGGCCGGGGAAGAGAAGCAAAGCGC
AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCTAACTTC
AGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAACCTCAGCCCCGCACATCCACGCGCGGCACAGG
CGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTCGGGCAGCTGGGCTCGGGC
GGCGGGAGTAGGGCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTCGCGGGCTGCGCCCTG
GGCAGAGGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCGCGCATGAGCCGCGGTG
TCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCCGCGCGCTGGTCAGC
GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCCTACTTCCATGAACT
GTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCGGCTTGTGAGAGTGAGGGGAGGAGTCCCTCTCA
GCCTTGAGAAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG
ACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGAATGGAGATGGGCAAACATCTGG
TGCTTGCCAGATCTCTACCACTGGTCTGATGGAAGCAATTCCCAGTACCGAAACTGGTACACAG
ATGAACCTTCCCTGCGGAAGTGAAAAGTGTGTGTGATGTATCACCACCAACTGCCAATCCTGGC
CTTGGGGGTCCCTACCTTTACCAGTGGAATGATGACAGGTGTAACATGAAGCACAATATATTTG
CAAGTATGAACCAGAGATTAATCCAACAGCCCTGTAGAAAAGCCTTATCTTACAAATCAACCTAG
GAGACACCCATCAGAATGTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTT
ATACCAACAATACCCCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCT
GCATAAAAGTAAAGGAAGAACAACAACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTA
CCAGAAAAGAAAGTGGCATGGAAGTATAATAACTCATTGACTTGGTTCCAGAATTTTGTAAATCT
GGATCTGTATAAGGAATGGCATCAGAACAAATAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGC
AAGATGAACTGTAAGCTCCCCCTTGAGGCAAATATTAAAGTAATTTTTATATGTCTATTATTCA
TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAA
ACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTA
TGTGTGTTAGAAGCAATTCCTTTTATTTCTTTACCTTTCATAAGTTGTTATCTAGTCAATGTAA
TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTTGTTTGATAAAA
ATGAACTGTTCTAATATTTATTTTATGGCATCTCATTTTCAATACATGCTCTTTTGATTAAAG
AACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTGT
TTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTCAGA
AATAAGAAGCTATTTCAATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGAT
TGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTATAGCTTAAATTAACAGATT
TTGTAATAATGTAACTTTGTTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAG
TGACATACACAATATAAATCATATGTCTTCACACGTTGCCATATAATGAGAAGCAGCTCTCTGA
GGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCACTAAACAAAGATGGTTGTTTCGGGGTTTGGG
ATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTG
ACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG
ACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACACGAAATCGTGTGAAAATGGGTTGG
AACCCTCAGTGATCGCATATTCATTGATGAGGGTTTGTCTTGAGATAGAAAATGGTGGCTCCTTT
CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCCTTGTCTTCTCAAGAGAAAGTTGTAACCT
CTGGTCTTCATATGTCCCTGTGCTCCTTTAACCATAAAGAGTTCTTGTCTTCTGGGGGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 168

MSRVVSLLLGAALLCGHGAFRRVVSQGKVCFADFKHPCYKMAYFHELSSRVSFQEARLACESE
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSGACPDLYQWSDGSNSQ
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWDDRCNMKHNYICKYEPEINPTAPVEK
PYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLLILVAFGTCCFQMLHKSKGRTKTSPNQ
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. 10/006,867 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 Ser. Nos. 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 THE 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 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 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

1. 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 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 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 times the fraction 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:

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

[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, 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, _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, -2, 4, 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 *name[2]; /* seq names: getseqs() */
char *prog; /* prog name for err msgs */
char *seqs[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 */

```

TABLE 1-continued

```

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 an 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 */
    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 */

```

TABLE 1-continued

```

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;
        } else {
            delx -= ins1;
            ndelx++;
        }
    }
    else {
        if (col1[yy-1] - (ins0+ins1) >= delx) {
            delx = col1[yy-1] - (ins0+ins1);

```


TABLE 1-continued

```

        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);
}

/*
 *
 * 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()

```

TABLE 1-continued

```

* 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++;
                n1++;
                siz0--;
            }
            else if (siz1) {
                p0++;
                n0++;
                siz1--;
            }
        }
    }
}

```

TABLE 1-continued

```

    }
    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)",
        gapx, (dna)? "base": "residue", (gapx == 1)? "" : "s");
    fprintf(fx, "%s", outx);
    fprintf(fx, ", gaps in second sequence: %d", gapy);
    if (gapy) {
        (void) sprintf(outx, "(%d %s%%s)",
            gapy, (dna)? "base": "residue", (gapy == 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;
    register i;
    for (i = 0, lmax = 0; i < 2; i++) {
        nn = stripname(namex[i]);
        if (nn > lmax)
            lmax = nn;
        nc[i] = 1;
        ni[i] = 1;
    }
}

```

...getmat

pr_align

TABLE 1-continued

```

        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])
                fprintf(fx, star);
            if (i == 1)
                nums(i);
        }
    }
}
}
/*

```

...pr_align

dumpblock

...dumpblock

TABLE 1-continued

```

/* put out a number line: dumpblock()
*/
static
nums(ix)                                     nums
{
    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)                                 putline
                                         ...putline
{
    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()                                     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++) {
        if (isalpha(*p0) && isalpha(*p1)) {
            if (xbm[*p0-'A']&xbm[*p1-'A']) {
                cx = '*';
                nm++;
            }
            else if (!dna && __day[*p0-'A'][*p1-'A'] > 0)
                cx = '.';

```

TABLE 1-continued

<pre> 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)) { if (*line == ';' *line == '<' *line == '>') continue; for (px = line; *px != '\n'; px++) if (isupper(*px) islower(*px)) tlen++; } if ((pseq = malloc((unsigned)(tlen+6))) == 0) {</pre>		stripname
		cleanup
		getseq

TABLE 1-continued

```

        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 ppl[], 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;
            }
            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];
        }
    }
}

```

...getseq

g__calloc

readjmps

...readjmps

TABLE 1-continued

```

        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	NNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNLLLLLLLL	(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	NNNNLLLV	(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

A. Full-Length PRO Polypeptides

[0253] 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.

[0254] 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.

B. PRO Polypeptide Variants

[0255] 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.

[0256] 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.

[0257] 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.

[0258] 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 restric-

tion enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase 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.

[0259] 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

[0260] 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:

- [0261] (1) hydrophobic: norleucine, met, ala, val, leu, ile;
- [0262] (2) neutral hydrophilic: cys, ser, thr;
- [0263] (3) acidic: asp, glu;
- [0264] (4) basic: asn, gln, his, lys, arg;
- [0265] (5) residues that influence chain orientation: gly, pro; and
- [0266] (6) aromatic: trp, tyr, phe.

[0267] 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.

[0268] 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.

[0269] 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.

C. Modifications of PRO

[0270] 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 (diazooacetyl)-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.

[0271] Other modifications include deamidation of glutaminyl 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.

[0272] 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.

[0273] 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.

[0274] 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 Sep. 11, 1987, and in Aplin and Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

[0275] 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.*

[0276] *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).

[0277] 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.

[0278] 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.

[0279] 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)].

[0280] 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.

D. Preparation of PRO

[0281] 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.

1. Isolation of DNA Encoding PRO

[0282] 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).

[0283] 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)].

[0284] 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.

[0285] 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.

[0286] 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.

2. Selection and Transformation of Host Cells

[0287] 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.

[0288] 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 Jun. 29, 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).

[0289] 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 Apr. 12, 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 Aug. 7, 1990. Alternatively, in vitro methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

[0290] 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 May 2, 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, 76:5259-5263 [1979]); Schwanniomycetes such as *Schwanniomycetes occidentalis* (EP 394,538 published Oct. 31, 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium* (WO 91/000357 published Jan. 10, 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]). Methylophilic 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 Methylophilic yeasts, 269 (1982).

[0291] 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.

3. Selection and Use of a Replicable Vector

[0292] 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.

[0293] 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 Apr. 4, 1990), or the signal described in WO 90/13646 published Nov. 15, 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.

[0294] 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.

[0295] 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*.

[0296] 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)].

[0297] 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.

[0298] 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.

[0299] 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.

[0300] 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 Jul. 5, 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.

[0301] 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.

[0302] 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.

[0303] 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.

4. Detecting Gene Amplification/Expression

[0304] 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.

[0305] 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.

5. Purification of Polypeptide

[0306] 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.

[0307] 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.

E. Uses for PRO

[0308] 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.

[0309] 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.

[0310] Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

[0311] 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).

[0312] 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.

[0313] 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 may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

[0314] 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 retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

[0315] 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.

[0316] Alternatively, a sense or an antisense oligonucleotide may be introduced into a 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.

[0317] 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.

[0318] The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO coding sequences.

[0319] 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.

[0320] 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.

[0321] 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.

[0322] 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 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.

[0323] 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.

[0324] 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).

[0325] 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.

[0326] 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.

[0327] 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.

[0328] 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.

[0329] 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.

[0330] 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.

[0331] 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.

[0332] 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.

[0333] 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.

[0334] 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.

[0335] The sustained-release formulations of these proteins were developed using polylactic-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.

[0336] 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.

[0337] 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.

[0338] 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.

[0339] 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.

[0340] 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-lacZ 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.

[0341] 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.

[0342] 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.

[0343] 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.

[0344] 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.

[0345] 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 antibodies, 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.

[0346] 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 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.

[0347] 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.

[0348] 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).

[0349] 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*.

[0350] 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.

[0351] Diagnostic and therapeutic uses of the herein disclosed molecules may also be based upon the positive functional assay hits disclosed and described below.

F. Anti-PRO Antibodies

[0352] The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

[0353] 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.

2. Monoclonal Antibodies

[0354] 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.

[0355] 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.

[0356] 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].

[0357] 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).

[0358] 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.

[0359] 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.

[0360] 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.

[0361] 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.

[0362] 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.

3. Human and Humanized Antibodies

[0363] 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)].

[0364] 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); Verhoeyen 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 corresponding 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.

[0365] 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).

[0366] 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.

4. Bispecific Antibodies

[0367] 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.

[0368] 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 May 13, 1993, and in Traunecker et al., *EMBO J.*, 10:3655-3659 (1991).

[0369] 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 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).

[0370] 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.

[0371] 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.

[0372] 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.

[0373] 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. Kostelný 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).

[0374] 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).

5. Heteroconjugate Antibodies

[0375] 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.

6. Effector Function Engineering

[0376] 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).

7. Immunoconjugates

[0377] 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).

[0378] 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, croton, *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.

[0379] 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 radionucleotide).

8. Immunoliposomes

[0380] 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.

[0381] Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition 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).

9. Pharmaceutical Compositions of Antibodies

[0382] 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.

[0383] 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.

[0384] 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.

[0385] The formulations to be used for in vivo administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

[0386] 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 65 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.

C. Uses for Anti-PRO Antibodies

[0387] 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, ¹⁴C, ³²P, ³⁵S, or ¹²⁵I, 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).

[0388] 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.

[0389] The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

[0390] All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

[0391] 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

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

[0392] 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.).

[0393] 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.

[0394] 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.

[0395] 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 Sall 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

Isolation of cDNA Clones by Amylase Screening

[0396] 1. Preparation of oligo dT primed cDNA library

[0397] 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 Sall/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.

[0398] 2. Preparation of random primed cDNA library

[0399] 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.

[0400] 3. Transformation and Detection

[0401] 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.

[0402] 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.

[0403] 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.

[0404] 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 2x10⁶ cells/ml (approx. OD₆₀₀=0.1) into fresh YEPD broth (500 ml) and regrown to 1x10⁷ cells/ml (approx. OD₆₀₀=0.4-0.5).

[0405] 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 Li₂OOCCH₃), and resuspended into LiAc/TE (2.5 ml).

[0406] 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 Li₂OOCCH₃, 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).

[0407] Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

[0408] 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.

[0409] 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).

[0410] 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.

[0411] 4. Isolation of DNA by PCR Amplification

[0412] 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:

[0413] 5'-TGTAACGACGGCCAGTTAAATA-GACCTGCAATTATTAATCT-3' (SEQ ID NO:169)

[0414] The sequence of reverse oligonucleotide 2 was:

[0415] 5'-CAGGAAACAGCTATGACCACCTG-CACACCTGCAAATCCATT-3' (SEQ ID NO:170)

[0416] 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

-continued			
e.	Extend Hold	72° C., 4° C.	60 seconds

[0417] 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.

[0418] Following the PCR, an aliquot of the reaction (5 µl) 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

Isolation of cDNA Clones Using Signal Algorithm Analysis

[0419] 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 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

Isolation of cDNA Clones Encoding Human PRO Polypeptides

[0420] 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
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

TABLE 7-continued

Material	ATCC Dep. No.	Deposit Date
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

[0421] 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).

[0422] 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

Use of PRO as a Hybridization Probe

[0423] The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

[0424] 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.

[0425] 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.

[0426] 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

Expression of PRO in *E. Coli*

[0427] This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

[0428] 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.

[0429] 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.

[0430] 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.

[0431] 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.

[0432] 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.

[0433] *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, Utrol 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.

[0434] 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 from the desired form, the reversed phase step also removes endotoxin from the samples.

[0435] 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.

[0436] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 7

Expression of PRO in Mammalian Cells

[0437] This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

[0438] 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.

[0439] 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 µg pRK5-PRO DNA is mixed with about 1 µg DNA encoding the VA RNA gene [Thimmappaya et al., Cell, 31:543 (1982)] and dissolved in 500 µl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl₂. To this mixture is added, dropwise, 500 µl 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.

[0440] Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 µCi/ml ³⁵S-cysteine and 200 µCi/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.

[0441] 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 µg 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 µg/ml bovine insulin and 0.1 µg/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.

[0442] 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.

[0443] 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 Ni^{2+} -chelate affinity chromatography.

[0444] 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.

[0445] 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.

[0446] 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.

[0447] 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.

[0448] 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 μm filtered PS20 with 5% 0.2 μm 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 μm filter. The filtrate was either stored at 4° C. or immediately loaded onto columns for purification.

[0449] 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.

[0450] Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned 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 μL 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.

[0451] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 8

Expression of PRO in Yeast

[0452] The following method describes recombinant expression of PRO in yeast.

[0453] 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.

[0454] 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.

[0455] Recombinant PRO can subsequently be isolated and purified by removing the 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.

[0456] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 9

Expression of PRO in Baculovirus-Infected Insect Cells

[0457] The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

[0458] The sequence coding for PRO is fused upstream of an epitope tag contained 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.

[0459] 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).

[0460] 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.

[0461] 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.

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

Example 10

Preparation of Antibodies That Bind PRO

[0463] This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

[0464] 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.

[0465] 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.

[0466] 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.

[0467] 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.

[0468] 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

Purification of PRO Polypeptides Using Specific Antibodies

[0469] 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.

[0470] 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 Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

[0471] 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.

[0472] 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

Drug Screening

[0473] 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.

[0474] 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.

[0475] 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.

[0476] 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

Rational Drug Design

[0477] 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)).

[0478] 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).

[0479] 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.

[0480] 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

Pericyte c-Fos Induction (Assay 93)

[0481] 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.

[0482] The following polypeptides tested positive in this assay: PRO1347 and PRO1340.

Example 15

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

[0483] The ability of various PRO polypeptides to stimulate the release of proteoglycans from cartilage tissue was tested as follows.

[0484] 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 100 U/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.

[0485] 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

Detection of Polypeptides That Affect Glucose or FFA Uptake in Skeletal Muscle (Assay 106)

[0486] 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.

[0487] 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 $\pm$ 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.

[0488] The following PRO polypeptides tested positive as either stimulators or inhibitors of glucose and/or FFA uptake in this assay: PRO4405.

Example 17

Identification of PRO Polypeptides That Stimulate TNF- α Release In Human Blood (Assay 128)

[0489] 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.

[0490] The following PRO polypeptides tested positive in this assay: PRO263, PRO295, PRO1282, PRO1063, PRO1356, PRO3543, and PRO5990.

Example 18

Tumor Versus Normal Differential Tissue Expression Distribution

[0491] 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 akin
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 normal akin	stomach tumor normal kidney melanoma tumor
DNA57827-1493	normal stomach normal skin	stomach tumor melanoma tumor
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 lung tumor rectum tumor melanoma tumor
DNA62815-1576	esophageal tumor	normal esophagus
DNA64881-1602	normal stomach normal lung	stomach tumor lung tumor
DNA64902-1667	esophageal tumor kidney 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

-continued		
Molecule	is more highly expressed in:	as compared to:
DNA66674-1599	kidney tumor	normal kidney
	normal lung	lung tumor
DNA68862-2546	melanoma tumor	normal skin
DNA68866-1644	normal stomach	stomach tumor
DNA68871-1638	lung tumor	normal lung
	normal skin	melanoma tumor
DNA68880-1676	normal lung	lung tumor
	normal skin	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 esophagus
	normal kidney	kidney tumor
	lung tumor	normal lung
	normal skin	melanoma tumor
DNA76393-1664	esophageal tumor	normal esophagus
	stomach tumor	normal stomach
	lung tumor	normal lung
	rectum tumor	normal rectum
DNA77568-1626	normal stomach	stomach tumor
DNA77626-1705	lung tumor	normal lung
	normal rectum	rectum tumor
DNA81754-2532	normal skin	melanoma tumor
DNA81757-2512	esophageal tumor	normal esophagus
	normal stomach	stomach tumor
	melanoma tumor	normal skin
	normal stomach	stomach tumor
DNA82302-2529	normal stomach	stomach tumor
	normal lung	lung tumor
DNA82340-2530	normal esophagus	esophageal tumor
DNA85066-2534	lung tumor	normal lung
	normal skin	melanoma tumor
DNA87991-2540	esophageal tumor	normal esophagus
DNA92238-2539	normal skin	melanoma tumor
DNA96787-2534	normal kidney	kidney tumor

Example 19

Identification of Receptor/Ligand Interactions

[0492] 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.

[0493] 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.

[0494] 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.

[0495] Using these assays, the following receptor/ligand interactions have been herein identified:

- [0496] (1) PRO10272 binds to PRO5801.
- [0497] (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.
- [0498] (3) PRO10096 binds to PRO20233.
- [0499] (4) PRO19670 binds to PRO1890.

[0500] 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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Asn Ile Ala Ala Val Leu Cys Ile Ala Thr Ile Tyr Val Arg Tyr
      65                      70                      75

Lys Gln Val His Ala Leu Ser Pro Glu Glu Asn Val Ile Ile Lys
      80                      85                      90

Leu Asn Lys Ala Gly Leu Val Leu Gly Ile Leu Ser Cys Leu Gly
      95                      100                     105

Leu Ser Ile Val Ala Asn Phe Gln Lys Thr Thr Leu Phe Ala Ala
     110                      115                     120

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Met Phe Val Gln Thr Ile Leu Ser Tyr Gln Met Gln Pro Lys Ile
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Cys Gly Val Ser Ala Leu Ser Met Leu Thr Cys Ser Ser Val Leu
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His Ser Gly Asn Phe Gly Thr Asp Leu Glu Gln Lys Leu His Trp
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Asn Pro Glu Asp Lys Gly Tyr Val Leu His Met Ile Thr Thr Ala
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Ala Glu Trp Ser Met Ser Phe Ser Phe Phe Gly Phe Phe Leu Thr
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Tyr Ile Arg Asp Phe Gln Lys Ile Ser Leu Arg Val Glu Ala Asn
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Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val	80	85	90
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Phe	Tyr	His	Arg	Trp	Phe	Asp	Val	Ile	Phe	Leu	Val	Ser	Ala	Leu
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ccagtggtaa aaaggcctcc tggctgtctg aggctagggtg ggttgaaagc      1500
caaggagtca ctgagaccaa ggctttctct actgattccg cagctcagac      1550
cctttcttca gctctgaaag agaaacacgt atcccacctg acatgtcctt      1600
ctgagcccgg taagagcaaa agaatggcag aaaagttag ccctgaaag      1650
ccatggagat ttcataact tgagacctaa tctctgtaaa gctaaaataa      1700
agaaatagaa caaggctgag gatacgacag tacactgtca gcagggactg      1750
taaacacaga cagggtcaaa gtgttttctc tgaacacatt gagttggaat      1800
cactgtttag aacacacaca ctacttttt ctggtctcta cactgctga      1850
tattttctct aggaaatata cttttacaag taacaaaaat aaaaactctt      1900
ataaatttct atttttatct gagttacaga aatgattact aaggaagatt      1950
actcagtaat ttgtttaaaa agtaataaaa ttcaacaaac atttgctgaa      2000
tagctactat atgtcaagtg ctgtgcaagg tattacactc tgtaattgaa      2050
tattattcct caaaaaattg cacatagtag aacgctatct gggaagctat      2100
ttttttcagt ttgatatatt ctagcttctc tacttccaaa ctaattttta      2150
tttttgctga gactaatctt attcatittc tctaatatgg caaccattat      2200
aaccttaatt tattattaac atacctaaga agtacattgt tacctctata      2250
taccaaagca cattttaaaa gtgccattaa caaatgtatc actagccctc      2300
ctttttccaa caagaaggga ctgagagatg cagaaatatt tgtgacaaaa      2350
aattaaagca tttgaaaaac tt                                     2372

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<210> SEQ ID NO 6

<211> LENGTH: 322

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 6

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

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	125		130		135
Thr Asn Ser Cys Ile Pro Glu Ile Ile Thr Thr Lys Asp Pro Ile					
	140		145		150
Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr Glu Phe Ile Val Ser					
	155		160		165
Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser Thr Ile Pro Ala					
	170		175		180
Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser Ile Pro Arg					
	185		190		195
Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu Thr Ser					
	200		205		210
Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala Ala					
	215		220		225
Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu					
	230		235		240
Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly					
	245		250		255
Phe Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn					
	260		265		270
Lys Asn Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu					
	275		280		285
Glu Lys Ala Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr					
	290		295		300
Asp Lys Asn Pro Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val					
	305		310		315
Arg Cys Leu Glu Ala Glu Val					
	320				

<210> SEQ ID NO 7
<211> LENGTH: 2586
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 7

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caccgcgcagc ccggcgccct ccggcgggga gcgagcagat ccagtcgggc	100
ccgcagcgca actcgggtcca gtcggggcgg cggtcgggg cgagagcg	150
agatgcagcg gcttggggcc accctgctgt gcctgctgct ggcggcggcg	200
gtccccacgg ccccgcgcc cgtccgcagc gcgacctcg ctccagtcaa	250
gcccggcccc gctctcagct acccgcagga ggaggccacc ctcaatgaga	300
tgttccgcga ggttgaggaa ctgatggagg acacgcagca caaattgcgc	350
agcgcggtgg aagagatgga ggcagaagaa gctgctgcta aagcatcatc	400
agaagtgaac ctggcaaact tacctcccag ctatcacaat gagaccaaca	450
cagacacgaa ggttggaat aataccatcc atgtgcaccg agaaattcac	500
aagataacca acaaccagac tggacaaatg gtcttttcag agacagttat	550
cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcatcatcg	600
acgaggactg tgggcccagc atgtactgcc agtttgccag cttccagtac	650
acctgccagc catgccgggg ccagaggatg ctctgcaccc gggacagtga	700

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gtgctgtgga gaccagctgt gtgtctggg tcaactgcacc aaaatggcca	750
ccaggggcag caatgggacc atctgtgaca accagaggga ctgccagccg	800
gggctgtgct gtgccttcca gagaggcctg ctgttccctg tgtgcacacc	850
cctgcccgtg gagggcgagc ttgtccatga ccccgccagc cggcttcttg	900
acctcatcac ctgggagcta gagcctgatg gagccttgga ccgatgccct	950
tgtgccagtg gcctcctctg ccagccccac agccacagcc tgggtgatgt	1000
gtgcaagccg accttcgtgg ggagccgtga ccaagatggg gagatcctgc	1050
tgcccagaga ggtccccgat gagtatgaag ttggcagctt catggaggag	1100
gtgccccagg agctggagga cctggagagg agcctgactg aagagatggc	1150
gctggggagg cctgcggctg ccgccgctgc actgctggga ggggaagaga	1200
tttagatctg gaccagcctg tgggtagatg tgcaatagaa atagctaatt	1250
tatttcccca ggtgtgtgct ttaggcgtgg gctgaccagg cttcttctca	1300
catcttcttc ccagtaagtt tcccctctgg cttgacagca tgagggtgtg	1350
tgcatattgt cagctcccc aggtgtttct ccaggcttca cagtctggtg	1400
cttgggagag tcaggcaggg ttaaactgca ggagcagttt gccaccctg	1450
tccagattat tggctgcttt gcctctacca gttggcagac agccgtttgt	1500
tctacatggc ttgataaatt gtttgagggg aggagatgga aacaatgtgg	1550
agtctccctc tgatttggtt tggggaatg tggagaagag tgccctgctt	1600
tgcaaacatc aacctggcaa aaatgcaaca aatgaatttt ccacgcagtt	1650
ctttccatgg gcataggtaa gctgtgcctt cagctgttgc agatgaaatg	1700
ttctgttcac cctgcattac atgtgtttat tcattccagca gtgttgctca	1750
gctcctacct ctgtgccagg gcagcatttt catatccaag atcaattccc	1800
tctctcagca cagcctgggg agggggtcat tgttctctc gtccatcagg	1850
gatctcagag gctcagagac tgcaagctgc ttgcccaagt cacacagcta	1900
gtgaagacca gagcagtttc atctggttgt gactctaagc tcagtgtctc	1950
ctccactacc ccacaccagc cttggtgcca ccaaagtgc tccccaaaag	2000
gaaggagaaat gggatttttc ttgaggcagc cacatctgga attaagggtca	2050
aactaattct cacatccctc taaaagtaaa ctactgttag gaacagcagt	2100
gttctcacag tgtggggcag ccgtccttct aatgaagaca atgatattga	2150
cactgtccct ctttggcagt tgcattagta actttgaaag gtatatgact	2200
gagcgtagca tacagggttaa cctgcagaaa cagtacttag gtaattgtag	2250
ggcgaggatt ataatgaaa ttgtcaaaat 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
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cttcaactgc aaaaaaaaa aaaaaaaaa aaaaaa	2586

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<210> SEQ ID NO 8

<211> LENGTH: 350

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 8

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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	

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	335	340	345
Gly Gly Glu Glu Ile			
	350		
<210> SEQ ID NO 9			
<211> LENGTH: 1395			
<212> TYPE: DNA			
<213> ORGANISM: Homo Sapien			
<400> SEQUENCE: 9			
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atcatgcaac cccacggccc accttgtgaa ctctcgtgc ccagggctga			100
tgtgcgtctt ccagggtac tcatccaaag gcctaatacca acgttctgtc			150
ttcaatctgc aaatctatgg ggtcctgggg ctcttctgga cccttaactg			200
ggtactggcc ctgggccaat gcgtcctcgc tggagccttt gcctccttct			250
actgggcctt ccacaagccc caggacatcc ctaccttccc cttaatatct			300
gccttcatcc gcacactccg ttaccacact gggtcattgg catttgagc			350
cctcatcctg acccttgtgc 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 agctgctggt			650
ggtcggaggc gtgggggtcc tgtccttctt ttttttctcc ggtcgcatcc			700
cggggctggg taaagacttt aagagcccc acctcaacta ttactggctg			750
cccattcatg cctccatcct gggggcctat gtcatcgcca gcggcttctt			800
cagcgttttc ggcatgtgtg tggacacgct ctctcctcgc ttcttggaag			850
acctggagcg gaacaacggc tccctggacc ggccctaacta catgtccaag			900
agccttctaa agattctggg caagaagaac gaggcgcccc cggacaacaa			950
gaagagggaag aagtgcacg tccggccctg atccaggact gcacccacc			1000
cccaccgtcc agccatccaa cctcacttcg ccttacaggt ctccattttg			1050
tggtaaaaaa aggttttagg ccaggcgccg tggctcacgc ctgtaatacca			1100
acactttgag aggctgaggc gggcggtatc cctgagtcag gagttcgaga			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			

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

gcccgcgcc cggcgcggg cgccgaagc cgggagccac cgccatggg

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gcctgcctgg gagcctgctc cctgctcagc tgcgcgtcct gcctctgcgg	100
ctctgcccc tgcctcctgt gcagctgctg ccccgccagc cgcaactcca	150
ccgtgagcgg cctcatcttc acgttcttcc tcttcctggg ggtgctgggtg	200
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc	250
ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca	300
tcgactgtgg ctccctgctt ggctaccgcg ctgtctaccg catgtgcttc	350
gccacggcgg ccttcttctt cttcttttcc accctgctca tgctctgcgt	400
gagcagcagc cgggaccccc gggctgccaat ccagaatggg ttttggttct	450
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gacggctcct tcaccaacat ctggtttctac ttgggcgtcg tgggtcctt	550
cctcttctac ctcatccagc tgggtgctgt catcgacttt gcgcactcct	600
ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg	650
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ggccgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg	750
agggcaaggt cttcatcagc ctcaacctca ccttctgtgt ctgcgtgtcc	800
atcgctgctg tcctgcccac ggtccaggac gccagccca actcgggtct	850
gctgcaggcc tcggtcatca ccctctacac catgtttgtc acctggtcag	900
ccctatccag tatccctgaa cagaaatgca accccattt gccaacccag	950
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tcttcatcag tctgcgtcc tcagaccacc ggcaggtgaa cagcctgatg	1100
cagaccgagg agtgcccacc tatgctagac gccacacagc agcagcagca	1150
gcaggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg	1200
tcacctacag ctactccttc ttccacttct gcctgggtgt ggctcactg	1250
cacgtcatga tgacgtcac caactggtag 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 ctggtgccca tactcagcat ctcggtgaa	1700
agggctccct tgtcctcagg ctccacggga gcggggctgc tggagagagc	1750
ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc	1800
tggtcacgtc cccagggga ccctgcccc ttcttggaact tcgtgcctta	1850
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a	1901

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<210> SEQ ID NO 12

<211> LENGTH: 457

<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

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Arg	Gln	Val	Asn	Ser	Leu	Met	Gln	Thr	Glu	Glu	Cys	Pro	Pro	Met
			350						355					360
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	caccogttaa	ggtgtcttct	50
ctttagggat	ggtgaggttg	gaaaaagact	cctgtaacct	tcctccagga	100
tgaaccacct	gccagaagac	atggagaacg	ctctcaccgg	gagccagagc	150
tcccatgctt	ctctgcgcaa	tatccattcc	atcaacccca	cacaactcat	200
ggccaggatt	gagtcctatg	aaggaaggga	aaagaaaggc	atatctgatg	250
tcaggaggac	tttctgtttg	tttgtcacct	ttgacctctt	attcgtaaca	300
ttactgtgga	taatagagtt	aaatgtgaat	ggaggcattg	agaacacatt	350
agagaaggag	gtgatgcagt	atgactacta	ttcttcatat	ttgatataat	400
ttcttctggc	agtttttcga	tttaaagtgt	taatacttgc	atatgctgtg	450
tgcagactgc	gccattgggtg	ggcaatagcg	ttgacaacgg	cagtgaccag	500
tgcccttttta	ctagcaaaaag	tgatcccttc	gaagcttttc	tctcaagggg	550
cttttggtcta	tgtgctgccc	atcatttcat	tcatccttgc	ctggattgag	600
acgtgggtcc	tggatttcaa	agtgttacct	caagaagcag	aagaagaaaa	650
cagactcctg	atagttcagg	atgcttcaga	gagggcagca	cttataacctg	700
gtggtctttc	tgatggtcag	ttttattccc	ctcctgaatc	cgaagcagga	750
tctgaagaag	ctgaagaaaa	acaggacagt	gagaaaccac	ttttagaact	800
atgagtacta	cttttggttaa	atgtgaaaaa	ccctcacaga	aagtcacga	850
ggcaaaaaga	ggcaggcagt	ggagtctccc	tgtcgacagt	aaagttgaaa	900
tggtgacgtc	cactgctggc	tttattgaac	agctaataaa	gattttattta	950
ttgtaataac	tcacaaacgt	tgtaccatat	ccatgcacat	ttagttgcct	1000
gcctgtggct	ggtaaggtaa	tgatcatgatt	catcctctct	tcagtgagac	1050
tgagcctgat	gtgttaacaa	atagggtgaag	aaagtcttgt	gctgtattcc	1100

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taatcaaaag acttaatata ttgaagtaac acttttttag taagcaagat      1150
acctttttat ttcaattcac agaatggaat ttttttgitt catgtctcag      1200
atttattttg tatttctttt ttaacactct acatttcctt tgttttttaa      1250
ctcatgcaca tgtgctcttt gtacagtttt aaaaagtgtg ataaaatctg      1300
acatgtcaat gtggctagtt ttatttttct tgttttgcat tatgtgtatg      1350
gcctgaagtg ttggacttgc aaaaggggaa gaaaggaatt gcgaatacat      1400
gtaaaatgtc accagacatt tgtattattt ttatcatgaa atcatgtttt      1450
tctctgattg ttctgaaatg ttctaaatac tcttattttg aatgcacaaa      1500
atgacttaaa ccattcatat catgtttcct ttgcgttcag ccaatttcaa      1550
ttaaatgaa 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
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<210> SEQ ID NO 15

<211> LENGTH: 2768

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 15

actcgaacgc agttgcttcg ggaccagga cccctcggg cccgaccgc	50
caggaaagac tgaggccgcg gcctgccccg cccggctccc tgcgcgcgcg	100
ccgcctcccg ggacagaaga tgtgtcccag ggtccctctg ctgctgccgc	150
tgtcctctgt actggccctg gggcctgggg tgcagggctg cccatccggc	200
tgccagtga gccagccaca gacagtcttc tgcactgcc gccaggggac	250
cacggtgcc cgagacgtgc caccgacac ggtggggctg tacgtctttg	300
agaacggcat caccatgctc gacgcaggca gctttgccg cctgccgggc	350
ctgcagctcc tggacctgtc acagaaccag atcgccagcc tgcccagcgg	400
ggtcttccag cactcgcca acctcagcaa cctggacctg acggccaaca	450
ggctgcata aatcaccaat gagaccttc gtggcctgcg gcgcctcgag	500
cgcctctacc tgggcaagaa ccgcctccgc cacatccagc ctggtgcctt	550
cgacacgtc gaccgcctcc tggagctcaa gctgcaggac aacgagctgc	600
gggactgccc cccgctgcgc ctgccccgcc tegtgtgtgt ggacctcagc	650
cacaacagcc tcctggccct ggagcccgcc atcctggaca ctgccaacgt	700
ggagggcgtg cggctggctg gtctggggct gcagcagctg gacgaggggc	750
tcctcagcgc 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 ggtgtctggc	1000
agctccccgc aacccttca actgcgtgtg cccctgagc tggtttgccc	1050
cctgggtgag 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 gccgccttc	1300
cactgcccc aagactgtag ggctgtccc ccagccccag gactgcccac	1350
cgctccactg cctcaatggg ggcacatgcc acctggggac acggcaccac	1400
ctggcgctgt tgtgccccga aggtctcagc ggctgtact gtgagagcca	1450
gatggggcag gggacacggc ccagccctac accagtacg ccgaggccac	1500
cacggtccct gaccctgggc atcgagccgg tgagccccc ctccctgcgc	1550
gtggggctgc agcgctacct ccaggggagc tccgtgcagc tcaggagcct	1600
ccgtctcaac tatcgcaacc tatcgggccc tgataagcgg ctggtgacgc	1650
tgcgactgcc tgcctcgctc gctgagtaca cggtcaccca gctgcggccc	1700

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aacgccactt actccgtctg tgtcatgcct ttggggcccg ggcgggtgcc      1750
ggagggcgag gaggcctgcg gggaggccca tacaccccca gccgtccact      1800
ccaaccacgc ccagtcacc caggcccgcg agggcaacct gccgctcctc      1850
attgcgcccg ccctggccgc ggtgctcctg gccgcgctgg ctgcggtggg      1900
ggcagcctac tgtgtgcggc gggggcgggc catggcagca gcggctcagg      1950
acaaagggca ggtggggcca ggggtctggc ccctggaact ggagggagtg      2000
aagggtccct tggagccagg ccggaaggca acagaggcg gtaggagggc      2050
cctgccacgc ggggtctgagt gtgaggtgcc actcatgggc tccccagggc      2100
ctggcctcca gtcaccctc caccgaaagc cctacatcta agccagagag      2150
agacagggca gctggggccg ggctctcagc cagtgcgatg gccagcccc      2200
tctctgtgcc acaccacgta agttctcagt cccaacctcg gggatgtgtg      2250
cagacagggc tgtgtgacca cagctgggco ctgttccctc tggacctcgg      2300
tctctctatc tgtgagatgc tgtggcccag ctgacgagcc ctaacgtccc      2350
cagaaccgag tgcctatgag gacagtgtcc gccctgccct ccgcaactg      2400
cagtcctctg gcacggcggg ccctgccatg tgctggtaac gcatgcctgg      2450
gtcctgtctg gctctccac tccagcgga ccctgggggc cagtgaagg      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
```

<210> SEQ ID NO 16
<211> LENGTH: 673
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 16

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

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Leu	Thr	Tyr	Arg	Asn	Leu	Ser	Gly	Pro	Asp	Lys	Arg	Leu	Val	Thr
				500					505					510
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	ggcggcggtg	gtggctgagt	ccgtggtggc	agaggcgaag	50
gcgacagctc	atgcgggtcc	ggatagggct	gacgctgctg	ctgtgtgcgg	100
tgctgctgag	cttggcctcg	gcgtcctcgg	atgaagaagg	cagccaggat	150
gaatccttag	attccaagac	tactttgaca	tcagatgagt	cagtaaagga	200
ccatactact	gcaggcagag	tagttgctgg	tcaaatat	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

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gaagctgact gaggaaggct ctccaaggg acagactgct cttggctttc	850
tgtatgcctc tggacttggg gttattcaa gtcaggcaaa ggctcttgta	900
tattatacat ttggagctct tgggggcaat ctaatagccc acatggtttt	950
ggtaagtaga ctttagtgga aggctaataa tattaacatc agaagaattt	1000
gtggtttata gcggccacaa ctttttcagc tttcatgac cagatttgct	1050
tgtattaaga ccaaataatc agttgaactt ccttcaaatt cttgttaatg	1100
gataatacac atggaatcta catgtaaatg aaagttgggt 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 gttatttggt	1400
cagaatgact ccagagagct ctactttctg ttttttactt ttcatgattg	1450
gctgtcttcc catttattct ggtcatttat tgctagtac actgtgcctg	1500
cttcagtag tctcattttc cctattttgc taatttgta ctttttcttt	1550
gctaatttgg aagattaact catttttaat 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

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Gly	Phe	Cys	Glu	Thr	Glu	Glu	Glu	Ala	Ala	Lys	Arg	Arg	Gln	Met
			170						175					180
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
ttctgtggac 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
agagaacctt ttgaagtga cctgtttgga ctcactcagt tgacactaaa	550
tatgcttcct ttggtcaaga aagctcaagg gagagttatt aatgtctcca	600
gtgttgaggg tcgccttgca atcgttggag gggctatac tccatccaaa	650
tatgcagtgg aaggtttcaa tgacagctta agacgggaca tgaaagcttt	700
tggtgtgcac gtctcatgca ttgaaccagg attgttcaa acaaaacttg	750
cagatccagt aaaggttaatt gaaaaaaac tcgccatttg ggagcagctg	800
tctccagaca tcaaacaaca atatggagaa gggttacattg aaaaaagtct	850
agacaaaactg aaaggcaata aatcctatgt gaacatggac ctctctccgg	900
tggttagagt catggaccac gctctaaca gtctcttccc taagactcat	950

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tatgccgctg gaaaagatgc caaaattttc tggatacctc tgtctcacat	1000
gccagcagct ttgcaagact ttttattgtt gaaacagaaa gcagagctgg	1050
ctaattcccaa ggcagtgatga ctacagtaac cacaatgtc tcctccaggc	1100
tatgaaattg gccgatttca agaacacatc tccttttcaa cccatttcct	1150
tatctgctcc aacctggact catttagatc gtgcttattt ggattgcaaa	1200
agggagtccc accatcgctg gtggtatccc agggtcctcg ctcaagtttt	1250
ctttgaaaag gagggtgga atggtacatc acataggcaa gtcctgccct	1300
gtatttaggc tttgcctgct tgggtgatg taagggaat tgaaagactt	1350
gcccattcaa aatgatcttt accgtggcct gcccctgct tatggtcccc	1400
agcattttaca gtaacttggt 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	

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Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu
230 235 240
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 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 tgtttataca attgacattc 200
agaaatatat tccatgctat cagcttttta gcttttataa ttcttcaggc 250
gaagtaaatg agcaagcact gaagaaaata ttatcaaatg tcaaaaagaa 300
tgtgtgtaggt tggtaacaaat tccgtcgtca ttcagatcag atcatgacgt 350
ttagagagag gctgcttcac aaaaacttgc aggagcattt ttcaaaccaa 400
gaccttgttt ttctgctatt aacaccaagt ataataacag aaagctgctc 450
tactcatcga ctggaacatt ccttatataa acctcaaaaa ggactttttc 500
acagggtacc tttagtgggt gccaatctgg gcatgtctga acaactgggt 550
tataaaactg tatcaggttc ctgtatgtcc actggtttta gccgagcagt 600
acaaacacac agctctaata tttttgaaga agatggatcc ttaaaggagg 650
tacataagat aaatgaaatg tatgcttcac 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

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aaagatgaag gggttttggtg aatattcacg gtctcctaca ttttgatcct      1250
tttaacctta caaggagatt tttttatttg gctgatgggt aaagccaaac      1300
atttctattg tttttactat gttgagctac ttgcagtaag ttcatttggt      1350
tttactatgt tcacctgttt gcagtaatac acagataact cttagtgcac      1400
ttacttcaca aagtactttt tcaaacatca gatgctttta tttccaaacc      1450
ttttttttcac ctttcactaa gttgttgagg ggaaggctta cacagacaca      1500
ttcttttagaa ttgaaaagt gagaccaggc acagtggctc acacctgtaa      1550
tcccagcact 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

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<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

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Glu Val His Lys Ile Asn Glu Met Tyr Ala Ser Leu Gln Glu Glu
215 220 225
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 cgcggcggag ggcagagtca gccgagccga gtccagcccg 50
acgagcggac cagcgcaggg cagcccaagc agcgcgcagc gaacgcccgc 100
cgccgcccac accctctgcg gtcccgcgg cgctgtccac ccttccctcc 150
ttccccgcgt cccgcctcg ccggccagtc agcttgccgg gttcgctgcc 200
ccgcgaaacc ccgaggtcac cagcccgcg ctctgtcttc ctgggcccgcg 250
cgccgcctcc acgcccctct tctcccctgg cccggcgctt ggcaccgggg 300
accgttgctt gacgcgaggc ccagctctac ttttcgcccc gcgtctcttc 350
cgctgtctcg cctcttccac caactccaac tccttctccc tccagctcca 400
ctcgctagtc cccgactccg ccagccctcg gcccgctgcc gtagcgccgc 450
ttcccgctcg gtcccaaagg tgggaacgag tccgcccgg cccgcacccat 500
ggcacgggtc ggcttgcccg cgcttctctg caccctggca gtgctcagcg 550
ccgcgctgct ggctgccgag ctcaagtcga aaagttgctc ggaagtgcga 600
cgtcttttag tgtccaaagg cttaacaag aacgatgccc cctccacga 650

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gatcaacggt gatcatttga agatctgtcc ccagggttct acctgctgct	700
ctcaagagat ggaggagaag tacagcctgc aaagtaaaga tgatttcaaa	750
agtgtggtca gcgaacagtgc 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
tcttgagcgc gatgttcgcg ctggtgaact ccagtagca ctttacagat	1050
gagtatctgg aatgtgtgag caagtatacg gagcagctga agcccttcgg	1100
agatgtccct cgcaaatga agctccaggt tactcgtgct ttgtagcag	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 ttgaatcgg catggatccc atcgatgtga	1450
agattttctga tgctattatg aacatgcagg ataatagtgt tcaagtgtct	1500
cagaaggttt tccagggatg tggaccccc aagcccctcc cagctggacg	1550
aatttctcgt tccatctctg aaagtgcctt cagtgtcgcg 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
gcagtgacag gaaatggatt agccaaccag ggcaacaacc cagaggtcca	1850
ggttgacacc agcaaaccag acatactgat ccttcgtcaa atcatggctc	1900
ttcagtgatg gaccagcaag atgaagaatg catacaatgg gaacgacgtg	1950
gacttctttg atatcagtga tgaaagtagt ggagaaggaa gtggaagtgg	2000
ctgtgagtat cagcagtgcc cttcagagtt tgactacaat gccactgacc	2050
atgctgggaa gagtgccaat gagaaagccg acagtgtggt gtccgtcct	2100
ggggcacagg cctacctcct cactgtcttc tgcattctgt tcttggttat	2150
gcagagagag tggagataat tctcaaaact tgagaaaaag tgttcacaa	2200
aaagttaaaa ggcaccagtt atcacttttc taccatccta gtgactttgc	2250
tttttaaatg aatggacaac aatgtacagt ttttactatg tggccactgg	2300
tttaagaagt gctgactttg ttttctcatt cagttttggg aggaaaagg	2350
actgtgcatt gagttggtc ctgctcccc aaaccatgtt aaacgtggct	2400
aacagtgtag gtacagaact atagttagtt gtgcatttgt gattttatca	2450
ctctattatt tgtttgtatg ttttttctc atttcgtttg tgggtttttt	2500
tttccaactg tgatctcgcc ttgtttctta caagcaaacc agggctccct	2550

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cttggcacgt aacatgtacg tatttctgaa atattaaata gctgtacaga      2600
agcagggtttt atttatcatg ttatcttatt aaaagaaaaa gcccaaaaag      2650
c                                                                2651

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<210> SEQ ID NO 24
<211> LENGTH: 556
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

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<400> SEQUENCE: 24

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```

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

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Asp Val Lys Ile Ser Asp Ala Ile Met Asn Met Gln Asp Asn Ser
320 325 330

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 cgcacagtgt	150
cgatgaaagt tctaattctct tccctcctcc tgttgctgcc actaatgctg	200
atgtccatgg tctctagcag cctgaatcca ggggtcgcca gaggccacag	250
ggaccgaggg caggcttcta ggagatggct ccaggaaggc ggccaagaat	300
gtgagtgcaa agattggttc ctgagagccc cgagaagaaa attcatgaca	350
gtgtctgggc tgccaaagaa gcagtgcgcc tgtgatcatt tcaagggcaa	400
tgtgaagaaa acaagacacc aaaggcacca cagaaagcca aacaagcatt	450

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ccagagcctg ccagcaattt ctcaacaat gtcagctaag aagctttgct      500
ctgcctttgt aggagctctg agcgccact cttccaatta aacattctca      550
gccaagaaga cagtgagcac acctaccaga cactcttctt ctcccacctc      600
actctcccac tgtaccacc cctaaatcat tccagtgtc tcaaaaagca      650
tgtttttcaa gatcattttg ttgttgctc tctctagtgt cttcttctct      700
cgtcagtctt agcctgtgcc ctccccttac ccaggcttag gcttaattac      750
ctgaaagatt ccaggaaact gtagcttcct agctagtgtc atttaacctt      800
aaatgcaatc aggaaagtag caaacagaag tcaataaata tttttaaatg      850
tcaaaaaaaa 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            115
```

<210> SEQ ID NO 27
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 27

```
ggacgccagc gcctgcagag gctgagcagg gaaaaagcca gtgcccacgc      50
ggaagcacag ctgagagctg gtctgccatg gacatcctgg tcccactcct      100
gcagctgctg gtgctgcttc ttacctgccc cctgcacctc atggctctgc      150
tgggctgctg gcagcccctg tgcaaaagct acttccccta cctgatggcc      200
gtgctgactc ccaagagcaa ccgcaagatg gagagcaaga aacgggagct      250
cttcagccag ataaaggggc ttacaggagc ctccgggaaa gtggccctac      300
tggaagctggg ctgcggaacc ggagccaact ttcagttcta cccaccgggc      350
tgcagggtca cctgcctaga cccaaatccc cactttgaga agttcctgac      400
aaagagcatg gctgagaaca ggcacctcca atatgagcgg tttgtggtgg      450
```

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ctcctggaga ggacatgaga cagctggctg atggctccat ggatgtggtg      500
gtctgcactc tgggtgctgtg ctctgtgcag agcccaagga aggtcctgca      550
ggaggtccgg agagtactga gaccgggagg tgtgctcttt ttctgggagc      600
atgtggcaga accatatgga agctgggcct tcatgtggca gcaagttttc      650
gagcccacct ggaacacat tggggatggc tgctgcctca ccagagagac      700
ctggaaggat cttgagaacg ccagtttctc cgaaatccaa atggaacgac      750
agccccctcc cttgaagtgg ctacctgttg ggccccacat catgggaaag      800
gctgtcaaac aatctttccc aagctccaag gcaactcatt gtccttccc      850
cagcctccaa ttagaacaag ccaccacca gcctatctat cttccactga      900
gagggacctc gcagaatgag agaagacatt catgtaccac ctactagtcc      950
ctctctcccc aacctctgcc agggcaatct ctaactcaa tccgccttc     1000
gacagtgaaa aagctctact tctacgtga ccagggagg aaacactagg     1050
accctgttgt atcctcaact gcaagtttct ggactagtct cccaacgttt     1100
gcctcccaat gttgtccctt tccttcgttc ccatggtaaa gtcctctctg     1150
ctttctcctt gaggctacac ccatgcgtct ctaggaactg gtcacaaaag     1200
tcatggtgcc tgcacccctg ccaagcccc ctgaccctct ctccccacta     1250
ccaccttctt cctgagctgg gggcaccagg gagaatcaga gatgctgggg     1300
atgccagagc aagactcaaa gaggcagagg tttgtttctc 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
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Gln Ser Pro Arg Lys Val Leu Gln Glu Val Arg Arg Val Leu Arg
155 160 165
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 ttcctttctg tgtctcctgc ctcatcggcc 200
tgcccatgacc tgcagccaag ccagccccg 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

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Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<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
tgccccctcaa acacctgagt gctactccct atttgcattct gttttgataa	150
atgatgttga caccctccac cgaattctaa gtggaatcat gtcgggaaga	200
gatacaatcc ttggcctgtg tatcctcgca ttgacctgtg ctttggccat	250
gatgtttacc ttacagattca tcaccaccct tctgggtcac attttcattt	300
cattgggttat tttgggattg ttgtttgtct gcggtgtttt atggtggctg	350
tattatgact ataccaacga cctcagcata gaattggaca cagaaaggga	400
aaatatgaag tgcgtgctgg ggtttgctat cgtatccaca ggcacacgg	450
cagtgcctgt cgtcttgatt tttgttctca gaaagagaat aaaattgaca	500
gttagctttt tccaaatcac aaataaagcc atcagcagtg ctcccttcct	550
gctgttccag ccactgtgga catttgccat cctcattttc tcttgggtcc	600
tcttgggtggc tgtgctgctg agcctgggaa ctgcaggagc tgcccagggt	650
atggaaggcg gccaaagtga atataagccc ctttcgggca ttcggtacat	700
gtggctgtac catttaattg gcctcatctg gactagttaa ttcattcctg	750
cgtgccagcaaatgactata gctggggcag tggttacttg ttatttcaac	800
agaagtaaaa atgatcctcc tgatcatccc atcctttcgt ctctctccat	850
tctcttcttc taccatcaag gaaccgttgt gaaagggta tttttaattct	900
ctgtggtgag gattccgaga atcattgtca tgtacatgca aaacgcactg	950
aaagaacagc agcatggtgc attgtccagg tacctgttcc gatgctgcta	1000
ctgctgtttt tggtgtcttg acaaatacct gctccatctc aaccagaatg	1050
catatactac aactgctatt aatgggacag atttctgtac atcagcaaaa	1100
gatgcattca aaatcttgtc caagaactca agtcacttta catctattaa	1150
ctgctttgga gacttcataa tttttctagg aaagggttta 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 gagggaggaa	1500
cagaactcca ggccattgtg agatagatac ccatttaggt atctgtacct	1550
ggaaaacatt tccttctaag agccatttac agaatagaag atgagaccac	1600
tagagaaaaa ttagtgaatt tttttttaa agacctata aacctattc	1650

-continued

ttcctcaaaa

1660

<210> SEQ ID NO 32

<211> LENGTH: 445

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 32

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	

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Gly	Lys	Val	Leu	Val	Val	Cys	Phe	Thr	Val	Phe	Gly	Gly	Leu	Met
			335						340					345
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 gaaaattttt tgaaaaaaaa	150
attgccttct tcaaacaagg gtgtcattct gatatttatg aggactgttg	200
ttctcactat gaaggcatct gttattgaaa tgttccttgt ttgctggtg	250
actggagtag attcaaacaa agaaacggca aagaagatta aaaggcccaa	300
gttcactgtg cctcagatca actgcgatgt caaagccgga aagatcatcg	350
atcctgagtt cattgtgaaa tgtccagcag gatgccaaaga ccccaaatac	400
catgtttatg gcactgacgt gtatgcatcc tactccagtg tgtgtggcgc	450
tgccgtacac agtggtgtgc ttgataatlc aggagggaaa atacttgttc	500
ggaagggttg tggacagtct gggtacaaag ggagttattc caacggtgtc	550
caatcgttat ccctaccacg atggagagaa tcctttatcg tcttagaaag	600
taaacccaaa aagggtgtaa cctaccatc agctcttaca tactcatcat	650
cgaaaagtcc agctgcccaa gcaggtgaga ccacaaaagc ctatcagagg	700
ccacctattc cagggacaac tgcacagccg gtcactctga tgcagcttct	750
ggctgtcact gtagctgtgg ccacccccac caccttgcca aggccatccc	800
cttctgtctg ttctaccacc agcatcccca gaccacaatc agtgggccac	850
aggagccagg agatggatct ctggtccact gccacctaca caagcagcca	900
aaacaggccc agagctgatc caggtatcca aaggcaagat ccttcaggag	950
ctgccttcca gaaacctggt ggagcggatg tcagcctggg acttgttcca	1000
aaagaagaat tgagcacaca gtctttggag ccagtatccc tgggagatcc	1050
aaactgcaaa attgacttgt cgtttttaat tgatggggagc accagcattg	1100

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gcaaacggcg attccgaatc cagaagcagc tcctggctga tgttgcccaa	1150
gctcttgaca ttggccctgc cggtcactg atgggtgttg tccagtatgg	1200
agacaaccct gctactcact ttaacctcaa gacacacacg aattctcgag	1250
atctgaagac agccatagag aaaattactc agagaggagg actttctaata	1300
gtaggtcggg ccatctcctt tgtgaccaag aacttctttt ccaaagccaa	1350
tggaaacaga agcggggctc ccaatgtggt ggtggtgatg gtggatggct	1400
ggccccagga caaagtggag gaggcttcaa gacttgcgag agagtcagga	1450
atcaacattt tcttcacac cattgaaggt gctgctgaaa atgagaagca	1500
gtatgtggtg gagcccaact ttgcaacaa ggccgtgtgc agaacaacg	1550
gcttctactc gctccacgtg cagagctggt ttggcctcca caagacctg	1600
cagcctcttg tgaagcgggt ctgcgacact gaccgcctgg cctgcagcaa	1650
gacctgcttg aactcggctg acattggctt cgtcatcgac ggctccagca	1700
gtgtggggac gggcaacttc cgcaccgtcc tccagtttgt gaccaacctc	1750
accaagagat ttgagatttc cgacacggac acgcgcctcg gggccgtgca	1800
gtacacctac gaacagcggc tggagtttgg gttcgacaag tacagcagca	1850
agcctgacat cctcaacgcc atcaagaggg tgggctactg gagtgtggc	1900
accagcacgg gggctgccat caacttcgcc ctggagcagc tcttcaagaa	1950
gtccaagccc aacaagagga agttaatgat cctcatcacc gacgggaggt	2000
cctacgacga cgtccggatc ccagccatgg ctgcccattc gaagggagt	2050
atcacctatg cgataggcgt tgctgggct gcccaagagg agctagaagt	2100
cattgccact caccocgcca gagaccactc cttctttgtg gacgagttt	2150
acaacctcca tcagtatgtc cccaggatca tccagaacat ttgtacagag	2200
ttcaactcac agcctcggaa ctgaattcag agcaggcaga gcaccagcaa	2250
gtgctgcttt actaactgac gtgttggaac accccaccgc ttaatggggc	2300
acgcacggtg catcaagtct tgggcagggc atggagaaac aaatgtcttg	2350
ttattattct ttgccatcat gctttttcat attccaaaac ttggagttac	2400
aaagatgatc acaaacgtat 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
aaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa	2700
aaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa	2750
aaaaaaaa aaaaaaaaa aag	2773

<210> SEQ ID NO 34

<211> LENGTH: 678

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 34

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Met	Arg	Thr	Val	Val	Leu	Thr	Met	Lys	Ala	Ser	Val	Ile	Glu	Met	1	5	10	15
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	

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Ile	Ser	Phe	Val	Thr	Lys	Asn	Phe	Phe	Ser	Lys	Ala	Asn	Gly	Asn	
				380					385					390	
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

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caacaaaaaa	cttaagcttt	aatttcacat	ggaattccac	agttttctta	200
gtcccttgga	cccgggtgac	ctgttggtc	ttcccgctgg	ctgctctatc	250
acgtggtgct	ctccgactac	tcaccccgag	tgtaaagaac	cttcggctcg	300
cggtgctctg	agctgctgtg	gatggcctcg	gctctctgga	ctgtccttcc	350
gagtaggatg	tactgagat	ccctcaaatg	gagcctcctg	ctgctgtcac	400
tcctgagttt	ctttgtgatg	tggtacctca	gccttcccca	ctacaatgtg	450
atagaacgcg	tgaactggat	gtacttctat	gagtatgagc	cgatttacag	500
acaagacttt	cacttcacac	ttcgagagca	ttcaaatgac	tctcatcaaa	550
atccatttct	ggtcattctg	gtgacctccc	acccttcaga	tgtgaaagcc	600
aggcaggcca	ttagagttac	ttggggtgaa	aaaaagtctt	ggtggggata	650
tgaggttctt	acatttttct	tattaggcca	agaggctgaa	aaggaagaca	700
aaatgttggc	attgtcctta	gaggatgaac	accttcttta	tggtgacata	750
atccgacaag	attttttaga	cacatataat	aacctgacct	tgaaaaccat	800
tatggcattc	aggtgggtaa	ctgagttttg	ccccaatgcc	aagtacgtaa	850
tgaagacaga	cactgatgtt	ttcatcaata	ctggcaattt	agtgaagtat	900
cttttaaacc	taaaccactc	agagaagttt	ttcacagggt	atcctctaata	950
tgataattat	tcctatagag	gattttacca	aaaaacccat	atttcttacc	1000
aggagtatcc	tttcaagggtg	ttccctccat	actgcagtgg	gttgggttat	1050
ataatgtcca	gagatttggg	gccaaaggatc	tatgaaatga	tggtgcacgt	1100
aaaaccatc	aagtttgaag	atgtttatgt	cgggatctgt	ttgaatttat	1150
taaaagtga	cattcatatt	ccagaagaca	caaatctttt	ctttctatat	1200
agaatccatt	tgatgtctg	tcaactgaga	cgtgtgattg	cagcccatgg	1250
cttttcttcc	aaggagatca	tcactttttg	gcaggctcatg	ctaaggaaca	1300
ccacatgcca	ttattaactt	cacattctac	aaaaagccta	gaaggacagg	1350
ataccttggt	gaaagtgtta	aataaagtag	gtactgtgga	aaattcatgg	1400
ggaggtcagt	gtgctggcct	acactgaact	gaaactcatg	aaaaaccag	1450
actggagact	ggagggttac	acttgtgatt	tattagtcag	gcccttcaaa	1500
gatgatattg	ggaggaatta	aatataaagg	aattggagggt	ttttgctaaa	1550
gaaattaata	ggaccaaaca	atttgacat	gtcattctgt	agactagaat	1600
ttcttaaaag	ggtgttactg	agttataagc	tcactaggct	gtaaaaacaa	1650
aacaatgtag	agttttattt	attgaacaat	gtagtcaatt	gaaggttttg	1700
tgtatatctt	atgtggatta	ccaatttaaa	aatatatgta	gttctgtgtc	1750
aaaaaacttc	ttactgaag	ttatactgaa	caaaatttta	cctgtttttg	1800
gtcattttata	aagtacttca	agatgttgca	gtatttcaca	gttattatta	1850
tttaaaatta	cttcaacttt	gtgtttttta	atgttttgac	gattttcaata	1900
caagataaaa	aggatagtga	atcattcttt	acatgcaaac	attttccagt	1950
tacttaactg	atcagtttat	tattgataca	tcactccatt	aatgtaaagt	2000
cataggtcatt	tattgcatat	cagtaatctc	ttggactttg	ttaaatattt	2050

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tactgtggta atatagagaa gaattaaagc aagaaaatct gaaaa

2095

<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

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Tyr

<210> SEQ ID NO 37

<211> LENGTH: 2846

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 37

cgctcgggca ccagcccgcg caaggatgga gctgggttgc tggacgcagt	50
tggggctcac ttttcttcag ctctcttctca tctcgtcctt gccaaagagag	100
tacacagtca ttaatgaagc ctgccctgga gcagagtgga atatcatgtg	150
tcgggagatgc tgtgaatatg atcagattga gtgcgtctgc cccggaaaga	200
gggaagtctg gggttatacc atcccttgct gcaggaaatga ggagaatgag	250
tgtgactcct gcctgatcca ccaggttgt accatctttg aaaactgcaa	300
gagctgccga aatggctcat ggggggttac cttggatgac ttctatgtga	350
aggggttcta ctgtgcagag tgccgagcag gctggtagcgg aggagactgc	400
atgcgatgtg gccaggttct gcgagcccca aagggtcaga tttgtttgga	450
aagctatccc ctaaagtctc actgtgaatg gaccattcat gctaaacctg	500
ggtttgtcat ccaactaaga tttgtcatgt tgagtctgga gtttgactac	550
atgtgccagt atgactatgt tgaggttctg 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 tgagtgcac tcacccttct accgccgctt gggcagcagc	1300
aggaggacat gtctgaggac tgggaagtgg agtgggcggg 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 caccatgac aagacagcag acctgaaagt tgttttgggg	1600
aaattctacc gggatgatga ccgggatgag aagaccatcc agagcctaca	1650

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gattttctgct atcattctgc atcccaacta tgaccccatc ctgcttgatg	1700
ctgacatcgc catcctgaag ctcttagaca aggcccgat cagcaccga	1750
gtccagccca tctgcctcgc tgccagtcgg gatctcagca cttccttcca	1800
ggagtcccac atcactgtgg ctggctggaa tgtcctggca gacgtgagga	1850
gccttggtt caagaacgac acactgcgct ctggggtggt cagtgtggtg	1900
gactcgctgc tgtgtgagga gcagcatgag gaccatggca 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
tgcccttttaa agactggatt gaaagaaata tgaatgaac catgctcatg	2200
cactccttga gaagtgttct tgtatatccg tctgtacgtg tgtcattgctg	2250
tgaagcagtg tgggcctgaa gtgtgatttg gcctgtgaac ttggctgtgc	2300
cagggtctct gacttcaggg aaaaaactca gtgaagggtg agtagacctc	2350
cattgctggt aggtgatgc cgcgtccact actaggacag ccaattggaa	2400
gatgccaggg cttgcaagaa gtaagtittct tcaaagaaga ccatatacaa	2450
aacctctcca ctccactgac ctgggtgtct tccccaactt tcagttatac	2500
gaatgccatc agcttgacca gggaagatct gggcttcatg agggcccttt	2550
tgaggctctc aagtictaga gagctgcctg tgggacagcc cagggcagca	2600
gagctgggat gtggtgcatg cttttgtgta catggccaca gtacagtctg	2650
gtccttttcc ttcccatct cttgtacaca ttttaataaa ataagggttg	2700
gtttctgaac 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

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Phe Tyr Val Lys Gly Phe Tyr Cys Ala	Glu Cys Arg Ala Gly Trp
110	115 120
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

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His	Lys	Gly	Ala	Trp	Phe	Leu	Val	Cys	Ser	Gly	Ala	Leu	Val	Asn
			485						490					495
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
cagtctgct aactacattg acaatgtggg caacctgcac ttcctgtatt	300
cagaactctg taaaggtgcc tccactacg gcctgaccaa agataggaag	350
aggcgtcac aagatggctg tccagacggc tgtgcgagcc tcacagccac	400
ggctccctcc ccagaggttt ctgcagctgc caccatctcc ttaatgacag	450
acgagcctgg cctagacaac cctgcctacg tgtcctcggc agaggacggg	500

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cagccagcaa tcagcccagt ggactctggc cggagcaacc gaactagggc	550
acggcccttt gagagatcca ctattagaag cagatcattt aaaaaataa	600
atcagagcttt gagtgttctt cgaaggacaa agagcgggag tgcagttgcc	650
aaccatgccg accagggcag ggaattctt gaaaacacca ctgccctga	700
agtctttcca aggttgtacc acctgattcc agatggtgaa attaccagca	750
tcaagatcaa tcgagtagat cccagtgaag gcctctctat taggctggtg	800
ggaggtagcg aaacccact ggtccatc attatccaac acatttatcg	850
tgatggggtg atcgccagag acggccggct actgccagga gacatcattc	900
taagggtcaa cgggatggac atcagcaatg tccctcaca ctacgctgtg	950
cgtctctcgtg ggcagccctg ccaggtgctg tggctgactg tgatgcgtga	1000
acagaagttc cgcagcagga acaatggaca ggcccggat gcctacagac	1050
cccagatga cagctttcat gtgattctca acaaaagtag ccccgaggag	1100
cagcttgga taaaactggt gcgcaagggt gatgagcctg gggttttcat	1150
cttcaatgtg ctggatggcg gtgtggcata tcgacatggt cagcttgagg	1200
agaatgaccg tgtgttagcc atcaatggac atgatcttcg atatggcagc	1250
ccagaaagtg cggctcatct gattcaggcc agtgaaagac gtgttcacct	1300
cgtcgtgtcc cgccaggttc ggcagcggag ccctgacatc ttccaggaag	1350
ccggctggaa cagcaatggc agctgggtccc cagggccagg ggagaggagc	1400
aacactccca agccctcca tcctacaatt acttgtcatg agaagtggt	1450
aaatatccaa aaagaccccg gtgaatctct cggcatgacc gtcgcagggg	1500
gagcatcaca tagagaatgg gatttgcta tctatgtcat cagtgttgag	1550
cccgaggagg tcataagcag agatggaaga ataaaaacag gtgacathtt	1600
gttgaatgtg gatggggtcg aactgacaga ggtcagccgg agtgaggcag	1650
tggcattatt gaaaagaaca tcctcctcga tagtactcaa agctttggaa	1700
gtcaagagat atgagcccca ggaagactgc agcagcccag cagccctgga	1750
ctccaaccac aacatggccc ccccagtgat ctggtcccca tcctgggtca	1800
tgtggctgga attaccacgg tgcttgata actgtaaaga tattgtatta	1850
cgaagaaaca cagctggaag tctgggcttc tgcattgtag gaggttatga	1900
agaatacaat ggaacaaac cttttttcat caaatccatt gttgaaggaa	1950
caccagcata caatgatgga agaattagat gtggtgatat tcttcttgct	2000
gtcaatggta gaagtacatc aggaatgata catgcttgct tggcaagact	2050
gctgaaagaa cttaaggaa gaattactct aactattggt tcttgccctg	2100
gcactttttt atagaatcaa tgatgggtca gaggaaca gaaaaatcac	2150
aaataggcta agaagttgaa acactatatt tatcttgta gtttttata	2200
ttaaagaaag aatacattgt aaaaatgtca ggaaaagtat gatcatctaa	2250
tgaagccag ttacacctca gaaaatatga ttccaaaaaa attaaaacta	2300
ctagtttttt ttcatgtgg aggattttct attactctac aacattgttt	2350
atattttttt tattcaataa aaagccctaa aacaactaaa atgattgatt	2400

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tgtatacccc actgaattca agctgattta aatttaaaat ttggtatatg	2450
ctgaagtctg ccaagggtac attatggcca tttttaattt acagctaaaa	2500
tatttttttaa aatgcattgc tgagaaacgt tgctttcatc aaacaagaat	2550
aaatatTTTT 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	15
Asn Tyr Ile Asp Asn Val Gly Asn Leu His Phe Leu Tyr Ser Glu	20	25	30	
Leu Cys Lys Gly Ala Ser His Tyr Gly Leu Thr Lys Asp Arg Lys	35	40	45	
Arg Arg Ser Gln Asp Gly Cys Pro Asp Gly Cys Ala Ser Leu Thr	50	55	60	
Ala Thr Ala Pro Ser Pro Glu Val Ser Ala Ala Ala Thr Ile Ser	65	70	75	
Leu Met Thr Asp Glu Pro Gly Leu Asp Asn Pro Ala Tyr Val Ser	80	85	90	
Ser Ala Glu Asp Gly Gln Pro Ala Ile Ser Pro Val Asp Ser Gly	95	100	105	
Arg Ser Asn Arg Thr Arg Ala Arg Pro Phe Glu Arg Ser Thr Ile	110	115	120	
Arg Ser Arg Ser Phe Lys Lys Ile Asn Arg Ala Leu Ser Val Leu	125	130	135	
Arg Arg Thr Lys Ser Gly Ser Ala Val Ala Asn His Ala Asp Gln	140	145	150	
Gly Arg Glu Asn Ser Glu Asn Thr Thr Ala Pro Glu Val Phe Pro	155	160	165	
Arg Leu Tyr His Leu Ile Pro Asp Gly Glu Ile Thr Ser Ile Lys	170	175	180	
Ile Asn Arg Val Asp Pro Ser Glu Ser Leu Ser Ile Arg Leu Val	185	190	195	
Gly Gly Ser Glu Thr Pro Leu Val His Ile Ile Ile Gln His Ile	200	205	210	
Tyr Arg Asp Gly Val Ile Ala Arg Asp Gly Arg Leu Leu Pro Gly	215	220	225	
Asp Ile Ile Leu Lys Val Asn Gly Met Asp Ile Ser Asn Val Pro	230	235	240	
His Asn Tyr Ala Val Arg Leu Leu Arg Gln Pro Cys Gln Val Leu	245	250	255	
Trp Leu Thr Val Met Arg Glu Gln Lys Phe Arg Ser Arg Asn Asn	260	265	270	
Gly Gln Ala Pro Asp Ala Tyr Arg Pro Arg Asp Asp Ser Phe His	275	280	285	
Val Ile Leu Asn Lys Ser Ser Pro Glu Glu Gln Leu Gly Ile Lys	290	295	300	

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Leu Val Arg Lys Val Asp Glu Pro Gly Val Phe Ile Phe Asn Val	305	310	315
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

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accaggcatt gtatcttcag ttgtcatcaa gttcgcaatc agattggaaa	50
agctcaactt gaagctttct tgcctgcagt gaagcagaga gatagatatt	100
attcacgtaa taaaaaacat gggcttcaac ctgactttcc accttccta	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
ttccccacog gaacagagag aaacacctga tgtacctgct ggaacatctg	550
catcccttcc tgcagaggca gcagctggat tatggcatct acgtcatcca	600
ccaggctgaa ggtaaaaagt ttaatcgagc caaactcttg aatgtgggct	650
atctagaagc cctcaaggaa gaaaattggg actgctttat attccacgat	700
gtggacctgg tacccgagaa tgactttaac ctttacaagt gtgaggagca	750
tccaagcat ctggtggttg gcaggaacag cactgggtac aggttacgtt	800
acagtggata ttttgggggt gttactgccc taagcagaga gcagtttttc	850
aagggtaatg gattctctaa caactactgg ggatggggag gcaagacga	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
ctcctgggtga 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 ggggtggagt tcggctgcaa aggcagcagt agctgagctg	1750
gttgacagtg ctgatagcct tcaggggag agctgccag gtatgccttc	1800
cagtgatgcc caccagagaa tacattctct attagtTTTT aaagagTTTT	1850
tgtaaaatga ttttgtacaa gtaggatag aattagcagt ttacaagttt	1900

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 acatattaac taataataaa tatgtctatc aaatacctct gtagtaaaat 1950

gtgaaaaagc aaaa 1964

<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

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gtgacccaaa atcgtaatag ggagagagta gacttcccag atggaggcta	300
ctccctgaag ctacgaaac 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 accttcacatc gcgttgccag gaaccctgtc agcagaaaact	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 atttgcctat gagaatgtta tctagacagc	1050
agtgcaactcc 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	

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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 tggttccag gaattatag	200
agcaggctctg atggccattc cagcaacaac aatgtccttg acagcaagaa	250
aaagagcgtg ctgcaacaac agaactggaa tgtttctttc atcatttttc	300
agtgtgatca cagtcattgg tgctctgtat tgcattgctga tatccatcca	350
ggctctctta aaaggtcctc tcatgtgtaa ttctccaagc aacagtaatg	400
ccaattgtga attttcattg aaaaacatca gtgacattca tccagaatcc	450
ttcaacttgc agtgggtttt caatgactct tgtgcacctc ctactggttt	500
caataaacc accagtaacg acaccatggc gagggtctgg agagcatcta	550
gtttccactt cgatttctgaa gaaaacaaac ataggcttat ccatttctca	600
gtatttttag gtctattgct tgttggaatt ctggaggctc tgtttgggct	650
cagtcagata gtcacgggtt tccttggtctg tctgtgtgga gtctctaagc	700
gaagaagtca aattgtgtag tttaattgga ataaatgta agtatcagta	750
gtttgaaaa 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
gcagacact ggtgaaggag cagtgaggaa cctgcagagt cacacagttg	100
ctgaccaatt gagctgtgag cctggagcag atccgtgggc tgcagacccc	150
cgccccagtg cctctcccc tgcagccctg cccctcgaac tgtgacatgg	200
agagagtgc cctggccctt ctctactgg caggcctgac tgccttgga	250
gccaatgacc catttgccaa taaagacgat cccttctact atgactggaa	300
aaacctgcag ctgagcggac tgatctgcgg agggctcctg gccattgctg	350

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ggatcgcggc agttctgagt ggcaaatgca aatacaagag cagccagaag 400
cagcacagtc ctgtacctga gaaggccatc ccactcatca ctccaggctc 450
tgccactact tgctgagcac aggactggcc tccagggatg gcctgaagcc 500
taacactggc ccccgagacc tcctcccctg ggaggcctta tcctcaagga 550
aggacttctc tccaagggca ggctgttagg cccctttctg atcaggaggc 600
ttctttatga attaaactcg ccccaccacc 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 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
gaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100
gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150
agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200
cctggcctgc ctctgctgg ccctctgcct gggcagtggg gaggctggcc 250
ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300
ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350
caaagaggcc ggaggggcag ctggctctaa agtcagttag gcccttggcc 400
aagggaccag agaagcagtt ggcactggag tcaggcaggt tccagcctt 450
ggcgacagc atgctttggg caacagggtc ggggaagcag cccatgctct 500
gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550
acggagcaga tgctgtccgc ggctcctggc aggggggtgcc tggccacagt 600
ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaaggtag 650
ccttgagggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700
tccacggata ccccgaaac tcagcaggca gctttggaat gaatcctcag 750

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ggagctccct ggggtcaagg aggcaatgga gggccaccaa actttgggac 800
caacactcag ggagctgtgg cccagcctgg ctatggttca gtgagagcca 850
gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900
ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtgg 950
cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050
agtgttgcca gcagtggcaa cagtgtgtgg agcagaggtg acagcggcag 1100
tgagtcctcc tggggatcca gcaccggctc ctctccggc aaccacggtg 1150
ggagcggcgg aggaaatgga cataaacccg ggtgtgaaaa gccagggaat 1200
gaagcccgcg ggagcgggga atctgggatt cagggcttca gaggacaggg 1250
agtttcacag aacatgaggg aaataagcaa agagggcaat cgcctccttg 1300
gaggctctgg agacaattat cgggggcaag ggtcgagctg gggcagtgga 1350
ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400
tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450
gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcac 1500
ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact 1550
ccctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600
aaataaacct tagctgcccc aaaaaaaaaa 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

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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 ccgacagaag gatgtcgtg	50
ctgagcctgc cctggctggg cctcagaccg gtggcaatgt ccccatggct	100
actcctgctg ctggttgtgg gctcctggct actcgccgc atcctggctt	150

-continued

ggacctatgc cttctataac aactgccgcc ggctccagtg tttcccacag 200
cccccaaaac ggaactgggt ttggggtcac ctgggcctga tcaactcctac 250
agaggagggc 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 tggagccgcc accgtcggat gctgacgccc 500
gccttcatt tcaacatcct gaagtctat ataacgatct tcaacaagag 550
tgcaaacatc atgcttgaca agtggcagca cctggcctca gagggcagca 600
gtcgtctgga catgtttgag cacatcagcc tcatgacctt ggacagtcta 650
cagaaatgca tcttcagctt tgacagccat tgtcaggaga ggcccagtga 700
atatattgcc accatcttgg agctcagtg ccttgtagag aaaagaagcc 750
agcatatcct ccagcacatg gactttctgt attacctctc ccatgacggg 800
cggcgcttcc acagggcctg ccgctgtgt catgacttca cagacgctgt 850
catccgggag cggcgctcga ccctcccccac tcagggtatt gatgattttt 900
tcaaagacaa agccaagtcc aagactttgg atttcattga tgtgcttctg 950
ctgagcaagg atgaagatgg gaaggcattg tcagatgagg atataagagc 1000
agaggctgac accttcatgt ttggaggcca tgacaccacg gccagtggcc 1050
tctcctgggt cctgtacaac cttgcgaggc acccagaata ccaggagcgc 1100
tgccgacagg aggtgcaaga gcttctgaag gaccgcatc ctaaagagat 1150
tgaatgggac gacctggccc agctgccctt cctgacctg tgcgtgaagg 1200
agagcctgag gttacatccc ccagctccct tcatctcccg atgctgcacc 1250
caggacattg ttctcccaga tggccgagtc atcccaaag gcattacctg 1300
cctcatcgat attatagggg tccatcacia cccaactgtg tggccggatc 1350
ctgagggtcta cgacccttc cgctttgacc cagagaacag caaggggagg 1400
tcacctctgg cttttattcc tttctccgca gggcccagga actgcatcgg 1450
gcaggcggtc gccatggcgg agatgaaagt ggtcctggcg ttgatgctgc 1500
tgcaacttccg gttcctgcca gaccacactg agccccgcag gaagctggaa 1550
ttgatcatgc gcgccgagg cggtctttgg ctgcgggtgg agccccgaa 1600
tgtaggcttg cagtgacttt ctgacctatc 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
Met Ser Pro Trp Leu Leu Leu Leu Val Val Gly Ser Trp Leu
20 25 30

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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
Leu	His	Pro	Pro	Ala	Pro	Phe	Ile	Ser	Arg	Cys	Cys	Thr	Gln	Asp	395	400	405

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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 tgaacacagct	50
gaagcgaatg tttaggccta ctcgtttgat tgcaactatc atggtgctgt	100
tgtgttttgc acttaccctg tgttctgcct tttggtggca taacaaggga	150
cttgacactta tcttctgcat tttagcagtct ttggcattga cgtggtacag	200
cctttccttc ataccatttg caagggatgc tgtgaagaag tgttttgccg	250
tgtgtctttg ataattcatg gccagtttta tgaagctttg gaaggcacta	300
tggaacagaag 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 agcaaaaaa aaaaaaaaa aaaaaaaaa	600
aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 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
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	tcggtctgag	gggcagtgga	gcaccacgca	50
ggccgccaac	atgctctgtc	tgtgcctgtg	cgtgccggtc	atcggggaag	100
cccagaccga	gttcaggtag	tttgagtoga	aggggctccc	tgccgagctg	150
aagtccattt	tcaaactcag	tgtcttcata	ccctcccagg	aattctccac	200
ctaccgccag	tggaagcaga	aaattgtaca	agctggagat	aaggaccttg	250
atgggcagct	agactttgaa	gaatttgtcc	attatctcca	agatcatgag	300
aagaagctga	ggctgggtgt	taagattttg	gacaaaaaga	atgatggacg	350
cattgacgcg	caggagatca	tgcagtcctc	gcgggacttg	ggagtcaaga	400
tatctgaaca	gcaggcagaa	aaaattctca	agagcatgga	taaaaacggc	450
acgatgacca	tcgactggaa	cgagtggaga	gactaccacc	tcctccaccc	500
cgtggaaaac	atccccgaga	tcctcctcta	ctggaagcat	tcacgatctt	550
ttgatgtggg	tgagaatcta	acggtccocg	atgagttcac	agtggaggag	600
aggcagacgg	ggatgtgggt	gagacacctg	gtggcaggag	gtggggcagg	650
ggccgtatcc	agaacctgca	cggccccctc	ggacaggctc	aaggtgctca	700
tgcaggcca	tgctctccgc	agcaacaaca	tgggcatact	tgggtgcttc	750
actcagatga	ttcgagaagg	aggggccagg	tcactctggc	ggggcaatgg	800
catcaacgtc	ctcaaaattg	ccccccaatc	agccatcaaa	ttcatggcct	850
atgagcagat	caagcgcctt	gttggtagtg	accaggagac	tctgaggatt	900
cacgagaggc	ttgtggcagg	gtccttgcca	ggggccatcg	cccagagcag	950
catctacceca	atggagggtcc	tgaagacccg	gatggcgctg	cggaagacag	1000
gccagtactc	aggaatgctg	gactgcgcga	ggaggatcct	ggccagagag	1050
ggggtggccg	ccttctacaa	aggctatgtc	cccaacatgc	tgggcatcat	1100
cccctatgcc	ggcatcgacc	ttgcagtcta	cgagacgctc	aagaatgcct	1150
ggctgcagca	ctatgcagtg	aacagcgocg	accccgccgt	gtttgtgctc	1200
ctggcctgtg	gcacatgtc	cagtacctgt	ggccagctgg	ccagctaccc	1250
cctggcccta	gtcaggaccc	ggatgcaggc	gcaagcctct	attgagggcg	1300
ctccggaggt	gaccatgagc	agcctcttca	aacatatcct	gcggaccgag	1350
ggggccttcg	ggctgtacag	ggggctggcc	cccaacttca	tgaaggatcat	1400
cccagctgtg	agcatcagct	acgtggtcta	cgagaacctg	aagatcacc	1450
tgggcgtgca	gtcgcggtga	cggggggagg	gccgcccggc	agtggactcg	1500
ctgatcctgg	gcgcagcctt	gggtgtgcca	gccatctcat	tctgtaatg	1550

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tgccaacact aagctgtctc gagccaagct gtgaaaaccc tagacgcacc	1600
cgcaggaggag gtggggagag ctggcaggcc cagggcttgt cctgctgacc	1650
ccagcagacc ctctgtttgg ttccagcgaa gaccacaggc attccttagg	1700
gtccagggtc agcaggctcc gggctcacat gtgtaaggac aggacatttt	1750
ctgcagtgcc tgccaatagt gagcttgagg cctggaggcc ggcttagttc	1800
ttccatttca cccttgagc cagctgttgg ccacggcccc tgccctctgg	1850
tctgccgtgc atctccctgt gccctcttgc tgcctgcctg tctgctgagg	1900
taagggtggga ggagggtac agcccacac ccacccctc gtccaatccc	1950
ataatccatg atgaaagggt aggtcacgtg gcctccagg cctgacttcc	2000
caacctacag cattgacgcc aacttggtg tgaaggaga ggaaggatc	2050
tgcccttgtg gtcactggca tctgagccct gctgatggct ggggctctcg	2100
ggcatgcttg ggagtgcagg gggctcgggc tgcctggcct ggctgcacag	2150
aaggcaagtg ctggggctca tgggtgctcg agctggcctg gaccctgtca	2200
ggatggggcc caccctagaa ccaactcac tgtccccact gtggcatgag	2250
ggcagtggag caccatgttt gagggcgaag ggcagagcgt ttgtgtgttc	2300
tggggaggga aggaaaagggt gttggaggcc ttaattatgg actgttggga	2350
aaagggtttt gtccagaagg acaagccgga caaatgagcg acttctgtgc	2400
ttccagagga agacgaggga gcaggagctt ggctgactgc tcagagtctg	2450
ttctgacgcc ctgggggttc ctgtccaacc ccagcagggg cgcagcggga	2500
ccagcccac attccacttg tgtcactgct tggaacctat ttattttgta	2550
tttatttgaa cagagttagt tcctaactat tttatagat ttgtttaatt	2600
aatagcttgt cattttcaag ttcatttttt attcataatt atgttcatgg	2650
ttgattgtac cttcccaagc ccgccagtg ggatgggagg aggaggagaa	2700
ggggggcctt gggccgctgc agtcacatct gtccagagaa attccttttg	2750
ggactggagg cagaaaagcg gccagaagcg agcagccctg gtccttttcc	2800
tttggcaggt tggggaagggt ctgtcccca gccttaggat ttcagggttt	2850
gactgggggc gtggagagag agggaggaac ctcaataacc ttgaagggtg	2900
aatccagtta tttcctgcgc tgcgagggtt tctttatttc actcttttct	2950
gaatgtcaag gcagtgaagt gcctctcact gtgaatttgt ggtgggcggg	3000
ggctggagga gaggtgggg ggctggctcc gtccctccca gccttctgct	3050
gcccttgctt aacaatgccg gccaaactgc gacctcacgg ttgcaactcc	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
aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaa	3334

<210> SEQ ID NO 58

<211> LENGTH: 469

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<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 58

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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

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

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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 acccagatac gctgggaacc 50
ttccccagcc atggcttccc tggggcagat cctcttcttg agcataatta 100
gcatcatcat tattctggct ggagcaattg cactcatcat tggotttgg 150
atttcaggga gacactccat cacagtcact actgtcgct cagctgggaa 200
cattggggag gatggaatcc tgagctgcac ttttgaacct gacatcaaac 250
tttctgatat cgtgatacaa tggctgaagg aaggtgtttt aggottggtc 300
catgagttaa aagaaggcaa agatgagctg tcggagcagg atgaaatgtt 350
cagaggccgg acagcagtgt ttgctgatca agtgatagtt ggcaatgcct 400
ctttgcggct gaaaaacgtg caactcacag atgctggcac ctacaaatgt 450
tatatcatca cttctaaagg caagggaat gctaaccttg agtataaaac 500
tgagaccttc agcatgccgg aagtgaatgt ggactataat gccagctcag 550
agaccttgcg gtgtgaggct ccccgatggt tccccagcc cacagtggtc 600
tgggcatccc aagttgacca gggagccaac ttctcggaag tctccaatac 650
cagctttgag ctgaactctg agaatgtgac catgaagggt gtgtctgtgc 700
tctacaatgt tacgatcaac aacacatact cctgtatgat tgaaaatgac 750
attgccaaag caacagggga tatcaaagt acagaatcgg agatcaaaag 800
gcggagtcac ctacagctgc taaactcaaa ggcttctctg tgtgtctctt 850
ctttctttgc catcagctgg gcaactctgc ctctcagccc ttacctgatg 900
ctaaaaatat gtgccttggc cacaaaaag catgcaaagt cattgttaca 950
acagggatct acagaactat ttcaccacca gatatgacct agttttatat 1000
ttctgggagg aaatgaattc atatctagaa gtctggagtg agcaacaag 1050
agcaagaaac aaaaagaagc caaaagcaga aggctccaat atgaacaaga 1100

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taaatctatc ttcaaagaca tattagaagt tgggaaaata attcatgtga	1150
actagacaag tgtgttaaga gtgataagta aaatgcacgt ggagacaagt	1200
gcatccccag atctcagga cctccccctg cctgtcacct ggggagtgag	1250
aggacaggat agtgcattgt ctttgtctct gaatttttag ttatatgtgc	1300
tgtaatgttg ctctgaggaa gcccttgaa agtctatccc aacatatcca	1350
catcttatat tccacaaatt aagctgtagt atgtacccta agacgtgct	1400
aattgactgc cacttcgcaa ctcaggggag gctgcatttt agtaatgggt	1450
caaatgattc actttttatg atgcttccaa aggtgccttg gcttctcttc	1500
ccaactgaca aatgccaaag ttgagaaaaa tgatcataat ttagcataa	1550
acagagcagt cggggacacc gattttataa ataaactgag caccttcttt	1600
ttaaacaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1650
aaaaaaaa	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
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

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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 ggagccccto cgggtagcta ctaccctgga	100
cccccaata gtggagggca gtatggtagt gggctacccc ctggtggtgg	150
ttatgggggt cctgccctg 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 ggccgcacg atgtctacgg cttctcagcc	550
ctgtggaaat tcatccagca gtggaagaac ctcttcagc agtatgaccg	600
ggaccgctcg ggctccatta gctacacaga gctgcagcaa gctctgtccc	650
aaatgggcta caacctgagc cccagttca ccagcttct ggtctcccgc	700
tactgcccac gctctgcca tcctgccatg cagcttgacc gttcatcca	750
ggtgtgcacc cagctgcagg tgctgacaga ggccttcgg gagaaggaca	800
cagctgtaca aggcaacatc cggctcagct tcgaggactt cgtcaccatg	850
acagcttctc ggatgctatg acccaaccat ctgtggagag tggagtgcac	900
cagggacctt tcctggcttc ttagagtgag agaagtatgt ggacatctct	950
tcttttctg tcctctaga agaacattct cccttgcttg atgcaacact	1000
gttccaaaag agggtgagaga gtccctgcac atagccacca aatagtgagg	1050
accggggctg agggcacaca gataggggccc tgatggagga gaggatagaa	1100
gttgaatgtc ctgatggcca tgagcagttg agtggcacag cctggcacca	1150
ggagcaggtc cttgtaatgg agttagtgtc cagtcagctg agctccaccc	1200
tgatgccagt ggtgagtgtt catcgccctg ttaccgtag tacctgtgtt	1250
ccctcaccag gccatcctgt caaacgagcc cattttctcc aaagtggaat	1300
ctgaccaagc atgagagaga tctgtctatg ggaccagtgg cttggattct	1350
gccacaccca taaatccttg tgtgttaact tctagctgcc tggggctggc	1400

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cctgctcaga caaatctgct ccctgggcat ctttggccag gcttctgccc	1450
cctgcagctg ggacccctca cttgcctgcc atgctctgct cggttcagt	1500
ctccaggaga cagtgggtcac ctctccctgc caatactttt tttaatttgc	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	
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						

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<210> SEQ ID NO 63
<211> LENGTH: 1234
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 63

caggatgcag ggcgcgtgg caggagctg cgctcctctg ggctgctcc	50
tggtctgtct tcatctccca ggctctttg cccggagcat cgggttgtg	100
gaggagaaa tttcccaaaa cttcgggacc aacttgctc agctcggaca	150
accttcctcc actggccct ctaactctga acatccgcag cccgctctgg	200
accctaggtc taatgacttg gcaagggttc ctctgaagct cagcgtgcct	250
ccatcagatg gcttcccacc tgcaggaggt tctgcagtgc agaggtggcc	300
tccatcgtgg gggctgcctg ccatggatto ctggccccct gaggatcctt	350
ggcagatgat ggctgctgcg gctgaggacc gcctggggga agcgtgcct	400
gaagaactct cttacctctc cagtgtctcg gccctcgtc cgggcagtgg	450
ccctttgcct ggggagtctt ctcccgatgc cacaggcctc tcacctgagg	500
cttcactcct ccaccaggac tcggagtcca gacgactgcc ccgttcta	550
tcactgggag ccgggggaaa aatcctttcc caacgccctc cctggtctct	600
catccacagg gttctgcctg atcacccctg gggtagccctg aatccagtg	650
tgctctgggg aggtggaggc cctgggactg gttggggaac gagggccatg	700
ccacaccctg agggaatctg gggatatcaat aatcaacccc caggtaccag	750
ctggggaaaat attaatcggg atccaggagg cagctgggga aatattaatc	800
ggtagccagg aggcagctgg gggaaatatta atcggtatcc aggaggcagc	850
tgggggaata ttcatctata cccaggatcc aataacccat ttctctcctg	900
agttctccgc cctcctgggt cttcttgga catccagct ggcttcccta	950
atcctccaag ccctaggttg cagtggggct agagcacgat agagggaaac	1000
ccaacattgg gagttagagt cctgtcccg ccccttgctg tgtgggctca	1050
atccaggccc tgtaacatg ttccagcac tatccccact ttccagtgc	1100
tcccctgctc 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	
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

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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

aaggagagggc caccgggact tcagtgtctc ctccatccca ggagcgcagt	50
ggccactatg gggctctgggc tgccccttg cctcctcttg accctccttg	100
gcagctcaca tggaacaggg ccgggtatga ctttgcaact gaagctgaag	150
gagtcttttc tgacaaattc ctctatgag tccagcttcc tggaattgct	200
tgaaaagctc tgcctcctcc tccatctccc ttcagggacc agcgtcaccc	250
tccaccatgc aagatctcaa caccatgttg tctgcaacac atgacagcca	300

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ttgaagcctg tgtccttctt ggcccgggct tttgggccgg ggatgcagga	350
ggcaggcccc gaccctgtct ttcagcaggc cccaccctc 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 gcccgcgc aggtgccct ggccggagat	100
gcggtagtag gggcgagcgc gagaagcccc ttcctcggcg ctgccaaacc	150
gccaccacgc ccatggcgaa ccccgggctg gggctgcttc tggcgtggg	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 ctcaggactc	500
caaggagacg gtgcagggct gcctgccc ataggtcccc tctcctgcat	550
ctgtctccct tcattgctgt gtgaccttgg ggaaaggcag tgccctctct	600
gggcagtcag atccaccag tgcttaatag cagggaagaa ggtacttcaa	650
agactctgcc cctgaggtca agagaggatg gggctattca cttttatata	700
tttatataaa attagtagtg agatgtaaaa aaaaaaaaaa aaaa	744

<210> SEQ ID NO 68
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 68

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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 ttcaaaatg	250
tatctatatt aattcctgag aattggaagg aaaatcctca gtacaaaagg	300
ccaaaacatg aaaccataa acatgctgat gttatagttg caccacctac	350
actcccaggt agagatgaac catacaccaa gcagttcaca gaatgtggag	400
agaaaggcga atacattcac ttcacccctg accttctact tggaaaaaaa	450
caaaatgaat atggaccacc aggcaaaactg 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 agtacaacaa gaaaaagcat ccataatggt tatgcaaagt	750
attgattctg ttgttgaatt ttgtaacgaa aaaaccata atcaagaagc	800
tccaagccta caaaacataa agtgaattt tagaagtaca tgggagggtga	850
ttagcaattc tgaggatttt aaaaacacca taccatggt gacaccacct	900
cctccacctg tcttctcatt gctgaagatc agtcaaagaa ttgtgtgctt	950
agttcttgat aagtctggaa gcatgggggg taaggaccgc ctaaatacgaa	1000
tgaatcaagc agcaaaacat ttcctgctgc agactgttga aaatggatcc	1050

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tggttgaggga tggttcactt tgatagtact gccactattg taaataagct	1100
aatccaaata aaaagcagtg atgaaagaaa cacactcatg gcaggattac	1150
ctacatatcc tctgggagga acttccatct gctctggaat taaatatgca	1200
tttcaggtga ttggagagct acattcccaa ctcgatggat ccgaagtact	1250
gctgctgact gatggggagg ataacactgc aagttcttgt attgatgaag	1300
tgaaacaaag tggggccatt gttcatttta ttgctttggg aagagctgct	1350
gatgaagcag taatagagat gagcaagata acaggaggaa gtcattttta	1400
tgtttcagat gaagctcaga acaatggcct cattgatgct tttggggctc	1450
ttacatcagg aaatactgat ctctcccaga agtcccttca gctcgaaagt	1500
aagggattaa cactgaatag taatgcctgg atgaacgaca ctgtcataat	1550
tgatagtaca gtgggaaagg acacgttctt tctcatcaca tggaacagtc	1600
tgccctccag tatttctctc tgggatccca gtggaacaat aatggaaaat	1650
ttcacagtg atgcaacttc caaaatggcc tatctcagta ttccaggaaac	1700
tgcaaagggt ggcacttggg cataaatct tcaagccaaa gcgaaccag	1750
aaacattaac tattacagta acttctcgag cagcaaatc ttctgtgcct	1800
ccaatcacag tgaatgctaa aatgaataag gacgtaaca gtttccccag	1850
cccaatgatt gtttacgcag aaattctaca aggatatgta cctgttcttg	1900
gagccaatgt gactgctttc attgaatcac agaatggaca tacagaagtt	1950
ttggaaactt tggataatgg tgcaggcgct gattctttca agaattgatg	2000
agtctactcc aggtatttta cagcatatac agaaaatggc agatatagct	2050
taaaagttcg ggctcatgga ggagcaaaca ctgccaggct aaaattacgg	2100
cctccactga atagagccgc gtacatacca ggctgggtag tgaacgggga	2150
aattgaagca aacccgcaa gacctgaaat tgatgaggat actcagacca	2200
ccttgaggga tttcagccga acagcatccg gaggtgcatt tgtggtatca	2250
caagtcccaa gccttccctt gcctgaccaa taccaccaa gtcaaatcac	2300
agaccttgat gccacagttc atgaggataa gattattctt acatggacag	2350
caccaggaga taattttgat gttggaaaag 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 aagtatccaa	2600
cattgcacaa gtaactttgt ttatccctca agcaaatcct gatgacattg	2650
atcctacacc tactcctact cctactccta ctctgataa aagtcataat	2700
tctggagtta atatttctac gctggtattg tctgtgattg ggtctgttgt	2750
aattgttaac tttattttaa gtaccacat ttgaacctta acgaagaaaa	2800
aaatcttcaa gtagacctag aagagagttt taaaaacaa aacaatgtaa	2850
gtaaaggata tttctgaatc ttaaaattca tcccatgtgt gatcataaac	2900
tcataaaaaa aattttaaga tgtcggaaaa ggatactttg attaaataaa	2950

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aacactcatg gatatgtaaa aactgtcaag attaaaaattt aatagtttca      3000
tttattttgtt attttatttg taagaaatag tgatgaacaa agatcctttt      3050
tcatactgat acctggttgt atattatttg atgcaacagt tttctgaaat      3100
gatattttcaa attgcatcaa gaaattaaaa tcacttatct gagtagtcaa      3150
aatacaagta aaggagagca aataaacaac atttgaaaaa 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
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
```

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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
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

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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
ctcgtgtgtg gctgccttc tatttcaagg aaagacgcca aggtaatttt	150
gaccagagg agcaatgatg tagccacctc ctaaccttc cttcttgaac	200
ccccagtat gccaggattt actagagagt gtcaactcaa ccagcaagcg	250
gtccttcgg cttaacttgt ggttgagga gagaacctt gtggggctgc	300

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gttctcttag	cagtgtctcag	aagtgacttg	cctgaggggtg	gaccagaaga	350
aaggaaaggt	cccctcttgc	tgttggtctg	acatcaggaa	ggctgtgatg	400
ggaatgaagg	tgaaaacttg	gagatttcac	ttcagtcatt	gcttctgcct	450
gcaagatcat	cctttaaag	tagagaagct	gctctgtgtg	gtggttaact	500
ccaagaggca	gaactcgttc	tagaaggaaa	tggatgcaag	cagctccggg	550
ggccccaac	gcatgcttcc	tgttggtctag	cccagggaag	cccttccgtg	600
ggggcccg	ctttgaggga	tgccaccggt	tctggacgca	tggtgatctc	650
ctgaatgatg	atggttcgcc	gggggtctgct	tgcgtggatt	tcccgggtgg	700
tggttttctg	ggtgctcctc	tgtgtgtcta	tctctgtcct	gtacatgttg	750
gcctgcacc	caaaagtgta	cgaggagcag	ctggcactgc	ccagggccaa	800
cagccccacg	gggaaggagg	ggtaccaggc	cgtccttcag	gagtgggagg	850
agcagcaccc	caactacgtg	agcagcctga	agcggcagat	cgcacagctc	900
aaggaggagc	tgcaggagag	gagtgtgagc	ctcaggaatg	ggcagtacca	950
agccagcgat	gctgctggcc	tgggtctgga	caggagcccc	ccagagaaaa	1000
cccaggccga	cctcctggcc	ttcctgcact	cgcaggtgga	caaggcagag	1050
gtgaatgctg	gcgtcaagct	ggccacagag	tatgcagcag	tgcctttcga	1100
tagctttact	ctacagaagg	tgtaccagct	ggagactggc	cttacccgcc	1150
accccgagga	gaagcctgtg	aggaaggaca	agcgggatga	gttgggtgaa	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
gaaagtga	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
gaattttctc	ggggaaaggg	acttgatgtt	ggagcccgtc	tctggaaggg	1700
aagcaacgtc	cttctctttt	tctgtgatgt	ggacatctac	ttcacatctg	1750
aattcctcaa	tacgtgtagg	ctgaatacac	agccagggaa	gaaggatatt	1800
tatccagttc	ttttcagtca	gtacaatcct	ggcataatat	acggccacca	1850
tgatgcagtc	cctcccttgg	aacagcagct	ggtcataaag	aaggaaactg	1900
gattttggag	agactttgga	tttgggatga	cgtgtcagta	tcggtcagac	1950
ttcatcaata	taggtgggtt	tgatctggac	atcaaaggct	ggggcgagga	2000
ggatgtgcac	ctttatcgca	agtatctcca	cagcaacctc	atagtggtag	2050
ggacgcctgt	gcgaggactc	ttccacctct	ggcatgagaa	gcgctgcatt	2100
gacgagctga	ccccgagca	gtacaagatg	tgcattgcagt	ccaaggccat	2150
gaacgaggca	tcccacggcc	agctgggcat	gctggtgttc	aggcacgaga	2200

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tagaggctca ccttcgcaaa cagaaacaga agacaagtag caaaaaaaca	2250
tgaactccca gagaaggatt gtgggagaca ctttttcttt ccttttgcaa	2300
ttactgaaa tggtctgaac agagaaaaga ctccataaa 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 aagaacccat aaatatcgtg tcatattttc	2800
cccaagatta accaaaaata atctgcttat ctttttggtt gtccttttaa	2850
ctgtctccgt ttttttcttt tatttaaaaa tgcacttttt ttcccttggt	2900
agttatagtc tgcttattta attaccactt tgcaagcctt acaagagagc	2950
acaagttggc ctacattttt atatttttta agaagatact ttgagatgca	3000
ttatgagaac tttcagttca aagcatcaaa ttgatgccat atccaaggac	3050
atgccaaatg ctgattctgt caggcactga atgtcaggca ttgagacata	3100
gggaaggaat ggtttgtact aatacagacg tacagatact ttctctgaag	3150
agtattttcg aagaggagca actgaacact ggaggaaaag aaaatgacac	3200
tttctgcttt acagaaaagg aaactcatte agactggtga tatcgtgatg	3250
tacctaaaag tcagaaacca ctttttctcc tcagaagtag ggaccgcttt	3300
cttacctgtt taataaaacc aaagtatacc gtgtgaacca aacaatctct	3350
tttcaaaaaca ggggtgctcct cctggcttct ggcttcata agaagaaatg	3400
gagaaaaata tatatatata tatatatatt gtgaaagatc aatccatctg	3450
ccagaatcta gtgggatgga agtttttgct acatgttatc caccacaggc	3500
cagggtggaag 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 tggtaaaaaa tgcattgtat tgatttgtac tggtagttta	3800
tgaaatttaa taaaacaca ggccatgaat ggaaggtggt attgcacagc	3850
taataaaata tgatttggtg atatgaa	3877

<210> SEQ ID NO 72

<211> LENGTH: 532

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 72

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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	
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				

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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
tgctctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc	100
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact	150
cacgccagga gctcgctcgc tctctctctc tctctctcac tcctccctcc	200
ctctctctct gctgtccta gtcctctagt cctcaaattc ccagtcccct	250
gcaccccttc ctgggacact atgttggttct cgcacctcct gctggagggtg	300
atttggatcc tggctgcaga tgggggtcaa cactggacgt atgaggggccc	350
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaacaatg	400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat	450
ttgctgtctc tgcagcccca cggatatgac cagcctggca ccgagccttt	500
ggacctgcac aacaatggcc acacagtgca actctctctg ccctctaccc	550
tgtatctggg tggacttccc cgaaaatatg tagctgccca gtcocacctg	600
cactggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag	650
tgaagccaca ttgcagagc tccacattgt acattatgac tctgattcct	700
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg	750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat	800

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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 cttgggtggc tgtctctgcc ttctcctggc tgtttatttc	1200
attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt	1250
cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac	1300
catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg	1350
gggtgtagga tctggccaga aacactgtag gagtagtaag 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
tttccctaga 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
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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	
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	

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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 tggcgcgccc ttggggacgg	50
gcagttccct gtgtctctgg tggtttgctt aaacctgcaa acatcacctt	100
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc	150
ttcaaggagt taaagttact tacactgtgc agtatattcat cacaaattgg	200
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgctc	250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc	300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac	350
taaatcaaac agaacgtggt ccagtggtgt gaccaaccac acgctgggtg	400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc	450
gtcccagggg ccctcgcgct tgctcagcct tctgagaagc agtgtgccag	500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt	550
atgttttgcc catatctatt accgtgttct ttttttctgt gatgggctat	600
tccatctacc gatatatcca cgttgcaaaa gagaaacacc cagcaaattt	650
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgctgctg	700
aaaaaatcgt gattaacttt atcacccctc atatctcgga tgattctaaa	750

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atttctcatc aggatatgag tt tactggga aaaagcagtg atgtatccag      800
ccttaatgat cctcagccca gcgggaacct gagggcccct caggaggaag      850
aggaggtgaa acatttaggg tatgtctcgc atttgatgga aattttttgt      900
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtcctt      950
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg     1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg     1050
caggaggagg tgtccacaca aggaacatta ttggagtgcg aggcagcgtt     1100
ggcagtcctg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc     1150
aagacttaga cccctggcg caggagcaca cagactcgga ggaggggccg     1200
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag     1250
gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg     1300
agccttctga gggggatggg ctcgagagg agggctctct atctagactc     1350
tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct     1400
catgcaattc atggaggaat gggggttata tgtgcagatg gaaaactgat     1450
gccaacactt ccttttcctt ttgtttcct gtgcaacaa gtgagtcacc     1500
cctttgatcc cagccataaa gtacctggga tgaagaagt tttttccagt     1550
ttgtcagtgt ctgtgagaat tacttatctt ttttctctat tctcatagca     1600
cgtgtgtgat tggttcatgc atgtaggctt cttacaatg atgggtgggc     1650
tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcaat     1700
aatgtttgc 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
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
```

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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											

<210> SEQ ID NO 77
<211> LENGTH: 1636
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 77

gaggagcggg ccgaggactc cagcgtgcc aggtctggca tctgcactt	50
gctgccctct gacacctggg aagatggccg gcccgggac cttcaccctt	100
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac	150

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```
tgcaagtctc atcctcggcc caaaagtcac caaagaaaag ctgacacagc      200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc      250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct      300
ggtgaacacc gtctgaagc acatcatctg gctgaaggtc atcacagcta      350
acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta      400
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctgggtcaa      450
gaccatcgtg gagtccaca tgacgactga ggcccaagcc accatccgca      500
tggacaccag tgcaagtggc cccaccgcgc tggctctcag tgactgtgcc      550
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttcct      600
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagtg ccatccctgc      650
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat      700
ggcatgtatg cagacctcct gcagctggtg aaggtgccca ttccctcag      750
cattgacctg ctggagtttg acctctctgta tcttgccatc aagggtgaca      800
ccattcagct ctacctgggg gccaaagttgt tggactcaca gggaaagggtg      850
accaagtggg tcaataactc tgcagcttcc ctgacaatgc cccacctgga      900
caacatcccg ttcagcctca tcgtgagtca ggacgtggtg aaagctgcag      950
tggctgctgt gctctctcca gaagaattca tggctctggt ggaactctgtg     1000
cttctctaga gtgcccatcg gctgaagtca agcatcgggc tgatcaatga     1050
aaaggctgca gataagctgg gatctaccca gatcgtgaag atcctaactc     1100
aggacactcc cgagtttttt atagaccaag gccatgccaa ggtggcccaa     1150
ctgatcgtgc tggaagtgtt tccctccagt gaagccctcc gccctttgtt     1200
caccctgggc atcgaagcca gctcgggaagc tcagttttac accaaagggtg     1250
accaacttat actcaacttg aataacatca gctctgatcg gatccagctg     1300
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat     1350
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa     1400
gatctggggg ccagtgctca ttggtgaagg ccttgggatt cgaggcagct     1450
gagtctcac  tgaccaagga tgcccttggt cttactccag cctccttggtg     1500
gaaaccacgc tctcctgtct ccagtgaaag acttggatgg cagccatcag     1550
ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc     1600
cctctctgca atcaataaac acttgctctg gaaaaa      1636
```

<210> SEQ ID NO 78

<211> LENGTH: 484

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 78

```
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
```


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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 aaatgaggga ttagaggtgt 50

tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100

gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150

ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200

tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250

gttggtcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300

catcacccag tgtgacatct atagcaccct tctgggcctg cccgctgaca 350

tccaggctgc ccaggccatg atggtgacat ccagtgaat ctctccctg 400

gctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atcccgaacc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500

ttggaggcct cctgggatcc attcctgttg cctggaatct tcatgggatc 550

ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600

tggagaggct ctttacttgg gcattatttc ttccctgttc tcctgatag 650

ctggaatcat cctctgcttt tcctgctcat ccagagaaaa tcgctccaac 700

tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750

gcctgggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800

cagggtatgt gtgaagaacc aggggccaga gctggggggt ggctgggtct 850

gtgaaaaaca gtggacagca ccccgagggc cacagggtgag ggacactacc 900

actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950

ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000

attgccaaag atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050

gtccccctgc cctaagtccc caacctcaa cttgaaacct cattccctta 1100

agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150

ccccaaacct actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200

ccctctctct ggctgaggtt ggctcttagc tcattgctgg ggaagggaag 1250

gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300

cctccaaaga aactgattgg ccctggaacc tocatccac tcttgttatg 1350

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actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc	1400
tacggtatcc agggaacaga aagcaggatg caggatggga ggacaggaag	1450
gcagcctggg acatttaaaa aaata	1475

<210> SEQ ID NO 80
<211> LENGTH: 230
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 80

Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu	15
1 5 10	
Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp	30
20 25	
Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly	45
35 40	
Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly	60
50 55	
Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala	75
65 70	
Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile	90
80 85	
Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr	105
95 100	
Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala	120
110 115	
Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro	135
125 130	
Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro	150
140 145	
Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr	165
155 160	
Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile	180
170 175	
Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr	195
185 190	
Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg	210
200 205	
Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser	225
215 220	
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 cttctgtctg gaccttcctt cgtctctcca	50
tctctccctc ctttccccgc gttctctttc cacctttctc ttcttccac	100
cttagacctc ctttctgtgc ctcttttctt gccaccgct gtttctgtgc	150

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ccttctccga ccccgctcta gcagcagacc tcctggggtc tgtgggttga	200
tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgaact	250
ccgctcccgg acccagggcc tgacctggg gaaaggatgg ttcccagggt	300
gagggtcctc tcctccttgc tgggactcgc gctgctctgg ttccccctgg	350
actcccacgc tcgagcccgcc ccagacatgt tctgcctttt ccatgggaag	400
agatactccc ccggcgagag ctggcaccct tacttgagc cacaaggcct	450
gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt	500
accgcctcca ctgtccgcct gtccactgcc ccagcctgt gacggagcca	550
cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg	600
ggccccacca aagtcctgcc agcacaacgg gaccatgtac caacacggag	650
agatcttcag tgcccatgag ctgttcccct ccgcctgcc caaccagtgt	700
gtcctctgca gctgcacaga ggccagatc tactgcggcc tcacaacctg	750
ccccgaacca ggctgcccag caccctctcc actgccagac tcctgctgcc	800
aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg	850
cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc	900
tgggagaaa agaggcccg gcacccacgc cccactggc ctacgcgcc	950
ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca	1000
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg	1050
cgggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct	1100
tcggcccctt gccctgcac ctatgcacct gtgaggatgg ccgccaggac	1150
tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa	1200
agtggtctgg aagtgtctga agatttgccc agaggacaaa gcagaccctg	1250
gccacagtga gatcagttct accagggtgc ccaaggcacc gggccgggtc	1300
ctcgtccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc	1350
cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg	1400
taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg	1450
ccacacagcc agaattctcc acttgactca gatcaagaaa gtcagggaagc	1500
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac	1550
gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac	1600
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

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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
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			

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	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 agtttgcct					50
ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca					100
gttctcctct tctctctaatt ccatccgtca cctctcctgt catccgtttc					150
catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt					200
ttggttctga gtctcctcaa gctgggatca gggcagtggc agtggtttgg					250
gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct					300
gtttcctgtc tcctaagacc aatgcagagg coatggaagt gcggttcttc					350
aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca					400
gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg					450
attctatttg ggagggcgcg atctctctga ggctggaaaa cattactgtg					500
ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca					550
gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca					600
tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtc					650
tcgggctggt tccccggcc cacagcgaag tggaaaggtc cacaaggaca					700
ggatttgtcc acagactcca ggacaaacag agacatgcat ggcctgtttg					750
atgtggagat ctctctgacc gtccaagaga acgcccggag catatcctgt					800
tccatgcggc atgctcatct gagccgagag gtggaatcca gggtagagat					850
aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac					900
tgggaatact ctgctgtggc ctattttttg gcattgttgg actgaagatt					950
ttcttctcca aattccagtg gaaaatccag gcggaactgg actggagaag					1000
aaagcacgga caggcagaat tgagagacgc ccggaaacac gcagtggagg					1050
tgactctgga tccagagacg gctcacccga agctctgcgt ttctgatctg					1100
aaaactgtaa cccatagaaa agctccccag gagtgcttc actctgagaa					1150
gagatttaca aggaagagtg tggtggtctc tcagagtttc caagcagggg					1200
aacattactg ggaggtggac ggaggacaca ataaaagggt gcgcgtggga					1250
gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc					1300
cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca					1350
cattaaatcc ccgttttatc agcgtcttcc ccaggacccc acctacaaaa					1400

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ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat	1450
aatgaccag tcccttattt ataccctgac atgtcggttt gaaggcttat	1500
tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaactccc	1550
atagtcatct gcccagtcac ccaggaatca gagaaagagg cctcttgcca	1600
aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg	1650
caaccacgcc cttcctcccc aggggtgaaa tgtaggatga atcacatccc	1700
acattcttct ttagggatat taaggctct ctcccagatc caaagtcg	1750
cagcagccgg ccaaggtggc ttccagatga agggggactg gcctgtccac	1800
atgggagtca ggtgtcatgg ctgccctgag ctgggaggga agaaggctga	1850
cattacattt agtttgcct cactccatct ggctaagtga tcttgaata	1900
ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg	1950
tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg	2000
acagagtgta 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	
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	

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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
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 ccctgctctt gggggaggga gagggcggaa ggacagacaa	100
gtaaactgct gacgatgcag agttccgtga cgggtcagga aggccctgtgt	150

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gtccatgtgc cctgctcctt ctccctacccc tcgcatggct ggatttaccc      200
tggtccagta gttcatggct actgggtccg ggaaggggcc aatacagacc      250
aggatgctcc agtggccaca aacaaccagc ctcgggcagt gtgggaggag      300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac      350
cctgagcatc agagatgcc aagaagtga tgcggggaga tacttctttc      400
gtatggagaa aggaagtata aaatggaatt ataacatca ccggctctct      450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac      500
cctggagtcg ggctgcccc agaactctgac ctgctctgtg ccttgggcct      550
gtgagcaggg gacacccct atgatctcct ggataggac ctcctgtgtc      600
ccccgggacc cctccaccac ccgctcctcg gtgctcacc tcacccaca      650
gcccaggac catggcacca gcctcacctg tcaggtgacc ttccctggg      700
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctaccgcct      750
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt      800
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc      850
tggtctgtgc agttgatgca gttgacagca atccccctgc caggctgagc      900
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg      950
gggtgtggag ctgccttggg tgcacctgag ggatgcagct gaattcacct     1000
gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc     1050
ctgcagagca aagccacatc aggagtgact cagggggtgg tcggggggagc     1100
tggaaccaca gccctggtct tcctgtcctt ctgcgtcatc ttcgttgtag     1150
tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat     1200
acgggcatag aggatgcaaa cgctgtcagg gggtcagcct ctcaggggcc     1250
cctgactgaa ccttgggcag aagacagtcc ccagaccag cctccccag      1300
cttctgcccc ctctcagtg ggggaaggag agtccagta tgcacccctc     1350
agcttcacga tggatgaagc ttgggactcg cggggacagg aggccactga     1400
caccgagtac tcggagatca agatccacag atgagaaact gcagagactc     1450
accctgattg agggatcaca gcccctccag gcaagggaga agtcagaggc     1500
tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaact      1550
atgaattatg tgcagagtga aaagcacaca ggcttttag tcaaagtatc      1600
tcaaacctga atccacactg tgccctccct tttatTTTTT taactaaaag      1650
acagacaaat tccta
```

<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
```

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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
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

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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 gcagtgagg gagggagtga	50
aggagctctc tgtaccaag gaaagtgcag ctgagactca gacaagatta	100
caatgaacca actcagcttc ctgctgtttc tcatagcgac caccagagga	150
tggagtacag atgaggctaa tacttacttc aaggaatgga cctgttcttc	200
gtctccatct ctgcccagaa gctgcaagga aatcaaagac gaatgtccta	250
gtgcatttga tggcctgtat tttctccgca ctgagaatgg tgttatctac	300
cagaccttct gtgacatgac ctctgggggt ggcggtgga ccctggtggc	350
cagcgtgcat gagaatgaca tgcgtgggaa gtgcacggtg ggcgatcgct	400
ggtccagtcg gcagggcagc aaagcagact acccagaggg ggaaggcaac	450
tgggccaact acaacacctt tggatctgca gaggcggcca cgagcgatga	500
ctacaagaac cctggctact acgacatcca ggccaaggac ctgggcatct	550
ggcacgtgcc caataagtcc cccatgcagc actggagaaa cagotccctg	600
ctgagggtacc gcacggacac tggcttcctc cagacactgg gacataatct	650
gtttggcatc taccagaaat atccagtga atatggagaa ggaagtgtt	700
ggactgacaa cggcccgggtg atccctgtgg tctatgattt tggcgacgcc	750
cagaaaacag catcttatta ctacacctat ggccagcggg aattcactgc	800
gggatttgtt cagttcaggg tatattaataa cgagagagca gccaacgcct	850
tgtgtgctgg aatgagggtc accggatgta aactgagca tctactgcatt	900
ggtggaggag gatactttcc agaggccagt cccagcagt gtggagattt	950
ttctggtttt gattggagtg gatatggaac tcatgttggt tacagcagca	1000
gccgtgagat aactgaggca gctgtgcttc tattctatcg ttgagagttt	1050
tgtgggaggg aaccagacc tctcctccca accatgagat cccaaggatg	1100
gagaacaact taccagtag ctagaatgtt aatggcagaa gagaaaacaa	1150
taaatcatat tgactcaaga aaaaaa	1176

<210> SEQ ID NO 88
<211> LENGTH: 313
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 88

-continued

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
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	cggcttgagg	ggagacttca	ggagtcgctg	tctctgaact	50
tccagcctca	gagaccgccg	cccttgcccc	cgagggccat	gggccgggtc	100
tcagggcttg	tgccctctcg	cttcctgacg	ctcctggcgc	atctggtggt	150

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```
cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc      200
ctctcacggt cacccccag gagtatgaca agcaggacat tcagctggtg      250
gccgcgctct ctgtcaccct gggcctcttt gcagtggagc tggccggttt      300
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg      350
gggctcactg tagtgcattc gtggccctgt ccttcttcat attcgagcgt      400
tgaggagtga ctacgtattg gtacattttt gtcttctgca gtgcccttcc      450
agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga      500
aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg      550
ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt      600
ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg      650
tcttgagctc gggattatcc gcattgtatt tagtgctttg taataaaata      700
tgttttgtag taacattaag acttatatac agttttaggg gacaattaa      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
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 gctgtctcgt gttcctggtg cagggtagcc      100
```

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tctatctggt catctgtggc caggatgatg gtcctcccg ctcagaggac	150
cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcggaa	200
gcggggccac atctcaccta agtcccgccc catggccaat tccactctcc	250
tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc	300
cccaaccgcc cgaaccacag cccccacccc tcagccaagg tgaagaaaat	350
ctttggctgg ggcgacttct actccaacat caagacgggt gcctgaacc	400
tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc	450
cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt	500
gcccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg	550
aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta	600
gaacggggcc gccggacctc gctttgcacc cagacccag ccaagatctg	650
ctcccagagc cagcctcaga gctcagccac ctggagctgc tcccagccct	700
tcaaagtcgt ctgtgtctac atgccttct acagcacgga ctatcggctg	750
gtccagaagg tgtgccaga ttacaactac catagtgata cccctacta	800
cccctctggg tgacccgggg caggccacag aggccaggcc agggctggaa	850
ggacaggcct gcccatgcag gagaccatct ggacaccggg cagggaaggg	900
gttgggcctc aggcagggag gggggtggag acgaggagat gccaagtggg	950
gccaggggcca agtctcaagt ggcagagaaa gggtoccaag tgctggcccc	1000
aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg	1050
ggctctctgt gcagcctcac agggctttgc caggagcca cagagagatg	1100
ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc ccagatcaa	1150
gtcatggggag gaagctaagc ccttggttct tgccatcctg aggaaagata	1200
gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg	1250
atggatggct gagaggcctt ctaggagcc agtcagcagg gtggggtggg	1300
gccagaggag ctctccagcc ctgcctagt ggcgccctga gcccctgtc	1350
gtgtgctgag catggcatga ggctgaagt gcaaccctgg ggtctttgat	1400
gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa	1450
ttccctcttc tgccagtact cccctgtac caccattgc tgatggcaca	1500
cccatcctta agctaagaca ggacgattgt ggtcctcca cactaaggcc	1550
acagcccac cgcgtgctgt gtgtccctct tccacccaa cccctgctgg	1600
ctcctctggg agcatccatg tcccggagag gggccctca acagtcagcc	1650
tcacctgtca gaccggggtt ctcccggatc tggatggcgc cgccctctca	1700
gcagcgggca cgggtggggc ggggcccggc 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

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<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

<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 atgccatcg agccgtgtcg	100
tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga	150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat	200
ggaccaaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta	250
tatccaagaa atgttcgat ttgcatatta taaactctta aaaaaagcca	300

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gtgaaggttt gaagagtata aaccagggtg agacagcacc ctctatgcga	350
ctgctggcct atgtttcttg cttgggcttt ggaatcatga gtggagtatt	400
ttccttttg t 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 cgctccagat 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	
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	

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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

aattttttcac cagagtaaacc ttgagaaacc aactggacct tgagtattgt	50
acatttttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac	100
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca	150
aacctgcttt gggactccct cccacaaaac tggctccgga tcaggaaca	200
ctaccaaaac aacagcagtc aaatcaggtc tttccttctt taagtctgat	250
accattaaca cagatgctca cactggggcc agatctgcat ctgttaaatc	300
ctgctgcagg aatgacacct ggtaccacaga cccaccatt gaccctggga	350
gggttgaatg tacaacagca actgcaccca catgtgttac caatttttgt	400
cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac	450
aaatcttcac gagcctcatc atccattcct tgttcccggg aggcatactg	500
cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc	550
agcaggagga gcagggtgtaa atcctgccac ccagggaacc ccagcaggcc	600
gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct	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
gaaaatatcc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa	900
cttttaaaaa caataattca atggataaat ctgtccttga 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

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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 cccaccacgc ccagcctggc cagagccccc	50
tggagaagga gctctcttct tgcttggcag ctggaccaag ggagccagtc	100
ttgggcgctg gagggcctgt cctgaccatg gtccctgcct ggctgtggct	150
gctttgtgtc tccgtccccc aggcctctcc caaggcccag cctgcagagc	200
tgtctgtgga agttccagaa aactatggtg gaaatttccc tttatacttg	250
accaagtgtc cgctgccccg tgagggggct gaaggccaga tcgtgctgtc	300
aggggactca ggcaaggcaa ctgagggccc atttgctatg gatccagatt	350
ctggcttctc gctggtgacc agggccctgg accgagagga gcaggcagag	400
taccagctac aggtcaccct ggagatgcag gatggacatg tcttgtgggg	450
tccacagcct gtgcttgtgc acgtgaagga tgagaatgac caggtgcccc	500
attttcttca agccatctac agagctcggc tgagccgggg taccaggcct	550
ggcatcccct tcctcttctc tgaggcttca gaccgggatg agccaggcac	600
agccaaactg gatcttcgat tccacatcct gagccaggct ccagcccagc	650
cttccccaga catgttccag ctggagcctc ggctgggggc tctggccctc	700
agccccaagg ggagcaccag ccttgaccac gccctggaga ggacctacca	750
gctgttggtg caggtcaagg acatgggtga ccaggcctca ggccaccagg	800

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ccactgccac cgtggaagtc tccatcatag agagcacctg ggtgtcccta	850
gagcctatcc acctggcaga gaatctcaaa gtcctatacc cgcaccacat	900
ggcccaggta cactggagtg ggggtgatgt gcactatcac ctggagagcc	950
atcccccggt accctttgaa gtgaatgcag agggaaacct ctacgtgacc	1000
agagagctgg acagagaagc ccaggctgag tacctgctcc aggtgcgggc	1050
tcagaattcc catggcgagg actatgcggc ccctctggag ctgcacgtgc	1100
tggtgatgga tgagaatgac aacgtgccta tctgccctcc ccgtgacccc	1150
acagtcagca tccctgagct cagtccacca ggtactgaag tgactagact	1200
gtcagcagag gatgcagatg cccccggctc cccaattcc cacgttgtgt	1250
atcagctcct gagccctgag cctgaggatg gggtagaggg gagagccttc	1300
caggtggacc ccacttcagg cagtgtgacg ctgggggtgc tcccaactcg	1350
agcaggccag aacatcctgc ttctggtgct ggccatggac ctggcaggcg	1400
cagaggggtg cttcagcagc acgtgtgaag tcgaagtgc agtcacagat	1450
atcaatgatc acgcccctga gttcatcact tcccagattg ggcctataag	1500
cctccctgag gatgtggagc ccgggactct ggtggccatg ctaacagcca	1550
ttgatgtga cctcgagccc gccttcggcc tcatggattt tgccattgag	1600
aggggagaca cagaagggac ttttggcctg gattgggagc cagactctgg	1650
gcatgttaga ctcagactct gcaagaacct cagttatgag gcagctccaa	1700
gtcatgaggt ggtggtggtg gtgcagagtg tggcgaagct ggtggggcca	1750
ggcccaggcc ctggagccac cgccacggtg actgtgctag tggagagagt	1800
gatgccaccc cccaagttgg accagagag ctacgaggcc agtgtcccca	1850
tcagtgcacc agccggtctt ttctgctga ccatccagcc ctccgacccc	1900
atcagccgaa ccctcaggtt ctccctagtc aatgactcag agggctggct	1950
ctgcattgag aaattctccg gggaggtgca caccgccag tcctgcagg	2000
gcgcccagcc tggggacacc tacacggtgc ttgtggaggc ccaggataca	2050
gccctgactc ttgcccctgt gccctccaa tacctctgca caccgcgcca	2100
agaccatggc ttgatcgtga gtggacccag caaggacccc gatctggcca	2150
gtgggcacgg tccctacagc ttcacccttg gtcccaaccc cacggtgcaa	2200
cgggattggc gcctccagac tctcaatggt tcccatgcct acctcacctt	2250
ggccctgcat tgggtggagc cacgtgaaca cataatccc gtgggtgtca	2300
gccacaatgc ccagatgtgg cagctcctgg ttcgagtgat cgtgtgtcgc	2350
tgcaacgtgg aggggcagtg catgcgaag gtgggccgca tgaaggcat	2400
ggccacgaag ctgtcggcag tgggcacctt tgtaggcacc ctggtagcaa	2450
taggaatctt cctcatcctc attttcaccc actggaccat gtcaaggaag	2500
aaggaccgg atcaaccagc agacagcgtg cccctgaagg cgactgtctg	2550
aatggcccag gcagctctag ctgggagctt ggccctctggc tccatctgag	2600
tcccctggga gagagcccag caccgaagat ccagcagggg acaggacaga	2650
gtagaagccc ctccatctgc cctgggggtg aggcaccatc accatcacca	2700

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ggcatgtctg cagagcctgg acaccaactt tatggactgc ccatgggagt 2750
gctccaaatg tcagggtgtt tgccaataa 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
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

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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	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
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

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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
gaccacagct 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 caaactgga tccagtgtga	350
tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc	400
agtggggtca gcacagccac catctcaggg tccagcgtga cctccaatgg	450
ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca	500
gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata	550
gccaccaact ctgagtccag cacaacctcc agtggggcca gcacagccac	600
caactctgag tccagcacac cctccagtgg ggccagcaca gtcaccaact	650
ctgggtccag tgtgacctcc agtgagcca gcaactgccac caactctgag	700
tccagcacag tgtccagtag ggccagcact gccaccaact ctgagtctag	750
cacctctccc 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 ggtgggcaca	1000
gccaccaact ctgagtccag cagcacctcc agtggggcca gcacagccac	1050
caactctgac tccagcacag tgtccagtgg ggccagcact gccaccaact	1100

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ctgagtccag cacgacctcc agtggggcca gcacagccac caactctgag      1150
tccagcacga cctccagtgg ggctagcaca gccaccaact ctgactccag      1200
cacaacctcc agtggggccg gcacagccac caactctgag tccagcacag      1250
tgtccagtgg gatcagcaca gtcaccaatt ctgagtccag cacacctcc      1300
agtggggcca acacagccac caactctgag tccagtacga cctccagtgg      1350
ggccaacaca gccaccaact ctgagtccag cacagtgtcc agtggggcca      1400
gcactgccac 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 totgactgga atgcacacaa      1700
cttcccatag tgcattctact gcagtgagtg aggcaaagcc tgggtgggtcc      1750
ctggtgcccgt gggaaatctt cctcatcacc ctggtctcgg ttgtggcggc      1800
cgtggggctc tttgctgggc tcttcttctg tgtgagaaac agcctgtccc      1850
tgagaaacac ctttaacaca gctgtctacc accctcatgg cctcaacctat      1900
ggccttggtc caggccctgg agggaatcat ggagccccc acaggcccg      1950
gtggagtcct aactggttct ggaggagacc agtatcatcg atagccatgg      2000
agatgagcgg gaggaacagc gggccctgag cagccccgga agcaagtgcc      2050
gcattcttca ggaaggaaga gacctgggca cccaagacct ggtttccttt      2100
cattcatccc aggagacccc tcccagcttt gtttgagatc ctgaaaatct      2150
tgaagaaggt attcctcacc tttcttgctt ttaccagaca ctggaaagag      2200
aatactatat tgctcattta gctaagaaat aaatacatct catctaacac      2250
acacgacaaa gagaagctgt gcttgccccg ggggtgggtat ctgactctga      2300
gatgaactca gttataggag aaaacctcca tgctggactc catctggcat      2350
tcaaaatctc cacagtaaaa tccaagacc tcaaaaaaaaa aaaaaaaaaa      2400
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa      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	
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	

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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

ggccggagcg	ctccgcgtta	cgggatgaat	taacggcggg	ttccgcacgg	50
agggtgtgac	ccctacggag	ccccagcttg	cccacgcacc	ccactcggcg	100
tcgcgcggcg	tgccctgctt	gtcacagggtg	ggaggctgga	actatcaggc	150
tgaaaaacag	agtgggtact	ctcttctggg	aagctggcaa	caaatggatg	200
atgtgatata	tgcattccag	gggaagggaa	atttgtgtgc	ttctgaaccc	250
atgggtcaatt	aacgaggcag	tttctagcta	ctgcacgtac	ttcataaagc	300
aggactctaa	aagctttgga	atcatggtgt	catggaaagg	gatttacttt	350
atactgactc	tgttttgggg	aagctttttt	ggaagcattt	tcatgctgag	400
tcccttttta	cctttgatgt	ttgtaaacc	atcttggtat	cgctggatca	450
acaaccgcct	tgtggcaaca	tggtcaccc	tacctgtggc	attattggag	500
accatgtttg	gtgtaaaagt	gattataact	ggggatgcat	ttgttcctgg	550
agaaagaagt	gtcattatca	tgaaccatcg	gacaagaatg	gactggatgt	600
tcctgtggaa	ttgcctgatg	cgatatagct	acctcagatt	ggagaaaatt	650
tgccctcaaag	cgagtctcaa	agggtgtcct	ggatttggtt	gggccatgca	700
ggctgctgcc	tatatcttca	ttcataggaa	atggaaggat	gacaagagcc	750
atttcgaaga	catgattgat	tacttttgtg	atattcacga	accacttcaa	800
ctcctcatat	tcccagaagg	gactgatctc	acagaaaaca	gcaagtctcg	850
aagtaatgoa	tttgctgaaa	aaaatggact	tcagaaatat	gaatatgttt	900
tacatccaag	aactacaggc	tttacttttg	tggtagaccg	tctaagagaa	950

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ggtaagaacc ttgatgctgt ccatgatatc actgtggcgt atcctcacia 1000
cattcctcaa tcagagaagc acctcctcca aggagacttt cccagggaaa 1050
tccactttca cgtccaccgg tatccaatag acaccctccc cacatccaag 1100
gaggaccttc aactctggtg ccacaaacgg tgggaagaga aagaagagag 1150
gctgcgttcc ttctatcaag gggagaagaa tttttatttt accggacaga 1200
gtgtcattcc accttgcaag tctgaactca gggtccttgt ggtcaaattg 1250
ctctctatac tgtattggac cctgttcagc cctgcaatgt gcctactcat 1300
atatttgtac agtcttgtaa agtgggtattt tataatcacc attgtaatct 1350
ttgtgctgca agagagaata tttggtggac tggagatcat agaacttgca 1400
tgtttaccgac ttttacacia acagccacat ttaaattcaa agaaaaatga 1450
gtaagattat aaggtttgcc atgtgaaaac ctagagcata ttttgaaat 1500
gttctaaacc tttctaagct cagatgcatt tttgcatgac tatgtcgaat 1550
atctcttact gccatcatta ttgtttaaag atattttgca cttaattttg 1600
tgggaaaaat attgctacia ttttttttaa tctctgaatg taatttcgat 1650
actgtgtaca tagcaggag tgatcggggt gaaataactt gggccagaat 1700
attattaaac aatcatcagg cttttaaa 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
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

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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
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 103

cggctcgagc ggctcgagtg aagagcctct ccacggctcc tgcgcctgag 50
acagctggcc tgacctcaa atcatccatc caccctgct gtcattgttt 100
ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150
tttggtttct agttttctac agctgggtgc aggacagtgg caagtcactg 200
gaccggggcaa gtttgtccag gccttggtgg gggaggacgc cgtgttctcc 250
tgctccctct ttcctgagac cagtgcagag gctatggaag tgcggttctt 300
caggaatcag ttccatgctg tgggtccact ctacagagat ggggaagact 350
gggaatctaa gcagatgcca cagtatcgag ggagaactga gtttgtgaag 400
gactccattg caggggggag tgtctctcta aggctaaaaa acatcactcc 450
ctcggacatc ggcctgtatg ggtgctggtt cagttcccag atttacgatg 500

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aggaggccac	ctgggagctg	cgggtggcag	cactgggctc	acttcctctc	550
atltccatcg	tgggatatgt	tgacggaggt	atccagttac	tctgcctgtc	600
ctcaggctgg	ttccccagc	ccacagccaa	gtgaaaggt	ccacaaggac	650
aggatttgtc	ttcagactcc	agagcaaatg	cagatgggta	cagcctgtat	700
gatgtggaga	tctccattat	agtccaggaa	aatgctggga	gcatattgtg	750
ttccatccac	cttgctgagc	agagtcata	ggtggaatcc	aaggatttga	800
taggagagac	gtttttccag	ccctcacctt	ggcgctggc	ttctatttta	850
ctcgggttac	tctgtgtgtc	cctgtgtggt	gttgtcatgg	ggatgataat	900
tgttttcttc	aaatccaaag	ggaaaatcca	ggcggaactg	gactggagaa	950
gaaagcacgg	acaggcagaa	ttgagagacg	cccggaaaca	cgcagtgagg	1000
gtgactctgg	atccagagac	ggctcacccg	aagctctcg	tttctgatct	1050
gaaaactgta	acccatagaa	aagctcccca	ggaggtgcct	cactctgaga	1100
agagatttac	aaggaagagt	gtggtggctt	ctcaggggtt	ccaagcaggg	1150
agacattact	gggaggtgga	cgtgggacaa	aatgtagggt	ggtatgtggg	1200
agtgtgtcgg	gatgacgtag	acagggggaa	gaacaatgtg	actttgtctc	1250
ccaacaatgg	gtattgggtc	ctcagactga	caacagaaca	tttgtatttc	1300
acattcaatc	cccattttat	cagcctcccc	cccagcacc	ctcctacacg	1350
agtgggggtc	ttcctggact	atgaggggtg	gaccatctcc	ttcttcaata	1400
caaatgacca	gtcccttatt	tataccctgc	tgacatgtca	gtttgaaggc	1450
ttgttgagac	cctatatcca	gcatgcgatg	tatgacgagg	aaaaggggac	1500
tcccatattc	atatgtccag	tgctctgggg	atgagacaga	gaagaccctg	1550
cttaaaaggg	cccacaccac	agaccagac	acagccaagg	gagagtgtct	1600
ccgacaggtg	gccccagctt	cctctccgga	gctgctgcac	agagagtcac	1650
gccccccact	ctcctttagg	gagctgaggt	tctctgtccc	tgagccctgc	1700
agcagcgcca	gtcacagctt	ccagatgagg	ggggattggc	ctgaccctgt	1750
gggagtgcga	agccatggct	gcctgaaagt	ggggacggaa	tagactcaca	1800
ttaggtttag	tttgtgaaaa	ctccatccag	ctaagcgatc	ttgaacaagt	1850
cacaacctcc	caggctcctc	atttgctagt	cacggacagt	gattcctgcc	1900
tcacagggtg	agattaaaga	gacaacgaat	gtgaatcatg	cttgacaggtt	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	aaaattttta	2250
caaattaaac	taaacaatat	atttaaagat	gatataatac	tactcagtgt	2300
ggtttgtccc	acaaatgcag	agttggttta	atatttaaat	atcaaccagt	2350
gtaattcagc	acattaataa	agtaaaaaag	aaaaccataa	aaaaaaaaaa	2400

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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	
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	

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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 gtttgtgtgg aaccctgggt 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
agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450
tgtttttacat gaaaagctgc aagatgctgt aggacccctt aaagtagatc 500
ctcactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550
ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600
caggatcggt ggtgggacag aagtagaaga gggatgaatg ccctggcagg 650
ctagcctgca gtgggatggg agtcatcgct gtggagcaac cttaattaat 700
gccacatggc ttgtgagtgc tgctcactgt tttacaacat ataagaacct 750
tgccagatgg actgcttcct ttggagtaac aataaaacct tcgaaaatga 800
aacggggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850
catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900
aatgcagta catagagttt gtctccctga tgcacccat gagtttcaac 950

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caggatgatgt gatgtttgtg acaggatttg gagcactgaa aaatgatggt	1000
tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac	1050
aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt	1100
tatgtgctgg ctcccttagaa ggaaaaacag atgcatgcc a ggtgactct	1150
ggaggaccac tggttagtgc agatgctaga gatatctggt accttgctgg	1200
aatagtgagc tggggagatg aatgtgcgaa acccaacaag cctggtgttt	1250
atactagagt tacggccttg cgggactgga ttacttcaaa aactggtatc	1300
taagagacaa aagcctcatg gaacagataa cttttttttt tgttttttgg	1350
gtgtggaggc cttttttaga gatacagaat tggagaagac ttgcaaaaca	1400
gctagatttg actgatctca ataaactgtt tgcttgatgc atgtattttc	1450
ttcccagctc tgttccgcac gtaagcatcc tgcttctgcc agatcaactc	1500
tgatcatctgt gagcaatagt tgaaacttta tgtacataga gaaatagata	1550
atacaatatt acattacagc ctgtattcat ttgttctcta gaagttttgt	1600
cagaattttg acttgttgac ataaatttgt aatgcatata tacaatttga	1650
agcactcctt ttcttcagtt cctcagctcc tctcatttca gcaaatatcc	1700
attttcaagg tgcagaacaa ggagtgaag aaaatataag aagaaaaaaa	1750
ttccctacat tttattggca cagaaaagta ttaggtgttt ttcttagtgg	1800
aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag	1850
aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag	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

<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	

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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	
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 cggctctccg

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cgaagaagtt ccctgcccc atgagcccc gccgtgcgtc cccgactatc	100
cccaggcggg cgtggggcac cgggccacg gccgacgac gctgccgttt	150
tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg	200
gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct	250
acgcctcaa tctgctcttt tggttaatgt ccatcagtgt gttggcagtt	300
tctgcttggg tgagggacta ctaaataat gttctcactt taactgcaga	350
aacgagggta gaggaagcag tcattttgac ttactttcct gtgggtcacc	400
cggtcacgat tgctgtttgc tgtttcctta tcattgtggg gatgttagga	450
tattgtgaa cggtgaaaag aaatctgttg cttcttgcac ggtactttgg	500
aagtttgctt gtcattttct gtgtagaact ggcttgtggc gtttgacat	550
atgaacagga acttatgggt ccagtacaat ggtcagatat ggtcactttg	600
aaagccagga tgacaaatta tggattacct agatatcggg ggttactca	650
tgcttggaa ttttttcaga gagagtttaa gtgctgtgga gtagtatatt	700
tcactgactg gttggaaatg acagagatgg actggcccc agattcctgc	750
tgtgttagag aattcccagg atgttccaaa caggcccacc aggaagatct	800
cagtgcctt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga	850
gaggaaccaa acaactgcag gtgctgaggt ttctgggaat ctccattggg	900
gtgacacaaa tcctggccat gattctcacc attactctgc tctgggctct	950
gtattatgat agaagggagc ctgggacaga ccaaatgatg tccttgaaga	1000
atgacaactc tcagcacctg tcatgtccct cagtagaact gttgaaacca	1050
agcctgtcaa gaatccttga acacacatcc atggcaaaca gctttaatac	1100
acactttgag atggaggagt tataaaaaga aatgtcacag aagaaaacca	1150
caaacttggt ttattggact tgtgaatttt tgagtacata ctatgtgttt	1200
cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata	1250
tactattcta tgctttaaaa tgaggatgga aaagtttcat gtcataagtc	1300
accacctgga caataattga tgcccttaaa atgctgaaga cagatgtcat	1350
accactgtg tagcctgtgt atgactttta ctgaacacag ttatgttttg	1400
aggcagcatg gtttgattag catttccgca tccatgcaa cgagtcacat	1450
atgggtgggac tggagccata gtaaagggtg atttacttct accaactagt	1500
atataaagta ctaattaaat gctaacatag gaagttagaa aatactaata	1550
acttttatta ctacgcgac tattcttctg atgctaaata aattatatat	1600
cagaaaactt tcaatattgg tgactacct aatgtgattt ttgctgggta	1650
ctaaaatatt cttaccactt aaaagagcaa gctaacacat tgtcttaagc	1700
tgatcaggga ttttttgat ataagtctgt gttaaactcg tataattcag	1750
tcgatttcag ttctgataat gttagaata accattatga aaaggaaaat	1800
ttgtcctgta tagcatcatt atttttagcc tttcctgtta ataaagcttt	1850
actattctgt cctgggctta tattacacat ataactgtta tttaaatact	1900
taaccactaa ttttgaaaat taccagtgtg atacatagga atcattattc	1950

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agaatgtagt ctggtcttta ggaagtatta ataagaaaat ttgcacataa      2000
cttagttgat tcagaaagga ctgtatgct gtttttctcc caaatgaaga      2050
ctctttttga cactaaacac tttttaaaaa gcttatcttt gccttctcca      2100
aacaagaagc aatagtctcc aagtcaatat aaattctaca gaaaatagtg      2150
ttctttttct ccagaaaaat gcttgtaga atcattaaaa catgtgacaa      2200
tttagagatt ctttgtttta tttcactgat taatatactg tggcaaatta      2250
cacagattat taaatttttt tacaagagta tagtatatit attgaaatg      2300
ggaaaagtgc attttactgt attttggtga ttttgtttat ttctcagaat      2350
atggaaagaa 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
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

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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 aaaaaaagt 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 tcaaggtcct cctctatgtg	350
acaaccatgt gaatggggag tggtagcact 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
gccagcgctg tgcttccacg tctactgtgg tcatttttat gacatctgcg	650
acgaggactg ccatggcagc tgctcagata ccagcgagtg cacatgcgct	700
ccaggaactg tgctaggccc tgacaggcag acatgctttg atgaaaatga	750
atgtgagcaa aacaacggtg gctgcagtga gatctgtgtg aacctcaaaa	800
actcctaccg ctgtgagtgt ggggttggcc gtgtgctaag aagtgtggc	850
aagacttgtg aagacgttga aggatgccac aataacaatg gtggctgcag	900
ccactcttgc cttggatctg agaaaggcta ccagtgtgaa tgtccccggg	950
gcctgtgtgt gtctgaggat aaccacactt gccaagtccc tgtgttgtgc	1000
aaatcaaatg ccattgaagt gaacatcccc agggagctgg ttggtggcct	1050
ggagctcttc ctgaccaaca cctcctgcg aggagtgtcc aacggcacc	1100
atgtcaacat cctcttctct ctcaagacat gtggtacagt ggtcgatgtg	1150
gtgaatgaca agattgtggc cagcaacctc gtgacaggtc tacccaagca	1200
gaccccgggg agcagcgggg acttcatcat cogaaccagc aagctgctga	1250
tcccggtgac ctgcgagttt ccacgcctgt acaccatttc tgaaggatac	1300
gttcccaacc ttcgaaactc cccactggaa atcatgagcc gaaatcatgg	1350
gatcttccca ttcactctgg agatcttcaa ggacaatgag tttgaagagc	1400

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cttaccggga agctctgccc accctcaagc ttcgtgactc cctctacttt      1450
ggcattgagc ccgtggtgca cgtgagcggc ttgaaaagct tggtgagagag      1500
ctgcttttgcc acccccacct ccaagatcga cgaggtcctg aaatactacc      1550
tcatccggga tggctgtgtt tcagatgact cggtaaagca gtacacatcc      1600
cgggatcacc tagcaaagca cttccaggtc cctgtcttca agtttgtggg      1650
caaagaccac aaggaagtgt ttctgcactg ccgggttctt gtctgtggag      1700
tgttggagca gcgttccgc tgtgccagg gttgccaccg gcgaatgcgt      1750
cgtggggcag gaggagagga ctacgccggt ctacagggcc agacgctaac      1800
aggcggcccg atccgcacg actgggagga ctagtctgta gccatacctc      1850
gagtcctgc attggacggc tctgtctttt ggagcttctc cccccaccgc      1900
cctctaagaa catctgccaa cagctgggtt cagacttcac actgtgagtt      1950
cagactccca gcaccaactc actctgatto tggtcattc agtgggcaca      2000
ggtcacagca ctgctgaaca atgtggcctg ggtggggttt catctttcta      2050
gggttgaaaa ctaactgtc caccagaaa gacactcacc ccatttcctt      2100
catttctttc ctacacttaa atacctcgtg tatggtgcaa tcagaccaca      2150
aatcagaag ctgggtataa tatttcaagt taaaaccct agaaaaatta      2200
aacagttact gaaattatga cttaaatacc caatgactcc ttaaatatgt      2250
aaattatagt tatacctga aatttcaatt caaatgcaga ctaattatag      2300
ggaatttgga agtgtatcaa taaaacagta tataatttt      2339
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<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      15
 1           5           10
Ser Val Ser Pro Val Ala Leu Asp Pro Cys Ser Ala Tyr Ile Ser      30
          20           25
Leu Asn Glu Pro Trp Arg Asn Thr Asp His Gln Leu Asp Glu Ser      45
          35           40
Gln Gly Pro Pro Leu Cys Asp Asn His Val Asn Gly Glu Trp Tyr      60
          50           55
His Phe Thr Gly Met Ala Gly Asp Ala Met Pro Thr Phe Cys Ile      75
          65           70
Pro Glu Asn His Cys Gly Thr His Ala Pro Val Trp Leu Asn Gly      90
          80           85
Ser His Pro Leu Glu Gly Asp Gly Ile Val Gln Arg Gln Ala Cys     105
          95          100
Ala Ser Phe Asn Gly Asn Cys Cys Leu Trp Asn Thr Thr Val Glu     120
          110          115
Val Lys Ala Cys Pro Gly Gly Tyr Tyr Val Tyr Arg Leu Thr Lys     135
          125          130
Pro Ser Val Cys Phe His Val Tyr Cys Gly His Phe Tyr Asp Ile     150
          140          145
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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
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

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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

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caaggcctgc cctgcactcg ggcctcctcc agccagtgct gaccagggac	100
ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctctgctgc	150
cttgggggtga caatctcagc tccaggctac agggagaccg ggaggatcac	200
agagccagca tgttacagga tcctgacagt gatcaacctc tgaacagcct	250
cgatgtcaaa cccctgcgca aaccccgat ccccatggag accttcagaa	300
aggtggggat ccccatcatc atagcactac tgagcctggc gagtatcatc	350
attgtggttg tcctcatcaa ggtgattctg gataaatact acttcctctg	400
cgggcagcct ctccacttca tcccgaggaa gcagctgtgt gacggagagc	450
tggactgtcc cttgggggag gacgaggagc actgtgtcaa gagcttcccc	500
gaagggcctg cagtggcagt ccgcctctcc aaggaccgat ccacactgca	550
ggtgtgtggc tcggccacag ggaactggtt ctctgcctgt ttcgacaact	600
tcacagaagc tctcgtgag acagcctgta ggcagatggg ctacagcaga	650
gctgtggaga ttggcccaga ccaggatctg gatgtgttg aaatcacaga	700
aaacagccag gagcttcgca tgcggaactc aagtgggccc tgtctctcag	750
gtcccttggt ctccctgcac tgtcttgct gtgggaagag cctgaagacc	800
ccccgtgtgg tgggtgggga ggaggcctct gtggattctt ggccttgga	850
ggtcagcatc cagtacgaca aacagcacgt ctgtggaggg agcatcctgg	900
acccccactg ggtcctcacg gcagccact gcttcaggaa acataccgat	950
gtgttcaact ggaaggtgcg ggcaggctca gacaaactgg gcagcttccc	1000
atccctggct gtggccaaga tcatcatcat tgaattcaac cccatgtacc	1050
ccaaagacaa tgacatcgcc ctcatgaagc tgcagttccc actcactttc	1100
tcaggcacag tcaggcccat ctgtctgccc ttctttgatg aggagctcac	1150
tccagccacc ccactctgga tcattggatg gggctttacg aagcagaatg	1200
gagggaagat gtctgacata ctgctgcagg cgtcagtcca ggtcattgac	1250
agcacacggt gcaatgcaga cgatcgctac cagggggaag tcaccgagaa	1300
gatgatgtgt gcaggcatcc cggaaggggg tgtggacacc tgccaggggtg	1350
acagtgggtg gccctgatg taccaatctg accagtggca tgtgggtggc	1400
atcgttagct ggggctatgg ctgcgggggc ccgagcacc caggagtata	1450
caccaaggtc tcagcctatc tcaactggat ctacaatgtc tggaaggctg	1500
agctgtaatg ctgctgcccc ttgcagtgc tgggagccgc ttccttctctg	1550

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ccctgccac ctgggatcc cccaaagtca gacacagagc aagagtcccc      1600
ttgggtacac ccctctgccc acagcctcag ctttcttg agcagcaaag      1650
ggcctcaatt cctgtaagag accctcgag cccagaggcg cccagaggaa      1700
gtcagcagcc ctagctcggc cacacttggt gctcccagca tcccaggag      1750
agacacagcc cactgaacaa ggtctcaggg gtattgctaa gccaagaagg      1800
aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga      1850
tcactgtggg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg      1900
tcttcaccca tcccgaagcc tactagagca agaaccagt tgtaataataa      1950
aatgcactgc cctactgttg gtatgactac cgttacctac tgttgtcatt      2000
gttattacag ctatggccac tattattaaa gagctgtgta acatctctgg      2050
caaaaaaaaa aaa                                             2063

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<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 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
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

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				230				235				240			
Cys	Phe	Arg	Lys	His 245	Thr	Asp	Val	Phe	Asn 250	Trp	Lys	Val	Arg	Ala 255	
Gly	Ser	Asp	Lys	Leu 260	Gly	Ser	Phe	Pro	Ser 265	Leu	Ala	Val	Ala	Lys 270	
Ile	Ile	Ile	Ile	Glu 275	Phe	Asn	Pro	Met	Tyr 280	Pro	Lys	Asp	Asn	Asp 285	
Ile	Ala	Leu	Met	Lys 290	Leu	Gln	Phe	Pro	Leu 295	Thr	Phe	Ser	Gly	Thr 300	
Val	Arg	Pro	Ile	Cys 305	Leu	Pro	Phe	Phe	Asp 310	Glu	Glu	Leu	Thr	Pro 315	
Ala	Thr	Pro	Leu	Trp 320	Ile	Ile	Gly	Trp	Gly 325	Phe	Thr	Lys	Gln	Asn 330	
Gly	Gly	Lys	Met	Ser 335	Asp	Ile	Leu	Leu	Gln 340	Ala	Ser	Val	Gln	Val 345	
Ile	Asp	Ser	Thr	Arg 350	Cys	Asn	Ala	Asp	Asp 355	Ala	Tyr	Gln	Gly	Glu 360	
Val	Thr	Glu	Lys	Met 365	Met	Cys	Ala	Gly	Ile 370	Pro	Glu	Gly	Gly	Val 375	
Asp	Thr	Cys	Gln	Gly 380	Asp	Ser	Gly	Gly	Pro 385	Leu	Met	Tyr	Gln	Ser 390	
Asp	Gln	Trp	His	Val 395	Val	Gly	Ile	Val	Ser 400	Trp	Gly	Tyr	Gly	Cys 405	
Gly	Gly	Pro	Ser	Thr 410	Pro	Gly	Val	Tyr	Thr 415	Lys	Val	Ser	Ala	Tyr 420	
Leu	Asn	Trp	Ile	Tyr 425	Asn	Val	Trp	Lys	Ala 430	Glu	Leu				

<210> SEQ ID NO 113
<211> LENGTH: 1768
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 113

ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc	50
aaggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac	100
tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac	150
tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgttt	200
tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca	250
ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt	300
ttctaccac accgtcccct cgaagccggg gacagcctca cttgctggc	350
ctctcgctgg agcagtgcc tcaccaactg tctcacgtct ggaggcactg	400
actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg	450
tgggccttgc cctggccgta gaagggattg acaagcccga agatttcata	500
ggcgatggct cccactgccc aggcacagc cttgctgtag tcaatcactg	550
ccctggggcc aggacgggcc gtggacacct gctcagaagc agtgggtgag	600
acatcacgct gcccgcccat ctaacctttt catgtcctgc acatcacctg	650
atccatgggc taatctgaac tctgtcccaa ggaaccaga gcttgagtga	700

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gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg      750
acaggacttg cattctcctg gaacatgagg gaacgccgga ggaaagcaaa      800
gtggcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt      850
gttgggttat cacaaggcat caggtctcct gcattcagtg gacatgtggg      900
ggaagggtcg ccgatggcgc atgacacact cgggactcac ctctggggcc      950
atcagacagc cgtttccgcc ccgatccagc taccagctgc tgaagggcaa     1000
ctgcaggccg atgtctcat cagccaggca gcagccaaaa tctgcgatca     1050
ccagccaggg gcagccgtct gggaaggagc aagcaaagtg accatttctc     1100
ctccctcctt tccctctgag aggccctcct atgtccctac taaagccacc     1150
agcaagacat agctgacagg ggctaattgg tcagtgttgg ccagggaggt     1200
cagcaaggcc tgagagctga tcagaagggc ctgctgtgcg aacacggaaa     1250
tgcctccagt aagcacaggc tgcaaatcc ccaggcaaag gactgtgtgg     1300
ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaggg     1350
agctagagct tggttcaaat gatctccaag ggcccttata cccagggaga     1400
ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccagggtgcat     1450
taagaatcag ttattgccgg gtgtggtggc ctgtaatgcc aacatttttg     1500
gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg     1550
gccaacatgg tgaaaccctt gtctctacta aaaatacaaa aaaactagcc     1600
aggcatgggt 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

<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
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<210> SEQ ID NO 115
<211> LENGTH: 1197
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 115

cagcagtggg ctctcagtc tctcaaagca aggaaagagt actgtgtgct 50
gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150
ttgtggactg gtgtttggta tcctggccct aactctaatt gtcctgtttt 200
gggggagcaa gcacttctgg ccggagggtac ccaaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatatctag aagcggaat ggactgatg 350
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
ctttctttga acagtcatg atttgggtcc cagcagaaaa gcctattgaa 550
aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600
gaccatgtat tggatcaatc ccactcta atcagtttct gagttacaag 650
actttgagga ggaggagaa gatcttctact ttctgcca cgaaaaaaaaa 700
gggattgaac aaaaatgaaca gtgggtggtc cctcaagtga aagtagagaa 750
gaccctgcac gccagacaag caagtgagga agaacttcca ataaatgact 800
atactgaaaa tggaaatagaa ttgatccca tgctggatga gagaggttat 850
tgttgtattt actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900
acctttacta ggctactacc catatccata ctgtaccaa ggaggacgag 950
tcatctgtcg tgtcatcatg ccttgtaact ggtgggtggc ccgcatgctg 1000
gggaggggtc aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050
atataataaa tgcatgctat tcaatgaatt tctgcctatg aggcatctgg 1100
cccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150
tgtttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> SEQ ID NO 116
<211> LENGTH: 317
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 116

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

-continued

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	
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 agggcgggc gccaggatca tgtccaccac	100
cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct	150
gcacgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac	200
aaccccgtoa cctccgtggt ccagtacgaa gggctctgga ggagctgcgt	250
gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg	300
gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcadc	350
gtcctgggtg ccattggcct cctggtatcc atctttgccc tgaatatgcat	400

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ccgcattggc agcatggagg actctgcca agccaacatg acactgacct	450
ccgggatcat gttcattgtc tcaggtcttt gtgcaattgc tggagtgtct	500
gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat	550
gtacaccggc atgggtggga tggcgagac tgttcagacc aggtacacat	600
ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt	650
gggggtgtga tgatgtgcat cgcctgccgg ggctggcac cagaagaaac	700
caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca	750
agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac	800
aagaagatat acgatggagg tgccgcaca gaggacgagg tacaatctta	850
tccttccaa cagcactatg tgtaatgctc taagacctct cagcacgggc	900
ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag	950
atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt	1000
catcttttga gaggccaaat ggtcttagcc tcagtctctg tctctaaata	1050
ttccaccata aaacagctga gttattttatg aattagaggc tatagctcac	1100
attttcaatc ctctatttct ttttttaaat ataactttct actctgatga	1150
gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact	1200
ccccctcttc ctctagtca ataaacccat tgatgatcta tttccagct	1250
tatccccaa aaaacttttg aaaggaaaga gtagaccaa agatgttatt	1300
ttctgctgtt tgaattttgt ctccccaccc ccaacttggc tagtaataaa	1350
cacttactga agaagaagca ataagagaaa gatatttgta atctctccag	1400
cccatgatct cggttttctt acactgtgat cttaaaagtt accaaaccaa	1450
agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct	1500
tccttattaca gcaacacccat tctaggagtt tctgagctc tccactggag	1550
tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt	1600
atttttttta atttaagtcc taaatatagt taaaaataat aatgttttag	1650
taaaatgata cactatctct gtgaaatagc ctacccccta catgtggata	1700
gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt	1750
aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct	1800
agcacttttg gaggtgagg aggaaggatc acttgagccc agaagttcga	1850
gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag	1900
aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg	1950
gaggctgagg tgggaggatc acttgagccc agggagggtg gggctgcagt	2000
gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct	2050
gtctaaaaaa ataaaaata aataatggaa cacagcaagt cctaggaagt	2100
aggttaaac taattcttta a	2121

<210> SEQ ID NO 118

<211> LENGTH: 261

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

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<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
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	aacctgctt	caaagcagaa	50
gtagcagttc	cggagtccag	ctggctaaaa	ctcatcccag	aggataatgg	100
caacccatgc	cttagaaatc	gctgggctgt	ttcttggtgg	tgttggaatg	150
gtgggcacag	tggtgtcac	tgtcatgcct	cagtgagag	tgtcgacctt	200
cattgaaaac	aacatcgtgg	tttttgaaaa	cttctgggaa	ggactgtgga	250
tgaattgcgt	gaggcaggct	aacatcagga	tgcaagtcaa	aatctatgat	300

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tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg	350
tgctgcttcc gtgatgtcct tcttggtttt catgatggcc atccttggca	400
tgaaatgcac caggtgcacg ggggacaatg agaagggtgaa ggctcacatt	450
ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tggtgctcat	500
ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa	550
tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga	600
tggaccacgg cactggtgct gattgttgga ggagctctgt tctgctgcgt	650
tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc	700
atcgcacaac ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc	750
tactccagaa gtcagtatgt gtagtgtgt atgttttttt aactttacta	800
taaagccatg caaatgacaa aaatctatat tactttctca aaatggaccc	850
caaagaaact ttgattttact gttcttaact gcctaactctt aattacagga	900
actgtgcac agctattttat gattctataa gctatttcag cagaatgaga	950
tattaaacc aatgctttga ttgttctaga aagtatagta atttgttttc	1000
taaggtgggt caagcatcta ctctttttat catttacttc aaaatgacat	1050
tgctaaagac tgcattattt tactactgta atttctccac gacatagcat	1100
tatgtacata gatgagtgtg acatttatat ctacacataga gacatgctta	1150
tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga	1200
actcaactat tgcttttcag ggaaatcatg gatagggttg aagaaggtta	1250
ctattaattg tttaaaaaca gcttagggat taatgtcctc cattttataat	1300
gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc	1350
tttctgatat gctgtttttt agcctaggag ttgaaatcc taacttcctt	1400
atcctcttct cccagaggct ttttttttct tgtgtattaa attaacattt	1450
ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc	1500
agggtatata tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg	1550
gttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat	1600
gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt	1650
gagtacagac tttgaggttt catcaatata aataaaagag cagaaaaata	1700
tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagtgtg	1750
cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc	1800
atttttgttc tgtgaaaaat aaatttcctt cttgtacat tctgttttag	1850
ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga	1900
tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta	1950
aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat	2000
ttttctaatt	2010

<210> SEQ ID NO 120

<211> LENGTH: 225

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

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<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

<210> SEQ ID NO 121
<211> LENGTH: 1257
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 121

ggagagagggc	gcgcgggtga	aaggcgcat	gatgcagcct	gcggcggcct	50
cgagagcgcg	cgagccaga	cgctgaccac	gttcctctcc	tcggtctcct	100
ccgcctccag	ctccgcgctg	cccggcagcc	gggagccatg	cgaccccagg	150
gccccgccgc	ctccccgcag	cggtccgcg	gcctcctgct	gctcctgctg	200
ctgcagctgc	ccgcgccgtc	gagcgctct	gagatcccca	aggggaagca	250
aaagcgcgca	ctccggcaga	gggaggtggt	ggacctgtat	aatggaatgt	300
gcttacaagg	gccagcagga	gtgcctggtc	gagacgggag	ccctggggcc	350
aatgttattc	cggttacacc	tgggatccca	ggtcgggatg	gattcaaagg	400
agaaaagggg	gaatgtctga	gggaaagctt	tgaggagtcc	tggacaccca	450
actacaagca	gtgttcattg	agttcattga	attatggcat	agatcttggg	500

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aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgctctaag	550
agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc	600
agcgttggtta tttcacattc aatggagctg aatgttcagg acctcttccc	650
attgaagcta taatttatatt ggaccaagga agccctgaaa tgaattcaac	700
aattaatatt catcgactt cttctgtgga aggactttgt gaaggaattg	750
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac	800
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat	850
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt	900
ttattatgcc ttggaatggt tcaactaaat gacattttta ataagtttat	950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagt	1000
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa	1050
aagtggtttc aatatttttt ttagttggtt agaatacttt cttcatagtc	1100
acattctctc aacctataat ttggaatatt gttgtgtct tttgttttt	1150
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac	1200
aatttgtaaa 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	
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	

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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 tgccttcttg gctccaacgc	50
agctctgttg ctgaactggg tgctcatcac gggaactgct gggctatgga	100
atacagatgt ggcagctcag gtagcccaa attgcctgga agaatacatc	150
atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc	200
ccccctccca cccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc	250
atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg	300
tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata	350
atgttccaaa atcgggtccat ctccaagggt gtccaatttt tcttcctggg	400
tgtcagcgag ccctgactca ctacagtgca gctgacaggg gctgtcatgc	450
aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat	500
acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag	550
cactggttat agccccact gtcttactga caatgctttc ttctgccgaa	600
cgaggatgcc ctaagggctg taggtgtgaa ggcaaaatgg tatattgtga	650
atctcagaaa ttacaggaga taccctcaag tatactctgct ggttgcttag	700
gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt	750
aaagggtcca accagctcac ctggctatac cttgaccata accatatcag	800
caatattgac gaaaatgctt ttaatggaat acgcgactc aaagagctga	850
ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct	900
gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct	950
gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac	1000
ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc	1050
aacctggaac ttttggacct gggatataac cggatccgaa gtttagccag	1100
gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca	1150
atcaattttc caagctcaac ctggcccttt ttccaaggtt ggtcagcctt	1200
cagaaccttt acttgcagtg gaataaaatc agtgtcatag gacagaccat	1250
gtcctggacc tggagctcct tacaaaggct tgatttatca ggcaatgaga	1300
tcgaagcttt cagtggacct agtgttttcc agtgtgtccc gaatctgcag	1350

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cgccctcaacc tggattccaa caagctcaca tttattgggc aagagatttt	1400
ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg	1450
aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagttttaaa	1500
ggctctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg	1550
agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta	1600
ctacagagag gtttgatctg gccagggctc tcccaaagcc gacgtttaag	1650
cccaagctcc ccaggccgaa gcatgagagc aaacccctt tgccccgac	1700
ggtgaggagcc acagagcccg gccagagagc cgatgctgac gccgagcaca	1750
tctctttcca taaaatcadc gcgggcagcg tggcgctttt cctgtccgtg	1800
ctcgtcatcc tgctggttat ctacgtgtca tggaagcggg accctgcgag	1850
catgaagcag ctgcagcagc gctccctcat gcgaaggcac aggaaaaaga	1900
aaagacagtc cctaaagcaa atgactccca gcacccagga attttatgta	1950
gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac	2000
gggaccctgc acctataaca aatcgggctc caggagtggt gaggtatgaa	2050
ccattgtgat aaaaagagct cttaaaagct gggaaataag tggtgcttta	2100
ttgaactctg gtgactatca agggaacgcg atgcccccc tcccttccc	2150
tctccctctc actttggtgg caagatcctt cctgtccgt ttagtgcat	2200
tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt	2250
aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta	2300
ttgtataaga ccctttactg attccattaa tgcgcattt gttttaagat	2350
aaaacttctt tcataggtaa aaaaaaaaa	2379

<210> SEQ ID NO 124

<211> LENGTH: 513

<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	

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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
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

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<210> SEQ ID NO 125
<211> LENGTH: 998
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien
```

c c g t t a t c g t	c t t g c g c t a c	t g c t g a a t g t	c c g t c c c g g a	g g a g g a g g a g	50
a g g c t t t t g c	c g c t g a c c c a	g a g a t g g c c c	c g a g c g a g c a	a a t t c c t a c t	100
g t c c g g c t g c	g c g g c t a c c g	t g g c c g a g c t	a g c a a c c t t t	c c c c t g g a t c	150
t c a c a a a a a c	t c g a c t c c a a	a t g c a a g g a g	a a g c a g c t c t	t g t c g g t t g	200
g g a g a c g g t g	c a a g a g a a t c	t g c c c c c t a t	a g g g g a a t g g	t g c g c a c a g c	250
c c t a g g g a t c	a t t g a a g a g g	a a g g c t t t c t	a a a g c t t t g g	c a a g g a g t g a	300
c a c c c g c c a t	t t a c a g a c a c	g t a g t g t a t t	c t g g a g g t c g	a a t g g t c a c a	350
t a t g a a c a t c	t c c g a g a g g t	t g t g t t t g g c	a a a a g t g a a g	a t g a g c a t t a	400
t c c c c t t t g g	a a a t c a g t c a	t t g g a g g g a t	g a t g g c t g g t	g t t a t t g g c c	450
a g t t t t t a g c	c a a t c c a a c t	g a c c t a g t g a	a g g t t c a g a t	g c a a a t g g a a	500
g g a a a a a g g a	a a c t g g a a g g	a a a a c c a t t g	c g a t t t c g t g	g t g t a c a t c a	550
t g c a t t t g c a	a a a a t c t t a g	c t g a a g g a g g	a a t a c a g a g g	c t t t g g g c a g	600
g c t g g g t a c c	c a a t a t a c a a	a g a g c a g c a c	t g g t g a a t a t	g g g a g a t t t a	650
a c c a c t t a t g	a t a c a g t g a a	a c a c t a c t t g	g t a t t g a a t a	c a c c a c t t g a	700
g g a c a a t a t c	a t g a c t c a c g	g t t t a t c a a g	t t t a t g t t c t	g g a c t g g t a g	750
c t t c t a t t c t	g g g a a c a c c a	g c c g a t g t c a	t c a a a a g c a g	a a t a a t g a a t	800
c a a c c a c g a g	a t a a a c a a g g	a a g g g g a c t t	t t g t a t a a a t	c a t c g a c t g a	850
c t g c t t g a t t	c a g g c t g t t c	a a g g t g a a g g	a t t c a t g a g t	c t a t a t a a a g	900
g c t t t t t a c c	a t c t t g g c t g	a g a a t g a c c c	c t t g g t c a a t	g g t g t t c t g g	950
c t t a c t t a t g	a a a a a a t c a g	a q a q a t q a g t	q q a q t c a q t c	c a t t t t t a a	990

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<210> SEQ ID NO 126
<211> LENGTH: 323
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien
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Met	Ser	Val	Pro	Glu	Glu	Glu	Glu	Arg	Leu	Leu	Pro	Leu	Thr	Gln
1				5					10					15
Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala
				20					25					30
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr
				35					40					45
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp
				50					55					60
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala
				65					70					75
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly
				80					85					90

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

cgcggtatcg acccaagcag gtcggcgggc gcggcaggag agcggccggg	50
cgtcagctcc tcgacccccg tgtcgggcta gtccagcgag gcggacgggc	100
ggcgtgggcc catggccagg cccggcatgg agcgggtggc cgaccggctg	150
gcgctgggtga cgggggcctc ggggggcata ggcgcggccg tggcccgggc	200
cctggtccag cagggaactga aggtggtggg ctgcgccgc actgtgggca	250
acatcgagga gctggctgct gaatgtaaga gtgcaggcta ccccgggact	300
ttgatccctt acagatgtga cctatcaaat gaagaggaca tcctctccat	350
gttctcagct atccgttctc agcacagcgg tgtagacatc tgcataaca	400
atgtcggctt ggcccgccct gacacctgc totcaggcag caccagtgtt	450
tggaaggaca tgttcaatgt gaacgtgctg gccctcagca tctgcacacg	500

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ggaagcctac cagtcctatga aggagcggaa tgtggacgat gggcacatca      550
ttaacatcaa tagcatgtct gccaccgag tgttaccct gtctgtgacc      600
cacttctata gtgccaccaa gtatgccgtc actgcgctga cagagggact      650
gaggcaagag cttcgggagg ccagaccca catccgagcc acgtgcatct      700
ctccaggtgt ggtggagaca caattgcct tcaaactcca cgacaaggac      750
cctgagaagg cagctgccac ctatgagcaa atgaagtgtc taaacccga      800
ggatgtggcc gaggtgtta tctacgtcct cagaccccc gcacacatcc      850
agattggaga catccagatg aggccacgg agcaggtgac ctagtgactg      900
tgaggagctcc tccttcctc cccacccttc atggcttgcc tcctgcctct      950
ggattttagg tgttgatttc tggatcacgg gataccactt cctgtccaca     1000
ccccgaccag gggctagaaa atttgttga gatttttata tcatcttgc     1050
aaattgcttc agttgtaaat gtgaaaaatg ggctggggaa aggaggtggt     1100
gtccctaatt gttttacttg ttaacttggt cttgtgcccc tgggcacttg     1150
gcctttgtct gctctcagt gcttcccttt gacatgggaa aggagttgtg     1200
gccaaaatcc ccatcttctt gcacctcaac gtctgtggct cagggctggg     1250
gtggcagagg gaggccttca cttatatct gtgtgttat ccagggctcc     1300
agacttcctc ctctgcctgc cccactgcac cctctcccc ttatctatct     1350
ccttctcggc tccccagccc agtcttggt tcttgcccc tcctggggtc     1400
atccctccac tctgactctg actatggcag cagaacacca gggcctggcc     1450
cagtggaattt catggtgatc attaaaaag aaaaatcgca accaaaaaaa     1500
aaaaa                                           1505

```

<210> SEQ ID NO 128

<211> LENGTH: 260

<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

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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 gctgctgggtg ctcttcctca gcctcctgcc 50
ggtggcctac accatcatgt ccctcccacc ctcccttgac tgcggggccgt 100
tcaggtgcag agtctcagtt gcccgggagc acctcccctc ccgaggcagt 150
ctgctcagag ggctcggcc cagaattcca gttctggttt catgccagcc 200
tgtaaaaggc catggaactt tgggtgaatc accgatgcca ttttaagaggg 250
ttttctgccg ggatggaaat gttaggtcgt tctgtgtctg cgtgtttcat 300
ttcagtagcc accagccacc tgtggccggt 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 tcaccaggc 550
tgaggtgcag tgggtccatc tcagcttact gcaacctctg cctgccaggt 600
tcaagcgatt ctcatgcctc cacctcccaa gtagctggga ctacaggcat 650
gcaccacaat gcccaactaa tttttgtatt tttagtagag acgggggtttt 700
gccatgttgc ccaggctggc ctggaactcc tggcctcaaa caatccactt 750
gcctcggcct cccaaagtgt tatgattaca ggcgtgagcc accgtgcctg 800
gcctaaacat ttatcttttc ttgtgttgg gaactttgaa attatacaat 850
gaattattgt taactgtcat ctccctgctg tgctatggaa cactgggact 900
tcttccctct atctaactgt atatttgtac cagttaacca accgtacttc 950
atccccactc ctctctatcc ttccaacct ctgatcacct cattctactc 1000

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tctacctcca tgagatccac ttttttagct cccacatgtg agtaagaaaa	1050
tgcaatatatt gtctttctgt gcctggctta tttcacttaa cataatgact	1100
tcctgtttcca tccatgttgc tgcaaatgac aggatttcgt tcttaatttc	1150
aattaaaaata accacacatg gcaaaaa	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

<400> SEQUENCE: 131

ttctgaagta acggaagcta ccttgataa 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 agatttgaaa aacttgctga	300
aagtagaaag aatataccta taccacaaca gtttagatga atttcctacc	350
aacctcccaa agtatgtaaa agagttacat ttgcaagaaa ataacataag	400
gactatcaact tatgattcac tttcaaaaat tccctatctg gaagaattac	450
atttagatga caactctgtc tctgcagtta gcatagaaga gggagcattc	500
cgagacagca actatctccg actgcttttc ctgtcccgta atcaccttag	550
cacaattccc tggggtttgc ccaggactat agaagaacta cgcttggatg	600
ataatcgcat atccactatt tcatcccat ctcttcaagg tctcactagt	650
ctaaaaagcc tgggttctaga tggaacctg ttgaacaatc atgggttagg	700

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tgacaaagtt ttcttcaacc tagttaattt gacagagctg tccctggtgc	750
ggaattccct gactgctgca ccagtaaacc ttccaggcac aaacctgagg	800
aagctttatc ttcaagataa ccacatcaat cgggtgcccc caaatgcttt	850
ttcttatcta aggcagctct atcgactgga tatgtccaat aataacctaa	900
gtaatttacc tcagggtatc tttgatgatt tggacaatat aacacaactg	950
attcttcgca acaatccctg gtattgctgg tgcaagatga aatgggtacg	1000
tgactggtta caatcactac ctgtgaaggt caacgtgcgt gggctcatgt	1050
gccaagcccc agaaaagggt cgtgggatgg ctattaagga tctcaatgca	1100
gaactgtttg attgtaagga cagtgggatt gtaagcacca ttcagataac	1150
cactgcaata cccaacacag tgtatcctgc ccaaggacag tggccagctc	1200
cagtgaccaa acagccagat attaagaacc ccaagctcac taaggatcaa	1250
caaaccacag ggagtccctc aagaaaaaca attacaatta ctgtgaagtc	1300
tgtcacctct gataccattc atatctcttg gaaacttgct ctacctatga	1350
ctgctttgag actcagctgg cttaactgg gccatagccc ggcatttgga	1400
tctataacag aaacaattgt aacaggggaa cgcagtgagt acttggtcac	1450
agccctggag cctgattcac cctataaagt atgcatgggt cccatggaaa	1500
ccagcaacct ctacctattt gatgaaactc ctgtttgtat tgagactgaa	1550
actgcacccc ttcgaatgta caaccctaca accaccctca atcgagagca	1600
agagaaagaa ccttacaaaa accccaattt acctttggct gccatcattg	1650
gtggggctgt ggccctgggt accattgccc ttcttgcttt agtgtgttg	1700
tatgttcata ggaatggatc gctcttctca aggaactgtg catatagcaa	1750
agggaggaga agaaaggatg actatgcaga agctggcact aagaaggaca	1800
actctatcct ggaaatcagg gaaacttctt ttcagatgtt accaataagc	1850
aatgaaccca tctcgaagga ggagtttgta atacacacca tatttcctcc	1900
taatggaatg aatctgtaca aaaacaatca cagtgaaagc agtagtaacc	1950
gaagctacag agacagtggg attccagact cagatcactc acactcatga	2000
tgctgaagga ctcacagcag acttgtgttt tgggtttttt aaacctaaag	2050
gaggtgatgg t	2061

<210> SEQ ID NO 132

<211> LENGTH: 649

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 132

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

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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
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			

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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		

<210> SEQ ID NO 133
<211> LENGTH: 1882
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 133

ccgtcatccc cctgcagcca ccctcccag agtcctttgc ccaggccacc	50
ccaggcttct tggcagccct gccggccac ttgtcttcat gtctgccagg	100
gggaggtggg aaggaggtgg gaggagggcg tgcagaggca gtctgggctt	150
ggccagagct cagggtgctg agcgtgtgac cagcagtgag cagaggccgg	200
ccatggccag cctggggctg ctgctcctgc tcttactgac agcactgccca	250
ccgctgtggt cctcctcact gcctgggctg gacactgctg aaagtaaagc	300
caccattgca gacctgatcc tgtctgcgct ggagagagcc accgtcttcc	350
tagaacagag gctgcctgaa atcaacctgg atggcatggt ggggggccga	400
gtgctggaag agcagctaaa aagtgtccgg gagaagtggg cccaggagcc	450
cctgctgcag ccgctgagcc tgcgcgtggg gatgctgggg gagaagctgg	500
aggctgccat ccagagatcc ctccactacc tcaagctgag tgatcccaag	550
tacctaagag agttccagct gaccctccag cccgggtttt ggaagctccc	600
acatgcctgg atccacactg atgcctcctt ggtgtacccc acgttcgggc	650

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cccaggactc attctcagag gagagaagtg acgtgtgcct ggtgcagctg      700
ctgggaaccg ggacggacag cagcgagccc tgcggcctct cagacctctg      750
caggagcctc atgaccaagc cgggtgctc aggctactgc ctgtcccacc      800
aactgctctt cttcctctgg gccagaatga ggggatgcac acagggacca      850
ctccaacaga gccaggacta tatcaacctc ttctgcgcc aatgatgga      900
cttgaaccgc agagctgagg ccatcgata cgcctaccct acccgggaca      950
tcttcatgga aaacatcatg ttctgtgga tggcggtt ctcgacttc     1000
tacaagctcc ggtggctgga ggccattctc agctggcaga aacagcagga     1050
aggatgcttc ggggagcctg atgctgaaga tgaagaatta tctaaagcta     1100
ttcaatatca gcagcathtt tcgaggagag tgaagaggcg agaaaaacaa     1150
tttccagatt ctgctctgt tgctcaggct ggagtacagt ggcgcaatct     1200
cggctcactg caacctttgc ctctgggtt caagcaattc tcttgcctca     1250
tcctcccag tagctgggac tacaggagcg tgccaccata cctggctaatt     1300
ttttatattt ttttagtaga gacagggttt catcatgttg ctcatgctgg     1350
tctcgaactc ctgatctcaa gagatccgcc cacctcaggc tcccaaagtg     1400
tggtattata ggtgtgagcc accgtgtctg gctgaaaagc actttcaaag     1450
agactgtgtt gaataaaggg ccaaggttct tgccaccag cactcatggg     1500
ggctctctcc cctagatggc tgctctctcc acaacacagc cacagcagtg     1550
gcagccctgg gtggcttct atacatcctg gcagaatacc cccagcaaaa     1600
cagagagcca caccatcca caccgccacc accaagcagc cgctgagacg     1650
gacggttcca tgccagctgc ctggaggagg aacagacccc tttagtctc     1700
atcccttaga tcctggaggg cacggatcac atcctgggaa gaaggcatct     1750
ggaggataag caaagccacc ccgacacca atcttggaag ccctgagtag     1800
gcagggccag ggtaggtggg ggccgggagg gacccagtg 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
```


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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
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

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<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 135

ggctctgagtg cagagctgct gtcattggcgg ccgctctgtg gggcttcttt 50
cccgtcctgc tgctgctgct gctatcgggg gatgtccaga gctcggagggt 100
gcccggggct gctgctgagg gatcgggagg gagtggggtc ggcataggag 150
atcgcttcaa gattgagggg cgtgcagttg ttccaggggt gaagcctcag 200
gactggatct cggcggcccc agtgctggtg gacggagaag agcacgtcgg 250
tttccttaag acagatggga gttttgtggt tcatgatata ccttctggat 300
cttatgtagt ggaagttgta tctccagctt acagattga tcccgttcga 350
gtggatatca cttcgaaagg aaaaatgaga gcaagatatg tgaattacat 400
caaaacatca gaggttgtca gactgcccta tcctctccaa atgaaatctt 450
cagggtccacc ttcttacttt attaaaaggg aatcgtgggg ctggacagac 500
tttctaatag acccaatggt tatgatgatg gttcttcctt tattgatatt 550
tgtgcttctg cctaaagtgg tcaacacaag tgatcctgac atgagacggg 600
aaatggagca gtcaatgaat atgctgaatt ccaacctga gttgcctgat 650
gtttctgagt tcatgacaag actcttctct tcaaaatcat ctggcaaata 700
tagcagcggc agcagtaaaa caggcaaaa tggggctggc aaaaggagggt 750
agtcaggccg tccagagctg gcatttgcac aaacacggca acactgggtg 800
gcatccaagt cttggaaaac cgtgtgaagc aactactata aacttgagtc 850
atccccgacg tgatctctta caactgtgta tggt 884

<210> SEQ ID NO 136
<211> LENGTH: 242
<212> TYPE: PRT
<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

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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 tctggaagg	100
gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa	150
atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac	200
ctgctgggga ctaacggcgg agccaggatg gggacagaat aaaggagcca	250
cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc	300
ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga	350
tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg	400
ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat	450
ttgggaagct gtgtgatcgc cacaaacctt caggaaatac gaaatggatt	500
ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca	550
gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga	600
tgctgcctcc tgcgccattt gctaagactc tatctggaca ggtattttaa	650
aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg	700
ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgcccac	750
atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct	800
gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg	850
gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa	900
agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat	950
acctgcagag gaggcatgac cccaaaccac catctcttta ctgtactagt	1000
cttgtgtctg tcacagtgtg tcttatttat gcattacttg cttccttgca	1050
tgattgtctt tatgcatccc caatcttaat tgagaccata cttgtataag	1100
atTTTTGTAA tatctttctg ctattggata tatttattag ttaatatatt	1150

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tatttatttt ttgctattta atgtatttat ttttttactt ggacatgaaa	1200
ctttaaaaaa attcacagat tatattttata acctgactag agcaggtgat	1250
gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg	1300
ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct	1350
gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt	1400
tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga	1450
ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg	1500
aatcctacac ggccagcatg tattttctaca aataaagttt tctttgcata	1550
ccaaaaaaaa aaaaaaaaaa a	1571

<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
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

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	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 ggtggggtcg			50
gttcgcgcatc cagcctagcg tgtccacgat gcggctgggc tccgggactt			100
tcgctacctg ttgcgtagcg atcgagggtc tagggatcgc ggtcttctct			150
cggggattct tcccggctcc cgttcgttcc tctgccagag cggaacacgg			200
agcggagccc ccagcgcccc aaccctcggc tggagccagt tctaactgga			250
ccacgctgcc accacctctc ttcagtaaa ttgttattgt tctgatagat			300
gccttgagag atgattttgt gtttgggtca aaggggtgtg aatttatgcc			350
ctacacaact taccttgttg aaaaaggagc atctcacagt tttgtggctg			400
aagcaaaagg acctacagtt actatgcctc gaatcaaggc attgatgacg			450
gggagccttc ctggcctttgt cgacgtcatc aggaacctca attctcctgc			500
actgctggaa gacagtgtga taagacaagc aaaagcagct ggaaaaagaa			550
tagtctttta tggagatgaa acctggggtta aattattccc aaagcatttt			600
gtggaatatg atggaacaac ctcatTTTTt gtgtcagatt acacagaggt			650
ggataataat gtcacgaggc atttgataaa agtattaaaa agaggagatt			700
gggacatat attcctccac tacctggggc tggaccacat tggccacatt			750
tcagggccca acagccccct gattgggcag aagctgagcg agatggacag			800
cgtgctgatg aagatccaca cctcactgca gtcgaaggag agagagacgc			850
ctttacccaa tttgctgggt ctttgtgtg accatggcat gctgaaaca			900
ggaagtcaag gggcctcctc caccgaggag gtgaatacac ctctgatttt			950
aatcagttct gcgtttgaaa ggaaccgccg tgatatccga catccaaagc			1000
acgtccaata gacggatgtg gctgcgacac tggcgatagc acttggttta			1050
ccgattccaa aagacagtgt agggagcctc ctattcccag ttgtggaagg			1100
aagaccaatg agagagcagt tgagattttt acatttgaat acagtgcagc			1150
ttagtaaaact gttgcaagag aatgtgccgt catatgaaaa agatcctggg			1200
tttgagcagt ttaaaatgtc agaaagattg catgggaact ggatcagact			1250
gtacttgagg gaaaagcatt cagaagtctc attcaacctg ggctccaagg			1300
ttctcaggca gtacctggat gctctgaaga cgctgagctt gtccctgagt			1350
gcacaagtgg ccagttctc accctgctcc tgctcagcgt cccacaggca			1400
ctgcacagaa aggctgagct ggaagtccca ctgtcatctc ctgggttttc			1450
tctgctcttt tatttggtga tcctggttct ttcgccggtt cagtcatttg			1500
tgtgcacctc agctgaaagt tcgtgctact tctgtggcct ctctgtgctg			1550
gcggcaggct gcctttcgtt taccagactc tggttgaaca cctggtgtgt			1600

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gccaagtgct ggcagtgccc tggacagggg gcctcagga aggacgtgga      1650
gcagccttat cccaggcctc tgggtgtccc gacacaggtg ttcacatctg      1700
tgctgtcagg tcagatgcct cagttcttgg aaagctaggt tcctgcgact      1750
gttaccaagg tgattgtaaa gagctggcgg tcacagagga acaagcccc      1800
cagctgaggg ggtgtgtgaa tcggacagcc tcccagcaga ggtgtgggag      1850
ctgcagctga gggaagaaga gacaatcgcc ctggacactc aggaggggtca      1900
aaaggagact tggtcgcacc actcatcctg ccacccccag aatgcacacct      1950
gcctcatcag gtccagattt ctttccaagg cggacgtttt ctgttggaat      2000
tcttagtcct tggcctcgga caccttcatt cgtagctgg ggagtgggtg      2050
tgaggcagtg aagaagaggc ggatggtcac actcagatcc acagagccca      2100
ggatcaaggg acccactgca gtggcagcag gactgttggg cccccaccc      2150
aaccctgcac agccctcatc ccctcttggc ttgagccgtc agaggccctg      2200
tgctgagtgt ctgaccgaga cactcacagc tttgtcatca gggcacaggc      2250
ttcctcggag ccaggatgat ctgtgccacg cttgcacctc gggcccatct      2300
gggctcatgc tctctctcct gctattgaat tagtacctag ctgcacacag      2350
tatgtagtta ccaaagaat aaacggcaat aattgagaaa aaaaa      2395
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<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
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
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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

ggcacgaggc aagccttcca ggttatcgtg acgcaccttg aaagtctgag	50
agctactgcc ctacagaaag ttactagtgc cctaaagctg gcgctggcac	100
tgatgttact gctgctgttg gagtacaact tccctataga aaacaactgc	150
cagcacctta agaccactca caccttcaga gtgaagaact taaacccgaa	200
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 aagtcatcca tcccttcagc tgaagaagga gaaactgatg	450
aagctggctg cccaaaagga atcagcacgc cggcccttca tcttttatag	500
ggctcagggt ggctcctgga acatgctgga gtcggcggct caccocggat	550
ggttcatctg cacctcctgc aattgtaatg agcctgttgg ggtgacagat	600
aaatttgaga acaggaaca 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

-continued

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
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 143

ctagagagta tagggcagaa ggatgcgaca tgagtgactc cacatccaga	50
gctgcctccc tttaatccag gatcctgtcc ttcctgtcct gtaggagtgc	100
ctgttgccag tgtggggtga gacaagtttg tcccacaggg ctgtctgagc	150
agataagatt aagggtctgg tctgtgctca attaactcct gtgggcacgg	200
gggctgggaa gagcaaagtc agcggtcct acagtcagca ccatgctggg	250
cctgccgtgg aaggagggtc tgtcctgggc gctgctgtg cttctcttag	300
gtccccagat cctgctgata tatgcctggc atttccacga gcaaaggac	350
tgtgatgaac acaatgtcat ggctcggtac ctccctgcc cagtggagtt	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 agcaccagc cctggatgac tcagttcagc	650
ctcctgaaca agacctgctt ggagggatc cactgagtga aaccactca	700
caggcttgct catgtgtctg tcccacatto cgtggacatc agcactactc	750

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tcctgaggac tcttcagtgg ctgagcagct ttggacttgt ttgttatcct	800
atTTTgcAtg tGTTtgAgat ctcagatcag tGTTttagaa aatccacaca	850
tcttgagcct aatcatgtag ttagatcat taaacatcag cattttaaga	900
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	950
aaaaaaaaa a	961

<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 5 10 15
Leu Leu Leu Leu Gly Ser Gln Ile Leu Leu Ile Tyr Ala Trp His	20 25 30
Phe His Glu Gln Arg Asp Cys Asp Glu His Asn Val Met Ala Arg	35 40 45
Tyr Leu Pro Ala Thr Val Glu Phe Ala Val His Thr Phe Asn Gln	50 55 60
Gln Ser Lys Asp Tyr Tyr Ala Tyr Arg Leu Gly His Ile Leu Asn	65 70 75
Ser Trp Lys Glu Gln Val Glu Ser Lys Thr Val Phe Ser Met Glu	80 85 90
Leu Leu Leu Gly Arg Thr Arg Cys Gly Lys Phe Glu Asp Asp Ile	95 100 105
Asp Asn Cys His Phe Gln Glu Ser Thr Glu Leu Asn Asn Thr Phe	110 115 120
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
gctgtctctc agccacctct ctgcggtcca gacgaggggc atcaagcaca	150
gaatcaagtg gaaccggaag gccctgcca gcaactgcca gatcactgag	200
gcccagggtg ctgagaaccg cccgggagcc ttcatcaagc aaggccgcaa	250
gctcgacatt gacttcggag ccgagggcaa caggtactac gaggccaact	300
actggcagtt ccccgatggc atccactaca acggtgctc tgaggctaatt	350
gtgaccaagg aggcatttgt caccgctgc atcaatgcca cccaggcggc	400
gaaccagggg gagtccaga agccagacaa caagctccac cagcaggtgc	450
tctggcggct ggtccaggag ctctgctccc tcaagcattg cgagtttttg	500

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ttggagaggg gcgcaggact tcgggtcacc atgcaccagc cagtgtctcct 550
ctgccttctg gctttgatct ggctcatggt gaaataagct tgccaggagg 600
ctggcagtac agagcgcagc agcagcaaaa tcctggcaag tgaccagct 650
cttctcccc aaaccacgc gtgttctgaa ggtgccagg agcggcgatg 700
cactcgcact gcaaatgccg ctcccacgta tgcgccctgg tatgtgctg 750
cgttctgata gatgggggac tgtggttct cgcactcc attctcagcc 800
cctagcagag cgtctggcac actagattag tagtaaatgc ttgatgagaa 850
gaacacatca ggcactgcgc cacctgcttc acagtacttc ccaacaactc 900
ttagaggtag gtgtattccc gttttacaga taaggaaact gaggcccaga 950
gagctgaagt actgcaccca gcatcaccag ctagaaagtg gcagagccag 1000
gattcaacc tggtctgtct aacccaggt tttctgctct gtccaattcc 1050
agagctgtct ggtgatcact ttatgtctca cagggacca catocaaaca 1100
tgtatctcta atgaaattgt gaaagctcca tgttagaaa 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
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

-continued

<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 147

gccttggcct cccaaagggc tgggattata ggcgtgacca ccatgtctgg 50
tccagagtct catttcctga tgatttatag actcaaagaa aactcatggt 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 tgcatgatgc 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

<210> SEQ ID NO 149
<211> LENGTH: 1893
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 149

gtctccgcgt cacaggaact tcagcaccca cagggcggac agcgctcccc 50
tctacctgga gacttgactc ccgcgcgccc caaccctgct tatcccttga 100
ccgtcgagtg tcagagatcc tgcagccgcc cagtcccggc ccctctcccg 150
ccccacaccc accctcctgg ctcttcctgt ttttactcct ccttttcatt 200
cataacaaaa gctacagctc caggagccca gcgccgggct gtgacccaag 250
ccgagcgtgg aagaatgggg ttctcggga ccggcacttg gattctgggtg 300
ttagtgctcc cgattcaagc ttccccaaa cctggaggaa gccaaagacaa 350
atctctacat aatagagaat taagtgcaga aagaccttg aatgaacaga 400
ttgtgtaagc agaagaagac aagattaaaa aaacatatcc tccagaaaac 450
aagccaggtc agagcaacta ttcttttgtt gataactga acctgctaaa 500
ggcaataaca gaaaaggaaa aaattgagaa agaaagacaa tctataagaa 550
gtccccact tgataataag ttgaatgtgg aagatgttga ttcaaccaag 600
aatcgaaaac tgatcgatga ttatgactct actaagagtg gattggatca 650

```
<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

[illegible]

-continued

<210> SEQ ID NO 151

<211> LENGTH: 2598

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 151

cggtctgagg ctcccgccag gagaaaggaa cattctgagg ggagtctaca	50
ccctgtggag ctcaagatgg tcctgagtg ggcgtgtgc ttccgaatga	100
aggactcggc attgaagggtg ctttatctgc ataataacca gcttctagct	150
ggagggctgc atgcagggaa ggtcattaaa ggtgaagaga tcagcgtggg	200
ccccaatcgg tggctggatg ccagcctgtc ccccgtcac ctgggtgtcc	250
agggtggaag ccagtgcctg tcatgtgggg tggggcagga gccgactcta	300
acactagagc cagtgaacat catggagctc tatcttggtg ccaaggaatc	350
caagagcttc accttctacc ggcgggacat ggggtcacc tccagcttcg	400
agtcggctgc ctacccgggc tggttcctgt gcacgggtgcc tgaagccgat	450
cagcctgtca gactcaccca gcttcccag aatgggtggct ggaatgcccc	500
catcacagac ttctacttcc agcagtgtga ctagggcaac gtgccccca	550
gaactccctg ggcagagcca gctcgggtga ggggtgagtg gaggagacct	600
atggcggaac atcactctct ctgctctcag gacccccacg tctgacttag	650
tgggcacctg accactttgt cttctgggtc ccagtttga taaattctga	700
gatttggagc tcagtccacg gtccctcccc actggatggg gctactgctg	750
tggaaacctg taaaaccat gtggggtaaa ctgggaataa catgaaaaga	800
tttctgtggg ggtgggtggg gggagtgtg ggaatcattc ctgcttaatt	850
gtaactgaca agtgttaccc tgagccccgc aggccaaacc atccccagtt	900
gagccttata gggtcagtag ctctccacat gaagtcctgt cactcaccac	950
tgtgcaggag agggaggtgg tcatagatgc agggatctat ggccttggc	1000
ccagccccac ccccttccct ttaatcctgc cactgtcata tgctaccttt	1050
cctatctctt ccctcatcat cttgtgtgg gcacgaggag gtggtgatgt	1100
cagaagaaat ggctcgagct cagaagataa aagataagta gggtatgctg	1150
atcctctttt aaaaacccaa gatacaatca aaatcccaga tgctggtctc	1200
tattcccatg aaaaagtgt catgacatat tgagaagacc tacttacaaa	1250
gtggcatata ttgcaattta ttttaattaa aagataccta tttatatatt	1300
tctttataga aaaaagtctg gaagagtta cttcaattgt agcaatgtca	1350
gggtggtggc agtatagggtg atttttcttt taattctgtt aatttatctg	1400
tatttcctaa tttttctaca atgaagatga attccttgta taaaaataag	1450
aaaagaaatt aatcttgagg taagcagagc agacatcatc tctgattgtc	1500
ctcagcctcc acttccccag agtaaatca aattgaatcg agctctgctg	1550
ctctggttgg ttgtagtagt gatcaggaaa cagatctcag caaagccact	1600
gaggaggagg ctgtgctgag ttgtgtggc tggaatctct gggaaggaa	1650
cttaagaac aaaaatcatc tggtaattct ttcctagaag gatcacagcc	1700

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```
cctgggattc caaggcattg gatccagtct ctaagaaggc tgctgtactg      1750
gttgaattgt gtccccctca aattcacatc cttcttgga tctcagtctg      1800
tgagtttatt tggagataag gtctctgcag atgtagttag ttaagacaag      1850
gtcatgtctg atgaaggtag acctaaattc aatatgactg gtttccttgt      1900
atgaaaagga gaggacacag agacagagga gacgcgggga agactatgta      1950
aagatgaagg cagagatcgg agttttgcag ccacaagcta agaaacacca      2000
aggattgtgg caaccatcag aagcttgga gaggcaaaga agaattcttc      2050
cctagagggt ttagagggat aacggctctg ctgaaacctt aatctcagac      2100
ttccagcctc ctgaacgaag aaagaataaa tttcggctgt ttttaagccac      2150
caagataaat tggttacagc agctctagga aactaataca gctgctaaaa      2200
tgatccctgt ctctctgtgt ttacattctg tgtgtgtccc ctcccacaat      2250
gtaccaaagt tgtctttgtg accaatagaa tatggcagaa gtgatggcat      2300
gccacttcca agattaggtt ataaaagaca ctgcagcttc tacttgagcc      2350
ctctctctct gccaccacc gccccaatc tatcttggt cactcgtctt      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

<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
```

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155	
<210> SEQ ID NO 153	
<211> LENGTH: 1152	
<212> TYPE: DNA	
<213> ORGANISM: Homo Sapien	
<400> SEQUENCE: 153	
cttcagaaca ggttctcctt cccagtcac cagttgctcg agttagaatt	50
gtctgcaatg gccgccctgc agaaatctgt gagctctttc cttatgggga	100
ccctggccac cagctgcctc cttctcttgg ccctcttggg acagggagga	150
gcagctgcgc ccatcagctc cactgcagg cttgacaagt ccaacttcca	200
gcagccctat atcaccaacc gcaccttcac gctggctaag gaggctagct	250
tggctgataa caacacagac gttcgtctca ttggggagaa actgttcac	300
ggagtcagta tgagtgagcg ctgctatctg atgaagcagg tgctgaactt	350
cacccttgaa gaagtgtgtg tcctcaatc tgataggttc cagccttata	400
tgcaggaggt ggtgcccttc ctggccaggc tcagcaacag gctaagcaca	450
tgatcatattg aaggtgatga cctgcatatc cagaggaatg tgcaaaagct	500
gaaggacaca gtgaaaagc ttggagagag tggagagatc aaagcaattg	550
gagaactgga tttgctgttt atgtctctga gaaatgcctg catttgacca	600
gagcaaaagct gaaaaatgaa taactaacc cctttccctg ctagaaataa	650
caattagatg ccccaaagcg atttttttta accaaaagga agatgggaag	700
ccaaactcca tcatgatggg tggattccaa atgaaccctt gcgttagtta	750
caaaggaaac caatgccact tttgtttata agaccagaag gtagactttc	800
taagcataga tatttattga taacatttca ttgtaactgg tgttctatac	850
acagaaaaca atttattttt taaataattg tctttttcca taaaaagat	900
tactttccat tccttttaggg gaaaaaaccc ctaaatagct tcatgtttcc	950
ataatcagta ctttatattt ataatgtat ttattattat tataagactg	1000
cattttattt atatcatttt attaatatgg atttatttat agaacatca	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 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	

-continued

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 agtgcccgac ttgtgactga gtgtgcagtg	100
cccagcatgt accaggtcag tgcagagggc tgcctgaggg ctgtgctgag	150
agggagagga gcagagatgc tgctgagggg ggagggaggg caagctgcca	200
ggtttggggg tggggggcaa gtggagttag aaactgggat cccaggggga	250
gggtgcagat gagggagcga cccagattag gtgaggacag ttctctcatt	300
agccttttcc tacaggtggt tgcattcttg gcaatggtca tgggaaccca	350
cacctacagc cactggccca gctgtgccc cagcaaaggg caggacacct	400
ctgaggagct gctgaggtgg agcactgtgc ctgtgcctcc cctagagcct	450
gctagggcca accgccaccc agagtccctg agggccagtg aagatggacc	500
cctcaacagc agggccatct ccccctggag atatgagttg gacagagact	550
tgaaccggct cccccaggac ctgtaccacg cccgttgctt gtgcccgcac	600
tgcgtcagcc tacagacagg ctcccacatg gacccccggg gcaactcgga	650
gtgctcttac cacaaccaga ctgtcttcta caggcggcca tgccatggcg	700
agaagggcac ccacaagggc tactgcctgg agcgcaggct gtaccgtgtt	750
tccttagctt gtgtgtgtgt gcggccccgt gtgatgggct agccggacct	800
gtggagggct ggtccctttt tgggaaacct ggagccaggt gtacaaccac	850
ttgccatgaa gggccaggat gccagatgc ttggcccttg tgaagtgtg	900
tctggagcag caggatcccc ggacaggatg gggggctttg gggaaaacct	950
gcacttctgc acattttgaa aagagcagct gctgcttagg gccgcgggaa	1000
gctggtgtcc tgtcattttc tctcaggaaa ggttttcaaa gttctgcccc	1050

-continued

tttctggagg ccaccactcc tgtctcttcc tcttttccca tcccctgcta	1100
ccctggccca gcacaggcac tttctagata tttccccctt gctggagaag	1150
aaagagcccc tggttttatt tgtttgttta ctcactactc agtgagcatc	1200
tactttgggt gcattctagt gtagttacta gtcttttgac atggatgatt	1250
ctgaggagga agctgttatt gaatgtatag agatttatcc aaataaatat	1300
ctttatttaa aaatgaaaaa	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	
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
cgtacccega gagccgaccg ttcaatgtgg ctctgaaact gggccatctc	100
cagagtggat gctacaacat gatctaatacc ccggagactt gagggacctc	150
cgagtagaac ctgttacaac tagtggtgca acaggggact attcaatttt	200
gatgaatgta agctgggtac tccgggcaga tgccagcatc cgcttggtga	250
aggccaccaa gatttgtgtg acggggcaaaa gcaacttcca gtcctacagc	300

-continued

tgtgtgaggt gcaattacac agaggccttc cagactcaga ccagaccctc	350
tggtggtaaa tggacatttt cctacatcgg cttccctgta gagctgaaca	400
cagtctattt cattggggcc cataatattc ctaatgcaa tatgaatgaa	450
gatggccctt ccatgtctgt gaatttcacc tcaccaggt gcctagacca	500
cataatgaaa tataaaaaa agtgtgtcaa ggccggaagc ctgtgggatc	550
cgaacatcac tgcttctaag aagaatgagg agacagtaga agtgaacttc	600
acaaccactc ccctgggaaa cagatacatg gctcttatcc aacacagcac	650
tatcatcggg ttttctcagg tgtttgagcc acaccagaag aaacaaacgc	700
gagcttcagt ggtgattcca gtgactggg atagtgaagg tgctacggtg	750
cagctgactc catattttcc tacttgtggc agcgactgca tccgacataa	800
aggaacagtt gtgctctgcc cacaaacagg cgtcccttcc cctctggata	850
acaacaaaaa caagccggga ggctggctgc ctctcctcct gctgtctctg	900
ctggtggtcca catgggtgct ggtggcagg atctatctaa tgtggaggca	950
cgaaaggatc aagaagactt ccttttctac caccacacta ctgcccccca	1000
ttaaggttct tgtggtttac ccatctgaaa tatgtttcca tcacacaatt	1050
gtttacttca ctgaatttct tcaaaacat tgcagaagtg aggtcatcct	1100
tgaaaagtgg cagaaaaaga aaatagcaga gatgggtcca gtgcagtggc	1150
ttgccactca aaagaaggca gcagacaaag tcgtcttcct tctttccaat	1200
gacgtcaaca gtgtgtcga tggtagctgt ggcaagagcg agggcagtcc	1250
cagtgagaac tctcaagacc tcttccccct tgcctttaac cttttctgca	1300
gtgatctaag aagccagatt catctgcaca aatacgtggt ggtctacttt	1350
agagagattg atacaaaaga cgattacaat gctctcagtg tctgccccaa	1400
gtaccacctc atgaaggatg ccaactgctt ctgtgcagaa cttctccatg	1450
tcaagcagca ggtgtcagca ggaaaaagat cacaagcctg ccacgatggc	1500
tgctgctcct ttag	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

-continued

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	
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	

-continued

[illegible]

```
<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	tgcttttctg	agtgagcg	100
cagctcgga	aatcccaaa	gtaggacata	cttttttcca	aaagcctgag	150
agttgccgcg	ctgtgccagg	aggtagtatg	aagcttgaca	ttggcatcat	200
caatgaaaac	cagcgcgttt	ccatgtcacg	taacatcgag	agccgctcca	250
cctccccctg	gaattacact	gtcacttg	accccaaccg	gtacccccctg	300
gaagttgtac	aggcccagtg	taggaacttg	ggctgcatac	atgctcaagg	350
aaaggaagac	atctccatga	attccgttcc	catccagcaa	gagaccctgg	400
tcgtccggag	gaagaccaa	ggctgctctg	tttctttcca	gttgagaaag	450
gtgctggtga	ctgttggtcg	cacctgcgtc	acccctgtca	tccaccatgt	500
gcagtaaaag	gtgcataatc	actcagctga	agaaag		535

```
<210> SEQ ID NO 160
<211> LENGTH: 163
<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

-continued

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 aacaaaaacg aaagcactcc gtgctggaag taggaggaga	50
gtcaggactc ccaggacaga gagtgcacaa actaccacgc acagccccct	100
ccgccccctc tggaggctga agagggattc cagcccctgc caccacaga	150
cacgggctga ctgggggtgc tgccccctt gggggggggc agcacagggc	200
ctcaggcctg ggtgccacct ggcacctaga agatgcctgt gccctggttc	250
ttgtgtcctc tggcactggg ccgaagccca gtggtccttt ctctggagag	300
gcttggtggg cctcaggacg ctaccactg ctctccgggc ctctcctgcc	350
gcctctggga cagtgcacata ctctgcctgc ctggggacat cgtgcctgct	400
ccggggcccc tgctggcgcc tacgcacctg cagacagagc tgggtctgag	450
gtgccagaag gagaccgact gtgacctctg tctgcgtgtg gctgtccact	500
tggccgtgca tgggcactgg gaagagcctg aagatgagga aaagtttgga	550
ggagcagctg actcaggggg ggaggagcct aggaatgcct ctctccaggc	600
ccaagtctgt ctctccttcc aggcctaccc tactgccccg tgcgtcctgc	650
tggagggtgca agtgccctgct gcccttgtgc agtttggtca gtctgtgggc	700
tctgtggtat atgactgctt cgaggctgcc ctagggagtg aggtacgaat	750
ctggtcctat actcagccca ggtacgagaa ggaactcaac cacacacagc	800
agctgcctgc cctgccctgg ctcaacgtgt cagcagatgg tgacaacgtg	850
catctgtgtc tgaatgtctc tgaggagcag cacttcggcc tctccctgta	900
ctggaatcag gtccagggcc ccccaaaacc ccggtggcac aaaaacctga	950
ctggaccgca gatcattacc ttgaaccaca cagacctggt tccctgcctc	1000
tgtattcagg tgtggcctct ggaacctgac tccgttagga cgaacatctg	1050
ccccttcagg gaggaccccc gcgcacacca gaacctctgg caagccgccc	1100
gactgcgact gctgaccctg cagagctggc tgctggacgc accgtgctcg	1150
ctgcccgcag aagcggcact gtgctggcgg gctccgggtg gggaccctg	1200
ccagccactg gtcccaccgc ttctctggga gaacgtcact gtggacaagg	1250
ttctcgagtt ccattgctg aaaggccacc ctaacctctg tgttcaggtg	1300
aacagctcgg agaagctgca gctgcaggag tgcttggtgg ctgactccct	1350
ggggcctctc aaagacgatg tgctactgtt ggagacacga gggccccag	1400
acaacagatc cctctgtgcc ttggaacca gtggctgtac ttactaccc	1450
agcaaacgct ccacgagggc agctcgctt ggagagtact tactacaaga	1500
cctgcagtca ggccagtgtc tgcagctatg ggacgatgac ttgggagcgc	1550
tatgggcctg ccccatggac aaatacatcc acaagcgctg ggccctctg	1600
tggtggtgct gcctactctt tgccgctgcg ctttcctca tcctccttct	1650

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caaaaaggat cacgcgaaag ggtggctgag gctcttgaaa caggacgtcc      1700
gctcgggggg ggccgccagg ggccgcgcgg ctctgctcct ctactcagcc      1750
gatgactcgg gtttcgagcg cctgggtggc gccctggcgt cgccctgtg      1800
ccagctgcgg ctgcgcgtgg ccgtagacct gtggagccgt cgtgaactga      1850
gcgcgcaggg gcccggtggt tggtttcacg cgcagcggcg ccagaccctg      1900
caggagggcg gcgtggtggt ctgtctcttc tctcccggtg cgttggcgct      1950
gtgcagcgag tggctacagg atggggtgtc cgggcccggg gcgcacggcc      2000
cgcacgacgc cttccgcgcc tcgtcagct gcgtgctgcc cgaattcttg      2050
cagggccggg cgcccggcag ctacgtgggg gcctgcttcg acaggctgct      2100
ccacccggac gccgtaccgg cccttttcgg caccgtgccc gtcttcacac      2150
tgccctccca actgccagac ttctggggg cctgcagca gcctcgcgcc      2200
ccgcgttcgg ggcgggtcca 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
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
```

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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
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

-continued

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

gtcagtgccg gaggccggtc agccaccaag atgactgaca gggtcagctc 50
tctgcagcac actaccctca agccacctga tgtgacctgt atctccaaag 100
tgagatcgat tcagatgatt gttcatccta cccccacgcc aatccgtgca 150
ggcgatggcc accggctaac cctggaagac atcttccatg acctgttcta 200
ccacttagag ctccaggtca accgcacctc ccaaattgcac cttggaggga 250
agcagagaga atatgagttc ttcggcctga cccctgacac agagttcctt 300
ggcaccatca tgatttgcgt tcccacctgg gccaaaggaga gtgcccccta 350
catgtgccga gtgaagacac tgccagaccg gacatggacc tactccttct 400
ccggagcctt cctgttctcc atgggcttcc tcgtcgcagt actctgctac 450
ctgagctaca gatatgtcac caagccgcct gcacctccca actccctgaa 500
cgtccagcga gtcttgactt tccagccgct gcgcttcac caggagcacg 550
tcctgatccc tgtctttgac ctcagcggcc ccagcagttc ggcccagcct 600
gtccagtact ccagatcag ggtgtctgga ccaggggagc ccgacaggagc 650
tccacagcgg catagcctgt ccgagatcac ctacttaggg cagccagaca 700
tctccatcct ccagccctcc aacgtgccac ctccccagat cctctcccca 750
ctgtcctatg ccccaaacgc tgcccctgag gtcggggccc catcctatgc 800
acctcaggtg acccccgaag ctcaattccc attctacgcc ccacaggcca 850
tctctaaggt ccagccttcc tcctatgccc ctcaagccac tccggacagc 900
tggcctccct cctatggggt atgcatggaa ggttctggca aagactcccc 950
cactgggaca ctttctagtc ctaaaccact taggcctaaa ggtcagcttc 1000

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agaaagagcc accagctgga agctgcatgt taggtggcct ttctctgcag	1050
gaggtgacct ccttggtat ggaggaatcc caagaagcaa aatcattgca	1100
ccagcccctg gggatttgca cagacagaac atctgaccca aatgtgctac	1150
acagtgggga ggaaggga ccaagctacc taaagggcc gctccccctc	1200
ctctcctcag tccagatcga gggccacccc atgtccctcc ctttgcaacc	1250
tccttcgggt ccatgttccc cctcggaacca aggtccaagt cctgggggcc	1300
tgctggagtc ccttgtgtgt cccaaggatg aagccaagag cccagcccct	1350
gagacctcag acctggagca gccacagaa ctggattctc ttttcagagg	1400
cctggcccctg actgtgcagt gggagtcctg aggggaatgg gaaaggcttg	1450
gtgcttcctc cctgtcccta cccagtgtca catccttggc tgtcaatccc	1500
atgcctgccc atgccacaca ctctgcgato tggcctcaga cgggtgccct	1550
tgagagaagc agagggagtg gcatgcaggg cccctgccat gggtcgctc	1600
ctcaccgga caaagcagca tgataaggac tgcagcgggg gagctctggg	1650
gagcagcttg tgtagacaag cgcgtgctcg ctgagccctg caaggcagaa	1700
atgacagtgc aaggaggaaa tgcagggaaa ctcccagagt ccagagcccc	1750
acctcctaac accatggatt caaagtgtct aggggaatttg cctctccttg	1800
ccccattcct ggccagtttc acaatctagc tcgacagagc atgaggcccc	1850
tgctcttct gtcatgttc aaagggtgga agagagcctg gaaaagaacc	1900
aggcctggaa aagaaccaga aggaggctgg gcagaaccag aacaacctgc	1950
acttctgcca aggccagggc cagcaggacg gcaggactct agggaggggt	2000
gtggcctgca gctcattccc agccagggca actgcctgac gttgcacgat	2050
ttcagcttca ttctctgat agaacaagc gaaatgcagg tccaccaggg	2100
agggagacac acaagccttt tctgcaggca ggagtctcag accctatcct	2150
gagaatgggg tttgaaagga aggtgagggc tgtggcccct ggacgggtac	2200
aataacacac tgtactgatg tcacaacttt gcaagctctg ccttggttc	2250
agcccatctg ggctcaaatt ccagcctcac cactcacaag ctgtgtgact	2300
tcaaacaaat gaaatcagtg cccagaacct cggtttcctc atctgtaatg	2350
tgggatcat aacacctacc tcatggagtt gtggtgaaga tgaaatgaag	2400
tcatgtcttt aaagtgttta atagtgcctg gtacatgggc agtgcccaat	2450
aaacggtagc tatttaaaaa aaaaaaaa	2478

<210> SEQ ID NO 164

<211> LENGTH: 574

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 164

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

-continued

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
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

-continued

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

tggcctactg gaaaaaaaaa aaaaaaaaaa aaaagtcacc cgggcccgcg	50
gtggccacaa catggctgcg gcgccggggc tgctcttctg gctgttcgtg	100
ctggggggcgc tctgggtgggt cccggggccag tcggatctca gccacggacg	150
gcgttttctcg 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 tcgaagaaag ctgaagaagt ttctcagcac	550
agagagaaat ctctgagga gtctcggggg cgtgaacttg accctgtgcc	600
tgagcccgag 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 tctctgcct cggtggagcg ggagaagaca	850
gatgcttaca aagtcctgaa aacagaaatg agtcagagag gaagtggaca	900

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gtgcgttatt cattacagca aaggatttcg ttggcatcaa aatctaagtt	950
tgttttacaa agattgtttt tagtactaag ctgccttggc agtttgcatt	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	
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	

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Asp Cys Phe

<210> SEQ ID NO 167

<211> LENGTH: 2570

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 167

ccagaccag ggcgaccgg ctcagcctct cacttgctcag aggccgggga	50
agagaagcaa agcgcaacgg tgtggtccaa gccggggcctt ctgcttcgcc	100
tctaggacat acacgggacc ccctaacttc agtcccccaa acgcgacccc	150
tcgaagtctt gaactccagc cccgcacatc cacgcgcggc acaggcgcgg	200
caggcggcag gtcccggccg aaggcgatgc gcgcaggggg tcgggcagct	250
gggctcgggc ggccgggagta ggcccgggca gggaggcagg gaggctgcat	300
attcagagtc gcgggctgcg ccctgggcag aggcgcgcct cgctccacgc	350
aacacctgct gctgccaccg cgcgcgatg agccgcgtgg tctcgtgct	400
gctgggcgcc gcgctgctct gcggccacgg agccttctgc cgcgcgtgg	450
tcagcgccca aaaggtgtgt tttgctgact tcaagcatcc ctgctacaaa	500
atggcctact tccatgaact gtccagccga gtgagctttc aggaggcacg	550
cctggcttgt gagagtgagg gaggagtctt cctcagcctt gagaatgaag	600
cagaacagaa gttaatagag agcatgttgc aaaacctgac aaaacccggg	650
acagggattt ctgatggtga tttctggata gggctttgga ggaatggaga	700
tgggcaaaca tctggtgcct gccagatct ctaccagtgg tctgatggaa	750
gcaattccca gtaccgaaac tggtagacag atgaaccttc ctgcggaagt	800
gaaaagtgtg ttgtgatgta tcaccaacca actgccaatc ctggccttgg	850
gggtccctac ctttaccagt ggaatgatga caggtgtaac atgaagcaca	900
attatatatt caagtatgaa ccagagatta atccaacagc ccctgtagaa	950
aagccttata ttacaaatca accaggagac acccatcaga atgtggttgt	1000
tactgaagca ggtataattc ccaatctaata ttatgttgtt ataccaacaa	1050
taccctctgt cttactgata ctggttgctt ttggaacctg ttgtttccag	1100
atgtctcata 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 aatattaaag taatttttat	1350
atgtctatta tttcatttaa agaatatgct gtgctaataa tggagtgaga	1400
catgcttatt ttgctaaagg atgcacccaa acttcaaact tcaagcaaat	1450
gaaatggaca atgcagataa agttgttatc aacacgtcgg gagtatgtgt	1500
gttagaagca attcctttta tttctttcac ctttcataag ttgttatcta	1550
gtcaatgtaa tgtatatgtt attgaaattt acagtgtgca aaagtatatt	1600
acctttgcat aagtgtttga taaaatgaa ctgttctaata atttattttt	1650

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atggcatctc atttttcaat acatgctctt ttgattaaag aaacttatta	1700
ctgttgtcaa ctgaattcac acacacacaa atatagtacc atagaaaaag	1750
tttgttttct cgaaataatt catcttttcag 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 agatagttgc aaagttagtc taaggtttcc ctactgtgat	2200
ttagcctctg actatattag tatacaaaga ggtcatgtgg ttgagaccag	2250
gtgaatagtc actatcagtg tggagacaag cacagcacac agacatttta	2300
ggaaggaaaag gaactacgaa atcgtgtgaa aatgggttgg aacccatcag	2350
tgatgcgata ttcattgatg agggtttgct tgagatagaa aatgggtggct	2400
cctttctgtc ttatctccta gtttcttcaa tgcttacgcc ttgttcttct	2450
caagagaaaag ttgtaactct ctgggtcttca tatgtccctg tgctcctttt	2500
aaccaataaa agagttcttg tttctggggg aaaaaaaaaa aaaaaaaaaa	2550
aaaaaaaaaa aaaaaaaaaa	2570

<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	

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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 43

<210> SEQ ID NO 170
<211> LENGTH: 41
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide probe

<400> SEQUENCE: 170

caggaaacag ctatgaccac ctgcacacct gcaaatccat t 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. 144** (SEQ ID NO:144);

(b) a nucleic acid sequence encoding the polypeptide shown in **FIG. 144** (SEQ ID NO:144), lacking its associated signal peptide;

(c) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 144** (SEQ ID NO:144);

(d) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 144** (SEQ ID NO:144), lacking its associated signal peptide;

(e) the nucleic acid sequence shown in **FIG. 143** (SEQ ID NO:143);

(f) the full-length coding sequence of the nucleic acid sequence shown in **FIG. 143** (SEQ ID NO:143); or
- (g) the full-length coding sequence of the cDNA deposited under ATCC accession number 209788.

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. 144** (SEQ ID NO:144);

(b) a nucleic acid sequence encoding the polypeptide shown in **FIG. 144** (SEQ ID NO:144), lacking its associated signal peptide;

(c) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 144** (SEQ ID NO:144);

(d) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 144** (SEQ ID NO:144), lacking its associated signal peptide;

(e) the nucleic acid sequence shown in **FIG. 143** (SEQ ID NO:143);

3. The isolated nucleic acid of claim 1 having at least 90% nucleic acid sequence identity to:

(b) a nucleic acid sequence encoding the polypeptide shown in **FIG. 144** (SEQ ID NO:144), lacking its associated signal peptide;

(c) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 144** (SEQ ID NO:144);

(d) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 144** (SEQ ID NO:144), lacking its associated signal peptide;

(e)the nucleic acid sequence shown in **FIG. 143** (SEQ ID NO:143);

(f) the full-length coding sequence of the nucleic acid sequence shown in **FIG. 143** (SEQ ID NO:143); or

(g) the full-length coding sequence of the cDNA deposited under ATCC accession number 209788.

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. 144** (SEQ ID NO:144);

(b) a nucleic acid sequence encoding the polypeptide shown in **FIG. 144** (SEQ ID NO:144), lacking its associated signal peptide;

(c) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 144** (SEQ ID NO:144);

(d) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 144** (SEQ ID NO:144), lacking its associated signal peptide;

(e)the nucleic acid sequence shown in **FIG. 143** (SEQ ID NO:143);

(f) the full-length coding sequence of the nucleic acid sequence shown in **FIG. 143** (SEQ ID NO:143); or

(g) the full-length coding sequence of the cDNA deposited under ATCC accession number 209788.

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. 144** (SEQ ID NO:144);

(b) a nucleic acid sequence encoding the polypeptide shown in **FIG. 144** (SEQ ID NO:144), lacking its associated signal peptide;

(c) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 144** (SEQ ID NO:144);

(d) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 144** (SEQ ID NO:144), lacking its associated signal peptide;

(e)the nucleic acid sequence shown in **FIG. 143** (SEQ ID NO:143);

(f) the full-length coding sequence of the nucleic acid sequence shown in **FIG. 143** (SEQ ID NO:143); or

(g) the full-length coding sequence of the cDNA deposited under ATCC accession number 209788.

6. An isolated nucleic acid comprising:

(a) a nucleic acid sequence encoding the polypeptide shown in **FIG. 144** (SEQ ID NO:144);

(b) a nucleic acid sequence encoding the polypeptide shown in **FIG. 144** (SEQ ID NO:144), lacking its associated signal peptide;

(c) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 144** (SEQ ID NO:144);

(d) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 144** (SEQ ID NO:144), lacking its associated signal peptide;

(e)the nucleic acid sequence shown in **FIG. 143** (SEQ ID NO:143);

(f) the full-length coding sequence of the nucleic acid sequence shown in **FIG. 143** (SEQ ID NO:143); or

(g) the full-length coding sequence of the cDNA deposited under ATCC accession number 209788.

7. The isolated nucleic acid of claim 6 comprising a nucleic acid sequence encoding the polypeptide shown in **FIG. 144** (SEO ID NO:144).

8. The isolated nucleic acid of claim 6 comprising a nucleic acid sequence encoding the polypeptide shown in **FIG. 144** (SEQ ID NO:144), 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. 144** (SEQ ID NO:144).

10. The isolated nucleic acid of claim 6 comprising a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 144** (SEQ ID NO:144), lacking its associated signal peptide.

11. The isolated nucleic acid of claim 6 comprising the nucleic acid sequence shown in **FIG. 143** (SEQ ID NO:143).

12. The isolated nucleic acid of claim 6 comprising the full-length coding sequence of the nucleic acid sequence shown in **FIG. 143** (SEQ ID NO:143).

13. The isolated nucleic acid of claim 6 comprising the full-length coding sequence of the cDNA deposited under ATCC accession number 209788.

14. An isolated nucleic acid that hybridizes to:

(a) a nucleic acid sequence encoding the polypeptide shown in **FIG. 144** (SEQ ID NO:144);

(b) a nucleic acid sequence encoding the polypeptide shown in **FIG. 144** (SEQ ID NO:144), lacking its associated signal peptide;

(c) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 144** (SEQ ID NO:144);

- (d) a nucleic acid sequence encoding the extracellular domain of the polypeptide shown in **FIG. 144** (SEQ ID NO:144), lacking its associated signal peptide;
 - (e) the nucleic acid sequence shown in **FIG. 143** (SEQ ID NO:143);
 - (f) the full-length coding sequence of the nucleic acid sequence shown in **FIG. 143** (SEQ ID NO:143); or
 - (g) the full-length coding sequence of the cDNA deposited under ATCC accession number 209788.
- 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.
- * * * * *