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Konthur et al.

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(54) **BIOMARKER FOR THE PREDICTION OF RESPONSIVENESS TO AN ANTI-TUMOUR NECROSIS FACTOR ALPHA (TNF) TREATMENT**

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G01N 33/53 (2006.01)
G01N 33/564 (2006.01)
G01N 33/68 (2006.01)

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CPC ***G01N 33/564*** (2013.01); ***G01N 33/6854*** (2013.01); ***G01N 33/6863*** (2013.01); *G01N 2333/82* (2013.01); *G01N 2333/91171* (2013.01); *G01N 2333/9121* (2013.01); *G01N 2333/916* (2013.01); *G01N 2800/102* (2013.01); *G01N 2800/52* (2013.01); *G01N 2333/4703* (2013.01); *G01N 2333/705* (2013.01)

(58) **Field of Classification Search**
None
See application file for complete search history.

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(57) **ABSTRACT**

The invention refers to a method for diagnosing an individual who is to be subjected to or is being subjected to an anti-tumor necrosis factor alpha (TNFα or TNF) treatment to assess the responsiveness to an anti-TNF treatment which comprises the detection of immunoglobulin(s) against one or more biomarker proteins in a bodily fluid or an excrement of said patient, and sorting the individual into one of two categories based on detection of said immunoglobulin(s), wherein individuals are classified as NON-responder or responder. The invention refers to diagnostic kits comprising said one or more biomarker proteins and the use of these kits for assessing the responsiveness to an anti-TNF treatment of an individual who is to be subjected to or is being subjected to an anti-TNFα treatment.

5 Claims, 126 Drawing Sheets

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Fig. 1

SEQ ID No. 1
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AACGTGGAGCGCTGGCTGAAGGAGCTGCGGGACCACGCAGACAGCAACATCGTCATCATG
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GTAGAGGAAGCATTCAAGAACATCCTCACAGAGATCTACCGCATCGTGTCACAGAAACAG
ATCGCAGACCGCGCTGCCCACGACGAGTCCCCGGGGAACAACGTGGTGGACATCAGCGTG
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Fig. 2

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AAGATGAGGTCCTCCTGGCCCTGGCAGAACAGCTGGGAACCTTCACTACCCTGGTGGGAG
GCCCAGAGTACGTGCACTGCCTGCTGCCTCTTCTCCGTCTGCTACCCCCGAGTGTCCAGT
GCTGTGAAGGCGGAACTTCGACAGTACTTCCGGAACCTGTGCTCAGATGACACCCCCATG
GTGCGGCGGGCCGCAGCCTCCAAGCTGGGGGAGTTTGCCAAGGTGCTGGAGCTGGACAAC
GTCAAGAGTGAGATCATCCCCATGTTCTCCAACCTGGCCTCTGACGAGCAGGACTCGGTG
CGGCTGCTGGCGGTGGAGGCGTGCGTGAACATCGCCCAGCTTCTGCCCCAGGAGGATCTG
GAGGCCCTGGTGATGCCCACTCTGCGCCAGGCCGCTGAAGACAAGTCCTGGCGCGTCCGC
TACATGGTGGCTGACAAGTTCACAGAGCTCCAGAAAGCAGTGGGGCCTGAGATCACCAAG
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GCAGCCTCCCACAAGGTCAAAGAGTTCTGTGAAAACCTCTCAGCTGACTGTCGGGAGAAT
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ACCATCGAGCACCTCTTGCCCCTCTTCCTGGCTCAGCTGAAGGATGAGTGCCCTGAGGTA
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TCCCAGTCCCTGCTCCCTGCCATTGTGGAGCTGGCTGAGGACGCCAAGTGGCGGGTGCGG
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GAGAAACTTAACTCCTTGTGCATGGCCTGGCTTGTGGATCATGTATATGCCATCCGCGAG
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ACGCTCTTCTGCATCAATGTGCTGTCTGAGGTCTGTGGGCAGGACATCACCACCAAGCAC
ATGCTACCCACGGTTCTGCGCATGGCTGGGGACCCGGTTGCCAATGTCCGCTTCAATGTG
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GAGGCTCTGACTGTTCTGTCTCTCGCCTGA

Fig. 3

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GCCCTTGGGGTTGAAAGGACCCGAAGTGAGCTTCTGCCTTTCCTTACAGATACCATCTAT
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ATGCTACCCACGGTTCTGCGCATGGCTGGGGACCCGGTTGCCAATGTCCGCTTCAATGTG
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Fig. 4

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ATCAAGAACTCTTTGACATCTAAAGATCCAGATATCAAGGCACAATATCAGCAGAGGTGG
CTTGCTATTGATGCTAATGCTCGACGAGAAGTCAAGAACTATGTTTTGCAGACATTGGGT
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Fig. 5

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Fig. 6

SEQ ID No. 6
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Fig. 7

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Fig. 8

SEQ ID No. 8
COG4
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TCTGAGGGGGTGGGAGGTGGCCGCTGCTCCGAAATCTCCGCTGAGCTCATTCGCTCCCTG
ACAGAGCTGCAGGAGCTGGAGGCTGTATACGAACGGCTCTGCGGCGAGGAGAAAGTGGTG
GAGAGAGAGCTGGATGCTCTTTTGGAACAGCAAAACACCATTGAAAGTAAGATGGTCACT
CTCCACCGAATGGGTCCTAATCTGCAGCTGATTGAGGCCAACCTGAAATTGCTGCAGGAA
GCTGAGCAACGTCTCAAAGCCATTGTGGCAGAGAAGTTTGCCATTGCCACCAAGGAAGGT
GATCTGCCCCAGGTGGAGCGCTTCTTCAAGATCTTCCCACTGCTGGGTTTGCATGAGGAG
GGATTAAGAAAGTTCTCGGAGTACCTTTGCAAGCAGGTGGCCAGTAAAGCTGAGGAGAAT
CTGCTCATGGTGCTGGGGACAGACATGAGTGATCGGAGAGCTGCAGTCATCTTTGCAGAT
ACACTTACTCTTCTGTTTGAAGGGATTGCCCGCATTGTGGAGACCCACCAGCCAATAGTG
GAGACCTATTATGGGCCAGGGAGACTCTATACCCTGATCAAATATCTGCAGGTGGAATGT
GACAGACAGGTGGAGAAGGTGGTAGACAAGTTCATCAAGCAAAGGGACTACCACCAGCAG
TTCCGGCATGTTCAGAACAACCTGATGAGAAATTCTACAACAGAAAAAATCGAACCAAGA
GAACTGGACCCCATCCTGACTGAGGTCACCCTGATGAATGCCCGCAGTGAGCTATACTTA
CGCTTCCTCAAGAAGAGGATTAGCTCTGATTTTGAGGTGGGAGACTCCATGGCCTCAGAG
GAAGTAAAGCAAGAGCACCAGAAGTGTCTGGACAAACTCCTCAATAACTGCCTTTTGAGC
TGTACCATGCAGGAGCTAATTGGCTTATATGTTACCATGGAGGAGTACTTCATGAGGGAG
ACTGTCAATAAGGCTGTGGCTCTGGACACCTATGAGAAGGGCCAGCTGACATCCAGCATG
GTGGATGATGTCTTCTACATTGTTAAGAAGTGCATTGGGCGGGCTCTGTCCAGCTCCAGC
ATTGACTGTCTCTGTGCCATGATCAACCTCGCCACCACAGAGCTGGAGTCTGACTTCAGG
GATGTTCTGTGTAATAAGCTGCGGATGGGCTTTCCTGCCACCACCTTCCAGGACATCCAG
CGCGGGGTGACAAGTGCCGTGAACATCATGCACAGCAGCCTCCAGCAAGGCAAATTTGAC
ACAAAAGGCATCGAGAGTACTGACGAGGCGAAGATGTCCTTCCTGGTGACTCTGAACAAC
GTGGAAGTCTGCAGTGAAAACATCTCCACTCTGAAGAAGACACTGGAGAGTGACTGCACC
AAGCTCTTCAGCCAGGGCATTGGAGGGGAGCAGGCCCAGGCCAAGTTTGACAGCTGCCTT
TCTGACTTGGCCGCCGTGTCCAACAAATTCCGAGACCTCTTGCAGGAAGGGCTGACGGAG
CTCAACAGCACAGCCATCAAGCCACAGGTGCAGCCTTGGATCAACAGCTTTTTCTCCGTC
TCCCACAACATCGAGGAGGAAGAATTCAATGACTATGAGGCCAACGACCCTTGGGTACAA
CAGTTCATCCTTAACCTGGAGCAGCAAATGGCAGAGTTCAAGGCCAGCCTGTCCCCGGTC
ATCTACGACAGCCTAACCGGCCTCATGACTAGCCTTGTTGCCGTCGAGTTGGAGAAAGTG
GTGCTGAAATCCACCTTTAACCGGCTGGGTGGTCTGCAGTTTGACAAGGAGCTGAGGTCG
CTCATTGCCTACCTTACCACGGTGACCACCTGGACCATCCGAGACAAGTTTGCCCGGCTC
TCCCAGATGGCCACCATCCTCAATCTGGAGCGGGTGACCGAGATCCTCGATTACTGGGGA
CCCAATTCCGGCCCATTGACGTGGCGCCTCACCCCTGCTGAAGTGCGCCAGGTGCTGGCC
CTGCGGATAGACTTCCGCAGTGAAGATATCAAGAGGCTGCGCCTGTAG

Fig. 9

SEQ ID No. 9
FDFT1
>ENSG00000079459|8|protein_coding|ENST00000220584|ENSP00000220584
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ATCGGGGGCAAGCGGAAGGTGATGCCCAAGATGGACCAGGACTCGCTCAGCAGCAGCCTG
AAAACTTGCTACAAGTATCTCAATCAGACCAGTCGCAGTTTCGCAGCTGTTATCCAGGCG
CTGGATGGGGAAATGCGCAACGCAGTGTGCATATTTTATCTGGTTCTCCGAGCTCTGGAC
ACACTGGAAGATGACATGACCATCAGTGTGGAAAAGAAGGTCCCGCTGTTACACAACTTT
CACTCTTTCCTTTACCAACCAGACTGGCGGTTCATGGAGAGCAAGGAGAAGGATCGCCAG
GTGCTGGAGGACTTCCCAACGATCTCCCTTGAGTTTAGAAATCTGGCTGAGAAATACCAA
ACAGTGATTGCCGACATTTGCCGGAGAATGGGCATTGGGATGGCAGAGTTTTTGGATAAG
CATGTGACCTCTGAACAGGAGTGGGACAAGTACTGCCACTATGTTGCTGGGCTGGTCGGA
ATTGGCCTTTCCCGTCTTTTCTCAGCCTCAGAGTTTGAAGACCCCTTAGTTGGTGAAGAT
ACAGAACGTGCCAACTCTATGGGCCTGTTTTTGCAGAAAACAAACATCATCCGTGACTAT
CTGGAAGACCAGCAAGGAGGAAGAGAGTTCTGGCCTCAAGAGGTTTGGAGCAGGTATGTT
AAGAAGTTAGGGGATTTTGCTAAGCCGGAGAATATTGACTTGGCCGTGCAGTGCCTGAAT
GAACTTATAACCAATGCACTGCACCACATCCCAGATGTCATCACCTACCTTTCGAGACTC
AGAAACCAGAGTGTGTTTAACTTCTGTGCTATTCCACAGGTGATGGCCATTGCCACTTTG
GCTGCCTGTTATAATAACCAGCAGGTGTTCAAAGGGGCAGTGAAGATTCGGAAAGGGCAA
GCAGTGACCCTGATGATGGATGCCACCAATATGCCAGCTGTCAAAGCCATCATATATCAG
TATATGGAAGAGATTTATCATAGAATCCCCGACTCAGACCCATCTTCTAGCAAAACAAGG
CAGATCATCTCCACCATCCGGACGCAGAATCTTCCCAACTGTCAGCTGATTTCCCGAAGC
CACTACTCCCCCATCTACCTGTCGTTTGTCATGCTTTTGGCTGCCCTGAGCTGGCAGTAC
CTGACCACTCTCTCCCAGGTAACAGAAGACTATGTTCAGACTGGAGAACACTGA

Fig. 10

SEQ ID No. 10
PECI
>ENSG00000198721|6|protein_coding|ENST00000380125|ENSP00000369468
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GATCCAGGAAACGAAGTGAAGCTAAAACTCTACGCGCTATATAAGCAGGCCACTGAAGGA
CCTTGTAACATGCCCAAACCAGGTGTATTTGACTTGATCAACAAGGCCAAATGGGACGCA
TGGAATGCCCTTGGCAGCCTGCCCAAGGAAGCTGCCAGGCAGAACTATGTGGATTTGGTG
TCCAGTTTGAGTCCTTCATTGGAATCCTCTAGTCAGGTGGAGCCTGGAACAGACAGGAAA
TCAACTGGGTTTGAAACTCTGGTGGTGACCTCCGAAGATGGCATCACAAAGATCATGTTC
AACCGGCCCAAAAAGAAAAATGCCATAAACACTGAGATGTATCATGAAATTATGCGTGCA
CTTAAAGCTGCCAGCAAGGATGACTCAATCATCACTGTTTTAACAGGAAATGGTGACTAT
TACAGTAGTGGGAATGATCTGACTAACTTCACTGATATTCCCCCTGGTGGAGTAGAGGAG
AAAGCTAAAAATAATGCCGTTTTACTGAGGGAATTTGTGGGCTGTTTTATAGATTTTCCT
AAGCCTCTGATTGCAGTGGTCAATGGTCCAGCTGTGGGCATCTCCGTCACCCTCCTTGGG
CTATTCGATGCCGTGTATGCATCTGACAGGGCAACATTTCATACACCATTTAGTCACCTA
GGCCAAAGTCCGGAAGGATGCTCCTCTTACACTTTTCCGAAGATAATGAGCCCAGCCAAG
GCAACAGAGATGCTTATTTTTGGAAAGAAGTTAACAGCGGGAGAGGCATGTGCTCAAGGA
CTTGTTACTGAAGTTTTCCCTGATAGCACTTTTCAGAAAGAAGTCTGGACCAGGCTGAAG
GCATTTGCAAAGCTTCCCCCAAATGCCTTGAGAATTTCAAAAGAGGTAATCAGGAAAAGA
GAGAGAGAAAAACTACACGCTGTTAATGCTGAAGAATGCAATGTCCTTCAGGGAAGATGG
CTATCAGATGAATGCACAAATGCTGTGGTGAACTTCTTATCCAGAAAATCAAAACTGTGA

Fig. 11

SEQ ID No. 11
PECI
>ENSG00000198721|6|protein_coding|ENST00000380114|ENSP00000369457
ATGTATCATGAAATTATGCGTGCACTTAAAGCTGCCAGCAAGGATGACTCAATCATCACT
GTTTTAACAGGAAATGGTGACTATTACAGTAGTGGGAATGATCTGACTAACTTCACTGAT
ATTCCCCCTGGTGGAGTAGAGGAGAAAGCTAAAAATAATGCCGTTTTACTGAGGGAATTT
GTGGGCTGTTTTATAGATTTTCCTAAGCCTCTGATTGCAGTGGTCAATGGTCCAGCTGTG
GGCATCTCCGTCACCCTCCTTGGGCTATTCGATGCCGTGTATGCATCTGACAGGGCAACA
TTTCATACACCATTTAGTCACCTAGGCCAAAGTCCGGAAGGATGCTCCTCTTACACTTTT
CCGAAGATAATGAGCCCAGCCAAGGCAACAGAGATGCTTATTTTTGGAAAGAAGTTAACA
GCGGGAGAGGCATGTGCTCAAGGACTTGTTACTGAAGTTTTCCCTGATAGCACTTTTCAG
AAAGAAGTCTGGACCAGGCTGAAGGCATTTGCAAAGCTTCCCCCAAATGCCTTGAGAATT
TCAAAAGAGGTAATCAGGAAAAGAGAGAGAGAAAAACTACACGCTGTTAATGCTGAAGAA
TGCAATGTCCTTCAGGGAAGATGGCTATCAGATGAATGCACAAATGCTGTGGTGAACTTC
TTATCCAGAAAATCAAAACTGTGA

Fig. 12

SEQ ID No. 12
PECI
>ENSG00000198721|6|protein_coding|ENST00000380118|ENSP00000369461
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GTCACTAGTTTCCCGGTAGTTCAGCTGCACATGAATAGAACAGCAATGAGAGCCAGTCAG
AAGGACTTTGAAAATTCAATGAATCAAGTGAAACTCTTGAAAAAGGATCCAGGAAACGAA
GTGAAGCTAAAACTCTACGCGCTATATAAGCAGGCCACTGAAGGACCTTGTAACATGCCC
AAACCAGGTGTATTTGACTTGATCAACAAGGCCAAATGGGACGCATGGAATGCCCTTGGC
AGCCTGCCCAAGGAAGCTGCCAGGCAGAACTATGTGGATTTGGTGTCCAGTTTGAGTCCT
TCATTGGAATCCTCTAGTCAGGTGGAGCCTGGAACAGACAGGAAATCAACTGGGTTTGAA
ACTCTGGTGGTGACCTCCGAAGATGGCATCACAAAGATCATGTTCAACCGGCCCAAAAAG
AAAAATGCCATAAACACTGAGATGTATCATGAAATTATGCGTGCACTTAAAGCTGCCAGC
AAGGATGACTCAATCATCACTGTTTTAACAGGAAATGGTGACTATTACAGTAGTGGGAAT
GATCTGACTAACTTCACTGATATTCCCCCTGGTGGAGTAGAGGAGAAAGCTAAAAATAAT
GCCGTTTTACTGAGGGAATTTGTGGGCTGTTTTATAGATTTTCCTAAGCCTCTGATTGCA
GTGGTCAATGGTCCAGCTGTGGGCATCTCCGTCACCCTCCTTGGGCTATTCGATGCCGTG
TATGCATCTGACAGGGCAACATTTCATACACCATTTAGTCACCTAGGCCAAAGTCCGGAA
GGATGCTCCTCTTACACTTTTCCGAAGATAATGAGCCCAGCCAAGGCAACAGAGATGCTT
ATTTTTGGAAAGAAGTTAACAGCGGGAGAGGCATGTGCTCAAGGACTTGTTACTGAAGTT
TTCCCTGATAGCACTTTTCAGAAAGAAGTCTGGACCAGGCTGAAGGCATTTGCAAAGCTT
CCCCCAAATGCCTTGAGAATTTCAAAAGAGGTAATCAGGAAAAGAGAGAGAGAAAAACTA
CACGCTGTTAATGCTGAAGAATGCAATGTCCTTCAGGGAAGATGGCTATCAGATGAATGC
ACAAATGCTGTGGTGAACTTCTTATCCAGAAAATCAAAACTGTGA

Fig. 13

SEQ ID No. 13
PECI
>ENSG00000198721|6|protein_coding|ENST00000361538|ENSP00000354737
ATGAATAGAACAGCAATGAGAGCCAGTCAGAAGGACTTTGAAAATTCAATGAATCAAGTG
AAACTCTTGAAAAAGGATCCAGGAAACGAAGTGAAGCTAAAACTCTACGCGCTATATAAG
CAGGCCACTGAAGGACCTTGTAACATGCCCAAACCAGGTGTATTTGACTTGATCAACAAG
GCCAAATGGGACGCATGGAATGCCCTTGGCAGCCTGCCCAAGGAAGCTGCCAGGCAGAAC
TATGTGGATTTGGTGTCCAGTTTGAGTCCTTCATTGGAATCCTCTAGTCAGGTGGAGCCT
GGAACAGACAGGAAATCAACTGGGTTTGAAACTCTGGTGGTGACCTCCGAAGATGGCATC
ACAAAGATCATGTTCAACCGGCCCAAAAAGAAAAATGCCATAAACACTGAGATGTATCAT
GAAATTATGCGTGCACTTAAAGCTGCCAGCAAGGATGACTCAATCATCACTGTTTTAACA
GGAAATGGTGACTATTACAGTAGTGGGAATGATCTGACTAACTTCACTGATATTCCCCCT
GGTGGAGTAGAGGAGAAAGCTAAAAATAATGCCGTTTTACTGAGGGAATTTGTGGGCTGT
TTTATAGATTTTCCTAAGCCTCTGATTGCAGTGGTCAATGGTCCAGCTGTGGGCATCTCC
GTCACCCTCCTTGGGCTATTCGATGCCGTGTATGCATCTGACAGGGCAACATTTCATACA
CCATTTAGTCACCTAGGCCAAAGTCCGGAAGGATGCTCCTCTTACACTTTTCCGAAGATA
ATGAGCCCAGCCAAGGCAACAGAGATGCTTATTTTTGGAAAGAAGTTAACAGCGGGAGAG
GCATGTGCTCAAGGACTTGTTACTGAAGTTTTCCCTGATAGCACTTTTCAGAAAGAAGTC
TGGACCAGGCTGAAGGCATTTGCAAAGCTTCCCCCAAATGCCTTGAGAATTTCAAAAGAG
GTAATCAGGAAAAGAGAGAGAGAAAAACTACACGCTGTTAATGCTGAAGAATGCAATGTC
CTTCAGGGAAGATGGCTATCAGATGAATGCACAAATGCTGTGGTGAACTTCTTATCCAGA
AAATCAAAACTGTGA

Fig. 14

SEQ ID No. 14
PECI
>ENSG00000198721|6|protein_coding|ENST00000380120|ENSP00000369463
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CGTGCACTTAAAGCTGCCAGCAAGGATGACTCAATCATCACTGTTTTAACAGGAAATGGT
GACTATTACAGTAGTGGGAATGATCTGACTAACTTCACTGATATTCCCCCTGGTGGAGTA
GAGGAGAAAGCTAAAAATAATGCCGTTTTACTGAGGGAATTTGTGGGCTGTTTTATAGAT
TTTCCTAAGCCTCTGATTGCAGTGGTCAATGGTCCAGCTGTGGGCATCTCCGTCACCCTC
CTTGGGCTATTCGATGCCGTGTATGCATCTGACAGGGCAACATTTCATACACCATTTAGT
CACCTAGGCCAAAGTCCGGAAGGATGCTCCTCTTACACTTTTCCGAAGATAATGAGCCCA
GCCAAGGCAACAGAGATGCTTATTTTTGGAAAGAAGTTAACAGCGGGAGAGGCATGTGCT
CAAGGACTTGTTACTGAAGTTTTCCCTGATAGCACTTTTCAGAAAGAAGTCTGGACCAGG
CTGAAGGCATTTGCAAAGCTTCCCCCAAATGCCTTGAGAATTTCAAAAGAGGTAATCAGG
AAAAGAGAGAGAGAAAAACTACACGCTGTTAATGCTGAAGAATGCAATGTCCTTCAGGGA
AGATGGCTATCAGATGAATGCACAAATGCTGTGGTGAACTTCTTATCCAGAAAATCAAAA
CTGTGA

Fig. 15

SEQ ID No. 15
CTNND2
>ENSG00000169862|5|protein_coding|ENST00000359640|ENSP00000352661
ATGTTTGCGAGGAAGCCGCCGGGCGCCGCGCCTTTGGGAGCTATGCCTGTTCCAGACCAG
CCTTCATCAGCCTCAGAGAAGACGAGTTCCCTGAGCCCCGGCTTAAACACCTCCAACGGG
GATGGCTCTGAAACAGAAACCACCTCTGCCATCCTCGCCTCAGTCAAAGAACAGGAATTA
CAGTTTGAAAGGCTGACCCGAGAGCTGGAGGCTGAACGGCAGATCGTAGCCAGCCAGCTG
GAGCGATGCAAGCTCGGATCCGAGACTGGCAGCATGAGCAGCATGAGTTCAGCAGAAGAG
CAGTTTCAGTGGCAGTCACAAGATGGTCAAAAAGATATCGAAGATGAGCTTACAACAGGT
CTCGAGCTGGTGGACTCCTGTATTAGGTCACTACAGGAATCAGGAATACTTGACCCACAG
GATTATTCTACAGGTGAAAGGCCCAGCCTGCTCTCCCAGAGTGCACTTCAGCTCAATTCC
AAACCTGAAGGGTCTTTCCAGTATCCGGCCAGCTACCATAGCAACCAGACCCTGGCCCTG
GGGGAAACCACCCCTTCACAGCTCCCGGCCCGAGGCACACAAGCCCGAGCTACGGGCCAG
AGCTTCAGCCAGGGCACGACCAGCCGCGCCGGCCACCTGGCGGGGCCCGAGCCCGCGCCG
CCGCCGCCGCCGCCGCCGCCGGGAGCCGTTCGCGCCCAGCCTGGGCAGCGCCTTCCACCTG
CCCGACGCGCCGCCCGCCGCCGCCGCCGCCGCGCTCTACTACTCCAGCTCCACGCTGCCC
GCGCCGCCGCGCGGGGGCTCCCCGCTGGCCGCGCCCCAGGGCGGTTCGCCCACCAAGCTG
CAGCGCGGCGGCTCGGCCCCCGAGGGCGCCACCTACGCCGCGCCGCGCGGCTCCTCGCCC
AAGCAGTCGCCCAGCCGCCTGGCCAAGTCCTACAGCACCAGCTCGCCCATCAACATCGTC
GTGTCCTCGGCCGGCCTGTCCCCGATCCGCGTGACCTCGCCCCCCACCGTGCAGTCCACC
ATCTCCTCCTCGCCCATCCACCAGCTGAGCTCCACCATCGGCACGTACGCCACCCTGTCG
CCCACCAAGCGCCTGGTCCACGCGTCCGAGCAGTACAGCAAGCACTCGCAGGAGCTGTAT
GCCACGGCCACCCTCCAGAGGCCGGGCAGCCTGGCAGCTGGTTCCCGAGCCTCATACAGC
AGCCAGCATGGGCACCTGGGCCCAGAGTTGCGGGCCCTGCAGTCCCCAGAACACCACATA
GATCCCATCTATGAAGACCGCGTCTATCAGAAGCCCCCTATGAGGAGTCTCAGCCAGAGC
CAGGGGGACCCTCTGCCGCCAGCACACACCGGCACCTACCGCACGAGCACAGCCCCATCT
TCCCCTGGTGTCGACTCCGTCCCCTTGCAGCGCACAGGCAGCCAGCACGGCCCACAGAAT
GCCGCCGCGGCCACCTTCCAGAGGGCCAGCTATGCCGCCGGCCCAGCCTCCAATTACGCG
GACCCCTACCGACAGCTGCAGTATTGTCCCTCTGTTGAGTCTCCATACAGCAAATCCGGC
CCTGCTCTCCCGCCTGAAGGCACCTTGGCCAGGTCCCCGTCCATTGATAGCATTCAGAAA
GATCCCAGAGAATTTGGATGGAGAGACCCGGAACTGCCGGAAGTGATTCAGATGTTGCAG
CACCAGTTTCCCTCGGTCCAGTCTAACGCGGCAGCCTACTTGCAACACCTCTGTTTTGGA
GACAACAAAATTAAAGCCGAGATAAGGAGACAAGGAGGCATCCAGCTCCTGGTGGACCTG
TTGGATCATCGGATGACCGAAGTCCACCGTAGTGCCTGTGGAGCTCTGAGAAACCTGGTG
TATGGGAAGGCCAACGATGATAACAAAATTGCCCTGAAAAACTGTGGTGGCATCCCAGCA
CTGGTGAGGTTACTCCGCAAGACGACTGACCTGGAGATCCGGGAGCTGGTCACAGGAGTC
CTTTGGAACCTCTCCTCATGCGATGCACTCAAAATGCCAATCATCCAGGATGCCCTAGCA
GTACTGACCAACGCGGTGATTATCCCCCACTCAGGCTGGGAAAATTCGCCTCTTCAGGAT
GATCGGAAAATACAGCTGCATTCATCACAGGTGCTGCGTAACGCCACCGGGTGCCTAAGG
AATGTTAGTTCGGCCGGAGAGGAGGCCCGCAGAAGGATGAGAGAGTGTGATGGGCTTACG
GATGCCTTGCTGTACGTGATCCAGTCTGCGCTGGGGAGCAGTGAGATCGATAGCAAGACC
GTTGAAAACTGTGTGTGCATTTTAAGGAACCTCTCGTACCGGCTGGCGGCAGAAACGTCT
CAGGGACAGCACATGGGCACGGACGAGCTGGACGGGCTACTCTGTGGCGAGGCCAATGGC
AAGGATGCTGAGAGCTCTGGGTGCTGGGGCAAGAAGAAGAAGAAAAAGAAATCCCAAGAT
CAGTGGTCAGTATATATCCGAGCCGCTGTCCGAAAAGAGAAAGGCCTGCCCATCCTCGTG
GAGCTGCTCCGAATAGACAATGACCGTGTGGTGTGCGCGGTGGCCACTGCGCTGCGGAAC
ATGGCCTTGGACGTCAGAAATAAGGAGCTCATCGGCAAATACGCCATGCGAGACCTAGTC
CACAGGCTTCCAGGAGGGAACAACAGCAACAACACTGCAAGCAAGGCCATGTCGGATGAC
ACAGTGACAGCTGTCTGCTGCACACTGCACGAAGTGATTACCAAGAACATGGAGAACGCC
AAGGCCTTACGGGATGCCGGTGGCATCGAGAAGTTGGTCGGCATCTCCAAAAGCAAAGGA
GATAAACACTCTCCAAAAGTGGTCAAGGCTGCATCTCAGGTCCTCAACAGCATGTGGCAG
TACCGAGATCTGAGGAGTCTCTACAAAAAGGATGGATGGTCACAATACCACTTTGTAGCC
TCGTCTTCAACCATCGAGAGGGACCGGCAAAGGCCCTACTCCTCCTCCCGCACGCCCTCC
ATCTCCCCTGTGCGCGTGTCTCCCAACAACCGCTCAGCAAGTGCCCCAGCTTCACCTCGG
GAAATGATCAGCCTCAAAGAAAGGAAAACAGACTACGAGTGCACCGGCAGCAACGCCACC
TACCACGGAGCTAAAGGCGAACACACTTCCAGGAAAGATGCCATGACAGCTCAAAACACT
GGAATTTCAACTTTGTATAGGAATTCTTATGGTGCGCCCGCTGAAGACATCAAACACAAC
CAGGTTTCAGCACAGCCAGTCCCACAGGAGCCCAGCAGAAAAGATTACGAGACCTACCAG
CCATTTCAGAATTCCACAAGAAATTACGATGAGTCCTTCTTCGAGGACCAGGTCCACCAT
CGCCCTCCCGCCAGCGAGTACACCATGCACCTGGGTCTCAAGTCCACCGGCAACTACGTT
GACTTCTACTCAGCTGCCCGTCCCTACAGTGAACTGAACTATGAAACGAGCCACTACCCG
GCCTCCCCCGACTCCTGGGTGTGA

Fig. 16

SEQ ID No. 16
CTNND2
>ENSG00000169862|5|protein_coding|ENST00000304623|ENSP00000307134
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CCTTCATCAGCCTCAGAGAAGACGAGTTCCCTGAGCCCCGGCTTAAACACCTCCAACGGG
GATGGCTCTGAAACAGAAACCACCTCTGCCATCCTCGCCTCAGTCAAAGAACAGGAATTA
CAGTTTGAAAGGCTGACCCGAGAGCTGGAGGCTGAACGGCAGATCGTAGCCAGCCAGCTG
GAGCGATGCAAGCTCGGATCCGAGACTGGCAGCATGAGCAGCATGAGTTCAGCAGAAGAG
CAGTTTCAGTGGCAGTCACAAGATGGTCAAAAAGATATCGAAGATGAGCTTACAACAGGT
CTCGAGCTGGTGGACTCCTGTATTAGGTCACTACAGGAATCAGGAATACTTGACCCACAG
GATTATTCTACAGGTGAAAGGCCCAGCCTGCTCTCCCAGAGTGCACTTCAGCTCAATTCC
AAACCTGAAGGGTCTTTCCAGTATCCGGCCAGCTACCATAGCAACCAGACCCTGGCCCTG
GGGGAAACCACCCCTTCACAGCTCCCGGCCCGAGGCACACAAGCCCGAGCTACGGGCCAG
AGCTTCAGCCAGGGCACGACCAGCCGCGCCGGCCACCTGGCGGGGCCCGAGCCCGCGCCG
CCGCCGCCGCCGCCGCCGCCGCGGGAGCCGTTCGCGCCCAGCCTGGGCAGCGCCTTCCACCTG
CCCGACGCGCCGCCCGCCGCCGCCGCCGCCGCGCTCTACTACTCCAGCTCCACGCTGCCC
GCGCCGCCGCGCGGGGGCTCCCCGCTGGCCGCGCCCCAGGGCGGTTCGCCCACCAAGCTG
CAGCGCGGCGGCTCGGCCCCCGAGGGCGCCACCTACGCCGCGCCGCGCGGCTCCTCGCCC
AAGCAGTCGCCCAGCCGCCTGGCCAAGTCCTACAGCACCAGCTCGCCCATCAACATCGTC
GTGTCCTCGGCCGGCCTGTCCCCGATCCGCGTGACCTCGCCCCCCACCGTGCAGTCCACC
ATCTCCTCCTCGCCCATCCACCAGCTGAGCTCCACCATCGGCACGTACGCCACCCTGTCG
CCCACCAAGCGCCTGGTCCACGCGTCCGAGCAGTACAGCAAGCACTCGCAGGAGCTGTAT
GCCACGGCCACCCTCCAGAGGCCGGGCAGCCTGGCAGCTGGTTCCCGAGCCTCATACAGC
AGCCAGCATGGGCACCTGGGCCCAGAGTTGCGGGCCCTGCAGTCCCCAGAACACCACATA
GATCCCATCTATGAAGACCGCGTCTATCAGAAGCCCCCTATGAGGAGTCTCAGCCAGAGC
CAGGGGGACCCTCTGCCGCCAGCACACACCGGCACCTACCGCACGAGCACAGCCCCATCT
TCCCCTGGTGTCGACTCCGTCCCCTTGCAGCGCACAGGCAGCCAGCACGGCCCACAGAAT
GCCGCCGCGGCCACCTTCCAGAGGGCCAGCTATGCCGCCGGCCCAGCCTCCAATTACGCG
GACCCCTACCGACAGCTGCAGTATTGTCCCTCTGTTGAGTCTCCATACAGCAAATCCGGC
CCTGCTCTCCCGCCTGAAGGCACCTTGGCCAGGTCCCCGTCCATTGATAGCATTCAGAAA
GATCCCAGAGAATTTGGATGGAGAGACCCGGAACTGCCGGAAGTGATTCAGATGTTGCAG
CACCAGTTTCCCTCGGTCCAGTCTAACGCGGCAGCCTACTTGCAACACCTCTGTTTTGGA
GACAACAAAATTAAAGCCGAGATAAGGAGACAAGGAGGCATCCAGCTCCTGGTGGACCTG
TTGGATCATCGGATGACCGAAGTCCACCGTAGTGCCTGTGGAGCTCTGAGAAACCTGGTG
TATGGGAAGGCCAACGATGATAACAAAATTGCCCTGAAAAACTGTGGTGGCATCCCAGCA
CTGGTGAGGTTACTCCGCAAGACGACTGACCTGGAGATCCGGGAGCTGGTCACAGGAGTC
CTTTGGAACCTCTCCTCATGCGATGCACTCAAAATGCCAATCATCCAGGATGCCCTAGCA
GTACTGACCAACGCGGTGATTATCCCCCACTCAGGCTGGGAAAATTCGCCTCTTCAGGAT
GATCGGAAAATACAGCTGCATTCATCACAGGTGCTGCGTAACGCCACCGGGTGCCTAAGG
AATGTTAGTTCGGCCGGAGAGGAGGCCCGCAGAAGGATGAGAGAGTGTGATGGGCTTACG
GATGCCTTGCTGTACGTGATCCAGTCTGCGCTGGGGAGCAGTGAGATCGATAGCAAGACC
GTTGAAAACTGTGTGTGCATTTTAAGGAACCTCTCGTACCGGCTGGCGGCAGAAACGTCT
CAGGGACAGCACATGGGCACGGACGAGCTGGACGGGCTACTCTGTGGCGAGGCCAATGGC
AAGGATGCTGAGAGCTCTGGGTGCTGGGGCAAGAAGAAGAAGAAAAAGAAATCCCAAGAT
CAGTGGGATGGAGTAGGACCTCTTCCAGACTGTGCTGAACCACCAAAAGGGATCCAGATG
CTGTGGCACCCATCAATAGTCAAACCCTACCTCACACTGCTCTCTGAGTGCTCAAATCCA
GACACGCTGGAAGGGGCGGCAGGCGCCCTGCAGAACTTGGCTGCAGGGAGCTGGAAGTGG
TCAGTATATATCCGAGCCGCTGTCCGAAAAGAGAAAGGCCTGCCCATCCTCGTGGAGCTG
CTCCGAATAGACAATGACCGTGTGGTGTGCGCGGTGGCCACTGCGCTGCGGAACATGGCC
TTGGACGTCAGAAATAAGGAGCTCATCGGCAAATACGCCATGCGAGACCTAGTCCACAGG
CTTCCAGGAGGGAACAACAGCAACAACACTGCAAGCAAGGCCATGTCGGATGACACAGTG
ACAGCTGTCTGCTGCACACTGCACGAAGTGATTACCAAGAACATGGAGAACGCCAAGGCC
TTACGGGATGCCGGTGGCATCGAGAAGTTGGTCGGCATCTCCAAAAGCAAAGGAGATAAA
CACTCTCCAAAAGTGGTCAAGGCTGCATCTCAGGTCCTCAACAGCATGTGGCAGTACCGA
GATCTGAGGAGTCTCTACAAAAAGGATGGATGGTCACAATACCACTTTGTAGCCTCGTCT
TCAACCATCGAGAGGGACCGGCAAAGGCCCTACTCCTCCTCCCGCACGCCCTCCATCTCC
CCTGTGCGCGTGTCTCCCAACAACCGCTCAGCAAGTGCCCCAGCTTCACCTCGGGAAATG
ATCAGCCTCAAAGAAAGGAAAACAGACTACGAGTGCACCGGCAGCAACGCCACCTACCAC
GGAGCTAAAGGCGAACACACTTCCAGGAAAGATGCCATGACAGCTCAAAACACTGGAATT
TCAACTTTGTATAGGAATTCTTATGGTGCGCCCGCTGAAGACATCAAACACAACCAGGTT
TCAGCACAGCCAGTCCCACAGGAGCCCAGCAGAAAAGATTACGAGACCTACCAGCCATTT
CAGAATTCCACAAGAAATTACGATGAGTCCTTCTTCGAGGACCAGGTCCACCATCGCCCT

CCCGCCAGCGAGTACACCATGCACCTGGGTCTCAAGTCCACCGGCAACTACGTTGACTTC
TACTCAGCTGCCCGTCCCTACAGTGAACTGAACTATGAAACGAGCCACTACCCGGCCTCC
CCCGACTCCTGGGTGTGA

Fig. 16 (continued)

Fig. 17

SEQ ID No. 17
NSMCE1
>ENSG00000169189|16|protein_coding|ENST00000358787|ENSP00000351638
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AGCACAAGGAGAATGGGCGTCATGACTGATGTCCACCGGCGCTTCCTCCAGTTGCTGATG
ACCCATGGCGTGCTAGAGGAATGGGACGTGAAGCGCTTGCAGACGCACTGCTACAAGGTC
CATGACCGCAATGCCACCGTAGATAAGTTGGAGGACTTCATCAACAACATTAACAGTGTC
TTGGAGTCCTTGTATATTGAGATAAAGAGAGGAGTCACGGAAGATGATGGGAGACCCATT
TATGCGTTGGTGAATCTTGCTACAACTTCAATTTCCAAAATGGCTACGGATTTTGCAGAG
AATGAACTGGATTTGTTTAGAAAGGCTCTGGAACTGATTATTGACTCAGAAACCTTGCGT
CTTCCACAAACATATTGA

Fig. 18

SEQ ID No. 18
NSMCE1
>ENSG00000169189|16|protein_coding|ENST00000361439|ENSP00000355077
ATGCAGGGCAGCACAAGGAGAATGGGCGTCATGACTGATGTCCACCGGCGCTTCCTCCAG
TTGCTGATGACCCATGGCGTGCTAGAGGAATGGGACGTGAAGCGCTTGCAGACGCACTGC
TACAAGGTCCATGACCGCAATGCCACCGTAGATAAGTTGGAGGACTTCATCAACAACATT
AACAGTGTCTTGGAGTCCTTGTATATTGAGATAAAGAGAGGAGTCACGGAAGATGATGGG
AGACCCATTTATGCGTTGGTGAATCTTGCTACAACTTCAATTTCCAAAATGGCTACGGAT
TTTGCAGAGAATGAACTGGATTTGTTTAGAAAGGCTCTGGAACTGATTATTGACTCAGAA
ACCGGCTTTGCGTCTTCCACAAACATATTGAACCTGGTTGATCAACTTAAAGGCAAGAAG
ATGAGGAAGAAGGAAGCGGAGCAGGTGCTGCAGAAGTTTGTTCAAAACAAGTGGCTGATT
GAGAAGGAAGGGGAGTTCACCCTGCACGGCCGGGCCATCCTGGAGATGGAGCAATACATC
CGGGAGACGTACCCCGACGCGGTGAAGATCTGCAATATCTGTCACAGCCTCCTCATCCAG
GGTCAAAGCTGCGAAACCTGTGGGATCAGGATGCACTTACCCTGCGTGGCCAAGTACTTC
CAGTCGAATGCTGAACCGCGCTGCCCCCACTGCAACGACTACTGGCCCCACGAGATCCCA
AAAGTCTTCGACCCTGAGAAGGAGAGGGAGTCTGGTGTCTTGAAATCGAACAAAAAGTCC
CTGCGGTCCAGGCAGCATTAG

Fig. 19

SEQ ID No. 19
NSMCE1
>ENSG00000169189|16|protein_coding|ENST00000311505|ENSP00000310853
GTCCACCTTGCGACCGTATCCGCTAGCGCGGCCTGGGATGCGCTTGGGCTCCCTGTTCGT
TCCCACATGCAGGGCAGCACAAGGAGAATGGGCGTCATGACTGATGTCCACCGGCGCTTC
CTCCAGTTGCTGATGACCCATGGCGTGCTAGAGGAATGGGACGTGAAGCGCTTGCAGACG
CACTGCTACAAGGTCCATGACCGCAATGCCACCGTAGATAAGTTGGAGGACTTCATCAAC
AACATTAACAGTGTCTTGGAGTCCTTGTATATTGAGATAAAGAGAGGAGTCACGGAAGAT
GATGGGAGACCCATTTATGCGTTGGTGAATCTTGCTACAACTTCAATTTCCAAAATGGCT
ACGGATTTTGCAGAGAATGAACTGGATTTGTTTAGAAAGGCTCTGGAACTGATTATTGAC
TCAGAAACCGGCTTTGCGTCTTCCACAAACATATTGAACCTGGTTGATCAACTTAAAGGC
AAGAAGATGAGGAAGAAGGAAGCGAGGTGCTGCAGAAGTTTGTTCAAAACAAGTGGCTGA

Fig. 20

SEQ ID No. 20
KTELC1
>ENSG00000163389|3|protein_coding|ENST00000295588|ENSP00000295588
ATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTGGCTGCTGTTGTTCCTCCTGCCCTCA
GCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGAAAGTATTTATTGACCAAATTAAC
AGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAACTGCAGCTGCTACCATGGTGTC
ATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAGGAAGATGATGGCAGAGGTA
GTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACAGACTGTACCGGGAAAAT
GACTGCATGTTCCCCTCAAGGTGTAGTGGTGTTGAGCACTTTATTTTGGAAGTGATCGGG
CGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCAGGTTCCTAAATGG
ATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACCATGATATCATG
TATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTATCCTACAGGT
CTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTGGCCATGG
AAAAAGAAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAGATCCT
CTCATTCTTCTGTCTCGGAAAAACCCAAAACTTGTTGATGCAGAATACACCAAAAACCAG
GCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGTG
GATCACTGCAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTT
AAACACCTCTTCCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTC
TTCTATCCACAGCTGAAGCCATGGGTTCACTATATCCCAGTCAAAACAGATCTCTCCAAT
GTCCAAGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAA
AGGGGAAGCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAG
AACCTCTTGAGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTAT
GATCAAATTATTCCCAAAATGTTGAAAACTGAACTATAG

Fig. 21

SEQ ID No. 21
HS6ST1
>ENSG00000136720|2|protein_coding|ENST00000259241|ENSP00000259241
ATGCGGCGGCGGCGCGCCGGCGGCAGGACCATGGTTGAGCGCGCCAGCAAGTTCGTGCTG
GTGGTGGCGGGCTCGGTGTGCTTCATGCTCATCTTGTACCAGTACGCGGGCCCAGGACTG
AGCCTGGGCGCGCCCGGCGGCCGCGCGCCGCCCGACGACCTGGACCTGTTCCCCACACCC
GACCCCCACTACGAGAAGAAGTACTACTTCCCGGTCCGCGAGCTGGAGCGCTCGCTGCGC
TTCGACATGAAGGGCGACGACGTGATCGTCTTCCTGCACATCCAGAAGACGGGCGGCACC
ACCTTCGGCCGCCACCTCGTGCAGAACGTACGCCTCGAGGTGCCGTGCGACTGCCGGCCC
GGCCAGAAGAAGTGCACCTGCTACCGGCCCAACCGCCGCGAGACTTGGCTCTTCTCCCGC
TTCTCCACCGGCTGGAGCTGCGGGCTGCACGCCGACTGGACCGAGCTCACCAACTGCGTG
CCCGGCGTGCTGGACCGCCGCGACTCCGCCGCGCTGCGCACGCCCAGGAAGTTCTACTAC
ATCACCCTGCTACGAGACCCCGTGTCCCGCTACCTGAGCGAGTGGCGGCATGTGCAGAGG
GGTGCCACGTGGAAGACGTCGTTGCATATGTGTGATGGGCGCACGCCCACGCCTGAGGAG
CTGCCGCCCTGCTACGAGGGCACGGACTGGTCGGGCTGCACGCTACAGGAGTTCATGGAC
TGCCCGTACAACCTGGCCAACAACCGCCAGGTGCGCATGCTGGCCGACCTGAGCCTGGTG
GGCTGCTACAACCTGTCCTTCATCCCCGAGGGCAAGCGGGCCCAGCTGCTGCTCGAGAGC
GCCAAGAAGAACCTGCGGGGCATGGCCTTCTTCGGCCTGACCGAGTTCCAGCGCAAGACG
CAGTACCTGTTCGAGCGGACGTTCAACCTCAAGTTCATCCGGCCCTTCATGCAGTACAAT
AGCACGCGGGCGGGCGGCGTGGAGGTGGATGAAGACACCATCCGGCGCATCGAGGAGCTC
AACGACCTGGACATGCAGCTGTACGACTACGCCAAGGACCTCTTCCAGCAGCGCTACCAG
TACAAGCGGCAGCTGGAGCGCAGGGAGCAGCGCCTGAGGAGCCGCGAGGAGCGTCTGCTG
CACCGGGCCAAGGAGGCACTGCCGCGGGAGGATGCCGACGAGCCGGGCCGCGTGCCCACC
GAGGACTACATGAGCCACATCATTGAGAAGTGGTAG

Fig. 22

SEQ ID No. 22
ARMC6
>ENSG00000105676|19|protein_coding|ENST00000379532|ENSP00000368847
ATGACATCCTGCAGATGCTCAGTGACCTCCAGGAGTCTGTGGCCAGCTCTCGCCCCCAGG
AGGTGTCAGCATACCTCACCCGCTTCTGCGCAGTGCAAACAGGACAAGGCCTGCCGCTTC
CTCGCGGCCCAGAAGGGGGCCTACCCCATCATCTTCACTGCCTGGAAGCTGGCCACTGCA
GGTGACCAGGGCCTTCTGCTCCAGTCCCTCAATGCCCTGTCGGTGCTGACTGATGGACAG
CCAGACCTCCTGGATGCCCAGGGCCTGCAGCTCCTAGTGGCCACGCTGACCCAGAATGCT
GATGAGGCTGACCTGACCTGCTCTGGGATCCGCTGTGTGCGTCACGCTTGCCTGAAACAT
GAACAGAATCGGCAAGACCTGGTGAAAGCTGGCGTGCTGCCTCTGCTGACTGGTGCCATC
ACCCATCATGGCCACCACACTGACGTGGTCAGGGAAGCCTGCTGGGCCCTGCGTGTCATG
ACCTTCGATGACGACATCCGTGTGCCCTTTGGCCATGCCCACAACCATGCCAAGATGATT
GTGCAGGAGAACAAAGGCTTGAAGGTGCTCATCGAAGCCACCAAAGCGTTCCTGGATAAC
CCTGGCATCCTGAGCGAGCTCTGTGGAACCCTGTCCCGCCTGGCCATTCGCAACGAGTTC
TGCCAGGAGGTCGTCGACCTCGGGGGCCTGAGCATTCTGGTGTCCCTGCTAGCCGACTGC
AATGACCACCAGATGAGGGACCAGAGCGGCGTTCAGGAGCTCGTGAAGCAAGTGCTGAGC
ACCCTGCGAGCCATCGCAGGCAACGACGACGTGAAAGATGCTATTGTCCGTGCTGGTGGG
ACGGAGTCCATCGTGGCTGCTATGACCCAGCATCTGACCAGCCCCCAGGTGTGTGAGCAG
AGCTGCGCGGCCCTGTGCTTCCTGGCCCTGCGTAAGCCCGACAACAGCCGCATCATCGTG
GAGGGTGGCGGGGCTGTGGCAGCACTGCAGGCCATGAAGGCACACCCGCAGAAGGCCGGC
GTGCAGAAACAGGCTTGCATGCTGATCCGAAACCTGGTGGCCCACAGGCCTTCTCGAAGC
CCATCCTGGACCTGGGGGCTGAGGCACTCATCATGCAGGCCCGATCTGCCCACCGTGACT
GTGAGGACGTGGCCAAGGCCGCCCTGCGGGACCTGGGTTGTCATGTCGAGCTCCGAGAGC
TGTGGACAGGCCAGAGGGGCAACCTGGCGCCATGACCCCAGGCCCAGTCTGGTGACTCTG
GGTGAGTCGTGTGACTCAGGAATGGGGGTAGATCCATGTCCTCCACTGTCCCCCATTAGT
TCTGTCCCCTTCACAATGAGAAGTGTTTTCTGGCAGGCCCTAGGTAAAGGGTCGGGGGAG
GGGGGAGCCTTGTAG

Fig. 23

SEQ ID No. 23
ARMC6
>ENSG00000105676|19|protein_coding|ENST00000392335|ENSP00000376147
ATGGTCTCCAAGCGCATTGCCCAGGAGACCTTTGATGCAGCTGTGCGCGAGAACATCGAG
GAGTTTGCGATGGGGCCAGAGGAGGCAGTGAAAGAGGCCGTGGAGCAGTTTGAATCGCAA
GGGGTTGATCTGAGCAACATTGTAAAGACGGCACCTAAAGTCTCTGCAGACGGATCCCAG
GAGCCCACACATGACATCCTGCAGATGCTCAGTGACCTCCAGGAGTCTGTGGCCAGCTCT
CGCCCCCAGGAGGTGTCAGCATACCTCACCCGCTTCTGCGACCAGTGCAAACAGGACAAG
GCCTGCCGCTTCCTCGCGGCCCAGAAGGGGGCCTACCCCATCATCTTCACTGCCTGGAAG
CTGGCCACTGCAGGTGACCAGGGCCTTCTGCTCCAGTCCCTCAATGCCCTGTCGGTGCTG
ACTGATGGACAGCCAGACCTCCTGGATGCCCAGGGCCTGCAGCTCCTAGTGGCCACGCTG
ACCCAGAATGCTGATGAGGCTGACCTGACCTGCTCTGGGATCCGCTGTGTGCGTCACGCT
TGCCTGAAACATGAACAGAATCGGCAAGACCTGGTGAAAGCTGGCGTGCTGCCTCTGCTG
ACTGGTGCCATCACCCATCATGGCCACCACACTGACGTGGTCAGGGAAGCCTGCTGGGCC
CTGCGTGTCATGACCTTCGATGACGACATCCGTGTGCCCTTTGGCCATGCCCACAACCAT
GCCAAGATGATTGTGCAGGAGAACAAAGGCTTGAAGGTGCTCATCGAAGCCACCAAAGCG
TTCCTGGATAACCCTGGCATCCTGAGCGAGCTCTGTGGAACCCTGTCCCGCCTGGCCATT
CGCAACGAGTTCTGCCAGGAGGTCGTCGACCTCGGGGGCCTGAGCATTCTGGTGTCCCTG
CTAGCCGACTGCAATGACCACCAGATGAGGGACCAGAGCGGCGTTCAGGAGCTCGTGAAG
CAAGTGCTGAGCACCCTGCGAGCCATCGCAGGCAACGACGACGTGAAAGATGCTATTGTC
CGTGCTGGTGGGACGGAGTCCATCGTGGCTGCTATGACCCAGCATCTGACCAGCCCCCAG
GTGTGTGAGCAGAGCTGCGCGGCCCTGTGCTTCCTGGCCCTGCGTAAGCCCGACAACAGC
CGCATCATCGTGGAGGGTGGCGGGGCTGTGGCAGCACTGCAGGCCATGAAGGCACACCCG
CAGAAGGCCGGCGTGCAGAAACAGGCTTGCATGCTGATCCGAAACCTGGTGGCCCACGGC
CAGGCCTTCTCGAAGCCCATCCTGGACCTGGGGGCTGAGGCACTCATCATGCAGGCCCGA
TCTGCCCACCGTGACTGTGAGGACGTGGCCAAGGCCGCCCTGCGGGACCTGGGTTGTCAT
GTCGAGCTCCGAGAGCTGTGGACAGGCCAGAGGGGCAACCTGGCGCCATGA

Fig. 24

SEQ ID No. 24
ARMC6
>ENSG00000105676|19|protein_coding|ENST00000392336|ENSP00000376148
ATGAGTGAACGATGTTGCTCTAGATACAGCTCAGGAGCATCTATCGGCTGCACGCCAACA
TCAACACAGGCGAAGATGGTCTCCAAGCGCATTGCCCAGGAGACCTTTGATGCAGCTGTG
CGCGAGAACATCGAGGAGTTTGCGATGGGGCCAGAGGAGGCAGTGAAAGAGGCCGTGGAG
CAGTTTGAATCGCAAGGGGTTGATCTGAGCAACATTGTAAAGACGGCACCTAAAGTCTCT
GCAGACGGATCCCAGGAGCCCACACATGACATCCTGCAGATGCTCAGTGACCTCCAGGAG
TCTGTGGCCAGCTCTCGCCCCCAGGAGGTGTCAGCATACCTCACCCGCTTCTGCGACCAG
TGCAAACAGGACAAGGCCTGCCGCTTCCTCGCGGCCCAGAAGGGGGCCTACCCCATCATC
TTCACTGCCTGGAAGCTGGCCACTGCAGGTGACCAGGGCCTTCTGCTCCAGTCCCTCAAT
GCCCTGTCGGTGCTGACTGATGGACAGCCAGACCTCCTGGATGCCCAGGGCCTGCAGCTC
CTAGTGGCCACGCTGACCCAGAATGCTGATGAGGCTGACCTGACCTGCTCTGGGATCCGC
TGTGTGCGTCACGCTTGCCTGAAACATGAACAGAATCGGCAAGACCTGGTGAAAGCTGGC
GTGCTGCCTCTGCTGACTGGTGCCATCACCCATCATGGCCACCACACTGACGTGGTCAGG
GAAGCCTGCTGGGCCCTGCGTGTCATGACCTTCGATGACGACATCCGTGTGCCCTTTGGC
CATGCCCACAACCATGCCAAGATGATTGTGCAGGAGAACAAAGGCTTGAAGGTGCTCATC
GAAGCCACCAAAGCGTTCCTGGATAACCCTGGCATCCTGAGCGAGCTCTGTGGAACCCTG
TCCCGCCTGGCCATTCGCAACGAGTTCTGCCAGGAGGTCGTCGACCTCGGGGGCCTGAGC
ATTCTGGTGTCCCTGCTAGCCGACTGCAATGACCACCAGATGAGGGACCAGAGCGGCGTT
CAGGAGCTCGTGAAGCAAGTGCTGAGCACCCTGCGAGCCATCGCAGGCAACGACGACGTG
AAAGATGCTATTGTCCGTGCTGGTGGGACGGAGTCCATCGTGGCTGCTATGACCCAGCAT
CTGACCAGCCCCCAGGTGTGTGAGCAGAGCTGCGCGGCCCTGTGCTTCCTGGCCCTGCGT
AAGCCCGACAACAGCCGCATCATCGTGGAGGGTGGCGGGGCTGTGGCAGCACTGCAGGCC
ATGAAGGCACACCCGCAGAAGGCCGGCGTGCAGAAACAGGCTTGCATGCTGATCCGAAAC
CTGGTGGCCCACGGCCAGGCCTTCTCGAAGCCCATCCTGGACCTGGGGGCTGAGGCACTC
ATCATGCAGGCCCGATCTGCCCACCGTGACTGTGAGGACGTGGCCAAGGCCGCCCTGCGG
GACCTGGGTTGTCATGTCGAGCTCCGAGAGCTGTGGACAGGCCAGAGGGGCAACCTGGCG
CCATGA

Fig. 25

SEQ ID No. 25
ARMC6
>ENSG00000105676|19|protein_coding|ENST00000269932|ENSP00000269932
ATGGTCTCCAAGCGCATTGCCCAGGAGACCTTTGATGCAGCTGTGCGCGAGAACATCGAG
GAGTTTGCGATGGGGCCAGAGGAGGCAGTGAAAGAGGCCGTGGAGCAGTTTGAATCGCAA
GGGGTTGATCTGAGCAACATTGTAAAGACGGCACCTAAAGTCTCTGCAGACGGATCCCAG
GAGCCCACACATGACATCCTGCAGATGCTCAGTGACCTCCAGGAGTCTGTGGCCAGCTCT
CGCCCCCAGGAGGTGTCAGCATACCTCACCCGCTTCTGCGACCAGTGCAAACAGGACAAG
GCCTGCCGCTTCCTCGCGGCCCAGAAGGGGGCCTACCCCATCATCTTCACTGCCTGGAAG
CTGGCCACTGCAGGTGACCAGGGCCTTCTGCTCCAGTCCCTCAATGCCCTGTCGGTGCTG
ACTGATGGACAGCCAGACCTCCTGGATGCCCAGGGCCTGCAGCTCCTAGTGGCCACGCTG
ACCCAGAATGCTGATGAGGCTGACCTGACCTGCTCTGGGATCCGCTGTGTGCGTCACGCT
TGCCTGAAACATGAACAGAATCGGCAAGACCTGGTGAAAGCTGGCGTGCTGCCTCTGCTG
ACTGGTGCCATCACCCATCATGGCCACCACACTGACGTGGTCAGGGAAGCCTGCTGGGCC
CTGCGTGTCATGACCTTCGATGACGACATCCGTGTGCCCTTTGGCCATGCCCACAACCAT
GCCAAGATGATTGTGCAGGAGAACAAAGGCTTGAAGGTGCTCATCGAAGCCACCAAAGCG
TTCCTGGATAACCCTGGCATCCTGAGCGAGCTCTGTGGAACCCTGTCCCGCCTGGCCATT
CGCAACGAGTTCTGCCAGGAGGTCGTCGACCTCGGGGGCCTGAGCATTCTGGTGTCCCTG
CTAGCCGACTGCAATGACCACCAGATGAGGGACCAGAGCGGCGTTCAGGAGCTCGTGAAG
CAAGTGCTGAGCACCCTGCGAGCCATCGCAGGCAACGACGACGTGAAAGATGCTATTGTC
CGTGCTGGTGGGACGGAGTCCATCGTGGCTGCTATGACCCAGCATCTGACCAGCCCCCAG
GTGTGTGAGCAGAGCTGCGCGGCCCTGTGCTTCCTGGCCCTGCGTAAGCCCGACAACAGC
CGCATCATCGTGGAGGGTGGCGGGGCTGTGGCAGCACTGCAGGCCATGAAGGCACACCCG
CAGAAGGCCGGCGTGCAGAAACAGGCTTGCATGCTGATCCGAAACCTGGTGGCCCACGGC
CAGGCCTTCTCGAAGCCCATCCTGGACCTGGGGGCTGAGGCACTCATCATGCAGGCCCGA
TCTGCCCACCGTGACTGTGAGGACGTGGCCAAGGCCGCCCTGCGGGACCTGGGTTGTCAT
GTCGAGCTCCGAGAGCTGTGGACAGGCCAGAGGGGCAACCTGGCGCCATGA

Fig. 26

SEQ ID No. 26
TH1L
>ENSG00000101158|20|protein_coding|ENST00000344018|ENSP00000342300
ATGGCGGGGGCCGTGCCGGGCGCCATCATGGACGAGGACTACTACGGGAGCGCGGCCGAG
TGGGGCGACGAGGCTGACGGCGGCCAGCAGGAGGATGATTCTGGAGAAGGAGAGGATGAT
GCGGAGGTTCAGCAAGAATGCCTGCATAAATTTTCCACCCGGGATTATATCATGGAACCC
TCCATCTTCAACACTCTGAAGAGGTATTTTCAGGCAGGAGGGTCTCCAGAGAATGTTATC
CAGCTCTTATCTGAAAACTACACCGCTGTGGCCCAGACTGTGAACCTGCTGGCCGAGTGG
CTCATTCAGACAGGTGTTGAGCCAGTGCAGGTTCAGGAAACTGTGGAAAATCACTTGAAG
AGTTTGCTGATCAAACATTTTGACCCCCGCAAAGCAGATTCTATTTTTACTGAAGAAGGA
GAGACCCCAGCGTGGCTGGAACAGATGATTGCACATACCACGTGGCGGGACCTTTTTTAT
AAACTGGCTGAAGCCCATCCAGACTGTTTGATGCTGAACTTCACCGTTAAGCTTATTTCT
GACGCAGGGTACCAGGGGGAGATCACCAGTGTGTCCACAGCATGCCAGCAGCTAGAAGTG
TTCTCGAGAGTGCTCCGGACCTCTCTAGCTACAATTTTAGATGGAGGAGAAGAAAACCTT
GAAAAAAATCTCCCTGAGTTTGCCAAGATGGTGTGCCACGGGGAGCACACGTACCTGTTT
GCCCAGGCCATGATGTCCGTGCTGGCCCAGGAGGAGCAGGGGGGCTCCGCTGTGCGCAGG
ATCGCCCAGGAAGTGCAGCGCTTTGCCCAGGAGAAAGGTCATGACGCCAGTCAGATCACA
CTAGCCTTGGGCACAGCTGCCTCCTACCCCAGGGCCTGCCAGGCTCTCGGGGCCATGCTG
TCCAAAGGAGCCCTGAACCCTGCTGACATCACCGTCCTGTTCAAGATGTTCACAAGCATG
GACCCTCCTCCGGTTGAACTTATCCGCGTTCCAGCCTTCCTGGACCTGTTCATGCAGTCA
CTCTTTAAACCAGGGGCTCGGATCAACCAGGACCACAAGCACAAATACATCCACATCTTG
GCGTACGCAGCAAGCGTGGTTGAGACCTGGAAGAAGAACAAGCGAGTGAGCATCAATAAA
GATGAGCTGAAGTCAACGTCAAAAGCTGTCGAAACCGTTCACAATTTGTGTTGCAACGAG
AACAAAGGGGCCTCTGAACTAGTGGCAGAATTGAGCACACTTTATCAGTGTATTAGGTTT
CCAGTGGTAGCAATGGGTGTGCTGAAGTGGGTGGATTGGACTGTATCAGAACCAAGGTAC
TTTCAGCTGCAGACTGACCATACCCCTGTCCACCTGGCGTTGCTGGATGAGATCAGCACC
TGCCACCAGCTCCTGCACCCCCAGGTCCTGCAGCTGCTTGTTAAGCTTTTTGAGACTGAG
CACTCCCAGCTGGACGTGATGGAGCAGCTTGAGTTGAAGAAGACACTGCTGGACAGGATG
GTTCACCTGCTGAGTCGAGGTTATGTACTTCCTGTTGTCAGTTACATCCGAAAGTGTCTG
GAGAAGCTGGACACTGACATTTCACTCATTCGCTATTTTGTCACTGAGGTGCTGGACGTC
ATTGCTCCTCCTTATACCTCTGACTTCGTGCAACTTTTCCTCCCCATCCTGGAGAATGAC
AGCATCGCAGGTACCATCAAAACGGAAGGCGAGCATGACCCTGTGACGGAGTTTATAGCT
CACTGCAAATCTAACTTCATCATGGTGAACTAA

Fig. 27

SEQ ID No. 27
PSME1
>ENSG00000092010|14|protein_coding|ENST00000382708|ENSP00000372155
ATGGCCATGCTCAGGGTCCAGCCCGAGGCCCAAGCCAAGGTGGATGTGTTTCGTGAAGAC
CTCTGTACCAAGACAGAGAACCTGCTCGGGAGCTATTTCCCCAAGAAGATTTCTGAGCTG
GATGCATTTTTAAAGGAGCCAGCTCTCAATGAAGCCAACTTGAGCAATCTGAAGGCCCCA
TTGGACATCCCAGTGCCTGATCCAGTCAAGGAGAAAGAGAAAGAGGAGCGGAAGAAACAG
CAGGAGAAGGAAGACAAGGATGAAAAGAAGAAGGGGGAGGATGAAGACAAAGGTCCTCCC
TGTGGCCCAGTGAACTGCAATGAAAAGATCGTGGTCCTTCTGCAGCGCTTGAAGCCTGAG
ATCAAGGATGTCATTGAGCAGCTCAACCTGGTCACCACCTGGTTGCAGCTGCAGATACCT
CGGATTGAGGATGGTAACAATTTTGGAGTGGCTGTCCAGGAGAAGGTGTTTGAGCTGATG
ACCAGCCTCCACACCAAGCTAGAAGGCTTCCACACTCAAATCTCTAAGTATTTCTCTGAG
CGTGGTGATGCAGTGACTAAAGCAGCCAAGCAGCCCCATGTGGGTGATTATCGGCAGCTG
GTGCACGAGCTGGATGAGGCAGAGTACCGGGACATCCGGCTGATGGTCATGGAGATCCGC
AATGCTTATGTGAGGAGGCAAGGGCAGGGCAGGGGTGGGCAGAGGCAGCTTTCCCAGGCC
ACCCACTCCCTGACCCTGCAGGCTAGGGGTTAA

Fig. 28

SEQ ID No. 28
PSME1
>ENSG00000092010|14|protein_coding|ENST00000206451|ENSP00000206451
ATGGCCATGCTCAGGGTCCAGCCCGAGGCCCAAGCCAAGGTGGATGTGTTTCGTGAAGAC
CTCTGTACCAAGACAGAGAACCTGCTCGGGAGCTATTTCCCCAAGAAGATTTCTGAGCTG
GATGCATTTTTAAAGGAGCCAGCTCTCAATGAAGCCAACTTGAGCAATCTGAAGGCCCCA
TTGGACATCCCAGTGCCTGATCCAGTCAAGGAGAAAGAGAAAGAGGAGCGGAAGAAACAG
CAGGAGAAGGAAGACAAGGATGAAAAGAAGAAGGGGGAGGATGAAGACAAAGGTCCTCCC
TGTGGCCCAGTGAACTGCAATGAAAAGATCGTGGTCCTTCTGCAGCGCTTGAAGCCTGAG
ATCAAGGATGTCATTGAGCAGCTCAACCTGGTCACCACCTGGTTGCAGCTGCAGATACCT
CGGATTGAGGATGGTAACAATTTTGGAGTGGCTGTCCAGGAGAAGGTGTTTGAGCTGATG
ACCAGCCTCCACACCAAGCTAGAAGGCTTCCACACTCAAATCTCTAAGTATTTCTCTGAG
CGTGGTGATGCAGTGACTAAAGCAGCCAAGCAGCCCCATGTGGGTGATTATCGGCAGCTG
GTGCACGAGCTGGATGAGGCAGAGTACCGGGACATCCGGCTGATGGTCATGGAGATCCGC
AATGCTTATGCTGTGTTATATGACATCATCCTGAAGAACTTCGAGAAGCTCAAGAAGCCC
AGGGGAGAAACAAAGGGAATGATCTATTGA

Fig. 29

SEQ ID No. 29
GPC1
>ENSG00000063660|2|protein_coding|ENST00000264039|ENSP00000264039
ATGGAGCTCCGGGCCCGAGGCTGGTGGCTGCTATGTGCGGCCGCAGCGCTGGTCGCCTGC
GCCCGCGGGGACCCGGCCAGCAAGAGCCGGAGCTGCGGCGAGGTCCGCCAGATCTACGGA
GCCAAGGGCTTCAGCCTGAGCGACGTGCCCCAGGCGGAGATCTCGGGTGAGCACCTGCGG
ATCTGTCCCCAGGGCTACACCTGCTGCACCAGCGAGATGGAGGAGAACCTGGCCAACCGC
AGCCATGCCGAGCTGGAGACCGCGCTCCGGGACAGCAGCCGCGTCCTGCAGGCCATGCTT
GCCACCCAGCTGCGCAGCTTCGATGACCACTTCCAGCACCTGCTGAACGACTCGGAGCGG
ACGCTGCAGGCCACCTTCCCCGGCGCCTTCGGAGAGCTGTACACGCAGAACGCGAGGGCC
TTCCGGGACCTGTACTCAGAGCTGCGCCTGTACTACCGCGGTGCCAACCTGCACCTGGAG
GAGACGCTGGCCGAGTTCTGGGCCCGCCTGCTCGAGCGCCTCTTCAAGCAGCTGCACCCC
CAGCTGCTGCTGCCTGATGACTACCTGGACTGCCTGGGCAAGCAGGCCGAGGCGCTGCGG
CCCTTCGGGGAGGCCCCGAGAGAGCTGCGCCTGCGGGCCACCCGTGCCTTCGTGGCTGCT
CGCTCCTTTGTGCAGGGCCTGGGCGTGGCCAGCGACGTGGTCCGGAAAGTGGCTCAGGTC
CCCCTGGGCCCGGAGTGCTCGAGAGCTGTCATGAAGCTGGTCTACTGTGCTCACTGCCTG
GGAGTCCCCGGCGCCAGGCCCTGCCCTGACTATTGCCGAAATGTGCTCAAGGGCTGCCTT
GCCAACCAGGCCGACCTGGACGCCGAGTGGAGGAACCTCCTGGACTCCATGGTGCTCATC
ACCGACAAGTTCTGGGGTACATCGGGTGTGGAGAGTGTCATCGGCAGCGTGCACACGTGG
CTGGCGGAGGCCATCAACGCCCTCCAGGACAACAGGGACACGCTCACGGCCAAGGTCATC
CAGGGCTGCGGGAACCCCAAGGTCAACCCCCAGGGCCCCGGGCCTGAGGAGAAGCGGCGC
CGGGGCAAGCTGGCCCCGCGGGAGAGGCCACCTTCAGGCACGCTGGAGAAGCTGGTCTCC
GAAGCCAAGGCCCAGCTCCGCGACGTCCAGGACTTCTGGATCAGCCTCCCAGGGACACTG
TGCAGTGAGAAGATGGCCCTGAGCACTGCCAGTGATGACCGCTGCTGGAACGGGATGGCC
AGAGGCCGGTACCTCCCCGAGGTCATGGGTGACGGCCTGGCCAACCAGATCAACAACCCC
GAGGTGGAGGTGGACATCACCAAGCCGGACATGACCATCCGGCAGCAGATCATGCAGCTG
AAGATCATGACCAACCGGCTGCGCAGCGCCTACAACGGCAACGACGTGGACTTCCAGGAC
GCCAGTGACGACGGCAGCGGCTCGGGCAGCGGTGATGGCTGTCTGGATGACCTCTGCAGC
CGGAAGGTCAGCAGGAAGAGCTCCAGCTCCCGGACGCCCTTGACCCATGCCCTCCCAGGC
CTGTCAGAGCAGGAAGGACAGAAGACCTCGGCTGCCAGCTGCCCCCAGCCCCCGACCTTC
CTCCTGCCCCTCCTCCTCTTCCTGGCCCTTACAGTAGCCAGGCCCCGGTGGCGGTAA

Fig. 30

SEQ ID No. 30
EDC4
>ENSG00000038358|16|protein_coding|ENST00000041337|ENSP00000041337
ATGGCCTCCTGCGCGAGCATCGACATCGAGGACGCCACGCAGCACCTGCGGGACATCCTC
AAGCTGGACCGGCCCGCGGGCGGCCCCAGTGCAGAGAGCCCACGGCCATCCAGTGCCTAC
AATGGGGACCTCAATGGACTTCTGGTCCCAGACCCGCTCTGCTCAGGTGATAGTACCTCA
GCAAACAAGACTGGTCTTCGGACCATGCCACCCATTAACCTGCAAGAGAAGCAGGTCATC
TGTCTCTCAGGAGATGATAGCTCCACCTGCATTGGGATTTTGGCCAAGGAGGTGGAGATT
GTGGCTAGCAGTGACTCTAGCATTTCAAGCAAGGCCCGGGGAAGCAACAAGGTGAAAATT
CAGCCTGTCGCCAAGTATGACTGGGAACAGAAGTACTACTATGGCAACCTGATTGCTGTG
TCTAACTCCTTCTTGGCCTATGCCATTCGGGCTGCCAACAATGGCTCTGCCATGGTGCGG
GTGATCAGCGTCAGCACTTCGGAGCGGACCTTGCTCAAGGGCTTCACAGGCAGTGTGGCT
GATCTGGCTTTCGCGCACCTCAACTCTCCACAGCTGGCCTGCCTGGATGAGGCAGGCAAC
CTGTTCGTGTGGCGCTTGGCTCTGGTTAATGGCAAAATTCAAGAAGAGATCTTGGTCCAT
ATTCGGCAGCCAGAGGGCACGCCACTGAACCACTTTCGCAGGATCATCTGGTGCCCCTTC
ATCCCTGAGGAGAGCGAAGACTGCTGTGAGGAGAGCAGCCCAACAGTGGCCCTGCTGCAT
GAAGACCGGGCTGAGGTGTGGGACCTGGACATGCTCCGCTCCAGCCACAGTACCTGGCCT
GTGGATGTTAGCCAGATCAAGCAGGGCTTCATTGTGGTAAAAGGTCATAGCACGTGCCTC
AGTGAAGGAGCCCTCTCTCCTGATGGGACTGTGCTGGCTACTGCGAGCCACGATGGCTAT
GTCAAGTTCTGGCAGATCTACATTGAGGGGCAAGATGAGCCAAGGTGTCTGCACGAGTGG
AAACCTCATGATGGGCGGCCCCTCTCCTGCCTCCTGTTCTGTGACAACCATAAGAAACAA
GACCCTGATGTCCCTTTCTGGAGGTTCCTTATTACTGGTGCTGACCAGAACCGAGAGTTA
AAGATGTGGTGTACAGTATCCTGGACCTGCCTGCAGACTATTCGCTTCTCCCCAGATATC
TTCAGCTCAGTGAGTGTGCCCCCTAGCCTCAAGGTTTGCTTGGACCTCTCAGCAGAATAC
CTGATTCTCAGCGATGTGCAACGGAAGGTCCTCTATGTGATGGAGCTGCTGCAAAACCAG
GAGGAGGGCCACGCCTGCTTCAGCTCCATCTCGGAGTTCCTGCTCACCCACCCTGTGCTG
AGCTTTGGTATCCAGGTTGTGAGTCGCTGCCGGCTACGGCACACTGAGGTGCTGCCTGCC
GAAGAGGAAAATGACAGCCTGGGTGCTGATGGTACCCATGGAGCCGGTGCCATGGAGTCT
GCGGCCGGTGTGCTCATCAAGCTCTTTTGTGTGCATACTAAGGCACTGCAAGATGTGCAG
ATCCGCTTCCAGCCACAGCTGAACCCTGATGTGGTGGCCCCACTGCCCACCCACACTGCC
CACGAGGACTTCACATTTGGAGAGTCTCGGCCCGAACTGGGCTCTGAGGGCCTGGGGTCA
GCCGCTCACGGCTCCCAGCCTGACCTCCGACGAATCGTGGAGCTGCCTGCACCTGCCGAC
TTCCTCAGTCTGAGCAGTGAGACCAAGCCCAAGTTGATGACACCTGACGCCTTCATGACA
CCTAGCGCCTCCTTGCAGCAGATCACTGCCTCTCCCAGCAGCAGCAGCAGCGGTAGCAGC
AGCAGCAGCAGCAGTAGCAGCAGCTCCCTTACAGCTGTGTCTGCCATGAGCAGCACCTCA
GCTGTGGACCCCTCCTTGACCAGGCCACCTGAGGAGCTGACCTTGAGCCCCAAGCTGCAG
CTGGATGGCAGCCTGACAATGAGCAGCAGTGGCAGCCTTCAGGCAAGCCCGCGTGGCCTC
CTGCCTGGCCTGCTCCCAGCCCCAGCTGACAAACTGACTCCCAAGGGGCCGGGCCAGGTG
CCTACTGCCACCTCTGCACTGTCCCTGGAGCTGCAGGAAGTGGAGCCCCTGGGGCTACCC
CAAGCCTCCCCTAGCCGCACTCGTTCCCCTGATGTCATCTCCTCAGCTTCCACTGCCCTG
TCCCAGGACATCCCTGAGATTGCATCTGAGGCCCTGTCCCGTGGTTTTGGCTCCTCTGCA
CCAGAGGGCCTTGAGCCAGACAGTATGGCTTCAGCCGCCTCGGCACTGCACCTGCTGTCC
CCACGGCCCCGGCCAGGGCCCGAGCTCGGCCCCCAGCTCGGGCTTGATGGAGGCCCTGGG
GATGGAGATCGGCATAATACCCCCTCCCTCCTGGAGGCAGCCTTGACCCAGGAGGCCTCG
ACTCCTGACAGTCAGGTTTGGCCCACAGCACCTGACATTACTCGTGAGACCTGCAGCACC
CTGGCAGAAAGCCCCAGGAATGGCCTTCAGGAAAAGCACAAGAGCCTGGCCTTCCACCGA
CCACCATATCACCTGCTGCAGCAACGTGACAGCCAGGATGCCAGTGCTGAGCAAAGTGAC
CATGATGATGAGGTGGCCAGCCTTGCCTCTGCTTCAGGAGGCTTTGGCACCAAAGTTCCT
GCTCCACGGCTGCCTGCCAAGGACTGGAAGACCAAGGGATCCCCTCGAACCTCACCCAAG
CTCAAGAGGAAAAGCAAGAAGGATGATGGGGATGCAGCCATGGGATCCCGGCTCACAGAG
CACCAGGTGGCAGAGCCCCCTGAGGACTGGCCAGCACTAATTTGGCAACAGCAGAGAGAG
CTGGCAGAGCTGCGGCACAGCCAGGAAGAGCTGCTGCAGCGTCTGTGTACCCAACTCGAA
GGCCTGCAGAGCACAGTCACAGGCCACGTAGAACGTGCCCTTGAGACTCGGCACGAGCAG
GAACAGCGGCGGCTGGAGCGAGCACTGGCTGAGGGGCAGCAGCGGGGAGGGCAGCTGCAG
GAGCAGCTGACACAACAGTTGTCCCAAGCACTGTCGTCAGCTGTAGCTGGGCGGCTAGAG
CGCAGCATACGGGATGAGATCAAGAAGACAGTCCCTCCATGTGTCTCAAGGAGTCTGGAG
CCTATGGCAGGCCAACTGAGCAACTCAGTGGCTACCAAGCTCACAGCTGTGGAGGGCAGC
ATGAAAGAGAACATCTCCAAGCTGCTCAAGTCCAAGAACTTGACTGATGCCATCGCCCGA
GCAGCTGCAGACACATTACAAGGGCCGATGCAGGCTGCCTACCGGGAAGCCTTCCAGAGT
GTGGTGCTGCCGGCCTTTGAGAAGAGCTGCCAGGCCATGTTCCAGCAAATCAATGATAGC
TTCCGGCTGGGGACACAGGAATACTTGCAGCAGCTAGAAAGCCACATGAAGAGCCGGAAG
GCACGGGAACAGGAGGCCAGGGAGCCTGTGCTAGCCCAGCTGCGGGGCCTGGTCAGCACA

CTGCAGAGTGCCACTGAGCAGATGCCACCGTGGCCGGCAGTGTTCGTGCTGAGGTGCAGC
ACCAGCTGCATGTGGCTGTGGGCAGCCTGCAGGAGTCCATTTTAG

Fig. 30 (continued)

Fig. 31

SEQ ID No. 31
EDC4
>ENSG00000038358|16|protein_coding|ENST00000358933|ENSP00000351811
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AAGCTGGACCGGCCCCGCGGGCGGCCCCAGTGCAGAGAGCCCACGGCCATCCAGTGCCTAC
AATGGGGACCTCAATGGACTTCTGGTCCCAGACCCGCTCTGCTCAGGTGATAGTACCTCA
GCAAACAAGACTGGTCTTCGGACCATGCCACCCATTAACCTGCAAGAGAAGCAGGTCATC
TGTCTCTCAGGAGATGATAGCTCCACCTGCATTGGGATTTTGGCCAAGGAGGTGGAGATT
GTGGCTAGCAGTGACTCTAGCATTTCAAGCAAGGCCCGGGGAAGCAACAAGGTGAAAATT
CAGCCTGTCGCCAAGTATGACTGGGAACAGAAGTACTACTATGGCAACCTGATTGCTGTG
TCTAACTCCTTCTTGGCCTATGCCATTCGGGCTGCCAACAATGGCTCTGCCATGGTGCGG
GTGATCAGCGTCAGCACTTCGGAGCGGACCTTGCTCAAGGGCTTCACAGGCAGTGTGGCT
GATCTGGCTTTCGCGCACCTCAACTCTCCACAGCTGGCCTGCCTGGATGAGGCAGGCAAC
CTGTTCGTGTGGCGCTTGGCTCTGGTTAATGGCAAAATTCAAGAAGAGATCTTGGTCCAT
ATTCGGCAGCCAGAGGGCACGCCACTGAACCACTTTCGCAGGATCATCTGGTGCCCCTTC
ATCCCTGAGGAGAGCGAAGACTGCTGTGAGGAGAGCAGCCCAACAGTGGCCCTGCTGCAT
GAAGACCGGGCTGAGGTGTGGGACCTGGACATGCTCCGCTCCAGCCACAGTACCTGGCCT
GTGGATGTTAGCCAGATCAAGCAGGGCTTCATTGTGGTAAAAGGTCATAGCACGTGCCTC
AGTGAAGGAGCCCTCTCTCCTGATGGGACTGTGCTGGCTACTGCGAGCCACGATGGCTAT
GTCAAGTTCTGGCAGATCTACATTGAGGGGCAAGATGAGCCAAGGTGTCTGCACGAGTGG
AAACCTCATGATGGGCGGCCCCTCTCCTGCCTCCTGTTCTGTGACAACCATAAGAAACAA
GACCCTGATGTCCCTTTCTGGAGGTTCCTTATTACTGGTGCTGACCAGAACCGAGAGTTA
AAGATGTGGTGTACAGTATCCTGGACCTGCCTGCAGACTATTCGCTTCTCCCCAGATATC
TTCAGCTCAGTGAGTGTGCCCCCTAGCCTCAAGGTTTGCTTGGACCTCTCAGCAGAATAC
CTGATTCTCAGCGATGTGCAACGGAAGGTCCTCTATGTGATGGAGCTGCTGCAAAACCAG
GAGGAGGGCCACGCCTGCTTCAGCTCCATCTCGGAGTTCCTGCTCACCCACCCTGTGCTG
AGCTTTGGTATCCAGGTTGTGAGTCGCTGCCGGCTACGGCACACTGAGGTGCTGCCTGCC
GAAGAGGAAAATGACAGCCTGGGTGCTGATGGTACCCATGGAGCCGGTGCCATGGAGTCT
GCGGCCGGTGTGCTCATCAAGCTCTTTTGTGTGCATACTAAGGCACTGCAAGATGTGCAG
ATCCGCTTCCAGCCACAGCTGAACCCTGATGTGGTGGCCCCACTGCCCACCCACACTGCC
CACGAGGACTTCACATTTGGAGAGTCTCGGCCCGAACTGGGCTCTGAGGGCCTGGGGTCA
GCCGCTCACGGCTCCCAGCCTGACCTCCGACGAATCGTGGAGCTGCCTGCACCTGCCGAC
TTCCTCAGTCTGAGCAGTGAGACCAAGCCCAAGTTGATGACACCTGACGCCTTCATGACA
CCTAGCGCCTCCTTGCAGCAGATCACTGCCTCTCCCAGCAGCAGCAGCAGCGGTAGCAGC
AGCAGCAGCAGCAGTAGCAGCAGCTCCCTTACAGCTGTGTCTGCCATGAGCAGCACCTCA
GCTGTGGACCCCTCCTTGACCAGGCCACCTGAGGAGCTGACCTTGAGCCCCAAGCTGCAG
CTGGATGGCAGCCTGACAATGAGCAGCAGTGGCAGCCTTCAGGCAAGCCCGCGTGGCCTC
CTGCCTGGCCTGCTCCCAGCCCCAGCTGACAAACTGACTCCCAAGGGGCCGGGCCAGGTG
CCTACTGCCACCTCTGCACTGTCCCTGGAGCTGCAGGAAGTGGAGCCCCTGGGGCTACCC
CAAGCCTCCCCTAGCCGCACTCGTTCCCCTGATGTCATCTCCTCAGCTTCCACTGCCCTG
TCCCAGGACATCCCTGAGATTGCATCTGAGGCCCTGTCCCGTGGTTTTGGCTCCTCTGCA
CCAGAGGGCCTTGAGCCAGACAGTATGGCTTCAGCCGCCTCGGCACTGCACCTGCTGTCC
CCACGGCCCCGGCCAGGGCCCGAGCTCGGCCCCCAGCTCGGGCTTGATGGAGGCCCTGGG
GATGGAGATCGGCATAATACCCCCTCCCTCCTGGAGGCAGCCTTGACCCAGGAGGCCTCG
ACTCCTGACAGTCAGGTTTGGCCCACAGCACCTGACATTACTCGTGAGACCTGCAGCACC
CTGGCAGAAAGCCCCAGGAATGGCCTTCAGGAAAAGCACAAGAGCCTGGCCTTCCACCGA
CCACCATATCACCTGCTGCAGCAACGTGACAGCCAGGATGCCAGTGCTGAGCAAAGTGAC
CATGATGATGAGGTGGCCAGCCTTGCCTCTGCTTCAGGAGGCTTTGGCACCAAAGTTCCT
GCTCCACGGCTGCCTGCCAAGGACTGGAAGACCAAGGGATCCCCTCGAACCTCACCCAAG
CTCAAGAGGAAAAGCAAGAAGGATGATGGGGATGCAGCCATGGGATCCCGGCTCACAGAG
CACCAGGTGGCAGAGCCCCCTGAGGACTGGCCAGCACTAATTTGGCAACAGCAGAGAGAG
CTGGCAGAGCTGCGGCACAGCCAGGAAGAGCTGCTGCAGCGTCTGTGTACCCAACTCGAA
GGCCTGCAGAGCACAGTCACAGGCCACGTAGAACGTGCCCTTGAGACTCGGCACGAGCAG
GAACAGCGGCGGCTGGAGCGAGCACTGGCTGAGGGGCAGCAGCGGGGAGGGCAGCTGCAG
GAGCAGCTGACACAACAGTTGTCCCAAGCACTGTCGTCAGCTGTAGCTGGGCGGCTAGAG
CGCAGCATACGGGATGAGATCAAGAAGACAGTCCCTCCATGTGTCTCAAGGAGTCTGGAG
CCTATGGCAGGCCAACTGAGCAACTCAGTGGCTACCAAGCTCACAGCTGTGGAGGGCAGC
ATGAAAGAGAACATCTCCAAGCTGCTCAAGTCCAAGAACTTGACTGATGCCATCGCCCGA
GCAGCTGCAGACACATTACAAGGGCCGATGCAGGCTGCCTACCGGGAAGCCTTCCAGAGT
GTGGTGCTGCCGGCCTTTGAGAAGAGCTGCCAGGCCATGTTCCAGCAAATCAATGATAGC
TTCCGGCTGGGGACACAGGAATACTTGCAGCAGCTAGAAAGCCACATGAAGAGCCGGAAG
GCACGGGAACAGGAGGCCAGGGAGCCTGTGCTAGCCCAGCTGCGGGGCCTGGTCAGCACA

CTGCAGAGTGCCACTGAGCAGATGGCAGCCACCGTGGCCGGCAGTGTTCGTGCTGAGGTG
CAGCACCAGCTGCATGTGGCTGTGGGCAGCCTGCAGGAGTCCATTTTAGCACAGGTACAG
CGCATCGTTAAGGGTGAGGTGAGTGTGGCGCTCAAGGAGCAGCAGGCCGCCGTCACCTCC
AGCATCATGCAGGCCATGCGCTCAGCTGCTGGCACACCTGTCCCCTCTGCCCACCTTGAC
TGCCAGGCCCAGCAAGCCCATATCCTGCAGCTGCTGCAGCAGGGCCACCTCAATCAGGCC
TTCCAGCAGGCGCTGACAGCTGCTGACCTGAACCTGGTGCTGTATGTGTGTGAAACTGTG
GACCCAGCCCAGGTTTTTGGGCAGCCACCCTGCCCGCTCTCCCAGCCTGTGCTCCTTTCC
CTCATCCAGCAGCTGGCATCTGACCTTGGCACTCGAACTGACCTCAAGCTCAGCTACCTG
GAAGAGGCCGTGATGCACCTGGACCACAGTGACCCCATCACTCGGGACCACATGGGCTCC
GTTATGGCCCAGGTGCGCCAAAAGCTTTTTCAGTTCCTGCAGGCTGAGCCACACAACTCA
CTTGGCAAAGCAGCTCGGCGTCTCAGCCTCATGCTGCATGGCCTCGTGACCCCCAGCCTC
CCTTAG

Fig. 31 (continued)

Fig. 32

SEQ ID No. 32
PRC1
>ENSG00000198901|15|protein_coding|ENST00000361188|ENSP00000354679
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GTAGGTCTGGACCTGGACTCACGGCTGCTTGGAGCGTCCGCCATGAGGAGAAGTGAGGTG
CTGGCGGAGGAGTCCATAGTATGTCTGCAGAAAGCCCTAAATCACCTTCGGGAAATATGG
GAGCTAATTGGGATTCCAGAGGACCAGCGGTTACAAAGAACTGAGGTGGTAAAGAAGCAT
ATCAAGGAACTCCTGGATATGATGATTGCTGAAGAGGAAAGCCTGAAGGAAAGACTCATC
AAAAGCATATCCGTCTGTCAGAAAGAGCTGAACACTCTGTGCAGCGAGTTACATGTTGAG
CCATTTCAGGAAGAAGGAGAGACGACCATCTTGCAACTAGAAAAAGATTTGCGCACCCAA
GTGGAATTGATGCGAAAACAGAAAAAGGAGAGAAAACAGGAACTGAAGCTACTTCAAGAG
CAAGATCAAGAACTGTGCGAAATTCTTTGTATGCCCCACTATGATATTGACAGTGCCTCA
GTGCCCAGCTTAGAAGAGCTGAACCAGTTCAGGCAACATGTGACAACTTTGAGGGAAACA
AAGGCTTCTAGGCGTGAGGAGTTTGTCAGTATAAAGAGACAGATCATACTGTGTATGGAA
GCATTAGACCACACCCCAGACACAAGCTTTGAAAGAGATGTGGTGTGTGAAGACGAAGAT
GCCTTTTGTTTGTCTTTGGAGAATATTGCAACACTACAAAAGTTGCTACGGCAGCTGGAA
ATGCAGAAATCACAAAATGAAGCAGTGTGTGAGGGGCTGCGTACTCAAATCCGAGAGCTC
TGGGACAGGTTGCAAATACCTGAAGAAGAAAGAGAAGCTGTGGCCACCATTATGTCTGGG
TCAAAGGCCAAGGTCCGGAAAGCGCTGCAATTAGAAGTGGATCGGTTGGAAGAACTGAAA
ATGCAAAACATGAAGAAAGTGATTGAGGCAATTCGAGTGGAGCTGGTTCAGTACTGGGAC
CAGTGCTTTTATAGCCAGGAGCAGAGACAAGCTTTTGCCCCTTTCTGTGCTGAGGACTAC
ACAGAAAGTCTGCTCCAGCTCCACGATGCTGAGATTGTGCGGTTAAAAAACTACTATGAA
GTTCACAAGGAACTCTTTGAAGGTGTCCAGAAGTGGGAAGAAACCTGGAGGCTTTTCTTA
GAGTTTGAGAGAAAAGCTTCAGATCCAAATCGATTTACAAACCGAGGAGGAAATCTTCTA
AAAGAAGAAAAACAACGAGCCAAGCTCCAGAAAATGCTGCCCAAGCTGGAAGAAGAGTTG
AAGGCACGAATTGAATTGTGGGAACAGGAACATTCAAAGGCATTTATGGTGAATGGGCAG
AAATTCATGGAGTATGTGGCAGAACAATGGGAGATGCATCGATTGGAGAAAGAGAGAGCC
AAGCAGGAAAGACAACTGAAGAACAAAAAACAGACAGAGACAGAGATGCTGTATGGCAGC
GCTCCTCGAACACCTAGCAAGCGGCGAGGACTGGCTCCCAATACACCGGGCAAAGCACGT
AAGCTGAACACTACCACCATGTCCAATGCTACGGCCAATAGTAGCATTCGGCCTATCTTT
GGAGGGACAGTCTACCACTCCCCCGTGTCTCGACTTCCTCCTTCTGGCAGCAAGCCAGTC
GCTGCTTCCACCTGTTCAGGGAAGAAAACACCCCGTACTGGCAGGCATGGAGCCAACAAG
GAGAACCTGGAGCTCAACGGCAGCATCCTGAGTGGTGGGTACCCTGGCTCGGCCCCCCTC
CAGCGCAACTTCAGCATTAATTCTGTTGCCAGCACCTATTCTGAGTTTGCGCGAGAACTT
TCAAAGGCTTCCAAATCTGATGCTACTTCTGGAATCCTCAATTCAACCAACATCCAGTCC
TGA

Fig. 33

SEQ ID No. 33
PRC1
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GCTACGCGGAGTGACATCGCCGGTGTTTGCGGGTGGTTGTTGCTCTCGGGGCCGTGTGGA
GTAGGTCTGGACCTGGACTCACGGCTGCTTGGAGCGTCCGCCATGAGGAGAAGTGAGGTG
CTGGCGGAGGAGTCCATAGTATGTCTGCAGAAAGCCCTAAATCACCTTCGGGAAATATGG
GAGCTAATTGGGATTCCAGAGGACCAGCGGTTACAAAGAACTGAGGTGGTAAAGAAGCAT
ATCAAGGAACTCCTGGATATGATGATTGCTGAAGAGGAAAGCCTGAAGGAAAGACTCATC
AAAAGCATATCCGTCTGTCAGAAAGAGCTGAACACTCTGTGCAGCGAGTTACATGTTGAG
CCATTTCAGGAAGAAGGAGAGACGACCATCTTGCAACTAGAAAAAGATTTGCGCACCCAA
GTGGAATTGATGCGAAAACAGAAAAAGGAGAGAAAACAGGAACTGAAGCTACTTCAAGAG
CAAGATCAAGAACTGTGCGAAATTCTTTGTATGCCCCACTATGATATTGACAGTGCCTCA
GTGCCCAGCTTAGAAGAGCTGAACCAGTTCAGGCAACATGTGACAACTTTGAGGGAAACA
AAGGCTTCTAGGCGTGAGGAGTTTGTCAGTATAAAGAGACAGATCATACTGTGTATGGAA
GCATTAGACCACACCCCAGACACAAGCTTTGAAAGAGATGTGGTGTGTGAAGACGAAGAT
GCCTTTTGTTTGTCTTTGGAGAATATTGCAACACTACAAAAGTTGCTACGGCAGCTGGAA
ATGCAGAAATCACAAAATGAAGCAGTGTGTGAGGGGCTGCGTACTCAAATCCGAGAGCTC
TGGGACAGGTTGCAAATACCTGAAGAAGAAAGAGAAGCTGTGGCCACCATTATGTCTGGG
TCAAAGGCCAAGGTCCGGAAAGCGCTGCAATTAGAAGTGGATCGGTTGGAAGAACTGAAA
ATGCAAAACATGAAGAAAGTGATTGAGGCAATTCGAGTGGAGCTGGTTCAGTACTGGGAC
CAGTGCTTTTATAGCCAGGAGCAGAGACAAGCTTTTGCCCCTTTCTGTGCTGAGGACTAC
ACAGAAAGTCTGCTCCAGCTCCACGATGCTGAGATTGTGCGGTTAAAAAACTACTATGAA
GTTCACAAGGAACTCTTTGAAGGTGTCCAGAAGTGGGAAGAAACCTGGAGGCTTTTCTTA
GAGTTTGAGAGAAAAGCTTCAGATCCAAATCGATTTACAAACCGAGGAGGAAATCTTCTA
AAAGAAGAAAAACAACGAGCCAAGCTCCAGAAAATGCTGCCCAAGCTGGAAGAAGAGTTG
AAGGCACGAATTGAATTGTGGGAACAGGAACATTCAAAGGCATTTATGGTGAATGGGCAG
AAATTCATGGAGTATGTGGCAGAACAATGGGAGATGCATCGATTGGAGAAAGAGAGAGCC
AAGCAGGAAAGACAACTGAAGAACAAAAAACAGACAGAGACAGAGATGCTGTATGGCAGC
GCTCCTCGAACACCTAGCAAGCGGCGAGGACTGGCTCCCAATACACCGGGCAAAGCACGT
AAGCTGAACACTACCACCATGTCCAATGCTACGGCCAATAGTAGCATTCGGCCTATCTTT
GGAGGGACAGTCTACCACTCCCCCGTGTCTCGACTTCCTCCTTCTGGCAGCAAGCCAGTC
GCTGCTTCCACCTGTTCAGGGAAGAAAACACCCCGTACTGGCAGGCATGGAGCCAACAAG
GAGAACCTGGAGCTCAACGGCAGCATCCTGAGTGGTGGGTACCCTGGCTCGGCCCCCCTC
CAGCGCAACTTCAGCATTAATTCTGTTGCCAGCACCTATTCTGAGTTTGCGAAGGATCCG
TCCCTCTCTGACAGTTCCACTGTTGGGCTTCAGCGAGAACTTTCAAAGGCTTCCAAATCT
GATGCTACTTCTGGAATCCTCAATTCAACCAACATCCAGTCCTGA

Fig. 34

SEQ ID No. 34
PRC1
>ENSG00000198901|15|protein_coding|ENST00000361919|ENSP00000354618
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GAGGTGGTAAAGAAGCATATCAAGGAACTCCTGGATATGATGATTGCTGAAGAGGAAAGC
CTGAAGGAAAGACTCATCAAAAGCATATCCGTCTGTCAGAAAGAGCTGAACACTCTGTGC
AGCGAGTTACATGTTGAGCCATTTCAGGAAGAAGGAGAGACGACCATCTTGCAACTAGAA
AAAGATTTGCGCACCCAAGTGGAATTGATGCGAAAACAGAAAAAGGAGAGAAAACAGGAA
CTGAAGCTACTTCAAGAGCAAGATCAAGAACTGTGCGAAATTCTTTGTATGCCCCACTAT
GATATTGACAGTGCCTCAGTGCCCAGCTTAGAAGAGCTGAACCAGTTCAGGCAACATGTG
ACAACTTTGAGGGAAACAAAGGCTTCTAGGCGTGAGGAGTTTGTCAGTATAAAGAGACAG
ATCATACTGTGTATGGAAGCATTAGACCACACCCCAGACACAAGCTTTGAAAGAGATGTG
GTGTGTGAAGACGAAGATGCCTTTTGTTTGTCTTTGGAGAATATTGCAACACTACAAAAG
TTGCTACGGCAGCTGGAAATGCAGAAATCACAAAATGAAGCAGTGTGTGAGGGGCTGCGT
ACTCAAATCCGAGAGCTCTGGGACAGGTTGCAAATACCTGAAGAAGAAAGAGAAGCTGTG
GCCACCATTATGTCTGGGTCAAAGGCCAAGGTCCGGAAAGCGCTGCAATTAGAAGTGGAT
CGGTTGGAAGAACTGAAAATGCAAAACATGAAGAAAGTGATTGAGGCAATTCGAGTGGAG
CTGGTTCAGTACTGGGACCAGTGCTTTTATAGCCAGGAGCAGAGACAAGCTTTTGCCCCT
TTCTGTGCTGAGGACTACACAGAAAGTCTGCTCCAGCTCCACGATGCTGAGATTGTGCGG
TTAAAAAACTACTATGAAGTTCACAAGGAACTCTTTGAAGGTGTCCAGAAGTGGGAAGAA
ACCTGGAGGCTTTTCTTAGAGTTTGAGAGAAAAGCTTCAGATCCAAATCGATTTACAAAC
CGAGGAGGAAATCTTCTAAAAGAAGAAAAACAACGAGCCAAGCTCCAGAAAATGCTGCCC
AAGCTGGAAGAAGAGTTGAAGGCACGAATTGAATTGTGGGAACAGGAACATTCAAAGGCA
TTTATGGTGAATGGGCAGAAATTCATGGAGTATGTGGCAGAACAATGGGAGATGCATCGA
TTGGAGAAAGAGAGAGCCAAGCAGGAAAGACAACTGAAGAACAAAAAACAGACAGAGACA
GAGATGCTGTATGGCAGCGCTCCTCGAACACCTAGCAAGCGGCGAGGACTGGCTCCCAAT
ACACCGGGCAAAGCACGTAAGCTGAACACTACCACCATGTCCAATGCTACGGCCAATAGT
AGCATTCGGCCTATCTTTGGAGGGACAGTCTACCACTCCCCCGTGTCTCGACTTCCTCCT
TCTGGCAGCAAGCCAGTCGCTGCTTCCACCTGTTCAGGGAAGAAAACACCCCGTACTGGC
AGGCATGGAGCCAACAAGGAGAACCTGGAGCTCAACGGCAGCATCCTGAGTGGTGGGTAC
CCTGGCTCGGCCCCCCTCCAGCGCAACTTCAGCATTAATTCTGTTGCCAGCACCTATTCT
GAGTTTGCGAAGGATCCGTCCCTCTCTGACAGTTCCACTGTTGGGCTTCAGCGAGAACTT
TCAAAGGCTTCCAAATCTGATGCTACTTCTGGAATCCTCAATTCAACCAACATCCAGTCC
TGA

Fig. 35

SEQ ID No. 35
NAT6
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CACTGTGAGGCCCGCTTTGGTGTGCACCTGCCACTCAATGCTCTGGGCATCATAGCCAAC
CGTGGCCAGCATTTTCACGGTCAGAACATGACCATTTTCTACAAGAACCAACTCGGCCTC
TATCCCTACTTTGGACCCAGGGGCACAGCTCACAATGGGGGCATCCCCCAGGCTTTGCCC
CTTGACCGCCACCTGGCACTGGCTGCCTACCAGATCCACCACAGCCTGAGACCTGGCTTT
GCTGGCCCAGCAGTGCTGGATTGGGAGGAGTGGTGTCCACTCTGGGCTGGGAACTGGGGC
CGCCGCCGAGCTTATCAGGCAGCCTCTTGGGCTTGGGCACAGCAGGTATTCCCTGACCTG
GACCCTCAGGAGCAGCTCTACAAGGCCTATACTGGCTTTGAGCAGGCGGCCCGTGCACTG
ATGGAGGATACGCTGCGGGTGGCCCAGGCACTACGGCCCCATGGACTCTGGGGCTTCTAT
CACTACCCAGCCTGTGGCAATGGCTGGCATAGTATGGCTTCCAACTATACCGGCCGCTGC
CATGCAGCCACCCTTGCCCGCAACACTCAACTGCATTGGCTCTGGGCCGCCTCCAGTGCC
CTCTTCCCCAGCATCTACCTCCCACCCAGGCTGCCACCTGCCCACCACCAGGCCTTTGTC
CGACATCGCCTGGAGGAGGCCTTCCGTGTGGCCCTTGTTGGGCACCGACATCCCCTGCCT
GTCCTGGCCTATGTCCGCCTCACACACCGGAGATCTGGGAGGTTCCTGTCCCAGGAGGAG
TGCTGGCATCTCCATGACTACCTGGTGGACACCTTGGGCCCCTATGTGATCAATGTGACC
AGGGCAGCGATGGCCTGCAGTCACCAGCGGTGCCATGGCCACGGGCGCTGTGCCCGGCGA
GATCCAGGACAGATGGAAGCCTTTCTACACCTGTGGCCAGACGGCAGCCTTGGAGATTGG
AAGTCCTTCAGCTGCCACTGTTACTGGGGCTGGGCTGGCCCCACCTGCCAGGAGCCCAGG
CCTGGGCCTAAAGAAGCAGTATAA

Fig. 36

SEQ ID No. 36
NAT6
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CACTGTGAGGCCCGCTTTGGTGTGCACCTGCCACTCAATGCTCTGGGCATCATAGCCAAC
CGTGGCCAGCATTTTCACGGTCAGAACATGACCATTTTCTACAAGAACCAACTCGGCCTC
TATCCCTACTTTGGACCCAGGGGCACAGCTCACAATGGGGGCATCCCCCAGGCTTTGCCC
CTTGACCGCCACCTGGCACTGGCTGCCTACCAGATCCACCACAGCCTGAGACCTGGCTTT
GCTGGCCCAGCAGTGCTGGATTGGGAGGAGTGGTGTCCACTCTGGGCTGGGAACTGGGGC
CGCCGCCGAGCTTATCAGGCAGCCTCTTGGGCTTGGGCACAGCAGGTATTCCCTGACCTG
GACCCTCAGGAGCAGCTCTACAAGGCCTATACTGGCTTTGAGCAGGCGGCCCGTGCACTG
ATGGAGGATACGCTGCGGGTGGCCCAGGCACTACGGCCCCATGGACTCTGGGGCTTCTAT
CACTACCCAGCCTGTGGCAATGGCTGGCATAGTATGGCTTCCAACTATACCGGCCGCTGC
CATGCAGCCACCCTTGCCCGCAACACTCAACTGCATTGGCTCTGGGCCGCCTCCAGTGCC
CTCTTCCCCAGCATCTACCTCCCACCCAGGCTGCCACCTGCCCACCACCAGGCCTTTGTC
CGACATCGCCTGGAGGAGGCCTTCCGTGTGGCCCTTGTTGGGCACCGACATCCCCTGCCT
GTCCTGGCCTATGTCCGCCTCACACACCGGAGATCTGGGAGGTTCCTGTCCCAGGATGAC
CTTGTGCAGTCCATTGGTGTGAGTGCAGCACTAGGGGCAGCCGGCGTGGTGCTCTGGGGG
GACCTGAGCCTCTCCAGCTCTGAGGAGGAGTGCTGGCATCTCCATGACTACCTGGTGGAC
ACCTTGGGCCCCTATGTGATCAATGTGACCAGGGCAGCGATGGCCTGCAGTCACCAGCGG
TGCCATGGCCACGGGCGCTGTGCCCGGCGAGATCCAGGACAGATGGAAGCCTTTCTACAC
CTGTGGCCAGACGGCAGCCTTGGAGATTGGAAGTCCTTCAGCTGCCACTGTTACTGGGGC
TGGGCTGGCCCCACCTGCCAGGAGCCCCTGGGCCTAAAGAAGCAGTATAAAGCCAGGGCC
CCTGCCACTGCCTCTTCTTTTCCCTGCTGCCACTTTTCCAGTCCTGGAACTACTCTGTCC
CACTCTTGCTCTATTCAGTTTACAGTCAACCCTCCCAAGCACACACCCCGCTTCCCTTGG
AATCCCTGA

Fig. 37

SEQ ID No. 37
NAT6
>ENSG00000186792|3|protein_coding|ENST00000336307|ENSP00000337425
ATGACCACGCAACTGGGCCCAGCCCTGGTGCTGGGGGTGGCCCTGTGCCTGGGTTGTGGC
CAGCCCCTACCACAGGTCCCTGAACGCCCCTTCTCTGTGCTGTGGAATGTACCCTCAGCA
CACTGTGAGGCCCGCTTTGGTGTGCACCTGCCACTCAATGCTCTGGGCATCATAGCCAAC
CGTGGCCAGCATTTTCACGGTCAGAACATGACCATTTTCTACAAGAACCAACTCGGCCTC
TATCCCTACTTTGGACCCAGGGGCACAGCTCACAATGGGGGCATCCCCCAGGCTTTGCCC
CTTGACCGCCACCTGGCACTGGCTGCCTACCAGATCCACCACAGCCTGAGACCTGGCTTT
GCTGGCCCAGCAGTGCTGGATTGGGAGGAGTGGTGTCCACTCTGGGCTGGGAACTGGGGC
CGCCGCCGAGCTTATCAGGCAGCCTCTTGGGCTTGGGCACAGCAGGTATTCCCTGACCTG
GACCCTCAGGAGCAGCTCTACAAGGCCTATACTGGCTTTGAGCAGGCGGCCCGTGCACTG
ATGGAGGATACGCTGCGGGTGGCCCAGGCACTACGGCCCCATGGACTCTGGGGCTTCTAT
CACTACCCAGCCTGTGGCAATGGCTGGCATAGTATGGCTTCCAACTATACCGGCCGCTGC
CATGCAGCCACCCTTGCCCGCAACACTCAACTGCATTGGCTCTGGGCCGCCTCCAGTGCC
CTCTTCCCCAGCATCTACCTCCCACCCAGGCTGCCACCTGCCCACCACCAGGCCTTTGTC
CGACATCGCCTGGAGGAGGCCTTCCGTGTGGCCCTTGTTGGGCACCGACATCCCCTGCCT
GTCCTGGCCTATGTCCGCCTCACACACCGGAGATCTGGGAGGTTCCTGTCCCAGGATGAC
CTTGTGCAGTCCATTGGTGTGAGTGCAGCACTAGGGGCAGCCGGCGTGGTGCTCTGGGGG
GACCTGAGCCTCTCCAGCTCTGAGGAGGAGTGCTGGCATCTCCATGACTACCTGGTGGAC
ACCTTGGGCCCCTATGTGATCAATGTGACCAGGGCAGCGATGGCCTGCAGTCACCAGCGG
TGCCATGGCCACGGGCGCTGTGCCCGGCGAGATCCAGGACAGATGGAAGCCTTTCTACAC
CTGTGGCCAGACGGCAGCCTTGGAGATTGGAAGTCCTTCAGCTGCCACTGTTACTGGGGC
TGGGCTGGCCCCACCTGCCAGGAGCCCAGGCCTGGGCCTAAAGAAGCAGTATAA

Fig. 38

SEQ ID No. 38
EEF1AL3
>ENSG00000185637|9|protein_coding|ENST00000329018|ENSP00000332874
ATGGGAAAGGAAAAGACTCATATCAACATTGTCGTCATTGGACACGTAGATTCGGGCAAG
TCCACCACTACTGGCCATCTGATCTATAAATGCGGTGGCATCGACAAAAGAACCATTGAA
AAATTTGAGAAGGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGGGTCTTG
GATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAATTT
GAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTTCATCAAA
AACATGATTACAGGGACATCTCAGGCTGACTGTGCTGTCCTGATTGTTGCTGCTGGTGTT
GGTGAATTTGAAGCTGGTATCTCCAAGAATGGGCAGACCCGAGAGCATGCCCTTCTGGCT
TACACACTGGGTGTGAAACAACTAATTGTCGGTGTTAACAAAATGGATTCCACTGAGCCA
CCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAAGTCAGCACTTACATTAAGAAA
ATTGGCTACAACCCCGACACAGTAGCATTTGTGCCAATTTCTGGTTGGAATGGTGACAAC
ATGCTGGAGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCACCCGTAAGGAT
GGCAATGCCAGTGGAACCACGCTGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCGC
CCAACTGACAAGCCCTTGCGCCTGCCTCTCCAGGATGTCTACAAAATTGGTGGTATTGGT
ACTGTTCCTGTTGGCCGAGTGGAGACTGGTGTTCTCAAACCCGGTATGGTGGTCACCTTT
GCTCCAGTCAACGTTACAACGGAAGTAAAATCTGTCGAAATGCACCATGAAGCTTTGAGT
GAAGCTCTTCCTGGGGACAATGTGGGCTTCAAGGTCAAGAATGTGTCTGTCAAGGATGTT
CGTCGTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTGGCTTC
ACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCCGGCTATGCCCCTGTA
TTGGATTGCCACATGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGAT
CGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCC
ATTGTTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCT
TTGGGTCGCTTTGCTGTTCGTGATATGAGACAGACAGTTGCGGTGGGTGTCATCAAAGCA
GTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAG
GCTAAATGA

Fig. 39

SEQ ID No. 39
NP_612480.1
>ENSG00000168005|11|protein_coding|ENST00000294244|ENSP00000294244
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GAAGGGGAGGACGAGGAGGAGGCCATGGTGGTGGCCGTAATTCCGCGGCCCGAGCCGATG
CTCAGAGTGACCCAACAGGAGAAGACCCCACCGCCTAGACCCAGCCCGCTAGAGGCAGGC
AGTGATGGCTGTGAGGAGCCGAAGCAGCAGGTGTCTTGGGAGCAGGAGTTCCTGGTGGGC
AGCAGCCCAGGAGGCAGCGGGCGGGCACTGTGCATGGTGTGTGGCGCTGAGATCCGGGCA
CCCTCGGCCGACACAGCTCGCTCGCACATCTTGGAGCAGCACCCTCACACCTTGGACCTG
AGCCCTTCTGAGAAGAGCAATATCCTGGAGGCCTGGAGTGAAGGGGTGGCCCTCTTGCAA
GACGTGAGAGCTGAGCAGCCGTCCCCACCCAACTCAGACTCGGGCCAGGATGCCCACCCA
GACCCAGACGCCAACCCAGACGCTGCCAGAATGCCAGCCGAAATCGTCGTTCTCCTTGAC
TCTGAGGATAACCCATCCCTCCCTAAAAGGAGCCGGCCCAGGGGACTCCGCCCCCTCGAG
CTTCCTGCTGTCCCTGCCACAGAGCCAGGAAATAAGAAGCCCCGTGGTCAGAGATGGAAG
GAACCCCCAGGGGAAGAGCCAGTCAGAAAGAAAAGAGGCAGACCTATGACCAAAAACCTG
GACCCTGACCCAGAGCCCCCATCGCCAGACTCGCCCACGGAGACTTTCGCAGCACCAGCC
GAGGTCCGACACTTCACTGACGGCAGCTTCCCCGCCGGCTTCGTCTTGCAGCTCTTCTCC
CACACCCAGCTCAGGGGCCCAGACAGCAAGGACTCACCCAAAGACAGGGAAGTGGCAGAA
GGAGGCCTTCCCCGGGCGGAGAGCCCCTCTCCAGCTCCCCCTCCGGGGCTCCGCGGGACA
CTGGATCTCCAGGTTATCCGCGTGCGGATGGAGGAGCCCCCAGCGGTCAGCCTCCTGCAA
GACTGGTCCAGGCACCCCCAGGGCACCAAGCGTGTGGGAGCAGGTGACACCTCAGACTGG
CCCACAGTTCTGTCAGAATCCAGCACCACTGTGGCAGGGAAGCCGGAAAAAGGGAATGGA
GTGTAA

Fig. 40

SEQ ID No. 40
PLXNA2
>ENSG00000076356|1|protein_coding|ENST00000321063|ENSP00000323194
ATGAGCACACACAGGAGCCGTCTCCTCACCGCCGCCCCTCTCAGCATGGAACAGAGGCGG
CCCTGGCCCCGGGCCCTGGAGGTGGACAGCCGCTCTGTGGTCCTGCTCTCAGTGGTCTGG
GTGCTGCTGGCCCCCCCAGCAGCCGGCATGCCTCAGTTCAGCACCTTCCACTCTGAGAAT
CGTGACTGGACCTTCAACCACTTGACCGTCCACCAAGGGACGGGGGCCGTCTATGTGGGG
GCCATCAACCGGGTCTATAAGCTGACAGGCAACCTGACCATCCAGGTGGCTCATAAGACA
GGGCCAGAAGAGGACAACAAGTCTTGTTACCCGCCCCTCATCGTGCAGCCCTGCAGCGAA
GTGCTCACCCTCACCAACAATGTCAACAAGCTGCTCATCATTGACTACTCTGAGAACCGC
CTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCAAGCTGCTGCGGCTGGATGACCTC
TTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTACCTGTCCAGTGTCAACAAGACG
GGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGATGGCAAGCTCTTCATCGGC
ACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCCAGCCGGAAGCTGCCCCGA
GACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGATTTTGTCTCCTCTCTC
ATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACATCTTCTACATCTAC
GGCTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGACCCCTGAGGGT
GTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGGCTCTGCAAG
GATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGCCGGGGTG
GAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCCAGGCC
TTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAGCAG
TATCACCACCCGCCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTTG
CAGATCAAGGAGCGCCTGCAGTCCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGG
CTGCTGGGGAAGGACGTCCAGTGCACCAAGGCGCCTGTCCCCATCGATGATAACTTCTGT
GGACTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTAC
ACCACCAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTG
GTTTTTGTGGGGACTAAGAGTGGCAAGCTGAAAAAGATTCGGGCCGACGGTCCCCCCCAT
GGTGGGGTCCAGTACGAGATGGTCTCTGTGCTCAAGGACGGAAGCCCCATCCTCCGGGAC
ATGGCCTTCTCCATTGATCAGCGCTACCTGTACGTCATGTCTGAGAGACAGGTCACCAGG
GTCCCCGTGGAGTCATGTGAGCAGTATACGACTTGTGGGGAGTGCCTGAGCTCTGGGGAC
CCTCACTGTGGCTGGTGTGCCCTGCACAACATGTGCTCCCGCAGGGACAAATGCCAACAG
GCCTGGGAACCTAATCGATTTGCTGCCAGCATCAGCCAGTGTGTGAGCCTTGCAGTGCAT
CCCAGCAGCATCTCAGTATCTGAGCACAGCCGGTTGCTTAGCCTGGTAGTGAGTGATGCT
CCTGATCTATCTGCGGGTATCGCCTGTGCCTTTGGGAACCTGACAGAGGTGGAGGGGCAG
GTGTCCGGGAGCCAGGTCATCTGCATCTCACCTGGGCCCAAGGATGTCCCTGTCATCCCG
CTGGATCAAGACTGGTTTGGGCTGGAGCTACAGCTGAGGTCCAAGGAGACAGGGAAGATA
TTTGTCAGCACCGAGTTCAAGTTTTACAACTGCAGTGCCCACCAACTGTGCCTGTCCTGT
GTCAACAGCGCCTTCCGCTGCCATTGGTGCAAGTACCGCAACCTCTGCACTCATGACCCC
ACCACCTGCTCCTTCCAGGAGGGCCGGATCAATATTTCAGAGGACTGTCCCCAGCTGGTG
CCCACAGAGGAGATCTTGATTCCAGTCGGGGAGGTAAAGCCAATCACCCTTAAGGCGCGA
AATCTGCCCCAGCCGCAGTCCGGCCAGCGAGGCTATGAGTGTGTCCTCAACATACAAGGA
GCCATCCACCGGGTCCCCGCTCTGCGCTTCAACAGCTCCAGCGTTCAGTGTCAGAACAGC
TCGTACCAGTATGATGGCATGGACATCAGCAATCTGGCCGTGGATTTCGCTGTGGTGTGG
AACGGCAATTTCATCATTGACAACCCTCAGGACCTGAAAGTCCATCTCTACAAGTGTGCA
GCCCAGCGGGAGAGCTGCGGCCTCTGCCTCAAGGCCGACCGGAAGTTTGAGTGTGGCTGG
TGCAGCGGCGAGCGCAGGTGCACCCTCCACCAGCACTGTACCAGCCCTTCCAGCCCCTGG
CTCGACTGGTCCAGCCACAATGTCAAGTGCTCCAACCCTCAAATCACCGAGATTTTGACG
GTGTCTGGACCGCCGGAAGGAGGGACGCGAGTGACCATCCATGGCGTGAACCTGGGTCTG
GACTTCTCCGAGATCGCCCACCATGTGCAGGTGGCTGGGGTGCCCTGCACGCCCCTCCCA
GGGGAATACATCATCGCTGAGCAGATTGTCTGTGAGATGGGCCATGCCCTCGTGGGAACC
ACCTCCGGGCCAGTACGCCTGTGTATTGGCGAGTGTAAGCCAGAGTTCATGACGAAGTCC
CATCAGCAGTACACCTTCGTGAACCCTTCTGTGCTGTCACTCAACCCAATCCGAGGTCCC
GAGTCAGGAGGCACTATGGTGACCATTACCGGCCATTACCTTGGGGCTGGGAGCAGCGTG
GCAGTCTACCTGGGCAACCAGACCTGCGAGTTCTACGGGAGGTCAATGAGTGAGATCGTG
TGTGTCTCACCCCCATCATCCAATGGCCTTGGCCCGGTCCCTGTTTCTGTGAGTGTCGAC
CGAGCCCATGTGGATAGCAACCTGCAGTTTGAGTACATAGATGACCCTCGGGTCCAGCGC
ATCGAGCCAGAGTGGAGCATTGCCAGTGGCCACACACCCCTGACCATCACAGGCTTCAAC
CTGGATGTCATTCAGGAGCCAAGGATCCGAGTCAAATTCAATGGCAAAGAATCTGTCAAT
GTGTGTAAAGTTGTGAACACAACCACCCTCACCTGCCTGGCACCCTCTCTGACCACGGAC
TACCGCCCTGGCCTGGACACTGTGGAACGCCCAGATGAGTTTGGATTTGTCTTTAACAAT
GTCCAATCCTTGCTAATTTACAACGACACCAAGTTTATCTACTACCCCAACCCGACCTTT
GAACTGCTTAGCCCTACTGGAGTCTTGGATCAAAAGCCAGGATCGCCCATCATTCTGAAG

GGCAAAAACCTCTGCCCTCCTGCCTCTGGAGGGGCCAAACTCAACTACACTGTGCTCATC
GGAGAGACCCCTTGTGCTGTCACCGTATCTGAGACCCAGCTTCTCTGCGAGCCTCCCAAC
CTCACCGGGCAGCACAAGGTCATGGTTCACGTGGGCGGGATGGTGTTCTCGCCTGGCTCG
GTGAGTGTCATCTCAGACAGCTTGCTGACCCTGCCAGCCATCGTCAGCATCGCGGCCGGC
GGCAGCCTCCTCCTCATCATCGTCATCATCGTCCTCATTGCCTACAAGCGCAAGTCTCGA
GAAAATGACCTCACTCTCAAGCGGCTGCAAATGCAGATGGACAATCTGGAGTCCCGTGTG
GCCTTGGAGTGCAAGGAAGCTTTTGCTGAGCTCCAGACGGATATCAATGAGTTGACCAGT
GACCTGGACCGCTCAGGAATCCCTTACCTGGACTATCGTACCTACGCTATGCGAGTCCTG
TTCCCGGGCATCGAGGACCACCCCGTCCTGCGGGAGCTGGAGGTACAAGGAAACGGGCAG
CAGCACGTGGAGAAGGCCCTGAAGCTCTTTGCCCAGCTCATCAACAACAAGGTGTTCCTG
CTGACCTTCATCCGCACCCTGGAGCTGCAGCGCAGTTTCTCCATGCGCGACCGGGGCAAC
GTGGCTTCGCTCATCATGACCGGCCTGCAGGGCCGCCTGGAATATGCCACTGATGTCCTC
AAGCAGCTGCTCTCTGACCTCATCGATAAGAACCTGGAGAACAAGAACCACCCCAAGCTG
CTACTCCGGAGGACAGAGTCTGTGGCTGAAAAGATGCTGACCAATTGGTTCGCCTTCCTC
CTGCACAAGTTCCTAAAGGAGTGCGCAGGGGAGCCACTCTTCATGCTATACTGTGCCATC
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AGCGAGGACAAGCTCATCCGGCAGCAGATCGAGTACAAGACCCTGATCCTGAACTGCGTC
AACCCTGACAACGAGAACAGTCCAGAGATCCCAGTGAAGGTGTTAAACTGTGACACCATC
ACACAGGTCAAGGAGAAGATTCTTGATGCCGTGTATAAGAATGTGCCCTATTCCCAGCGG
CCGAGGGCAGTGGACATGGACTTGGAGTGGCGCCAAGGCCGGATCGCCCGGGTCGTGCTG
CAAGATGAGGACATCACCACCAAGATTGAGGGTGACTGGAAGCGGCTCAACACACTGATG
CATTATCAGGTGTCAGACAGGTCGGTGGTGGCTCTGGTCCCCAAACAGACCTCCTCCTAC
AACATCCCTGCCTCTGCCAGCATCTCCCGGACGTCCATCAGCAGATACGACTCCTCCTTC
AGGTATACGGGCAGCCCCGACAGCCTGCGGTCCCGGGCCCCGATGATCACCCCAGACCTG
GAAAGTGGGGTCAAGGTGTGGCATCTGGTGAAGAACCATGACCACGGTGACCAGAAGGAG
GGTGACCGGGGCAGCAAGATGGTGTCCGAGATCTACCTGACCCGGCTACTGGCCACCAAG
GGCACCCTGCAGAAGTTTGTGGACGACTTGTTTGAGACCTTGTTCAGCACTGTGCACCGG
GGCAGCGCTCTCCCCCTGGCCATCAAGTACATGTTTGATTTCCTAGATGAGCAGGCAGAC
AGGCACAGCATCCATGACACAGATGTGCGGCACACCTGGAAAAGCAACTGCCTCCCTCTG
CGCTTCTGGGTGAACGTGATTAAGAACCCCCAGTTCGTGTTTGACATCCACAAGGGCAGC
ATCACGGACGCCTGCCTCTCTGTGGTGGCCCAGACCTTCATGGACTCTTGTTCAACGTCA
GAGCACCGGCTGGGCAAGGACTCCCCCTCCAACAAGCTGCTCTATGCCAAGGACATCCCC
AGCTACAAGAGCTGGGTGGAGAGATACTACGCAGACATCGCCAAGCTCCCAGCCATCAGT
GACCAGGACATGAATGCCTACCTCGCCGAGCAGTCCCGCCTGCACGCCGTGGAGTTCAAC
ATGCTGAGTGCCCTCAATGAGATCTACTCCTATGTCAGCAAGTATAGTGAGGAGCTCATC
GGGGCCCTAGAGCAGGATGAGCAGGCACGGCGGCAGCGGCTGGCTTATAAGGTGGAGCAG
CTCATTAATGCCATGTCCATTGAGAGCTGA

Fig. 40 (continued)

Fig. 41

SEQ ID No. 41
PLXNA2
>ENSG00000076356|1|protein_coding|ENST00000367033|ENSP00000356000
ATGGAACAGAGGCGGCCCTGGCCCCGGGCCCTGGAGGTGGACAGCCGCTCTGTGGTCCTG
CTCTCAGTGGTCTGGGTGCTGCTGGCCCCCCCAGCAGCCGGCATGCCTCAGTTCAGCACC
TTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGTCCACCAAGGGACGGGG
GCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCAACCTGACCATCCAG
GTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTTGTTACCCGCCCCTCATCGTG
CAGCCCTGCAGCGAAGTGCTCACCCTCACCAACAATGTCAACAAGCTGCTCATCATTGAC
TACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCAAGCTGCTG
CGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTACCTGTCC
AGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGATGGC
AAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCCAGC
CGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGAC
ATCTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCC
GAGACCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATC
GTGCGGCTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGCTGC
ACCCGGGCCGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGAC
TCACTGGCCCAGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCC
AAAGGGCAGAAGCAGTATCACCACCCGCCCGATGACTCTGCCCTGTGTGCCTTCCCTATC
CGGGCCATCAACTTGCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAGGGCGAGGGCAAC
CTGGAGCTCAACTGGCTGCTGGGGAAGGACGTCCAGTGCACCAAGGCGCCTGTCCCCATC
GATGATAACTTCTGTGGACTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGTGGAG
GGCCTGACCCTGTACACCACCAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTAC
AACGGCTACAGCGTGGTTTTTGTGGGGACTAAGAGTGGCAAGCTGAAAAAGATTCGGGCC
GACGGTCCCCCCCATGGTGGGGTCCAGTACGAGATGGTCTCTGTGCTCAAGGACGGAAGC
CCCATCCTCCGGGACATGGCCTTCTCCATTGATCAGCGCTACCTGTACGTCATGTCTGAG
AGACAGGTCACCAGGGTCCCCGTGGAGTCATGTGAGCAGTATACGACTTGTGGGGAGTGC
CTGAGCTCTGGGGACCCTCACTGTGGCTGGTGTGCCCTGCACAACATGTGCTCCCGCAGG
GACAAATGCCAACAGGCCTGGGAACCTAATCGATTTGCTGCCAGCATCAGCCAGTGTGTG
AGCCTTGCAGTGCATCCCAGCAGCATCTCAGTATCTGAGCACAGCCGGTTGCTTAGCCTG
GTAGTGAGTGATGCTCCTGATCTATCTGCGGGTATCGCCTGTGCCTTTGGGAACCTGACA
GAGGTGGAGGGGCAGGTGTCCGGGAGCCAGGTCATCTGCATCTCACCTGGGCCCAAGGAT
GTCCCTGTCATCCCGCTGGATCAAGACTGGTTTGGGCTGGAGCTACAGCTGAGGTCCAAG
GAGACAGGGAAGATATTTGTCAGCACCGAGTTCAAGTTTTACAACTGCAGTGCCCACCAA
CTGTGCCTGTCCTGTGTCAACAGCGCCTTCCGCTGCCATTGGTGCAAGTACCGCAACCTC
TGCACTCATGACCCCACCACCTGCTCCTTCCAGGAGGGCCGGATCAATATTTCAGAGGAC
TGTCCCCAGCTGGTGCCCACAGAGGAGATCTTGATTCCAGTCGGGGAGGTAAAGCCAATC
ACCCTTAAGGCGCGAAATCTGCCCCAGCCGCAGTCCGGCCAGCGAGGCTATGAGTGTGTC
CTCAACATACAAGGAGCCATCCACCGGGTCCCCGCTCTGCGCTTCAACAGCTCCAGCGTT
CAGTGTCAGAACAGCTCGTACCAGTATGATGGCATGGACATCAGCAATCTGGCCGTGGAT
TTCGCTGTGGTGTGGAACGGCAATTTCATCATTGACAACCCTCAGGACCTGAAAGTCCAT
CTCTACAAGTGTGCAGCCCAGCGGGAGAGCTGCGGCCTCTGCCTCAAGGCCGACCGGAAG
TTTGAGTGTGGCTGGTGCAGCGGCGAGCGCAGGTGCACCCTCCACCAGCACTGTACCAGC
CCTTCCAGCCCCTGGCTCGACTGGTCCAGCCACAATGTCAAGTGCTCCAACCCTCAAATC
ACCGAGATTTTGACGGTGTCTGGACCGCCGGAAGGAGGGACGCGAGTGACCATCCATGGC
GTGAACCTGGGTCTGGACTTCTCCGAGATCGCCCACCATGTGCAGGTGGCTGGGGTGCCC
TGCACGCCCCTCCCAGGGGAATACATCATCGCTGAGCAGATTGTCTGTGAGATGGGCCAT
GCCCTCGTGGGAACCACCTCCGGGCCAGTACGCCTGTGTATTGGCGAGTGTAAGCCAGAG
TTCATGACGAAGTCCCATCAGCAGTACACCTTCGTGAACCCTTCTGTGCTGTCACTCAAC
CCAATCCGAGGTCCCGAGTCAGGAGGCACTATGGTGACCATTACCGGCCATTACCTTGGG
GCTGGGAGCAGCGTGGCAGTCTACCTGGGCAACCAGACCTGCGAGTTCTACGGGAGGTCA
ATGAGTGAGATCGTGTGTGTCTCACCCCCATCATCCAATGGCCTTGGCCCGGTCCCTGTT
TCTGTGAGTGTCGACCGAGCCCATGTGGATAGCAACCTGCAGTTTGAGTACATAGATGAC
CCTCGGGTCCAGCGCATCGAGCCAGAGTGGAGCATTGCCAGTGGCCACACACCCCTGACC
ATCACAGGCTTCAACCTGGATGTCATTCAGGAGCCAAGGATCCGAGTCAAATTCAATGGC
AAAGAATCTGTCAATGTGTGTAAAGTTGTGAACACAACCACCCTCACCTGCCTGGCACCC
TCTCTGACCACGGACTACCGCCCTGGCCTGGACACTGTGGAACGCCCAGATGAGTTTGGA
TTTGTCTTTAACAATGTCCAATCCTTGCTAATTTACAACGACACCAAGTTTATCTACTAC
CCCAACCCGACCTTTGAACTGCTTAGCCCTACTGGAGTCTTGGATCAAAAGCCAGGATCG
CCCATCATTCTGAAGGGCAAAAACCTCTGCCCTCCTGCCTCTGGAGGGGCCAAACTCAAC

TACACTGTGCTCATCGGAGAGACCCCTTGTGCTGTCACCGTATCTGAGACCCAGCTTCTC
TGCGAGCCTCCCAACCTCACCGGGCAGCACAAGGTCATGGTTCACGTGGGCGGGATGGTG
TTCTCGCCTGGCTCGGTGAGTGTCATCTCAGACAGCTTGCTGACCCTGCCAGCCATCGTC
AGCATCGCGGCCGGCGGCAGCCTCCTCCTCATCATCGTCATCATCGTCCTCATTGCCTAC
AAGCGCAAGTCTCGAGAAAATGACCTCACTCTCAAGCGGCTGCAAATGCAGATGGACAAT
CTGGAGTCCCGTGTGGCCTTGGAGTGCAAGGAAGCTTTTGCTGAGCTCCAGACGGATATC
AATGAGTTGACCAGTGACCTGGACCGCTCAGGAATCCCTTACCTGGACTATCGTACCTAC
GCTATGCGAGTCCTGTTCCCGGGCATCGAGGACCACCCCGTCCTGCGGGAGCTGGAGGTA
CAAGGAAACGGGCAGCAGCACGTGGAGAAGGCCCTGAAGCTCTTTGCCCAGCTCATCAAC
AACAAGGTGTTCCTGCTGACCTTCATCCGCACCCTGGAGCTGCAGCGCAGTTTCTCCATG
CGCGACCGGGGCAACGTGGCTTCGCTCATCATGACCGGCCTGCAGGGCCGCCTGGAATAT
GCCACTGATGTCCTCAAGCAGCTGCTCTCTGACCTCATCGATAAGAACCTGGAGAACAAG
AACCACCCCAAGCTGCTACTCCGGAGGACAGAGTCTGTGGCTGAAAAGATGCTGACCAAT
TGGTTCGCCTTCCTCCTGCACAAGTTCCTAAAGGAGTGCGCAGGGGAGCCACTCTTCATG
CTATACTGTGCCATCAAGCAGCAGATGGAGAAGGGCCCCATTGATGCCATCACGGGCGAG
GCCCGCTACTCCCTGAGCGAGGACAAGCTCATCCGGCAGCAGATCGAGTACAAGACCCTG
ATCCTGAACTGCGTCAACCCTGACAACGAGAACAGTCCAGAGATCCCAGTGAAGGTGTTA
AACTGTGACACCATCACACAGGTCAAGGAGAAGATTCTTGATGCCGTGTATAAGAATGTG
CCCTATTCCCAGCGGCCGAGGGCAGTGGACATGGACTTGGAGTGGCGCCAAGGCCGGATC
GCCCGGGTCGTGCTGCAAGATGAGGACATCACCACCAAGATTGAGGGTGACTGGAAGCGG
CTCAACACACTGATGCATTATCAGGTGTCAGACAGGTCGGTGGTGGCTCTGGTCCCCAAA
CAGACCTCCTCCTACAACATCCCTGCCTCTGCCAGCATCTCCCGGACGTCCATCAGCAGA
TACGACTCCTCCTTCAGGTATACGGGCAGCCCCGACAGCCTGCGGTCCCGGGCCCCGATG
ATCACCCCAGACCTGGAAAGTGGGGTCAAGGTGTGGCATCTGGTGAAGAACCATGACCAC
GGTGACCAGAAGGAGGGTGACCGGGGCAGCAAGATGGTGTCCGAGATCTACCTGACCCGG
CTACTGGCCACCAAGGGCACCCTGCAGAAGTTTGTGGACGACTTGTTTGAGACCTTGTTC
AGCACTGTGCACCGGGGCAGCGCTCTCCCCCTGGCCATCAAGTACATGTTTGATTTCCTA
GATGAGCAGGCAGACAGGCACAGCATCCATGACACAGATGTGCGGCACACCTGGAAAAGC
AACTGCCTCCCTCTGCGCTTCTGGGTGAACGTGATTAAGAACCCCCAGTTCGTGTTTGAC
ATCCACAAGGGCAGCATCACGGACGCCTGCCTCTCTGTGGTGGCCCAGACCTTCATGGAC
TCTTGTTCAACGTCAGAGCACCGGCTGGGCAAGGACTCCCCCTCCAACAAGCTGCTCTAT
GCCAAGGACATCCCCAGCTACAAGAGCTGGGTGGAGAGATACTACGCAGACATCGCCAAG
CTCCCAGCCATCAGTGACCAGGACATGAATGCCTACCTCGCCGAGCAGTCCCGCCTGCAC
GCCGTGGAGTTCAACATGCTGAGTGCCCTCAATGAGATCTACTCCTATGTCAGCAAGTAT
AGTGAGGAGCTCATCGGGGCCCTAGAGCAGGATGAGCAGGCACGGCGGCAGCGGCTGGCT
TATAAGGTGGAGCAGCTCATTAATGCCATGTCCATTGAGAGCTGA

Fig. 41 (continued)

Fig. 42

SEQ ID No. 42
ELMO2
>ENSG00000062598|20|protein_coding|ENST00000290246|ENSP00000290246
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CTCCTTGAAATCGACCAGAAACGGCCCCTGGCATCCATTATCAAGGAAGTTTGTGATGGG
TGGTCGTTGCCAAACCCAGAGTATTATACCCTCCGTTATGCAGATGGTCCTCAGCTGTAC
ATCACCGAACAGACTCGCAGTGACATTAAGAATGGGACAATCTTACAACTGGCTATCTCC
CCGTCCCGGGCTGCACGCCAGCTGATGGAGAGGACCCAGTCATCCAACATGGAGACCCGG
CTGGATGCCATGAAGGAGCTGGCCAAGCTCTCTGCCGACGTGACTTTCGCTACTGAGTTC
ATCAACATGGATGGCATCATTGTGCTGACAAGGCTCGTGGAAAGTGGAACCAAGCTCTTG
TCCCACTACAGTGAGATGCTGGCATTCACCCTGACTGCCTTCCTAGAGCTCATGGACCAT
GGCATTGTCTCCTGGGACATGGTTTCAATCACCTTTATTAAGCAGATTGCAGGGTATGTG
AGCCAGCCCATGGTGGACGTGTCAATCCTTCAGAGGTCCCTGGCCATCCTGGAGAGCATG
GTCTTGAACAGCCAGAGTCTGTACCAGAAGATAGCCGAGGAAATCACCGTGGGACAGCTC
ATCTCACACCTCCAGGTCTCCAACCAGGAGATTCAGACCTACGCCATTGCACTGATTAAT
GCACTTTTTCTGAAGGCTCCTGAGGACAAACGACAGGATATGGCAAATGCATTTGCACAG
AAGCATCTCCGGTCTATAATCCTGAATCATGTGATCCGAGGGAACCGCCCCATCAAAACT
GAGATGGCCCATCAGCTATATGTCCTTCAAGTCCTAACCTTTAACCTTCTGGAAGAAAGG
ATGATGACCAAGATGGACCCCAATGACCAGGCTCAAAGGGACATCATATTTGAACTGAGG
AGGATTGCATTTGACGCAGAGTCTGATCCTAGCAATGCCCCTGGGAGTGGGACCGAAAAA
CGCAAAGCCATGTACACAAAGGACTACAAAATGCTGGGATTTACCAACCACATCAATCCA
GCCATGGACTTTACCCAGACTCCTCCTGGAATGCTGGCCTTGGACAACATGCTGTACTTG
GCTAAAGTCCACCAGGACACCTACATCCGGATTGTCTTGGAGAACAGTAGCCGGGAAGAC
AAACATGAATGCCCCTTTGGCCGCAGTGCCATTGAGCTCACCAAAATGCTCTGTGAAATC
CTGCAGGTTGGGGAACTACCAAATGAAGGACGCAATGACTACCACCCGATGTTCTTTACC
CATGACCGAGCCTTTGAAGAGCTCTTTGGAATCTGCATCCAGCTGTTGAACAAGACCTGG
AAGGAGATGAGGGCAACAGCAGAGGACTTCAACAAGGTTATGCAAGTCGTCCGAGAGCAA
ATCACTCGAGCTTTGCCCTCCAAACCCAACTCTTTGGATCAGTTCAAGAGCAAATTGCGT
AGCCTGAGTTACTCTGAGATTCTACGACTGCGCCAGTCTGAGAGGATGAGTCAGGATGAC
TTCCAGTCCCCGCCAATTGTGGAGCTGAGGGAGAAGATCCAGCCCGAGATCCTTGAGCTG
ATCAAGCAGCAGCGCCTGAACCGGCTCTGTGAGGGCAGCAGCTTCCGAAAGATTGGGAAC
CGCCGAAGGCAAGAACGGTTCTGGTACTGCCGGTTGGCACTGAACCACAAGGTCCTTCAC
TATGGTGACTTGGATGACAACCCACAAGGGGAGGTGACATTTGAATCCCTGCAGGAGAAA
ATTCCTGTTGCAGACATTAAGGCCATTGTCACTGGGAAAGATTGTCCCCACATGAAAGAG
AAAAGTGCTCTGAAACAGAACAAGGAGGTGTTGGAATTGGCCTTCTCCATCCTGTATGAC
CCTGATGAGACCTTAAACTTCATCGCACCTAATAAATATGAGTACTGCATCTGGATTGAT
GGCCTCAGTGCCCTTCTGGGGAAGGACATGTCCAGTGAGCTGACCAAGAGTGACCTGGAC
ACCCTGCTGAGCATGGAGATGAAGCTGCGGCTCCTGGACCTGGAGAACATCCAGATTCCC
GAAGCCCCACCCCCCATCCCCAAGGAGCCCAGCAGCTATGACTTTGTCTATCACTATGGC
TGA

Fig. 43

SEQ ID No. 43
ELMO2
>ENSG00000062598|20|protein_coding|ENST00000396391|ENSP00000379673
ATGCCACCACCGTCAGACATTGTCAAAGTGGCCATTGAGTGGCCAGGTGCTAACGCCCAG
CTCCTTGAAATCGACCAGAAACGGCCCCTGGCATCCATTATCAAGGAAGTTTGTGATGGG
TGGTCGTTGCCAAACCCAGAGTATTATACCCTCCGTTATGCAGATGGTCCTCAGCTGTAC
ATCACCGAACAGACTCGCAGTGACATTAAGAATGGGACAATCTTACAACTGGCTATCTCC
CCGTCCCGGGCTGCACGCCAGCTGATGGAGAGGACCCAGTCATCCAACATGGAGACCCGG
CTGGATGCCATGAAGGAGCTGGCCAAGCTCTCTGCCGACGTGACTTTCGCTACTGAGTTC
ATCAACATGGATGGCATCATTGTGCTGACAAGGCTCGTGGAAAGTGGAACCAAGCTCTTG
TCCCACTACAGTGAGATGCTGGCATTCACCCTGACTGCCTTCCTAGAGCTCATGGACCAT
GGCATTGTCTCCTGGGACATGGTTTCAATCACCTTTATTAAGCAGATTGCAGGGTATGTG
AGCCAGCCCATGGTGGACGTGTCAATCCTTCAGAGGTCCCTGGCCATCCTGGAGAGCATG
GTCTTGAACAGCCAGAGTCTGTACCAGAAGATAGCCGAGGAAATCACCGTGGGACAGCTC
ATCTCACACCTCCAGGTCTCCAACCAGGAGATTCAGACCTACGCCATTGCACTGATTAAT
GCACTTTTTCTGAAGGCTCCTGAGGACAAACGACAGGATATGGCAAATGCATTTGCACAG
AAGCATCTCCGGTCTATAATCCTGAATCATGTGATCCGAGGGAACCGCCCCATCAAAACT
GAGATGGCCCATCAGCTATATGTCCTTCAAGTCCTAACCTTTAACCTTCTGGAAGAAAGG
ATGATGACCAAGATGGACCCCAATGACCAGGCTCAAAGGGACATCATATTTGAACTGAGG
AGGATTGCATTTGACGCAGAGTCTGATCCTAGCAATGCCCCTGGGAGTGGGACCGAAAAA
CGCAAAGCCATGTACACAAAGGACTACAAAATGCTGGGATTTACCAACCACATCAATCCA
GCCATGGACTTTACCCAGACTCCTCCTGGAATGCTGGCCTTGGACAACATGCTGTACTTG
GCTAAAGTCCACCAGGACACCTACATCCGGATTGTCTTGGAGAACAGTAGCCGGGAAGAC
AAACATGAATGCCCCTTTGGCCGCAGTGCCATTGAGCTCACCAAAATGCTCTGTGAAATC
CTGCAGGTTGGGGAACTACCAAATGAAGGACGCAATGACTACCACCCGATGTTCTTTACC
CATGACCGAGCCTTTGAAGAGCTCTTTGGAATCTGCATCCAGCTGTTGAACAAGACCTGG
AAGGAGATGAGGGCAACAGCAGAGGACTTCAACAAGGTTATGCAAGTCGTCCGAGAGCAA
ATCACTCGAGCTTTGCCCTCCAAACCCAACTCTTTGGATCAGTTCAAGAGCAAATTGCGT
AGCCTGAGTTACTCTGAGATTCTACGACTGCGCCAGTCTGAGAGGATGAGTCAGGATGAC
TTCCAGTCCCCGCCAATTGTGGAGCTGAGGGAGAAGATCCAGCCCGAGATCCTTGAGCTG
ATCAAGCAGCAGCGCCTGAACCGGCTCTGTGAGGGCAGCAGCTTCCGAAAGATTGGGAAC
CGCCGAAGGCAAGAACGGTTCTGGTACTGCCGGTTGGCACTGAACCACAAGGTCCTTCAC
TATGGTGACTTGGATGACAACCCACAAGGGGAGGTGACATTTGAATCCCTGCAGGAGAAA
ATTCCTGTTGCAGACATTAAGGCCATTGTCACTGGGAAAGATTGTCCCCACATGAAAGAG
AAAAGTGCTCTGAAACAGAACAAGGAGGTGTTGGAATTGGCCTTCTCCATCCTGTATGAC
CCTGATGAGACCTTAAACTTCATCGCACCTAATAAATATGAGTACTGCATCTGGATTGAT
GGCCTCAGTGCCCTTCTGGGGAAGGACATGTCCAGTGAGCTGACCAAGAGTGACCTGGAC
ACCCTGCTGAGCATGGAGATGAAGCTGCGGCTCCTGGACCTGGAGAACATCCAGATTCCC
GAAGCCCCACCCCCCATCCCCAAGGAGCCCAGCAGCTATGACTTTGTCTATCACTATGGC
TGA

Fig. 44

SEQ ID No. 44
ELMO2
>ENSG00000062598|20|protein_coding|ENST00000372176|ENSP00000361249
ATGGAGAGGACCCAGTCATCCAACATGGAGACCCGGCTGGATGCCATGAAGGAGCTGGCC
AAGCTCTCTGCCGACGTGACTTTCGCTACTGAGTTCATCAACATGGATGGCATCATTGTG
CTGACAAGGCTCGTGGAAAGTGGAACCAAGCTCTTGTCCCACTACAGTGAGATGCTGGCA
TTCACCCTGACTGCCTTCCTAGAGCTCATGGACCATGGCATTGTCTCCTGGGACATGGTT
TCAATCACCTTTATTAAGCAGATTGCAGGGTATGTGAGCCAGCCCATGGTGGACGTGTCA
ATCCTTCAGAGGTCCCTGGCCATCCTGGAGAGCATGGTCTTGAACAGCCAGAGTCTGTAC
CAGAAGATAGCCGAGGAAATCACCGTGGGACAGCTCATCTCACACCTCCAGGTCTCCAAC
CAGGAGATTCAGACCTACGCCATTGCACTGATTAATGCACTTTTTCTGAAGGCTCCTGAG
GACAAACGACAGGATATGGCAAATGCATTTGCACAGAAGCATCTCCGGTCTATAATCCTG
AATCATGTGATCCGAGGGAACCGCCCCATCAAAACTGAGATGGCCCATCAGCTATATGTC
CTTCAAGTCCTAACCTTTAACCTTCTGGAAGAAAGGATGATGACCAAGATGGACCCCAAT
GACCAGGCTCAAAGGGACATCATATTTGAACTGAGGAGGATTGCATTTGACGCAGAGTCT
GATCCTAGCAATGCCCCTGGGAGTGGGACCGAAAAACGCAAAGCCATGTACACAAAGGAC
TACAAAATGCTGGGATTTACCAACCACATCAATCCAGCCATGGACTTTACCCAGACTCCT
CCTGGAATGCTGGCCTTGGACAACATGCTGTACTTGGCTAAAGTCCACCAGGACACCTAC
ATCCGGATTGTCTTGGAGAACAGTAGCCGGGAAGACAAACATGAATGCCCCTTTGGCCGC
AGTGCCATTGAGCTCACCAAAATGCTCTGTGAAATCCTGCAGGTTGGGGAACTACCAAAT
GAAGGACGCAATGACTACCACCCGATGTTCTTTACCCATGACCGAGCCTTTGAAGAGCTC
TTTGGAATCTGCATCCAGCTGTTGAACAAGACCTGGAAGGAGATGAGGGCAACAGCAGAG
GACTTCAACAAGGTTATGCAAGTCGTCCGAGAGCAAATCACTCGAGCTTTGCCCTCCAAA
CCCAACTCTTTGGATCAGTTCAAGAGCAAATTGCGTAGCCTGAGTTACTCTGAGATTCTA
CGACTGCGCCAGTCTGAGAGGATGAGTCAGGATGACTTCCAGTCCCCGCCAATTGTGGAG
CTGAGGGAGAAGATCCAGCCCGAGATCCTTGAGCTGATCAAGCAGCAGCGCCTGAACCGG
CTCTGTGAGGGCAGCAGCTTCCGAAAGATTGGGAACCGCCGAAGGCAAGAACGGTTCTGG
TACTGCCGGTTGGCACTGAACCACAAGGTCCTTCACTATGGTGACTTGGATGACAACCCA
CAAGGGGAGGTGACATTTGAATCCCTGCAGGAGAAAATTCCTGTTGCAGACATTAAGGCC
ATTGTCACTGGGAAAGATTGTCCCCACATGAAAGAGAAAAGTGCTCTGAAACAGAACAAG
GAGGTGTTGGAATTGGCCTTCTCCATCCTGTATGACCCTGATGAGACCTTAAACTTCATC
GCACCTAATAAATATGAGTACTGCATCTGGATTGATGGCCTCAGTGCCCTTCTGGGGAAG
GACATGTCCAGTGAGCTGACCAAGAGTGACCTGGACACCCTGCTGAGCATGGAGATGAAG
CTGCGGCTCCTGGACCTGGAGAACATCCAGATTCCCGAAGCCCCACCCCCCATCCCCAAG
GAGCCCAGCAGCTATGACTTTGTCTATCACTATGGCTGA

Fig. 45

SEQ ID No. 45
ELMO2
>ENSG00000062598|20|protein_coding|ENST00000352077|ENSP00000326172
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CTCCTTGAAATCGACCAGAAACGGCCCCTGGCATCCATTATCAAGGAAGTTTGTGATGGG
TGGTCGTTGCCAAACCCAGAGTATTATACCCTCCGTTATGCAGATGGTCCTCAGCTGTAC
ATCACCGAACAGACTCGCAGTGACATTAAGAATGGGACAATCTTACAACTGGCTATCTCC
CCGTCCCGGGCTGCACGCCAGCTGATGGAGAGGACCCAGTCATCCAACATGGAGACCCGG
CTGGATGCCATGAAGGAGCTGGCCAAGCTCTCTGCCGACGTGACTTTCGCTACTGAGTTC
ATCAACATGGATGGCATCATTGTGCTGACAAGGCTCGTGGAAAGTGGAACCAAGCTCTTG
TCCCATGAGATGCTGGCATTCACCCTGACTGCCTTCCTAGAGCTCATGGACCATGGCATT
GTCTCCTGGGACATGGTTTCAATCACCTTTATTAAGCAGATTGCAGGGTATGTGAGCCAG
CCCATGGTGGACGTGTCAATCCTTCAGAGGTCCCTGGCCATCCTGGAGAGCATGGTCTTG
AACAGCCAGAGTCTGTACCAGAAGATAGCCGAGGAAATCACCGTGGGACAGCTCATCTCA
CACCTCCAGGTCTCCAACCAGGAGATTCAGACCTACGCCATTGCACTGATTAATGCACTT
TTTCTGAAGGCTCCTGAGGACAAACGACAGGATATGGCAAATGCATTTGCACAGAAGCAT
CTCCGGTCTATAATCCTGAATCATGTGATCCGAGGGAACCGCCCCATCAAAACTGAGATG
GCCCATCAGCTATATGTCCTTCAAGTCCTAACCTTTAACCTTCTGGAAGAAAGGATGATG
ACCAAGATGGACCCCAATGACCAGGCTCAAAGGGACATCATATTTGAACTGAGGAGGATT
GCATTTGACGCAGAGTCTGATCCTAGCAATGCCCCTGGGAGTGGGACCGAAAAACGCAAA
GCCATGTACACAAAGGACTACAAAATGCTGGGATTTACCAACCACATCAATCCAGCCATG
GACTTTACCCAGACTCCTCCTGGAATGCTGGCCTTGGACAACATGCTGTACTTGGCTAAA
GTCCACCAGGACACCTACATCCGGATTGTCTTGGAGAACAGTAGCCGGGAAGACAAACAT
GAATGCCCCTTTGGCCGCAGTGCCATTGAGCTCACCAAAATGCTCTGTGAAATCCTGCAG
GTTGGGGAACTACCAAATGAAGGACGCAATGACTACCACCCGATGTTCTTTACCCATGAC
CGAGCCTTTGAAGAGCTCTTTGGAATCTGCATCCAGCTGTTGAACAAGACCTGGAAGGAG
ATGAGGGCAACAGCAGAGGACTTCAACAAGGTTATGCAAGTCGTCCGAGAGCAAATCACT
CGAGCTTTGCCCTCCAAACCCAACTCTTTGGATCAGTTCAAGAGCAAATTGCGTAGCCTG
AGTTACTCTGAGATTCTACGACTGCGCCAGTCTGAGAGGATGAGTCAGGATGACTTCCAG
TCCCCGCCAATTGTGGAGCTGAGGGAGAAGATCCAGCCCGAGATCCTTGAGCTGATCAAG
CAGCAGCGCCTGAACCGGCTCTGTGAGGGCAGCAGCTTCCGAAAGATTGGGAACCGCCGA
AGGCAAGAACGGTTCTGGTACTGCCGGTTGGCACTGAACCACAAGGTCCTTCACTATGGT
GACTTGGATGACAACCCACAAGGGGAGGTGACATTTGAATCCCTGCAGGAGAAAATTCCT
GTTGCAGACATTAAGGCCATTGTCACTGGGAAAGATTGTCCCCACATGAAAGAGAAAAGT
GCTCTGAAACAGAACAAGGAGGTGTTGGAATTGGCCTTCTCCATCCTGTATGACCCTGAT
GAGACCTTAAACTTCATCGCACCTAATAAATATGAGTACTGCATCTGGATTGATGGCCTC
AGTGCCCTTCTGGGGAAGGACATGTCCAGTGAGCTGACCAAGAGTGACCTGGACACCCTG
CTGAGCATGGAGATGAAGCTGCGGCTCCTGGACCTGGAGAACATCCAGATTCCCGAAGCC
CCACCCCCCATCCCCAAGGAGCCCAGCAGCTATGACTTTGTCTATCACTATGGCTGA

Fig. 46

SEQ ID No. 46
NDUFS2
>ENSG00000158864|1|protein_coding|ENST00000367993|ENSP00000356972
ATGGCGGCGCTGAGGGCTTTGTGCGGCTTCCGGGGCGTCGCGGCCCAGGTGCTGCGGCCT
GGGGCTGGAGTCCGATTGCCGATTCAGCCCAGCAGAGGTGTTCGGCAGTGGCAGCCAGAT
GTGGAATGGGCACAGCAGTTTGGGGGAGCTGTTATGTACCCAAGCAAAGAAACAGCCCAC
TGGAAGCCTCCACCTTGGAATGATGTGGACCCTCCAAAGGACACAATTGTGAAGAACATT
ACCCTGAACTTTGGGCCCCAACACCCAGCAGCGCATGGTGTCCTGCGACTAGTGATGGAA
TTGAGTGGGGAGATGGTGCGGAAGTGTGATCCTCACATCGGGCTCCTGCACCGAGGCACT
GAGAAGCTCATTGAATACAAGACCTATCTTCAGGCCCTTCCATACTTTGACCGGCTAGAC
TATGTGTCCATGATGTGTAACGAACAGGCCTATTCTCTAGCTGTGGAGAAGTTGCTAAAC
ATCCGGCCTCCTCCTCGGGCACAGTGGATCCGAGTGCTGTTTGGAGAAATCACACGTTTG
TTGAACCACATCATGGCTGTGACCACACATGCCCTGGACCTTGGGGCCATGACCCCTTTC
TTCTGGCTGTTTGAAGAAAGGGAGAAGATGTTTGAGTTCTACGAGCGAGTGTCTGGAGCC
CGAATGCATGCTGCTTATATCCGGCCAGGAGGAGTGCACCAGGACCTACCCCTTGGGCTT
ATGGATGACATTTATCAGTTTTCTAAGAACTTCTCTCTTCGGCTTGATGAGTTGGAGGAG
TTGCTGACCAACAATAGGATCTGGCGAAATCGGACAATTGACATTGGGGTTGTAACAGCA
GAAGAAGCACTTAACTATGGTTTTAGTGGAGTGATGCTTCGGGGCTCAGGCATCCAGTGG
GACCTGCGGAAGACCCAGCCCTATGATGTTTACGACCAGGTTGAGTTTGATGTTCCTGTT
GGTTCTCGAGGGGACTGCTATGATAGGTACCTGTGCCGGGTGGAGGAGATGCGCCAGTCC
CTGAGAATTATCGCACAGTGTCTAAACAAGATGCCTCCTGGGGAGATCAAGGTTGATGAT
GCCAAAGTGTCTCCACCTAAGCGAGCAGAGATGAAGACTTCCATGGAGTCACTGATTCAT
CACTTTAAGTTGTATACTGAGGGCTACCAAGTTCCTCCAGGAGCCACATATACTGCCATT
GAGGCTCCCAAGGGAGAGTTTGGGGTGTACCTGGTGTCTGATGGCAGCAGCCGCCCTTAT
CGATGCAAGATCAAGGCTCCTGGTTTTGCCCATCTGGCTGGTTTGGACAAGATGTCTAAG
GGACACATGTTGGCAGATGTCGTTGCCATCATAGGTACCCAAGATATTGTATTTGGAGAA
GTAGATCGGTGA

Fig. 47

SEQ ID No. 47
NDUFS2
>ENSG00000158864|1|protein_coding|ENST00000392179|ENSP00000376018
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GGGGCTGGAGTCCGATTGCCGATTCAGCCCAGCAGAGGTGTTCGGCAGTGGCAGCCAGAT
GTGGAATGGGCACAGCAGTTTGGGGGAGCTGTTATGTACCCAAGCAAAGAAACAGCCCAC
TGGAAGCCTCCACCTTGGAATGATGTGGACCCTCCAAAGGACACAATTGTGAAGAACATT
ACCCTGAACTTTGGGCCCCAACACCCAGCAGCGCATGGTGTCCTGCGACTAGTGATGGAA
TTGAGTGGGGAGATGGTGCGGAAGTGTGATCCTCACATCGGGCTCCTGCACCGAGGCACT
GAGAAGCTCATTGAATACAAGACCTATCTTCAGGCCCTTCCATACTTTGACCGGCTAGAC
TATGTGTCCATGATGTGTAACGAACAGGCCTATTCTCTAGCTGTGGAGAAGTTGCTAAAC
ATCCGGCCTCCTCCTCGGGCACAGTGGATCCGAGTGCTGTTTGGAGAAATCACACGTTTG
TTGAACCACATCATGGCTGTGACCACACATGCCCTGGACCTTGGGGCCATGACCCCTTTC
TTCTGGCTGTTTGAAGAAAGGGAGAAGATGTTTGAGTTCTACGAGCGAGTGTCTGGAGCC
CGAATGCATGCTGCTTATATCCGGCCAGGAGGAGTGCACCAGGACCTACCCCTTGGGCTT
ATGGATGACATTTATCAGTTTTCTAAGAACTTCTCTCTTCGGCTTGATGAGTTGGAGGAG
TTGCTGACCAACAATAGGATCTGGCGAAATCGGACAATTGACATTGGGGTTGTAACAGCA
GAAGAAGCACTTAACTATGGTTTTAGTGGAGTGATGCTTCGGGGCTCAGGCATCCAGTGG
GACCTGCGGAAGACCCAGCCCTATGATGTTTACGACCAGGTTGAGTTTGATGTTCCTGTT
GGTTCTCGAGGGGACTGCTATGATAGGTACCTGTGCCGGGTGGAGGAGATGCGCCAGTCC
CTGAGAATTATCGCACAGTGTCTAAACAAGATGCCTCCTGGGGAGATCAAGGTTGATGAT
GCCAAAGTGTCTCCACCTAAGCGAGCAGAGATGAAGACTTCCATGGAGTCACTGATTCAT
CACTTTAAGTTGTATACTGAGGGCTACCAAGTTCCTCCAGGAGCCACATATACTGCCATT
GAGGCTCCCAAGGGAGAGTTTGGGGTGTACCTGGTGTCTGATGGCAGCAGCCGCCCTTAT
CGATGCAAGATCAAGGCTCCTGGTTTTGCCCATCTGGCTGGTTTGGACAAGATGTCTAAG
GGACACATGTTGGCAGATGTCGTTGCCATCATAGGTACCCAAGATATTGTATTTGGAGAA
GTAGATCGGTGA

Fig. 48

SEQ ID No. 48
IRAK1
>ENSG00000184216|X|protein_coding|ENST00000369980|ENSP00000358997
ATGGCCGGGGGGCCGGGCCCGGGGGAGCCCGCAGCCCCCGGCGCCCAGCACTTCTTGTAC
GAGGTGCCGCCCTGGGTCATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCCCGCC
GACTGGTGCCAGTTCGCCGCCCTGATCGTGCGCGACCAGACCGAGCTGCGGCTGTGCGAG
CGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAACGCCCGTGTG
GCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGTGCGCGGGACATCATCACA
GCCTGGCACCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACTGCCCCGAGGCCCAGCAGC
ATCCCTGCACCCGCCGAGGCCGAGGCCTGGAGCCCCCGGAAGTTGCCATCCTCAGCCTCC
ACCTTCCTCTCCCCAGCTTTTCCAGGCTCCCAGACCCATTCAGGGCCTGAGCTCGGCCTG
GTCCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCCATCTCCAGCCCCTTCTTCTACCAAG
CCAGGCCCAGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGCCCCTTTCCGTTTTGCTGG
CCCCTCTGTGAGATTTCCCGGGGCACCCACAACTTCTCGGAGGAGCTCAAGATCGGGGAG
GGTGGCTTTGGGTGCGTGTACCGGGCGGTGATGAGGAACACGGTGTATGCTGTGAAGAGG
CTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAGAGCTTCCTGACCGAGGTG
GAGCAGCTGTCCAGGTTTCGTCACCCAAACATTGTGGACTTTGCTGGCTACTGTGCTCAG
AACGGCTTCTACTGCCTGGTGTACGGCTTCCTGCCCAACGGCTCCCTGGAGGACCGTCTC
CACTGCCAGACCCAGGCCTGCCCACCTCTCTCCTGGCCTCAGCGACTGGACATCCTTCTG
GGTACAGCCCGGGCAATTCAGTTTCTACATCAGGACAGCCCCAGCCTCATCCATGGAGAC
ATCAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCCAAGCTGGGAGACTTTGGC
CTGGCCCGGTTCAGCCGCTTTGCCGGGTCCAGCCCCAGCCAGAGCAGCATGGTGGCCCGG
ACACAGACAGTGCGGGGCACCCTGGCCTACCTGCCCGAGGAGTACATCAAGACGGGAAGG
CTGGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTGCTAGAGACCTTGGCTGGT
CAGAGGGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTGAAAGACCTGGTGGAAGAG
GAGGCTGAGGAGGCTGGAGTGGCTTTGAGAAGCACCCAGAGCACACTGCAAGCAGGTCTG
GCTGCAGATGCCTGGGCTGCTCCCATCGCCATGCAGATCTACAAGAAGCACCTGGACCCC
AGGCCCGGGCCCTGCCCACCTGAGCTGGGCCTGGGCCTGGGCCAGCTGGCCTGCTGCTGC
CTGCACCGCCGGGCCAAAAGGAGGCCTCCTATGACCCAGGTGTACGAGAGGCTAGAGAAG
CTGCAGGCAGTGGTGGCGGGGGTGCCCGGGCATTCGGAGGCCGCCAGCTGCATCCCCCCT
TCCCCGCAGGAGAACTCCTACGTGTCCAGCACTGGCAGAGCCCACAGTGGGGCTGCTCCA
TGGCAGCCCCTGGCAGCGCCATCAGGAGCCAGTGCCCAGGCAGCAGAGCAGCTGCAGAGA
GGCCCCAACCAGCCCGTGGAGAGTGACGAGAGCCTAGGCGGCCTCTCTGCTGCCCTGCGC
TCCTGGCACTTGACTCCAAGCTGCCCTCTGGACCCAGCACCCCTCAGGGAGGCCGGCTGT
CCTCAGGGGGACACGGCAGGAGAATCGAGCTGGGGGAGTGGCCCAGGATCCCGGCCCACA
GCCGTGGAAGGACTGGCCCTTGGCAGCTCTGCATCATCGTCGTCAGAGCCACCGCAGATT
ATCATCAACCCTGCCCGACAGAAGATGGTCCAGAAGCTGGCCCTGTACGAGGATGGGGCC
CTGGACAGCCTGCAGCTGCTGTCGTCCAGCTCCCTCCCAGGCTTGGGCCTGGAACAGGAC
AGGCAGGGGCCCGAAGAAAGTGATGAATTTCAGAGCTGA

Fig. 49

SEQ ID No. 49
IRAK1
>ENSG00000184216|X|protein_coding|ENST00000369973|ENSP00000358990
ATGGCCGGGGGGCCGGGCCCGGGGGAGCCCGCAGCCCCCGGCGCCCAGCACTTCTTGTAC
GAGGTGCCGCCCTGGGTCATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCCCGCC
GACTGGTGCCAGTTCGGTGGGTGGCGGCGGGCTGCCGGGGGGCGGGAGGCGCGCGGGCTC
CTGGCGCCGACGCCTGACGCCCCCCGCCCCGCAGCCGCCCTGATCGTGCGCGACCAGACC
GAGCTGCGGCTGTGCGAGCGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATC
AACCGCAACGCCCGTGTGGCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGT
GCGCGGGACATCATCACAGCCTGGCACCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACT
GCCCCGAGGCCCAGCAGCATCCCTGCACCCGCCGAGGCCGAGGCCTGGAGCCCCCGGAAG
TTGCCATCCTCAGCCTCCACCTTCCTCTCCCCAGCTTTTCCAGGCTCCCAGACCCATTCA
GGGCCTGAGCTCGGCCTGGTCCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCCATCTCCA
GCCCCTTCTTCTACCAAGCCAGGCCCAGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGC
CCCTTTCCGTTTTGCTGGCCCCTCTGTGAGATTTCCCGGGGCACCCACAACTTCTCGGAG
GAGCTCAAGATCGGGGAGGGTGGCTTTGGGTGCGTGTACCGGGCGGTGATGAGGAACACG
GTGTATGCTGTGAAGAGGCTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAG
AGCTTCCTGACCGAGGTGGAGCAGCTGTCCAGGTTTCGTCACCCAAACATTGTGGACTTT
GCTGGCTACTGTGCTCAGAACGGCTTCTACTGCCTGGTGTACGGCTTCCTGCCCAACGGC
TCCCTGGAGGACCGTCTCCACTGCCAGACCCAGGCCTGCCCACCTCTCTCCTGGCCTCAG
CGACTGGACATCCTTCTGGGTACAGCCCGGGCAATTCAGTTTCTACATCAGGACAGCCCC
AGCCTCATCCATGGAGACATCAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCC
AAGCTGGGAGACTTTGGCCTGGCCCGGTTCAGCCGCTTTGCCGGGTCCAGCCCCAGCCAG
AGCAGCATGGTGGCCCGGACACAGACAGTGCGGGGCACCCTGGCCTACCTGCCCGAGGAG
TACATCAAGACGGGAAGGCTGGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTG
CTAGAGACCTTGGCTGGTCAGAGGGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTG
AAAGACCTGGTGGAAGAGGAGGCTGAGGAGGCTGGAGTGGCTTTGAGAAGCACCCAGAGC
ACACTGCAAGCAGGTCTGGCTGCAGATGCCTGGGCTGCTCCCATCGCCATGCAGATCTAC
AAGAAGCACCTGGACCCCAGGCCCGGGCCCTGCCCACCTGAGCTGGGCCTGGGCCTGGGC
CAGCTGGCCTGCTGCTGCCTGCACCGCCGGGCCAAAAGGAGGCCTCCTATGACCCAGGAG
AACTCCTACGTGTCCAGCACTGGCAGAGCCCACAGTGGGGCTGCTCCATGGCAGCCCCTG
GCAGCGCCATCAGGAGCCAGTGCCCAGGCAGCAGAGCAGCTGCAGAGAGGCCCCAACCAG
CCCGTGGAGAGTGACGAGAGCCTAGGCGGCCTCTCTGCTGCCCTGCGCTCCTGGCACTTG
ACTCCAAGCTGCCCTCTGGACCCAGCACCCCTCAGGGAGGCCGGCTGTCCTCAGGGGGAC
ACGGCAGGAGAATCGAGCTGGGGGAGTGGCCCAGGATCCCGGCCCACAGCCGTGGAAGGA
CTGGCCCTTGGCAGCTCTGCATCATCGTCGTCAGAGCCACCGCAGATTATCATCAACCCT
GCCCGACAGAAGATGGTCCAGAAGCTGGCCCTGTACGAGGATGGGGCCCTGGACAGCCTG
CAGCTGCTGTCGTCCAGCTCCCTCCCAGGCTTGGGCCTGGAACAGGACAGGCAGGGGCCC
GAAGAAAGTGATGAATTTCAGAGCTGA

Fig. 50

SEQ ID No. 50
IRAK1
>ENSG00000184216|X|protein_coding|ENST00000369974|ENSP00000358991
ATGGCCGGGGGGCCGGGCCCGGGGGAGCCCGCAGCCCCCGGCGCCCAGCACTTCTTGTAC
GAGGTGCCGCCCTGGGTCATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCCCGCC
GACTGGTGCCAGTTCGCCGCCCTGATCGTGCGCGACCAGACCGAGCTGCGGCTGTGCGAG
CGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAACGCCCGTGTG
GCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGTGCGCGGGACATCATCACA
GCCTGGCACCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACTGCCCCGAGGCCCAGCAGC
ATCCCTGCACCCGCCGAGGCCGAGGCCTGGAGCCCCCGGAAGTTGCCATCCTCAGCCTCC
ACCTTCCTCTCCCCAGCTTTTCCAGGCTCCCAGACCCATTCAGGGCCTGAGCTCGGCCTG
GTCCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCCATCTCCAGCCCCTTCTTCTACCAAG
CCAGGCCCAGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGCCCCTTTCCGTTTTGCTGG
CCCCTCTGTGAGATTTCCCGGGGCACCCACAACTTCTCGGAGGAGCTCAAGATCGGGGAG
GGTGGCTTTGGGTGCGTGTACCGGGCGGTGATGAGGAACACGGTGTATGCTGTGAAGAGG
CTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAGAGCTTCCTGACCGAGGTG
GAGCAGCTGTCCAGGTTTCGTCACCCAAACATTGTGGACTTTGCTGGCTACTGTGCTCAG
AACGGCTTCTACTGCCTGGTGTACGGCTTCCTGCCCAACGGCTCCCTGGAGGACCGTCTC
CACTGCCAGACCCAGGCCTGCCCACCTCTCTCCTGGCCTCAGCGACTGGACATCCTTCTG
GGTACAGCCCGGGCAATTCAGTTTCTACATCAGGACAGCCCCAGCCTCATCCATGGAGAC
ATCAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCCAAGCTGGGAGACTTTGGC
CTGGCCCGGTTCAGCCGCTTTGCCGGGTCCAGCCCCAGCCAGAGCAGCATGGTGGCCCGG
ACACAGACAGTGCGGGGCACCCTGGCCTACCTGCCCGAGGAGTACATCAAGACGGGAAGG
CTGGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTGCTAGAGACCTTGGCTGGT
CAGAGGGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTGGTGTACGAGAGGCTAGAG
AAGCTGCAGGCAGTGGTGGCGGGGGTGCCCGGGCATTCGGAGGCCGCCAGCTGCATCCCC
CCTTCCCCGCAGGAGAACTCCTACGTGTCCAGCACTGGCAGAGCCCACAGTGGGGCTGCT
CCATGGCAGCCCCTGGCAGCGCCATCAGGAGCCAGTGCCCAGGCAGCAGAGCAGCTGCAG
AGAGGCCCCAACCAGCCCGTGGAGAGTGACGAGAGCCTAGGCGGCCTCTCTGCTGCCCTG
CGCTCCTGGCACTTGACTCCAAGCTGCCCTCTGGACCCAGCACCCCTCAGGGAGGCCGGC
TGTCCTCAGGGGGACACGGCAGGAGAATCGAGCTGGGGGAGTGGCCCAGGATCCCGGCCC
ACAGCCGTGGAAGGACTGGCCCTTGGCAGCTCTGCATCATCGTCGTCAGAGCCACCGCAG
ATTATCATCAACCCTGCCCGACAGAAGATGGTCCAGAAGCTGGCCCTGTACGAGGATGGG
GCCCTGGACAGCCTGCAGCTGCTGTCGTCCAGCTCCCTCCCAGGCTTGGGCCTGGAACAG
GACAGGCAGGGGCCCGAAGAAAGTGATGAATTTCAGAGCTGA

Fig. 51

SEQ ID No. 51
IRAK1
>ENSG00000184216|X|protein_coding|ENST00000393682|ENSP00000377287
ATGGCCGGGGGGCCGGGCCCGGGGGAGCCCGCAGCCCCCGGCGCCCAGCACTTCTTGTAC
GAGGTGCCGCCCTGGGTCATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCCCGCC
GACTGGTGCCAGTTCGGTGGGTGGCGGCGGGCTGCCGGGGGGCGGGAGGCGCGCGGGCTC
CTGGCGCCGACGCCTGACGCCCCCCGCCCCGCAGCCGCCCTGATCGTGCGCGACCAGACC
GAGCTGCGGCTGTGCGAGCGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATC
AACCGCAACGCCCGTGTGGCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGT
GCGCGGGACATCATCACAGCCTGGCACCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACT
GCCCCGAGGCCCAGCAGCATCCCTGCACCCGCCGAGGCCGAGGCCTGGAGCCCCCGGAAG
TTGCCATCCTCAGCCTCCACCTTCCTCTCCCCAGCTTTTCCAGGCTCCCAGACCCATTCA
GGGCCTGAGCTCGGCCTGGTCCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCCATCTCCA
GCCCCTTCTTCTACCAAGCCAGGCCCAGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGC
CCCTTTCCGTTTTGCTGGCCCCTCTGTGAGATTTCCCGGGGCACCCACAACTTCTCGGAG
GAGCTCAAGATCGGGGAGGGTGGCTTTGGGTGCGTGTACCGGGCGGTGATGAGGAACACG
GTGTATGCTGTGAAGAGGCTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAG
AGCTTCCTGACCGAGGTGGAGCAGCTGTCCAGGTTTCGTCACCCAAACATTGTGGACTTT
GCTGGCTACTGTGCTCAGAACGGCTTCTACTGCCTGGTGTACGGCTTCCTGCCCAACGGC
TCCCTGGAGGACCGTCTCCACTGCCAGACCCAGGCCTGCCCACCTCTCTCCTGGCCTCAG
CGACTGGACATCCTTCTGGGTACAGCCCGGGCAATTCAGTTTCTACATCAGGACAGCCCC
AGCCTCATCCATGGAGACATCAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCC
AAGCTGGGAGACTTTGGCCTGGCCCGGTTCAGCCGCTTTGCCGGGTCCAGCCCCAGCCAG
AGCAGCATGGTGGCCCGGACACAGACAGTGCGGGGCACCCTGGCCTACCTGCCCGAGGAG
TACATCAAGACGGGAAGGCTGGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTG
CTAGAGACCTTGGCTGGTCAGAGGGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTG
AAAGACCTGGTGGAAGAGGAGGCTGAGGAGGCTGGAGTGGCTTTGAGAAGCACCCAGAGC
ACACTGCAAGCAGGTCTGGCTGCAGATGCCTGGGCTGCTCCCATCGCCATGCAGATCTAC
AAGAAGCACCTGGGCCAGCTGGCCTGCTGCTGCCTGCACCGCCGGGCCAAAAGGAGGCCT
CCTATGACCCAGGAGAACTCCTACGTGTCCAGCACTGGCAGAGCCCACAGTGGGGCTGCT
CCATGGCAGCCCCTGGCAGCGCCATCAGGAGCCAGTGCCCAGGCAGCAGAGCAGCTGCAG
AGAGGCCCCAACCAGCCCGTGGAGAGTGACGAGAGCCTAGGCGGCCTCTCTGCTGCCCTG
CGCTCCTGGCACTTGACTCCAAGCTGCCCTCTGGACCCAGCACCCCTCAGGGAGGCCGGC
TGTCCTCAGGGGGACACGGCAGGAGAATCGAGCTGGGGGAGTGGCCCAGGATCCCGGCCC
ACAGCCGTGGAAGGACTGGCCCTTGGCAGCTCTGCATCATCGTCGTCAGAGCCACCGCAG
ATTATCATCAACCCTGCCCGACAGAAGATGGTCCAGAAGCTGGCCCTGTACGAGGATGGG
GCCCTGGACAGCCTGCAGCTGCTGTCGTCCAGCTCCCTCCCAGGCTTGGGCCTGGAACAG
GACAGGCAGGGGCCCGAAGAAAGTGATGAATTTCAGAGCTGA

Fig. 52

SEQ ID No. 52
IRAK1
>ENSG00000184216|X|protein_coding|ENST00000393687|ENSP00000377291
ATGGCCGGGGGGCCGGGCCCGGGGGAGCCCGCAGCCCCCGGCGCCCAGCACTTCTTGTAC
GAGGTGCCGCCCTGGGTCATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCCCGCC
GACTGGTGCCAGTTCGCCGCCCTGATCGTGCGCGACCAGACCGAGCTGCGGCTGTGCGAG
CGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAACGCCCGTGTG
GCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGTGCGCGGGACATCATCACA
GCCTGGCACCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACTGCCCCGAGGCCCAGCAGC
ATCCCTGCACCCGCCGAGGCCGAGGCCTGGAGCCCCCGGAAGTTGCCATCCTCAGCCTCC
ACCTTCCTCTCCCCAGCTTTTCCAGGCTCCCAGACCCATTCAGGGCCTGAGCTCGGCCTG
GTCCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCCATCTCCAGCCCCTTCTTCTACCAAG
CCAGGCCCAGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGCCCCTTTCCGTTTTGCTGG
CCCCTCTGTGAGATTTCCCGGGGCACCCACAACTTCTCGGAGGAGCTCAAGATCGGGGAG
GGTGGCTTTGGGTGCGTGTACCGGGCGGTGATGAGGAACACGGTGTATGCTGTGAAGAGG
CTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAGAGCTTCCTGACCGAGGTG
GAGCAGCTGTCCAGGTTTCGTCACCCAAACATTGTGGACTTTGCTGGCTACTGTGCTCAG
AACGGCTTCTACTGCCTGGTGTACGGCTTCCTGCCCAACGGCTCCCTGGAGGACCGTCTC
CACTGCCAGACCCAGGCCTGCCCACCTCTCTCCTGGCCTCAGCGACTGGACATCCTTCTG
GGTACAGCCCGGGCAATTCAGTTTCTACATCAGGACAGCCCCAGCCTCATCCATGGAGAC
ATCAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCCAAGCTGGGAGACTTTGGC
CTGGCCCGGTTCAGCCGCTTTGCCGGGTCCAGCCCCAGCCAGAGCAGCATGGTGGCCCGG
ACACAGACAGTGCGGGGCACCCTGGCCTACCTGCCCGAGGAGTACATCAAGACGGGAAGG
CTGGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTGCTAGAGACCTTGGCTGGT
CAGAGGGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTGAAAGACCTGGTGGAAGAG
GAGGCTGAGGAGGCTGGAGTGGCTTTGAGAAGCACCCAGAGCACACTGCAAGCAGGTCTG
GCTGCAGATGCCTGGGCTGCTCCCATCGCCATGCAGATCTACAAGAAGCACCTGGACCCC
AGGCCCGGGCCCTGCCCACCTGAGCTGGGCCTGGGCCTGGGCCAGCTGGCCTGCTGCTGC
CTGCACCGCCGGGCCAAAAGGAGGCCTCCTATGACCCAGGAGAACTCCTACGTGTCCAGC
ACTGGCAGAGCCCACAGTGGGGCTGCTCCATGGCAGCCCCTGGCAGCGCCATCAGGAGCC
AGTGCCCAGGCAGCAGAGCAGCTGCAGAGAGGCCCCAACCAGCCCGTGGAGAGTGACGAG
AGCCTAGGCGGCCTCTCTGCTGCCCTGCGCTCCTGGCACTTGACTCCAAGCTGCCCTCTG
GACCCAGCACCCCTCAGGGAGGCCGGCTGTCCTCAGGGGGACACGGCAGGAGAATCGAGC
TGGGGGAGTGGCCCAGGATCCCGGCCCACAGCCGTGGAAGGACTGGCCCTTGGCAGCTCT
GCATCATCGTCGTCAGAGCCACCGCAGATTATCATCAACCCTGCCCGACAGAAGATGGTC
CAGAAGCTGGCCCTGTACGAGGATGGGGCCCTGGACAGCCTGCAGCTGCTGTCGTCCAGC
TCCCTCCCAGGCTTGGGCCTGGAACAGGACAGGCAGGGGCCCGAAGAAAGTGATGAATTT
CAGAGCTGA

Fig. 53

SEQ ID No. 53
C20orf149
>ENSG00000125534|20|protein_coding|ENST00000370177|ENSP00000359196
ATGGCGGCCATCCCCTCCAGCGGCTCGCTCGTGGCCACCCACGACTACTACCGGCGCCGC
CTGGGTTCCACTTCCAGCAACAGCTCCTGCAGCAGTACCGAGTGCCCCGGGGAAGCCATT
CCCCACCCCCCAGGTGAGTGCAGGATCGCCCCTTTCTCCCCCCGCTCCTCCAGGAGCTGG
CAGCATCAAGACCCCACTTCGCTTCTCTCAGGTCTCCCCAAGGCTGACCCGGGTCATTGG
TGGGCCAGCTTCTTTTTCGGGAAGTCCACCCTCCCGTTCATGGCCACGGTGTTGGAGTCC
GCAGAGCACTCGGAACCTCCCCAGGCCTCCAGCAGCATGACCGCCTGTGGCCTGGCTCGG
GACGCCCCGAGGAAGCAGCCCGGCGGTCAGTCCAGCACAGCCAGCGCTGGGCCCCCGTCC
TGA

Fig. 54

SEQ ID No. 54
C20orf149
>ENSG00000125534|20|protein_coding|ENST00000370178|ENSP00000359197
ATGGCGGCCATCCCCTCCAGCGGCTCGCTCGTGGCCACCCACGACTACTACCGGCGCCGC
CTGGGTTCCACTTCCAGCAACAGCTCCTGCAGCAGTACCGAGTGCCCCGGGGAAGCCATT
CCCCACCCCCCAGGTCTCCCCAAGGCTGACCCGGGTCATTGGTGGGCCAGCTTCTTTTTC
GGGAAGTCCACCCTCCCACCCCCCACCCTGTAA

Fig. 55

SEQ ID No. 55
C20orf149
>ENSG00000125534|20|protein_coding|ENST00000370179|ENSP00000359198
ATGGCGGCCATCCCCTCCAGCGGCTCGCTCGTGGCCACCCACGACTACTACCGGCGCCGC
CTGGGTTCCACTTCCAGCAACAGCTCCTGCAGCAGTACCGAGTGCCCCGGGGAAGCCATT
CCCCACCCCCCAGGTCTCCCCAAGGCTGACCCGGGTCATTGGTGGGCCAGCTTCTTTTTC
GGGAAGTCCACCCTCCCGTTCATGGCCACGGTGTTGGAGTCCGCAGAGCACTCGGAACCT
CCCCAGGCCTCCAGCAGCATGACCGCCTGTGGCCTGGCTCGGGACGCCCCGAGGAAGCAG
CCCGGCGGTCAGTCCAGCACAGCCAGCGCTGGGCCCCCGTCCTGA

Fig. 56

SEQ ID No. 56
PSCD2L
>ENSG00000105443|19|protein_coding|ENST00000325139|ENSP00000314566
ATGGAGGACGGCGTCTATGAACCCCCAGACCTGACTCCGGAGGAGCGGATGGAGCTGGAG
AACATCCGGCGGCGGAAGCAGGAGCTGCTGGTGGAGATTCAGCGCCTGCGGGAGGAGCTC
AGTGAAGCCATGAGCGAGGTGGAGGGGCTGGAGGCCAATGAGGGCAGTAAGACCTTGCAA
CGGAACCGGAAGATGGCAATGGGCAGGAAGAAGTTCAACATGGACCCCAAGAAGGGGATC
CAGTTCTTGGTGGAGAATGAACTGCTGCAGAACACACCCGAGGAGATCGCCCGCTTCCTG
TACAAGGGCGAGGGGCTGAACAAGACAGCCATCGGGGACTACCTGGGGGGAGAGGGAAGAA
CTGAACCTGGCAGTGCTCCATGCTTTTGTGGATCTGCATGAGTTCACCGACCTCAATCTG
GTGCAGGCCCTCAGGCAGTTTCTATGGAGCTTTCGCCTACCCGGAGAGGCCCAGAAAATT
GACCGGATGATGGAGGCCTTCGCCCAGCGATACTGCCTGTGCAACCCTGGGGTTTTCCAG
TCCACAGACACGTGCTATGTGCTGTCCTTCGCCGTCATCATGCTCAACACCAGTCTCCAC
AATCCCAATGTCCGGGACAAGCCGGGCCTGGAGCGCTTTGTGGCCATGAACCGGGGCATC
AACGAGGGCGGGGACCTGCCTGAGGAGCTGCTCAGGAACCTGTACGACAGCATCCGAAAT
GAGCCCTTCAAGATTCCTGAGGATGACGGGAATGACCTGACCCACACCTTCTTCAACCCG
GACCGGGAGGGCTGGCTCCTGAAGCTGGGTAGGGGCCGGGTGAAGACGTGGAAGCGGCGC
TGGTTTATCCTCACAGACAACTGCCTCTACTACTTTGAGTACACCACGGACAAGGAGCCC
CGAGGAATCATCCCCCTGGAGAATCTGAGCATCCGAGAGGTGGACGACCCCCGGAAACCG
AACTGCTTTGAACTTTACATCCCCAACAACAAGGGGCAGCTCATCAAAGCCTGCAAAACT
GAGGCGGACGGCCGAGTGGTGGAGGGAAACCACATGGTGTACCGGATCTCGGCCCCCACG
CAGGAGGAGAAGGACGAGTGGATCAAGTCCATCCAGGCGGCTGTGAGTGTGGACCCCTTC
TATGAGATGCTGGCAGCGAGAAAGAAGCGGATTTCAGTCAAGAAGAAGCAGGAGCAGCCC
TGA

Fig. 57

SEQ ID No. 57
PSCD2L
>ENSG00000105443|19|protein_coding|ENST00000391881|ENSP00000375753
ATGGAGGACGGCGTCTATGAACCCCCAGACCTGACTCCGGAGGAGCGGATGGAGCTGGAG
AACATCCGGCGGCGGAAGCAGGAGCTGCTGGTGGAGATTCAGCGCCTGCGGGAGGAGCTC
AGTGAAGCCATGAGCGAGGTGGAGGGGCTGGAGGCCAATGAGGGCAGTAAGACCTTGCAA
CGGAACCGGAAGATGGCAATGGGCAGGAAGAAGTTCAACATGGACCCCAAGAAGGGGATC
CAGTTCTTGGTGGAGAATGAACTGCTGCAGAACACACCCGAGGAGATCGCCCGCTTCCTG
TACAAGGGCGAGGGGCTGAACAAGACAGCCATCGGGGACTACCTGGGGGAGAGGGAAGAA
CTGAACCTGGCAGTGCTCCATGCTTTTGTGGATCTGCATGAGTTCACCGACCTCAATCTG
GTGCAGGCCCTCAGGCAGTTTCTATGGAGCTTTCGCCTACCCGGAGAGGCCCAGAAAATT
GACCGGATGATGGAGGCCTTCGCCCAGCGATACTGCCTGTGCAACCCTGGGGTTTTCCAG
TCCACAGACACGTGCTATGTGCTGTCCTTCGCCGTCATCATGCTCAACACCAGTCTCCAC
AATCCCAATGTCCGGGACAAGCCGGGCCTGGAGCGCTTTGTGGCCATGAACCGGGGCATC
AACGAGGGCGGGGACCTGCCTGAGGAGCTGCTCAGGAACCTGTACGACAGCATCCGAAAT
GAGCCCTTCAAGATTCCTGAGGATGACGGGAATGACCTGACCCACACCTTCTTCAACCCG
GACCGGGAGGGCTGGCTCCTGAAGCTGGGGGGCCGGGTGAAGACGTGGAAGCGGCGCTGG
TTTATCCTCACAGACAACTGCCTCTACTACTTTGAGTACACCACGGACAAGGAGCCCCGA
GGAATCATCCCCCTGGAGAATCTGAGCATCCGAGAGGTGGACGACCCCCGGAAACCGAAC
TGCTTTGAACTTTACATCCCCAACAACAAGGGGCAGCTCATCAAAGCCTGCAAAACTGAG
GCGGACGGCCGAGTGGTGGAGGGAAACCACATGGTGTACCGGATCTCGGCCCCCACGCAG
GAGGAGAAGGACGAGTGGATCAAGTCCATCCAGGCGGCTGTGAGTGTGGACCCCTTCTAT
GAGATGCTGGCAGCGAGAAAGAAGCGGATTTCAGTCAAGAAGAAGCAGGAGCAGCCCTGA

Fig. 58

SEQ ID No. 58
PPIA
>ENSG00000198618|21|protein_coding|ENST00000358455|ENSP00000351238
ATGGTCAACCCCACCGTGTTCTTCGACATTGCCGTCGACGGCGAGCCCTTGGGCCGCGTC
TCCTTTGAGCTGTTTGCAGACAAGGTCCCAAAGACAGCAGAAAATTTTCGTGCTCTGAGC
ACTGGAGAGAAAGGATTTGGTTATAAGGGTTCCTGCTTTCACAGAATTATTCCAGGGTTT
ATGTGTCAGGGTGGTGACTTCACACGCCATAATGGCACTGGTGGCAAGTCCATCTATGGG
GAGAAATTTGAAGATGAGAACTTCATCCTAAAGCATACAGGTCCTGGCATCTTGTCCATG
GCAAATGCTGGACCCAACACAAATGGATCCCAGTTTTTCATCTGCACTGCCAAGACTGAG
TGGTTGGATGGCAAGCATGTGGTGTTTGGCAAAGTGAAAGAAGGCATGAATATTGTGGAG
GCCATGGAGCGCTTTGGGTCCAGGAATGGCAAGACCAGCAAGAAGATCACCATTGCTGAC
TGTGGACAACTCGAATAA

Fig. 59

SEQ ID No. 59
MGTRDDEYDYLFKVVLIGDSGVGKSNLLSRFTRNEFNLESKSTIGVEFATRSIQVDGKTI
KAQIWDTAGQERYRAITSAYYRGAVGALLVYDIAKHLTYENVERWLKELRDHADSNIVIM
LVGNKSDLRHLRAVPTDEARAFAEKNNLSFIETSALDSTNVEEAFKNILTEIYRIVSQKQ
IADRAAHDESPGNNVVDISVPPTTDGQKPNKLQCCQNL*

Fig. 60

SEQ ID No. 60
MAAADGDDSLYPIAVLIDELRNEDVQLRLNSIKKLSTIALALGVERTRSELLPFLTDTIY
DEDEVLLALAEQLGTFTTLVGGPEYVHCLLPPLESLATVEETVVRDKAVESLRAISHEHS
PSDLEAHFVPLVKRLAGGDWFTSRTSACGLFSVCYPRVSSAVKAELRQYFRNLCSDDTPM
VRRAAASKLGEFAKVLELDNVKSEIIPMFSNLASDEQDSVRLLAVEACVNIAQLLPQEDL
EALVMPTLRQAAEDKSWRVRYMVADKFTELQKAVGPEITKTDLVPAFQNLMKDCEAEVRA
AASHKVKEFCENLSADCRENVIMSQILPCIKELVSDANQHVKSALASVIMGLSPILGKDN
TIEHLLPLFLAQLKDECPEVRLNIISNLDCVNEVIGIRQLSQSLLPAIVELAEDAKWRVR
LAIIEYMPLLAGQLGVEFFDEKLNSLCMAWLVDHVYAIREAATSNLKKLVEKFGKEWAHA
TIIPKVLAMSGDPNYLHRMTTLFCINVLSEVCGQDITTKHMLPTVLRMAGDPVANVRFNV
AKSLQKIGPILDNSTLQSEVKPILEKLTQDQDVDVKYFAQEALTVLSLA*

Fig. 61

SEQ ID No. 61
MRTFSFASTASRSCPPSPWPLGLKGPEVSFCLSLQIPSMMKMRSSWPWQNSWEPSLPWWE
AQSTCTACCLFSVCYPRVSSAVKAELRQYFRNLCSDDTPMVRRAAASKLGEFAKVLELDN
VKSEIIPMFSNLASDEQDSVRLLAVEACVNIAQLLPQEDLEALVMPTLRQAAEDKSWRVR
YMVADKFTELQKAVGPEITKTDLVPAFQNLMKDCEAEVRAAASHKVKEFCENLSADCREN
VIMSQILPCIKELVSDANQHVKSALASVIMGLSPILGKDNTIEHLLPLFLAQLKDECPEV
RLNIISNLDCVNEVIGIRQLSQSLLPAIVELAEDAKWRVRLAIIEYMPLLAGQLGVEFFD
EKLNSLCMAWLVDHVYAIREAATSNLKKLVEKFGKEWAHATIIPKVLAMSGDPNYLHRMT
TLFCINVLSEVCGQDITTKHMLPTVLRMAGDPVANVRFNVAKSLQKIGPILDNSTLQSEV
KPILEKLTQDQDVDVKYFAQEALTVLSLA*

Fig. 62

SEQ ID No. 62
MELITILEKTVSPDRLELEAAQKFLERAAVENLPTFLVELSRVLANPGNSQVARVAAGLQ
IKNSLTSKDPDIKAQYQQRWLAIDANARREVKNYVLQTLGTETYRPSSASQCVAGIACAE
IPVNQWPELIPQLVANVTNPNSTEHMKESTLEAIGYICQDIDPEQLQDKSNEILTAIIQG
MRKEEPSNNVKLAATNALLNSLEFTKANFDKESERHFIMQVVCEATQCPDTRVRVAALQN
LVKIMSLYYQYMETYMGPALFAITIEAMKSDIDEVALQGIEFWSNVCDEEMDLAIEASEA
AEQGRPPEHTSKFYAKGALQYLVPILTQTLTKQDENDDDDDWNPCKAAGVCLMLLATCCE
DDIVPHVLPFIKEHIKNPDWRYRDAAVMAFGCILEGPEPSQLKPLVIQAMPTLIELMKDP
SVVVRDTAAWTVGRICELLPEAAINDVYLAPLLQCLIEGLSAEPRVASNVCWAFSSLAEA
AYEAADVADDQEEPATYCLSSSFELIVQKLLETTDRPDGHQNNLRSSAYESLMEIVKNSA
KDCYPAVQKTTLVIMERLQQVLQMESHIQSTSDRIQFNDLQSLLCATLQNVLRKVQHQDA
LQISDVVMASLLRMFQSTAGSGGVQEDALMAVSTLVEVLGGEFLKYMEAFKPFLGIGLKN
YAEYQVCLAAVGLVGDLCRALQSNIIPFCDEVMQLLLENLGNENVHRSVKPQILSVFGDI
ALAIGGEFKKYLEVVLNTLQQASQAQVDKSDYDMVDYLNELRESCLEAYTGIVQGLKGDQ
ENVHPDVMLVQPRVEFILSFIDHIAGDEDHTDGVVACAAGLIGDLCTAFGKDVLKLVEAR
PMIHELLTEGRRSKTNKAKTLATWATKELRKLKNQA*

Fig. 64

SEQ ID No. 64
MGTKMADLDSPPKLSGVQQPSEGVGGGRCSEISAELIRSLTELQELEAVYERLCGEEKVV
ERELDALLEQQNTIESKMVTLHRMGPNLQLIEGDAKQLAGMITFTCNLAENVSSKVRQLD
LAKNRLYQAIQRADDILDLKFCMDGVQTALRSEDYEQAAAHTHRYLCLDKSVIELSRQGK
EGSMIDANLKLLQEAEQRLKAIVAEKFAIATKEGDLPQVERFFKIFPLLGLHEEGLRKFS
EYLCKQVASKAEENLLMVLGTDMSDRRAAVIFADTLTLLFEGIARIVETHQPIVETYYGP
GRLYTLIKYLQVECDRQVEKVVDKFIKQRDYHQQFRHVQNNLMRNSTTEKIEPRELDPIL
TEVTLMNARSELYLRFLKKRISSDFEVGDSMASEEVKQEHQKCLDKLLNNCLLSCTMQEL
IGLYVTMEEYFMRETVNKAVALDTYEKGQLTSSMVDDVFYIVKKCIGRALSSSSIDCLCA
MINLATTELESDFRDVLCNKLRMGFPATTFQDIQRGVTSAVNIMHSSLQQGKFDTKGIES
TDEAKMSFLVTLNNVEVCSENISTLKKTLESDCTKLFSQGIGGEQAQAKFDSCLSDLAAV
SNKFRDLLQEGLTELNSTAIKPQVQPWINSFFSVSHNIEEEEFNDYEANDPWVQQFILNL
EQQMAEFKASLSPVIYDSLTGLMTSLVAVELEKVVLKSTFNRLGGLQFDKELRSLIAYLT
TVTTWTIRDKFARLSQMATILNLERVTEILDYWGPNSGPLTWRLTPAEVRQVLALRIDFR
SEDIKRLRL*

Fig. 65

SEQ ID No. 65
MADLDSPPKLSGVQQPSEGVGGGRCSEISAELIRSLTELQELEAVYERLCGEEKVVEREL
DALLEQQNTIESKMVTLHRMGPNLQLIEGDAKQLAGMITFTCNLAENVSSKVRQLDLAKN
RLYQAIQRADDILDLKFCMDGVQTALRSEDYEQAAAHTHRYLCLDKSVIELSRQGKEGSM
IDANLKLLQEAEQRLKAIVAEKFAIATKEGDLPQVERFFKIFPLLGLHEEGLRKFSEYLC
KQVASKAEENLLMVLGTDMSDRRAAVIFADTLTLLFEGIARIVETHQPIVETYYGPGRLY
TLIKYLQVECDRQVEKVVDKFIKQRDYHQQFRHVQNNLMRNSTTEKIEPRELDPILTEVT
LMNARSELYLRFLKKRISSDFEVGDSMASEEVKQEHQKCLDKLLNNCLLSCTMQELIGLY
VTMEEYFMRETVNKAVALDTYEKGQLTSSMVDDVFYIVKKCIGRALSSSSIDCLCAMINL
ATTELESDFRDVLCNKLRMGFPATTFQDIQRGVTSAVNIMHSSLQQGKFDTKGIESTDEA
KMSFLVTLNNVEVCSENISTLKKTLESDCTKLFSQGIGGEQAQAKFDSCLSDLAAVSNKF
RDLLQEGLTELNSTAIKPQVQPWINSFFSVSHNIEEEEFNDYEANDPWVQQFILNLEQQM
AEFKASLSPVIYDSLTGLMTSLVAVELEKVVLKSTFNRLGGLQFDKELRSLIAYLTTVTT
WTIRDKFARLSQMATILNLERVTEILDYWGPNSGPLTWRLTPAEVRQVLALRIDFRSEDI
KRLRL*

Fig. 66

SEQ ID No. 66
MADLDSPPKLSGVQQPSEGVGGGRCSEISAELIRSLTELQELEAVYERLCGEEKVVEREL
DALLEQQNTIESKMVTLHRMGPNLQLIEGDAKQLAGMITFTCNLAENVSSKVRQLDLAKN
RLYQAIQRADDILDLKFCMDGVQTALRSEDYEQAAAHTHRYLCLDKSVIELSRQGKEGSM
IDANLKLLQEAEQRLKAIVAEKFAIATKEGDLPQVERFFKIFPLLGLHEEGLRKFSEYLC
KQVASKAEENLLMVLGTDMSDRRAAVIFADTLTLLFEGIARIVETHQPIVETYYGPGRLY
TLIKYLQVECDRQVEKVVDKFIKQRDYHQQNFVFSFF*

Fig. 67

SEQ ID No. 67

MGTKMADLDSPPKLSGVQQPSEGVGGGRCSEISAELIRSLTELQELEAVYERLCGEEKVV
ERELDALLEQQNTIESKMVTLHRMGPNLQLIEANLKLLQEAEQRLKAIVAEKFAIATKEG
DLPQVERFFKIFPLLGLHEEGLRKFSEYLCKQVASKAEENLLMVLGTDMSDRRAAVIFAD
TLTLLFEGIARIVETHQPIVETYYGPGRLYTLIKYLQVECDRQVEKVVDKFIKQRDYHQQ
FRHVQNNLMRNSTTEKIEPRELDPILTEVTLMNARSELYLRFLKKRISSDFEVGDSMASE
EVKQEHQKCLDKLLNNCLLSCTMQELIGLYVTMEEYFMRETVNKAVALDTYEKGQLTSSM
VDDVFYIVKKCIGRALSSSSIDCLCAMINLATTELESDFRDVLCNKLRMGFPATTFQDIQ
RGVTSAVNIMHSSLQQGKFDTKGIESTDEAKMSFLVTLNNVEVCSENISTLKKTLESDCT
KLFSQGIGGEQAQAKFDSCLSDLAAVSNKFRDLLQEGLTELNSTAIKPQVQPWINSFFSV
SHNIEEEEFNDYEANDPWVQQFILNLEQQMAEFKASLSPVIYDSLTGLMTSLVAVELEKV
VLKSTFNRLGGLQFDKELRSLIAYLTTVTTWTIRDKFARLSQMATILNLERVTEILDYWG
PNSGPLTWRLTPAEVRQVLALRIDFRSEDIKRLRL*

Fig. 68

SEQ ID No. 68
MEFVKCLGHPEEFYNLVRFRIGGKRKVMPKMDQDSLSSSLKTCYKYLNQTSRSFAAVIQA
LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ
VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG
IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDQQGGREFWPQEVWSRYV
KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL
AACYNNQQVFKGAVKIRKGQAVTLMMDATNMPAVKAIIYQYMEEIYHRIPDSDPSSSKTR
QIISTIRTQNLFNCQLISRSHYSPIYLSFVMLLAALSWQYLTTLSQVTEDYVQTGEH*

Fig. 69

SEQ ID No. 69
MRASQKDFENSMNQVKLLKKDPGNEVKLKLYALYKQATEGPCNMPKPGVFDLINKAKWDA
WNALGSLPKEAARQNYVDLVSSLSPSLESSSQVEPGTDRKSTGFETLVVTSEDGITKIMF
NRPKKKNAINTEMYHEIMRALKAASKDDSIITVLTGNGDYYSSGNDLTNFTDIPPGGVEE
KAKNNAVLLREFVGCFIDFPKPLIAVVNGPAVGISVTLLGLFDAVYASDRATFHTPFSHL
GQSPEGCSSYTFPKIMSPAKATEMLIFGKKLTAGEACAQGLVTEVFPDSTFQKEVWTRLK
AFAKLPPNALRISKEVIRKREREKLHAVNAEECNVLQGRWLSDECTNAVVNFLSRKSKL*

Fig. 70

SEQ ID No. 70
MYHEIMRALKAASKDDSIITVLTGNGDYYSSGNDLTNFTDIPPGGVEEKAKNNAVLLREF
VGCFIDFPKPLIAVVNGPAVGISVTLLGLFDAVYASDRATFHTPFSHLGQSPEGCSSYTF
PKIMSPAKATEMLIFGKKLTAGEACAQGLVTEVFPDSTFQKEVWTRLKAFAKLPPNALRI
SKEVIRKREREKLHAVNAEECNVLQGRWLSDECTNAVVNFLSRKSKL*

Fig. 71

SEQ ID No. 71
MAMAYLAWRLARRSCPSSLQVTSFPVVQLHMNRTAMRASQKDFENSMNQVKLLKKDPGNE
VKLKLYALYKQATEGPCNMPKPGVFDLINKAKWDAWNALGSLPKEAARQNYVDLVSSLSP
SLESSSQVEPGTDRKSTGFETLVVTSEDGITKIMFNRPKKKNAINTEMYHEIMRALKAAS
KDDSIITVLTGNGDYYSSGNDLTNFTDIPPGGVEEKAKNNAVLLREFVGCFIDFPKPLIA
VVNGPAVGISVTLLGLFDAVYASDRATFHTPFSHLGQSPEGCSSYTFPKIMSPAKATEML
IFGKKLTAGEACAQGLVTEVFPDSTFQKEVWTRLKAFAKLPPNALRISKEVIRKREREKL
HAVNAEECNVLQGRWLSDECTNAVVNFLSRKSKL*

Fig. 72

SEQ ID No. 72
MNRTAMRASQKDFENSMNQVKLLKKDPGNEVKLKLYALYKQATEGPCNMPKPGVFDLINK
AKWDAWNALGSLPKEAARQNYVDLVSSLSPSLESSSQVEPGTDRKSTGFETLVVTSEDGI
TKIMFNRPKKKNAINTEMYHEIMRALKAASKDDSIITVLTGNGDYYSSGNDLTNFTDIPP
GGVEEKAKNNAVLLREFVGCFIDFPKPLIAVVNGPAVGISVTLLGLFDAVYASDRATFHT
PFSHLGQSPEGCSSYTFPKIMSPAKATEMLIFGKKLTAGEACAQGLVTEVFPDSTFQKEV
WTRLKAFAKLPPNALRISKEVIRKREREKLHAVNAEECNVLQGRWLSDECTNAVVNFLSR
KSKL*

Fig. 73

SEQ ID No. 73
MFNRPKKKNAINTEMYHEIMRALKAASKDDSIITVLTGNGDYYSSGNDLTNFTDIPPGGV
EEKAKNNAVLLREFVGCFIDFPKPLIAVVNGPAVGISVTLLGLFDAVYASDRATFHTPFS
HLGQSPEGCSSYTFPKIMSPAKATEMLIFGKKLTAGEACAQGLVTEVFPDSTFQKEVWTR
LKAFAKLPPNALRISKEVIRKREREKLHAVNAEECNVLQGRWLSDECTNAVVNFLSRKSK
L*

Fig. 74

SEQ ID No. 74
MFARKPPGAAPLGAMPVPDQPSSASEKTSSLSPGLNTSNGDGSETETTSAILASVKEQEL
QFERLTRELEAERQIVASQLERCKLGSETGSMSSMSSAEEQFQWQSQDGQKDIEDELTTG
LELVDSCIRSLQESGILDPQDYSTGERPSLLSQSALQLNSKPEGSFQYPASYHSNQTLAL
GETTPSQLPARGTQARATGQSFSQGTTSRAGHLAGPEPAPPPPPPPREPFAPSLGSAFHL
PDAPPAAAAAAALYYSSSTLPAPPRGGSPLAAPQGGSPTKLQRGGSAPEGATYAAPRGSSP
KQSPSRLAKSYSTSSPINIVVSSAGLSPIRVTSPPTVQSTISSSPIHQLSSTIGTYATLS
PTKRLVHASEQYSKHSQELYATATLQRPGSLAAGSRASYSSQHGHLGPELRALQSPEHHI
DPIYEDRVYQKPPMRSLSQSQGDPLPPAHTGTYRTSTAPSSPGVDSVPLQRTGSQHGPQN
AAAATFQRASYAAGPASNYADPYRQLQYCPSVESPYSKSGPALPPEGTLARSPSIDSIQK
DPREFGWRDPELPEVIQMLQHQFPSVQSNAAAYLQHLCFGDNKIKAEIRRQGGIQLLVDL
LDHRMTEVHRSACGALRNLVYGKANDDNKIALKNCGGIPALVRLLRKTTDLEIRELVTGV
LWNLSSCDALKMPIIQDALAVLTNAVIIPHSGWENSPLQDDRKIQLHSSQVLRNATGCLR
NVSSAGEEARRRMRECDGLTDALLYVIQSALGSSEIDSKTVENCVCILRNLSYRLAAETS
QGQHMGTDELDGLLCGEANGKDAESSGCWGKKKKKKKSQDQWDGVGPLPDCAEPPKGIQM
LWHPSIVKPYLTLLSECSNPDTLEGAAGALQNLAAGSWKWSVYIRAAVRKEKGLPILVEL
LRIDNDRVVCAVATALRNMALDVRNKELIGKYAMRDLVHRLPGGNNSNNTASKAMSDDTV
TAVCCTLHEVITKNMENAKALRDAGGIEKLVGISKSKGDKHSPKVVKAASQVLNSMWQYR
DLRSLYKKDGWSQYHFVASSSTIERDRQRPYSSSRTPSISPVRVSPNNRSASAPASPREM
ISLKERKTDYECTGSNATYHGAKGEHTSRKDAMTAQNTGISTLYRNSYGAPAEDIKHNQV
SAQPVPQEPSRKDYETYQPFQNSTRNYDESFFEDQVHHRPPASEYTMHLGLKSTGNYVDF
YSAARPYSELNYETSHYPASPDSWV*

Fig. 75

SEQ ID No. 75
MFARKPPGAAPLGAMPVPDQPSSASEKTSSLSPGLNTSNGDGSETETTSAILASVKEQEL
QFERLTRELEAERQIVASQLERCKLGSETGSMSSMSSAEEQFQWQSQDGQKDIEDELTTG
LELVDSCIRSLQESGILDPQDYSTGERPSLLSQSALQLNSKPEGSFQYPASYHSNQTLAL
GETTPSQLPARGTQARATGQSFSQGTTSRAGHLAGPEPAPPPPPPPREPFAPSLGSAFHL
PDAPPAAAAAALYYSSSTLPAPPRGGSPLAAPQGGSPTKLQRGGSAPEGATYAAPRGSSP
KQSPSRLAKSYSTSSPINIVVSSAGLSPIRVTSPPTVQSTISSSPIHQLSSTIGTYATLS
PTKRLVHASEQYSKHSQELYATATLQRPGSLAAGSRASYSSQHGHLGPELRALQSPEHHI
DPIYEDRVYQKPPMRSLSQSQGDPLPPAHTGTYRTSTAPSSPGVDSVPLQRTGSQHGPQN
AAAATFQRASYAAGPASNYADPYRQLQYCPSVESPYSKSGPALPPEGTLARSPSIDSIQK
DPREFGWRDPELPEVIQMLQHQFPSVQSNAAAYLQHLCFGDNKIKAEIRRQGGIQLLVDL
LDHRMTEVHRSACGALRNLVYGKANDDNKIALKNCGGIPALVRLLRKTTDLEIRELVTGV
LWNLSSCDALKMPIIQDALAVLTNAVIIPHSGWENSPLQDDRKIQLHSSQVLRNATGCLR
NVSSAGEEARRRMRECDGLTDALLYVIQSALGSSEIDSKTVENCVCILRNLSYRLAAETS
QGQHMGTDELDGLLCGEANGKDAESSGCWGKKKKKKKSQDQWSVYIRAAVRKEKGLPILV
ELLRIDNDRVVCAVATALRNMALDVRNKELIGKYAMRDLVHRLPGGNNSNNTASKAMSDD
TVTAVCCTLHEVITKNMENAKALRDAGGIEKLVGISKSKGDKHSPKVVKAASQVLNSMWQ
YRDLRSLYKKDGWSQYHFVASSSTIERDRQRPYSSSRTPSISPVRVSPNNRSASAPASPR
EMISLKERKTDYECTGSNATYHGAKGEHTSRKDAMTAQNTGISTLYRNSYGAPAEDIKHN
QVSAQPVPQEPSRKDYETYQPFQNSTRNYDESFFEDQVHHRPPASEYTMHLGLKSTGNYV
DFYSAARPYSELNYETSHYPASPDSWV*

Fig. 76

SEQ ID No. 76
MQGSTRRMGVMTDVHRRFLQLLMTHGVLEEWDVKRLQTHCYKVHDRNATVDKLEDFINNI
NSVLESLYIEIKRGVTEDDGRPIYALVNLATTSISKMATDFAENELDLFRKALELIIDSE
TGFASSTNILNLVDQLKGKKMRKKEAEQVLQKFVQNKWLIEKEGEFTLHGRAILEMEQYI
RETYPDAVKICNICHSLLIQGQSCETCGIRMHLPCVAKYFQSNAEPRCPHCNDYWPHEIP
KVFDPEKERESGVLKSNKKSLRSRQH*

Fig. 77

SEQ ID No. 77
PYPLARWDALGLPVRSHMQGSTRRMGVMTDVHRRFLQLLMTHGVLEEWDVKRLQTHCYKV
HDRNATVDKLEDFINNINSVLESLYIEIKRGVTEDDGRPIYALVNLATTSISKMATDFAE
NELDLFRKALELIIDSETLRLPQTY*

Fig. 78

SEQ ID No. 78
VHLATVSASAAWDALGLPVRSHMQGSTRRMGVMTDVHRRFLQLLMTHGVLEEWDVKRLQT
HCYKVHDRNATVDKLEDFINNINSVLESLYIEIKRGVTEDDGRPIYALVNLATTSISKMA
TDFAENELDLFRKALELIIDSETGFASSTNILNLVDQLKGKKMRKKEARCCRSLFKTSG*

Fig. 79

SEQ ID No. 79
MEWWASSPLRLWLLLFLLPSAQGRQKESGSKWKVFIDQINRSLENYEPCSSQNCSCYHGV
IEEDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIG
RLPDMEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTG
LGRWDLFREDLVRSAAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQ
AWKSMKDTLGKPAAKDVHLVDHCKYKYLFNFRGVAASFRFKHLFLCGSLVFHVGDEWLEF
FYPQLKPWVHYIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWE
NLLSEYSKFLSYNVTRRKGYDQIIPKMLKTEL*

Fig. 80

SEQ ID No. 80
MRRRRAGGRTMVERASKFVLVVAGSVCFMLILYQYAGPGLSLGAPGGRAPPDDLDLFPTP
DPHYEKKYYFPVRELERSLRFDMKGDDVIVFLHIQKTGGTTFGRHLVQNVRLEVFCDCRP
GQKKCTCYRPNRRETWLFSRFSTGWSCGLHADWTELTNCVPGVLDRRDSAALRTPRKFYY
ITLLRDPVSRYLSEWRHVQRGATWKTSLHMCDGRTPTPEELPPCYEGTDWSGCTLQEFMD
CPYNLANNRQVRMLADLSLVGCYNLSFIPEGKRAQLLLESAKKNLRGMAFFGLTEFQRKT
QYLFERTFNLKFIRPFMQYNSTRAGGVEVDEDTIRRIEELNDLDMQLYDYAKDLFQQRYQ
YKRQLERREQRLRSREERLLHRAKEALPREDADEPGRVPTEDYMSHIIEKW*

Fig. 81

SEQ ID No. 81
MTSCRCSVTSRSLWPALAPRRCQHTSPASAQCKQDKACRFLAAQKGAYPIIFTAWKLATA
GDQGLLLQSLNALSVLTDGQPDLLDAQGLQLLVATLTQNADEADLTCSGIRCVRHACLKH
EQNRQDLVKAGVLPLLTGAITHHGHHTDVVREACWALRVMTFDDDIRVPFGHAHNHAKMI
VQENKGLKVLIEATKAFLDNPGILSELCGTLSRLAIRNEFCQEVVDLGGLSILVSLLADC
NDHQMRDQSGVQELVKQVLSTLRAIAGNDDVKDAIVRAGGTESIVAAMTQHLTSPQVCEQ
SCAALCFLALRKPDNSRIIVEGGGAVAALQAMKAHPQKAGVQKQACMLIRNLVAHRPSRS
PSWTWGLRHSSCRPDLPTVTVRTWPRPPCGTWVVMSSSESCGQARGATWRHDPRPSLVTL
GESCDSGMGVDPCPPLSPISSVPFTMRSVFWQALGKGSGEGGAL*

Fig. 82

SEQ ID No. 82
MSERCCSRYSSGASIGCTPTSTQAKMVSKRIAQETFDAAVRENIEEFAMGPEEAVKEAVE
QFESQGVDLSNIVKTAPKVSADGSQEPTHDILQMLSDLQESVASSRPQEVSAYLTRFCDQ
CKQDKACRFLAAQKGAYPIIFTAWKLATAGDQGLLLQSLNALSVLTDGQPDLLDAQGLQL
LVATLTQNADEADLTCSGIRCVRHACLKHEQNRQDLVKAGVLPLLTGAITHHGHHTDVVR
EACWALRVMTFDDDIRVPFGHAHNHAKMIVQENKGLKVLIEATKAFLDNPGILSELCGTL
SRLAIRNEFCQEVVDLGGLSILVSLLADCNDHQMRDQSGVQELVKQVLSTLRAIAGNDDV
KDAIVRAGGTESIVAAMTQHLTSPQVCEQSCAALCFLALRKPDNSRIIVEGGGAVAALQA
MKAHPQKAGVQKQACMLIRNLVAHGQAFSKPILDLGAEALIMQARSAHRDCEDVAKAALR
DLGCHVELRELWTGQRGNLAP*

Fig. 83

SEQ ID No. 83
MVSKRIAQETFDAAVRENIEEFAMGPEEAVKEAVEQFESQGVDLSNIVKTAPKVSADGSQ
EPTHDILQMLSDLQESVASSRPQEVSAYLTRFCDQCKQDKACRFLAAQKGAYPIIFTAWK
LATAGDQGLLLQSLNALSVLTDGQPDLLDAQGLQLLVATLTQNADEADLTCSGIRCVRHA
CLKHEQNRQDLVKAGVLPLLTGAITHHGHHTDVVREACWALRVMTFDDDIRVPFGHAHNH
AKMIVQENKGLKVLIEATKAFLDNPGILSELCGTLSRLAIRNEFCQEVVDLGGLSILVSL
LADCNDHQMRDQSGVQELVKQVLSTLRAIAGNDDVKDAIVRAGGTESIVAAMTQHLTSPQ
VCEQSCAALCFLALRKPDNSRIIVEGGGAVAALQAMKAHPQKAGVQKQACMLIRNLVAHG
QAFSKPILDLGAEALIMQARSAHRDCEDVAKAALRDLGCHVELRELWTGQRGNLAP*

Fig. 84

SEQ ID No. 84
MVSKRIAQETFDAAVRENIEEFAMGPEEAVKEAVEQFESQGVDLSNIVKTAPKVSADGSQ
EPTHDILQMLSDLQESVASSRPQEVSAYLTRFCDQCKQDKACRFLAAQKGAYPIIFTAWK
LATAGDQGLLLQSLNALSVLTDGQPDLLDAQGLQLLVATLTQNADEADLTCSGIRCVRHA
CLKHEQNRQDLVKAGVLPLLTGAITHHGHHTDVVREACWALRVMTFDDDIRVPFGHAHNH
AKMIVQENKGLKVLIEATKAFLDNPGILSELCGTLSRLAIRNEFCQEVVDLGGLSILVSL
LADCNDHQMRDQSGVQELVKQVLSTLRAIAGNDDVKDAIVRAGGTESIVAAMTQHLTSPQ
VCEQSCAALCFLALRKPDNSRIIVEGGGAVAALQAMKAHPQKAGVQKQACMLIRNLVAHG
QAFSKPILDLGAEALIMQARSAHRDCEDVAKAALRDLGCHVELRELWTGQRGNLAP*

Fig. 85

SEQ ID No. 85
MAGAVPGAIMDEDYYGSAAEWGDEADGGQQEDDSGEGEDDAEVQQECLHKFSTRDYIMEP
SIFNTLKRYFQAGGSPENVIQLLSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLK
SLLIKHFDPRKADSIFTEEGETPAWLEQMIAHTTWRDLFYKLAEAHPDCLMLNFTVKLIS
DAGYQGEITSVSTACQQLEVFSRVLRTSLATILDGGEENLEKNLPEFAKMVCHGEHTYLF
AQAMMSVLAQEEQGGSAVRRIAQEVQRFAQEKGHDASQITLALGTAASYPRACQALGAML
SKGALNPADITVLFKMFTSMDPPPVELIRVPAFLDLFMQSLFKPGARINQDHKHKYIHIL
AYAASVVETWKKNKRVSINKDELKSTSKAVETVHNLCCNENKGASELVAELSTLYQCIRF
PVVAMGVLKWVDWTVSEPRYFQLQTDHTPVHLALLDEISTCHQLLHPQVLQLLVKLFETE
HSQLDVMEQLELKKTLLDRMVHLLSRGYVLPVVSYIRKCLEKLDTDISLIRYFVTEVLDV
IAPPYTSDFVQLFLPILENDSIAGTIKTEGEHDPVTEFIAHCKSNFIMVN*

Fig. 86

SEQ ID No. 86
MAMLRVQPEAQAKVDVFREDLCTKTENLLGSYFPKKISELDAFLKEPALNEANLSNLKAP
LDIPVPDPVKEKEKEERKKQQEKEDKDEKKKGEDEDKGPPCGPVNCNEKIVVLLQRLKPE
IKDVIEQLNLVTTWLQLQIPRIEDGNNFGVAVQEKVFELMTSLHTKLEGFHTQISKYFSE
RGDAVTKAAKQPHVGDYRQLVHELDEAEYRDIRLMVMEIRNAYVRRQGQGRGGQRQLSQA
THSLTLQARG*

Fig. 87

SEQ ID No. 87
MAMLRVQPEAQAKVDVFREDLCTKTENLLGSYFPKKISELDAFLKEPALNEANLSNLKAP
LDIPVPDPVKEKEKEERKKQQEKEDKDEKKKGEDEDKGPPCGPVNCNEKIVVLLQRLKPE
IKDVIEQLNLVTTWLQLQIPRIEDGNNFGVAVQEKVFELMTSLHTKLEGFHTQISKYFSE
RGDAVTKAAKQPHVGDYRQLVHELDEAEYRDIRLMVMEIRNAYAVLYDIILKNFEKLKKP
RGETKGMIY*

Fig. 88

SEQ ID No. 88
MELRARGWWLLCAAAALVACARGDPASKSRSCGEVRQIYGAKGFSLSDVPQAEISGEHLR
ICPQGYTCCTSEMEENLANRSHAELETALRDSSRVLQAMLATQLRSFDDHFQHLLNDSER
TLQATFPGAFGELYTQNARAFRDLYSELRLYYRGANLHLEETLAEFWARLLERLFKQLHP
QLLLPDDYLDCLGKQAEALRPFGEAPRELRLRATRAFVAARSFVQGLGVASDVVRKVAQV
PLGPECSRAVMKLVYCAHCLGVPGARPCPDYCRNVLKGCLANQADLDAEWRNLLDSMVLI
TDKFWGTSGVESVIGSVHTWLAEAINALQDNRDTLTAKVIQGCGNPKVNPQGPGPEEKRR
RGKLAPRERPPSGTLEKLVSEAKAQLRDVQDFWISLPGTLCSEKMALSTASDDRCWNGMA
RGRYLPEVMGDGLANQINNPEVEVDITKPDMTIRQQIMQLKIMTNRLRSAYNGNDVDFQD
ASDDGSGSGSGDGCLDDLCSRKVSRKSSSSRTPLTHALPGLSEQEGQKTSAASCPQPPTF
LLPLLLFLALTVARPRWR*

Fig. 89

SEQ ID No. 89

MASCASIDIEDATQHLRDILKLDRPAGGPSAESPRPSSAYNGDLNGLLVPDPLCSGDSTS
ANKTGLRTMPPINLQEKQVICLSGDDSSTCIGILAKEVEIVASSDSSISSKARGSNKVKI
QPVAKYDWEQKYYYGNLIAVSNSFLAYAIRAANNGSAMVRVISVSTSERTLLKGFTGSVA
DLAFAHLNSPQLACLDEAGNLFVWRLALVNGKIQEEILVHIRQPEGTPLNHFRRIIWCPF
IPEESEDCCEESSPTVALLHEDRAEVWDLDMLRSSHSTWPVDVSQIKQGFIVVKGHSTCL
SEGALSPDGTVLATASHDGYVKFWQIYIEGQDEPRCLHEWKPHDGRPLSCLLFCDNHKKQ
DPDVPFWRFLITGADQNRELKMWCTVSWTCLQTIRFSPDIFSSVSVPPSLKVCLDLSAEY
LILSDVQRKVLYVMELLQNQEEGHACFSSISEFLLTHPVLSFGIQVVSRCRLRHTEVLPA
EEENDSLGADGTHGAGAMESAAGVLIKLFCVHTKALQDVQIRFQPQLNPDVVAPLPTHTA
HEDFTFGESRPELGSEGLGSAAHGSQPDLRRIVELPAPADFLSLSSETKPKLMTPDAFMT
PSASLQQITASPSSSSSGSSSSSSSSSSLTAVSAMSSTSAVDPSLTRPPEELTLSPKLQ
LDGSLTMSSSGSLQASPRGLLPGLLPAPADKLTPKGPGQVPTATSALSLELQEVEPLGLP
QASPSRTRSPDVISSASTALSQDIPEIASEALSRGFGSSAPEGLEPDSMASAASALHLLS
PRPRPGPELGPQLGLDGGPGDGDRHNTPSLLEAALTQEASTPDSQVWPTAPDITRETCST
LAESPRNGLQEKHKSLAFHRPPYHLLQQRDSQDASAEQSDHDDEVASLASASGGFGTKVP
APRLPAKDWKTKGSPRTSPKLKRKSKKDDGDAAMGSRLTEHQVAEPPEDWPALIWQQQRE
LAELRHSQEELLQRLCTQLEGLQSTVTGHVERALETRHEQEQRRLERALAEGQQRGGQLQ
EQLTQQLSQALSSAVAGRLERSIRDEIKKTVPPCVSRSLEPMAGQLSNSVATKLTAVEGS
MKENISKLLKSKNLTDAIARAAADTLQGPMQAAYREAFQSVVLPAFEKSCQAMFQQINDS
FRLGTQEYLQQLESHMKSRKAREQEAREPVLAQLRGLVSTLQSATEQMPPWPAVFVLRCS
TSCMWLWAACRSPF*

Fig. 90

SEQ ID No. 90

MASCASIDIEDATQHLRDILKLDRPAGGPSAESPRPSSAYNGDLNGLLVPDPLCSGDSTS
ANKTGLRTMPPINLQEKQVICLSGDDSSTCIGILAKEVEIVASSDSSISSKARGSNKVKI
QPVAKYDWEQKYYYGNLIAVSNSFLAYAIRAANNGSAMVRVISVSTSERTLLKGFTGSVA
DLAFAHLNSPQLACLDEAGNLFVWRLALVNGKIQEEILVHIRQPEGTPLNHFRRIIWCPF
IPEESEDCCEESSPTVALLHEDRAEVWDLDMLRSSHSTWPVDVSQIKQGFIVVKGHSTCL
SEGALSPDGTVLATASHDGYVKFWQIYIEGQDEPRCLHEWKPHDGRPLSCLLFCDNHKKQ
DPDVPFWRFLITGADQNRELKMWCTVSWTCLQTIRFSPDIFSSVSVPPSLKVCLDLSAEY
LILSDVQRKVLYVMELLQNQEEGHACFSSISEFLLTHPVLSFGIQVVSRCRLRHTEVLPA
EEENDSLGADGTHGAGAMESAAGVLIKLFCVHTKALQDVQIRFQPQLNPDVVAPLPTHTA
HEDFTFGESRPELGSEGLGSAAHGSQPDLRRIVELPAPADFLSLSSETKPKLMTPDAFMT
PSASLQQITASPSSSSSGSSSSSSSSSSSLTAVSAMSSTSAVDPSLTRPPEELTLSPKLQ
LDGSLTMSSSGSLQASPRGLLPGLLPAPADKLTPKGPGQVPTATSALSLELQEVEPLGLP
QASPSRTRSPDVISSASTALSQDIPEIASEALSRGFGSSAPEGLEPDSMASAASALHLLS
PRPRPGPELGPQLGLDGGPGDGDRHNTPSLLEAALTQEASTPDSQVWPTAPDITRETCST
LAESPRNGLQEKHKSLAFHRPPYHLLQQRDSQDASAEQSDHDDEVASLASASGGFGTKVP
APRLPAKDWKTKGSPRTSPKLKRKSKKDDGDAAMGSRLTEHQVAEPPEDWPALIWQQQRE
LAELRHSQEELLQRLCTQLEGLQSTVTGHVERALETRHEQEQRRLERALAEGQQRGGQLQ
EQLTQQLSQALSSAVAGRLERSIRDEIKKTVPPCVSRSLEPMAGQLSNSVATKLTAVEGS
MKENISKLLKSKNLTDAIARAAADTLQGPMQAAYREAFQSVVLPAFEKSCQAMFQQINDS
FRLGTQEYLQQLESHMKSRKAREQEAREPVLAQLRGLVSTLQSATEQMAATVAGSVRAEV
QHQLHVAVGSLQESILAQVQRIVKGEVSVALKEQQAAVTSSIMQAMRSAAGTPVPSAHLD
CQAQQAHILQLLQQGHLNQAFQQALTAADLNLVLYVCETVDPAQVFGQPPCPLSQPVLLS
LIQQLASDLGTRTDLKLSYLEEAVMHLDHSDPITRDHMGSVMAQVRQKLFQFLQAEPHNS
LGKAARRLSLMLHGLVTPSLP*

Fig. 91

SEQ ID No. 91

MRRSEVLAEESIVCLQKALNHLREIWELIGIPEDQRLQRTEVVKKHIKELLDMMIAEEES
LKERLIKSISVCQKELNTLCSELHVEPFQEEGETTILQLEKDLRTQVELMRKQKKERKQE
LKLLQEQDQELCEILCMPHYDIDSASVPSLEELNQFRQHVTTLRETKASRREEFVSIKRQ
IILCMEALDHTPDTSFERDVVCEDEDAFCLSLENIATLQKLLRQLEMQKSQNEAVCEGLR
TQIRELWDRLQIPEEEREAVATIMSGSKAKVRKALQLEVDRLEELKMQNMKKVIEAIRVE
LVQYWDQCFYSQEQRQAFAPFCAEDYTESLLQLHDAEIVRLKNYYEVHKELFEGVQKWEE
TWRLFLEFERKASDPNRFTNRGGNLLKEEKQRAKLQKMLPKLEEELKARIELWEQEHSKA
FMVNGQKFMEYVAEQWEMHRLEKERAKQERQLKNKKQTETEMLYGSAPRTPSKRRGLAPN
TPGKARKLNTTTMSNATANSSIRPIFGGTVYHSPVSRLPPSGSKPVAASTCSGKKTPRTG
RHGANKENLELNGSILSGGYPGSAPLQRNFSINSVASTYSEFAKDPSLSDSSTVGLQREL
SKASKSDATSGILNSTNIQS*

Fig. 92

SEQ ID No. 92
TRLRPVARFEILRGSTARGAATRSDIAGVCGWLLLSGPCGVGLDLDSRLLGASAMRRSEV
LAEESIVCLQKALNHLREIWELIGIPEDQRLQRTEVVKKHIKELLDMMIAEEESLKERLI
KSISVCQKELNTLCSELHVEPFQEEGETTILQLEKDLRTQVELMRKQKKERKQELKLLQE
QDQELCEILCMPHYDIDSASVPSLEELNQFRQHVTTLRETKASRREEFVSIKRQIILCME
ALDHTPDTSFERDVVCEDEDAFCLSLENIATLQKLLRQLEMQKSQNEAVCEGLRTQIREL
WDRLQIPEEEREAVATIMSGSKAKVRKALQLEVDRLEELKMQNMKKVIEAIRVELVQYWD
QCFYSQEQRQAFAPFCAEDYTESLLQLHDAEIVRLKNYYEVHKELFEGVQKWEETWRLFL
EFERKASDPNRFTNRGGNLLKEEKQRAKLQKMLPKLEEELKARIELWEQEHSKAFMVNGQ
KFMEYVAEQWEMHRLEKERAKQERQLKNKKQTETEMLYGSAPRTPSKRRGLAPNTPGKAR
KLNTTTMSNATANSSIRPIFGGTVYHSPVSRLPPSGSKPVAASTCSGKKTPRTGRHGANK
ENLELNGSILSGGYPGSAPLQRNFSINSVASTYSEFAKDPSLSDSSTVGLQRELSKASKS
DATSGILNSTNIQS*

Fig. 93

SEQ ID No. 93
TRLRPVARFEILRGSTARGAATRSDIAGVCGWLLLSGPCGVGLDLDSRLLGASAMRRSEV
LAEESIVCLQKALNHLREIWELIGIPEDQRLQRTEVVKKHIKELLDMMIAEEESLKERLI
KSISVCQKELNTLCSELHVEPFQEEGETTILQLEKDLRTQVELMRKQKKERKQELKLLQE
QDQELCEILCMPHYDIDSASVPSLEELNQFRQHVTTLRETKASRREEFVSIKRQIILCME
ALDHTPDTSFERDVVCEDEDAFCLSLENIATLQKLLRQLEMQKSQNEAVCEGLRTQIREL
WDRLQIPEEEREAVATIMSGSKAKVRKALQLEVDRLEELKMQNMKKVIEAIRVELVQYWD
QCFYSQEQRQAFAPFCAEDYTESLLQLHDAEIVRLKNYYEVHKELFEGVQKWEETWRLFL
EFERKASDPNRFTNRGGNLLKEEKQRAKLQKMLPKLEEELKARIELWEQEHSKAFMVNGQ
KFMEYVAEQWEMHRLEKERAKQERQLKNKKQTETEMLYGSAPRTPSKRRGLAPNTPGKAR
KLNTTTMSNATANSSIRPIFGGTVYHSPVSRLPPSGSKPVAASTCSGKKTPRTGRHGANK
ENLELNGSILSGGYPGSAPLQRNFSINSVASTYSEFARELSKASKSDATSGILNSTNIQS
*

Fig. 94

SEQ ID No. 94
MTTQLGPALVLGVALCLGCGQPLPQVPERPFSVLWNVPSAHCEARFGVHLPLNALGIIAN
RGQHFHGQNMTIFYKNQLGLYPYFGPRGTAHNGGIPQALPLDRHLALAAYQIHHSLRPGF
AGPAVLDWEEWCPLWAGNWGRRRAYQAASWAWAQQVFPDLDPQEQLYKAYTGFEQAARAL
MEDTLRVAQALRPHGLWGFYHYPACGNGWHSMASNYTGRCHAATLARNTQLHWLWAASSA
LFPSIYLPPRLPPAHHQAFVRHRLEEAFRVALVGHRHPLPVLAYVRLTHRRSGRFLSQDD
LVQSIGVSAALGAAGVVLWGDLSLSSSEEECWHLHDYLVDTLGPYVINVTRAAMACSHQR
CHGHGRCARRDPGQMEAFLHLWPDGSLGDWKSFSCHCYWGWAGPTCQEPRPGPKEAV*

Fig. 95

SEQ ID No. 95
MTTQLGPALVLGVALCLGCGQPLPQVPERPFSVLWNVPSAHCEARFGVHLPLNALGIIAN
RGQHFHGQNMTIFYKNQLGLYPYFGPRGTAHNGGIPQALPLDRHLALAAYQIHHSLRPGF
AGPAVLDWEEWCPLWAGNWGRRRAYQAASWAWAQQVFPDLDPQEQLYKAYTGFEQAARAL
MEDTLRVAQALRPHGLWGFYHYPACGNGWHSMASNYTGRCHAATLARNTQLHWLWAASSA
LFPSIYLPPRLPPAHHQAFVRHRLEEAFRVALVGHRHPLPVLAYVRLTHRRSGRFLSQDD
LVQSIGVSAALGAAGVVLWGDLSLSSSEEECWHLHDYLVDTLGPYVINVTRAAMACSHQR
CHGHGRCARRDPGQMEAFLHLWPDGSLGDWKSFSCHCYWGWAGPTCQEPLGLKKQYKARA
PATASSFPCCHFSSPGTTLSHSCSIQFTVNPPKHTPRFPWNP*

Fig. 96

SEQ ID No. 96
MTTQLGPALVLGVALCLGCGQPLPQVPERPFSVLWNVPSAHCEARFGVHLPLNALGIIAN
RGQHFHGQNMTIFYKNQLGLYPYFGPRGTAHNGGIPQALPLDRHLALAAYQIHHSLRPGF
AGPAVLDWEEWCPLWAGNWGRRRAYQAASWAWAQQVFPDLDPQEQLYKAYTGFEQAARAL
MEDTLRVAQALRPHGLWGFYHYPACGNGWHSMASNYTGRCHAATLARNTQLHWLWAASSA
LFPSIYLPPRLPPAHHQAFVRHRLEEAFRVALVGHRHPLPVLAYVRLTHRRSGRFLSQEE
CWHLHDYLVDTLGPYVINVTRAAMACSHQRCHGHGRCARRDPGQMEAFLHLWPDGSLGDW
KSFSCHCYWGWAGPTCQEPRPGPKEAV*

Fig. 97

SEQ ID No. 97
MGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAEMGKGSFKYAWVL
DKLKAERERGITIDISLWKFETSKYYVTIIDAPGHRDFIKNMITGTSQADCAVLIVAAGV
GEFEAGISKNGQTREHALLAYTLGVKQLIVGVNKMDSTEPPYSQKRYEEIVKEVSTYIKK
IGYNPDTVAFVPISGWNGDNMLEPSANMPWFKGWKVTRKDGNASGTTLLEALDCILPPTR
PTDKPLRLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVTFAPVNVTTEVKSVEMHHEALS
EALPGDNVGFKVKNVSVKDVRRGNVAGDSKNDPPMEAAGFTAQVIILNHPGQISAGYAPV
LDCHMAHIACKFAELKEKIDRRSGKKLEDGPKFLKSGDAAIVDMVPGKPMCVESFSDYPP
LGRFAVRDMRQTVAVGVIKAVDKKAAGAGKVTKSAQKAQKAK*

Fig. 98

SEQ ID No. 98
MALKAEGAALDCFEVTLKCEEGEDEEEAMVVAVIPRPEPMLRVTQQEKTPPPRPSPLEAG
SDGCEEPKQQVSWEQEFLVGSSPGGSGRALCMVCGAEIRAPSADTARSHILEQHPHTLDL
SPSEKSNILEAWSEGVALLQDVRAEQPSPPNSDSGQDAHPDPDANPDAARMPAEIVVLLD
SEDNPSLPKRSRPRGLRPLELPAVPATEPGNKKPRGQRWKEPPGEEPVRKKRGRPMTKNL
DPDPEPPSPDSPTETFAAPAEVRHFTDGSFPAGFVLQLFSHTQLRGPDSKDSPKDREVAE
GGLPRAESPSPAPPPGLRGTLDLQVIRVRMEEPPAVSLLQDWSRHPQGTKRVGAGDTSDW
PTVLSESSTTVAGKPEKGNGV*

Fig. 99

SEQ ID No. 99

MSTHRSRLLTAAPLSMEQRRPWPRALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSEN
RDWTFNHLTVHQGTGAVYVGAINRVYKLTGNLTIQVAHKTGPEEDNKSCYPPLIVQPCSE
VLTLTNNVNKLLIIDYSENRLLACGSLYQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKT
GTMYGVIVRSEGEDGKLFIGTAVDGKQDYFPTLSSRKLPRDPESSAMLDYELHSDFVSSL
IKIPSDTLALVSHFDIFYIYGFASGGFVYFLTVQPETPEGVAINSAGDLFYTSRIVRLCK
DDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKPGDSLAQAFNITSQDDVLFAIFSKGQKQ
YHHPPDDSALCAFPIRAINLQIKERLQSCYQGEGNLELNWLLGKDVQCTKAPVPIDDNFC
GLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNGYSVVFVGTKSGKLKKIRADGPPH
GGVQYEMVSVLKDGSPILRDMAFSIDQRYLYVMSERQVTRVPVESCEQYTTCGECLSSGD
PHCGWCALHNMCSRRDKCQQAWEPNRFAASISQCVSLAVHPSSISVSEHSRLLSLVVSDA
PDLSAGIACAFGNLTEVEGQVSGSQVICISPGPKDVPVIPLDQDWFGLELQLRSKETGKI
FVSTEFKFYNCSAHQLCLSCVNSAFRCHWCKYRNLCTHDPTTCSFQEGRINISEDCPQLV
PTEEILIPVGEVKPITLKARNLPQPQSGQRGYECVLNIQGAIHRVPALRFNSSSVQCQNS
SYQYDGMDISNLAVDFAVVWNGNFIIDNPQDLKVHLYKCAAQRESCGLCLKADRKFECGW
CSGERRCTLHQHCTSPSSPWLDWSSHNVKCSNPQITEILTVSGPPEGGTRVTIHGVNLGL
DFSEIAHHVQVAGVPCTPLPGEYIIAEQIVCEMGHALVGTTSGPVRLCIGECKPEFMTKS
HQQYTFVNPSVLSLNPIRGPESGGTMVTITGHYLGAGSSVAVYLGNQTCEFYGRSMSEIV
CVSPPSSNGLGPVPVSVSVDRAHVDSNLQFEYIDDPRVQRIEPEWSIASGHTPLTITGFN
LDVIQEPRIRVKFNGKESVNVCKVVNTTTLTCLAPSLTTDYRPGLDTVERPDEFGFVFNN
VQSLLIYNDTKFIYYPNPTFELLSPTGVLDQKPGSPIILKGKNLCPPASGGAKLNYTVLI
GETPCAVTVSETQLLCEPPNLTGQHKVMVHVGGMVFSPGSVSVISDSLLTLPAIVSIAAG
GSLLLIIVIIVLIAYKRKSRENDLTLKRLQMQMDNLESRVALECKEAFAELQTDINELTS
DLDRSGIPYLDYRTYAMRVLFPGIEDHPVLRELEVQGNGQQHVEKALKLFAQLINNKVFL
LTFIRTLELQRSFSMRDRGNVASLIMTGLQGRLEYATDVLKQLLSDLIDKNLENKNHPKL
LLRRTESVAEKMLTNWFAFLLHKFLKECAGEPLFMLYCAIKQQMEKGPIDAITGEARYSL
SEDKLIRQQIEYKTLILNCVNPDNENSPEIPVKVLNCDTITQVKEKILDAVYKNVPYSQR
PRAVDMDLEWRQGRIARVVLQDEDITTKIEGDWKRLNTLMHYQVSDRSVVALVPKQTSSY
NIPASASISRTSISRYDSSFRYTGSPDSLRSRAPMITPDLESGVKVWHLVKNHDHGDQKE
GDRGSKMVSEIYLTRLLATKGTLQKFVDDLFETLFSTVHRGSALPLAIKYMFDFLDEQAD
RHSIHDTDVRHTWKSNCLPLRFWVNVIKNPQFVFDIHKGSITDACLSVVAQTFMDSCSTS
EHRLGKDSPSNKLLYAKDIPSYKSWVERYYADIAKLPAISDQDMNAYLAEQSRLHAVEFN
MLSALNEIYSYVSKYSEELIGALEQDEQARRQRLAYKVEQLINAMSIES*

Fig. 100

SEQ ID No. 100

MEQRRPWPRALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTG
AVYVGAINRVYKLTGNLTIQVAHKTGPEEDNKSCYPPLIVQPCSEVLTLTNNVNKLLIID
YSENRLLACGSLYQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDG
KLFIGTAVDGKQDYFPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFD
IFYIYGFASGGFVYFLTVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGC
TRAGVEYRLLQAAYLAKPGDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPI
RAINLQIKERLQSCYQGEGNLELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVE
GLTLYTTSRDRMTSVASYVYNGYSVVFVGTKSGKLKKIRADGPPHGGVQYEMVSVLKDGS
PILRDMAFSIDQRYLYVMSERQVTRVPVESCEQYTTCGECLSSGDPHCGWCALHNMCSRR
DKCQQAWEPNRFAASISQCVSLAVHPSSISVSEHSRLLSLVVSDAPDLSAGIACAFGNLT
EVEGQVSGSQVICISPGPKDVPVIPLDQDWFGLELQLRSKETGKIFVSTEFKFYNCSAHQ
LCLSCVNSAFRCHWCKYRNLCTHDPTTCSFQEGRINISEDCPQLVPTEEILIPVGEVKPI
TLKARNLPQPQSGQRGYECVLNIQGAIHRVPALRFNSSSVQCQNSSYQYDGMDISNLAVD
FAVVWNGNFIIDNPQDLKVHLYKCAAQRESCGLCLKADRKFECGWCSGERRCTLHQHCTS
PSSPWLDWSSHNVKCSNPQITEILTVSGPPEGGTRVTIHGVNLGLDFSEIAHHVQVAGVP
CTPLPGEYIIAEQIVCEMGHALVGTTSGPVRLCIGECKPEFMTKSHQQYTFVNPSVLSLN
PIRGPESGGTMVTITGHYLGAGSSVAVYLGNQTCEFYGRSMSEIVCVSPPSSNGLGPVPV
SVSVDRAHVDSNLQFEYIDDPRVQRIEPEWSIASGHTPLTITGFNLDVIQEPRIRVKFNG
KESVNVCKVVNTTTLTCLAPSLTTDYRPGLDTVERPDEFGFVFNNVQSLLIYNDTKFIYY
FNPTFELLSPTGVLDQKPGSPIILKGKNLCPPASGGAKLNYTVLIGETPCAVTVSETQLL
CEPPNLTGQHKVMVHVGGMVFSPGSVSVISDSLLTLPAIVSIAAGGSLLLIIVIIVLIAY
KRKSRENDLTLKRLQMQMDNLESRVALECKEAFAELQTDINELTSDLDRSGIPYLDYRTY
AMRVLFPGIEDHPVLRELEVQGNGQQHVEKALKLFAQLINNKVFLLTFIRTLELQRSFSM
RDRGNVASLIMTGLQGRLEYATDVLKQLLSDLIDKNLENKNHPKLLLRRTESVAEKMLTN
WFAFLLHKFLKECAGEPLFMLYCAIKQQMEKGPIDAITGEARYSLSEDKLIRQQIEYKTL
ILNCVNPDNENSPEIPVKVLNCDTITQVKEKILDAVYKNVPYSQRPRAVDMDLEWRQGRI
ARVVLQDEDITTKIEGDWKRLNTLMHYQVSDRSVVALVPKQTSSYNIPASASISRTSISR
YDSSFRYTGSPDSLRSRAPMITPDLESGVKVWHLVKNHDHGDQKEGDRGSKMVSEIYLTR
LLATKGTLQKFVDDLFETLFSTVHRGSALPLAIKYMFDFLDEQADRHSIHDTDVRHTWKS
NCLPLRFWVNVIKNPQFVFDIHKGSITDACLSVVAQTFMDSCSTSEHRLGKDSPSNKLLY
AKDIPSYKSWVERYYADIAKLPAISDQDMNAYLAEQSRLHAVEFNMLSALNEIYSYVSKY
SEELIGALEQDEQARRQRLAYKVEQLINAMSIES*

Fig. 101

SEQ ID No. 101
MPPPSDIVKVAIEWPGANAQLLEIDQKRPLASIIKEVCDGWSLPNPEYYTLRYADGPQLY
ITEQTRSDIKNGTILQLAISPSRAARQLMERTQSSNMETRLDAMKELAKLSADVTFATEF
INMDGIIVLTRLVESGTKLLSHYSEMLAFTLTAFLELMDHGIVSWDMVSITFIKQIAGYV
SQPMVDVSILQRSLAILESMVLNSQSLYQKIAEEITVGQLISHLQVSNQEIQTYAIALIN
ALFLKAPEDKRQDMANAFAQKHLRSIILNHVIRGNRPIKTEMAHQLYVLQVLTFNLLEER
MMTKMDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTEKRKAMYTKDYKMLGFTNHINP
AMDFTQTPPGMLALDNMLYLAKVHQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEI
LQVGELPNEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFNKVMQVVREQ
ITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSERMSQDDFQSPPIVELREKIQPEILEL
IKQQRLNRLCEGSSFRKIGNRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEK
IPVADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNFIAPNKYEYCIWID
GLSALLGKDMSSELTKSDLDTLLSMEMKLRLLDLENIQIPEAPPPIPKEPSSYDFVYHYG
*

Fig. 102

SEQ ID No. 102
MPPPSDIVKVAIEWPGANAQLLEIDQKRPLASIIKEVCDGWSLPNPEYYTLRYADGPQLY
ITEQTRSDIKNGTILQLAISPSRAARQLMERTQSSNMETRLDAMKELAKLSADVTFATEF
INMDGIIVLTRLVESGTKLLSHYSEMLAFTLTAFLELMDHGIVSWDMVSITFIKQIAGYV
SQPMVDVSILQRSLAILESMVLNSQSLYQKIAEEITVGQLISHLQVSNQEIQTYAIALIN
ALFLKAPEDKRQDMANAFAQKHLRSIILNHVIRGNRPIKTEMAHQLYVLQVLTFNLLEER
MMTKMDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTEKRKAMYTKDYKMLGFTNHINP
AMDFTQTPPGMLALDNMLYLAKVHQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEI
LQVGELPNEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFNKVMQVVREQ
ITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSERMSQDDFQSPPIVELREKIQPEILEL
IKQQRLNRLCEGSSFRKIGNRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEK
IPVADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNFIAPNKYEYCIWID
GLSALLGKDMSSELTKSDLDTLLSMEMKLRLLDLENIQIPEAPPPIPKEPSSYDFVYHYG
*

Fig. 103

SEQ ID No. 103
MPPPSDIVKVAIEWPGANAQLLEIDQKRPLASIIKEVCDGWSLPNPEYYTLRYADGPQLY
ITEQTRSDIKNGTILQLAISPSRAARQLMERTQSSNMETRLDAMKELAKLSADVTFATEF
INMDGIIVLTRLVESGTKLLSHEMLAFTLTAFLELMDHGIVSWDMVSITFIKQIAGYVSQ
PMVDVSILQRSLAILESMVLNSQSLYQKIAEEITVGQLISHLQVSNQEIQTYAIALINAL
FLKAPEDKRQDMANAFAQKHLRSIILNHVIRGNRPIKTEMAHQLYVLQVLTFNLLEERMM
TKMDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTEKRKAMYTKDYKMLGFTNHINPAM
DFTQTPPGMLALDNMLYLAKVHQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQ
VGELPNEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFNKVMQVVREQIT
RALPSKPNSLDQFKSKLRSLSYSEILRLRQSERMSQDDFQSPPIVELREKIQPEILELIK
QQRLNRLCEGSSFRKIGNRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIP
VADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNFIAPNKYEYCIWIDGL
SALLGKDMSSELTKSDLDTLLSMEMKLRLLDLENIQIPEAPPPIPKEPSSYDFVYHYG*

Fig. 104

SEQ ID No. 104
MERTQSSNMETRLDAMKELAKLSADVTFATEFINMDGIIVLTRLVESGTKLLSHYSEMLA
FTLTAFLELMDHGIVSWDMVSITFIKQIAGYVSQPMVDVSILQRSLAILESMVLNSQSLY
QKIAEEITVGQLISHLQVSNQEIQTYAIALINALFLKAPEDKRQDMANAFAQKHLRSIIL
NHVIRGNRPIKTEMAHQLYVLQVLTFNLLEERMMTKMDPNDQAQRDIIFELRRIAFDAES
DPSNAPGSGTEKRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKVHQDTY
IRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELPNEGRNDYHPMFFTHDRAFEEL
FGICIQLLNKTWKEMRATAEDFNKVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEIL
RLRQSERMSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIGNRRRQERFW
YCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPVADIKAIVTGKDCPHMKEKSALKQNK
EVLELAFSILYDPDETLNFIAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMK
LRLLDLENIQIPEAPPPIPKEPSSYDFVYHYG*

Fig. 105

SEQ ID No. 105
MAALRALCGFRGVAAQVLRPGAGVRLPIQPSRGVRQWQPDVEWAQQFGGAVMYPSKETAH
WKPPPWNDVDPPKDTIVKNITLNFGPQHPAAHGVLRLVMELSGEMVRKCDPHIGLLHRGT
EKLIEYKTYLQALPYFDRLDYVSMMCNEQAYSLAVEKLLNIRPPPRAQWIRVLFGEITRL
LNHIMAVTTHALDLGAMTPFFWLFEEREKMFEFYERVSGARMHAAYIRPGGVHQDLPLGL
MDDIYQFSKNFSLRLDELEELLTNNRIWRNRTIDIGVVTAEEALNYGFSGVMLRGSGIQW
DLRKTQPYDVYDQVEFDVPVGSRGDCYDRYLCRVEEMRQSLRIIAQCLNKMPPGEIKVDD
AKVSPPKRAEMKTSMESLIHHFKLYTEGYQVPPGATYTAIEAPKGEFGVYLVSDGSSRPY
RCKIKAPGFAHLAGLDKMSKGHMLADVVAIIGTQDIVFGEVDR*

Fig. 106

SEQ ID No. 106
MAALRALCGFRGVAAQVLRPGAGVRLPIQPSRGVRQWQPDVEWAQQFGGAVMYPSKETAH
WKPPPWNDVDPPKDTIVKNITLNFGPQHPAAHGVLRLVMELSGEMVRKCDPHIGLLHRGT
EKLIEYKTYLQALPYFDRLDYVSMMCNEQAYSLAVEKLLNIRPPPRAQWIRVLFGEITRL
LNHIMAVTTHALDLGAMTPFFWLFEEREKMFEFYERVSGARMHAAYIRPGGVHQDLPLGL
MDDIYQFSKNFSLRLDELEELLTNNRIWRNRTIDIGVVTAEEALNYGFSGVMLRGSGIQW
DLRKTQPYDVYDQVEFDVPVGSRGDCYDRYLCRVEEMRQSLRIIAQCLNKMPPGEIKVDD
AKVSPPKRAEMKTSMESLIHHFKLYTEGYQVPPGATYTAIEAPKGEFGVYLVSDGSSRPY
RCKIKAPGFAHLAGLDKMSKGHMLADVVAIIGTQDIVFGEVDR*

Fig. 107

SEQ ID No. 107
MAGGPGPGEPAAPGAQHFLYEVPPWVMCRFYKVMDALEPADWCQFGGWRRAAGGREARGL
LAPTPDAPRPAAALIVRDQTELRLCERSGQRTASVLWPWINRNARVADLVHILTHLQLLR
ARDIITAWHPPAPLPSPGTTAPRPSSIPAPAEAEAWSPRKLPSSASTFLSPAFPGSQTHS
GPELGLVPSPASLWPPPPSPAPSSTKPGPESSVSLLQGARPFPFCWPLCEISRGTHNFSE
ELKIGEGGFGCVYRAVMRNTVYAVKRLKENADLEWTAVKQSFLTEVEQLSRFRHPNIVDF
AGYCAQNGFYCLVYGFLPNGSLEDRLHCQTQACPPLSWPQRLDILLGTARAIQFLHQDSP
SLIHGDIKSSNVLLDERLTPKLGDFGLARFSRFAGSSPSQSSMVARTQTVRGTLAYLPEE
YIKTGRLAVDTDTFSFGVVVLETLAGQRAVKTHGARTKYLKDLVEEEAEEAGVALRSTQS
TLQAGLAADAWAAPIAMQIYKKHLGQLACCCLHRRAKRRPPMTQENSYVSSTGRAHSGAA
PWQPLAAPSGASAQAAEQLQRGPNQPVESDESLGGLSAALRSWHLTPSCPLDPAPLREAG
CPQGDTAGESSWGSGPGSRPTAVEGLALGSSASSSSEPPQIIINPARQKMVQKLALYEDG
ALDSLQLLSSSSLPGLGLEQDRQGPEESDEFQS*

Fig. 108

SEQ ID No. 108
MAGGPGPGEPAAPGAQHFLYEVPPWVMCRFYKVMDALEPADWCQFAALIVRDQTELRLCE
RSGQRTASVLWPWINRNARVADLVHILTHLQLLRARDIITAWHPPAPLPSPGTTAPRPSS
IPAPAEAEAWSPRKLPSSASTFLSPAFPGSQTHSGPELGLVPSPASLWPPPPSPAPSSTK
PGPESSVSLLQGARPFPFCWPLCEISRGTHNFSEELKIGEGGFGCVYRAVMRNTVYAVKR
LKENADLEWTAVKQSFLTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLEDRL
HCQTQACPPLSWPQRLDILLGTARAIQFLHQDSPSLIHGDIKSSNVLLDERLTPKLGDFG
LARFSRFAGSSPSQSSMVARTQTVRGTLAYLPEEYIKTGRLAVDTDTFSFGVVVLETLAG
QRAVKTHGARTKYLKDLVEEEAEEAGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHLDP
RPGPCPPELGLGLGQLACCCLHRRAKRRPPMTQVYERLEKLQAVVAGVPGHSEAASCIPP
SPQENSYVSSTGRAHSGAAPWQPLAAPSGASAQAAEQLQRGPNQPVESDESLGGLSAALR
SWHLTPSCPLDPAPLREAGCPQGDTAGESSWGSGPGSRPTAVEGLALGSSASSSSEPPQI
IINPARQKMVQKLALYEDGALDSLQLLSSSSLPGLGLEQDRQGPEESDEFQS*

Fig. 109

SEQ ID No. 109
MAGGPGPGEPAAPGAQHFLYEVPPWVMCRFYKVMDALEPADWCQFAALIVRDQTELRLCE
RSGQRTASVLWPWINRNARVADLVHILTHLQLLRARDIITAWHPPAPLPSPGTTAPRPSS
IPAPAEAEAWSPRKLPSSASTFLSPAFPGSQTHSGPELGLVPSPASLWPPPPSPAPSSTK
PGPESSVSLLQGARPFPFCWPLCEISRGTHNFSEELKIGEGGFGCVYRAVMRNTVYAVKR
LKENADLEWTAVKQSFLTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLEDRL
HCQTQACPPLSWPQRLDILLGTARAIQFLHQDSPSLIHGDIKSSNVLLDERLTPKLGDFG
LARFSRFAGSSPSQSSMVARTQTVRGTLAYLPEEYIKTGRLAVDTDTFSFGVVVLETLAG
QRAVKTHGARTKYLKDLVEEEAEEAGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHLDP
RPGPCPPELGLGLGQLACCCLHRRAKRRPPMTQENSYVSSTGRAHSGAAPWQPLAAPSGA
SAQAAEQLQRGPNQPVESDESLGGLSAALRSWHLTPSCPLDPAPLREAGCPQGDTAGESS
WGSGPGSRPTAVEGLALGSSASSSSEPPQIIINPARQKMVQKLALYEDGALDSLQLLSSS
SLPGLGLEQDRQGPEESDEFQS*

Fig. 110

SEQ ID No. 110
MAGGPGPGEPAAPGAQHFLYEVPPWVMCRFYKVMDALEPADWCQFAALIVRDQTELRLCE
RSGQRTASVLWPWINRNARVADLVHILTHLQLLRARDIITAWHPPAPLPSPGTTAPRPSS
IPAPAEAEAWSPRKLPSSASTFLSPAFPGSQTHSGPELGLVPSPASLWPPPPSPAPSSTK
PGPESSVSLLQGARPFPFCWPLCEISRGTHNFSEELKIGEGGFGCVYRAVMRNTVYAVKR
LKENADLEWTAVKQSFLTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLEDRL
HCQTQACPPLSWPQRLDILLGTARAIQFLHQDSPSLIHGDIKSSNVLLDERLTPKLGDFG
LARFSRFAGSSPSQSSMVARTQTVRGTLAYLPEEYIKTGRLAVDTDTFSFGVVVLETLAG
QRAVKTHGARTKYLVYERLEKLQAVVAGVPGHSEAASCIPPSPQENSYVSSTGRAHSGAA
PWQPLAAPSGASAQAAEQLQRGPNQPVESDESLGGLSAALRSWHLTPSCPLDPAPLREAG
CPQGDTAGESSWGSGPGSRPTAVEGLALGSSASSSSEPPQIIINPARQKMVQKLALYEDG
ALDSLQLLSSSSLPGLGLEQDRQGPEESDEFQS*

Fig. 111

SEQ ID No. 111
MAGGPGPGEPAAPGAQHFLYEVPPWVMCRFYKVMDALEPADWCQFGGWRRAAGGREARGL
LAPTPDAPRPAAALIVRDQTELRLCERSGQRTASVLWPWINRNARVADLVHILTHLQLLR
ARDIITAWHPPAPLPSPGTTAPRPSSIPAPAEAEAWSPRKLPSSASTFLSPAFPGSQTHS
GPELGLVPSPASLWPPPPSPAPSSTKPGPESSVSLLQGARPFPFCWPLCEISRGTHNFSE
ELKIGEGGFGCVYRAVMRNTVYAVKRLKENADLEWTAVKQSFLTEVEQLSRFRHPNIVDF
AGYCAQNGFYCLVYGFLPNGSLEDRLHCQTQACPPLSWPQRLDILLGTARAIQFLHQDSP
SLIHGDIKSSNVLLDERLTPKLGDFGLARFSRFAGSSPSQSSMVARTQTVRGTLAYLPEE
YIKTGRLAVDTDTFSFGVVVLETLAGQRAVKTHGARTKYLKDLVEEEAEEAGVALRSTQS
TLQAGLAADAWAAPIAMQIYKKHLDPRPGPCPPELGLGLGQLACCCLHRRAKRRPPMTQE
NSYVSSTGRAHSGAAPWQPLAAPSGASAQAAEQLQRGPNQPVESDESLGGLSAALRSWHL
TPSCPLDPAPLREAGCPQGDTAGESSWGSGPGSRPTAVEGLALGSSASSSSEPPQIIINP
ARQKMVQKLALYEDGALDSLQLLSSSSLPGLGLEQDRQGPEESDEFQS*

Fig. 112

SEQ ID No. 112
MAAIPSSGSLVATHDYYRRRLGSTSSNSSCSSTECPGEAIPHPPGECRIAPFSPRSSRSW
QHQDPTSLLSGLPKADPGHWWASFFFGKSTLPFMATVLESAEHSEPPQASSSMTACGLAR
DAPRKQPGGQSSTASAGPPS*

Fig. 113

SEQ ID No. 113
MAAIPSSGSLVATHDYYRRRLGSTSSNSSCSSTECPGEAIPHPPGLPKADPGHWWASFFF
GKSTLPPPTL*

Fig. 114

SEQ ID No. 114
MAAIPSSGSLVATHDYYRRRLGSTSSNSSCSSTECPGEAIPHPPGLPKADPGHWWASFFF
GKSTLPFMATVLESAEHSEPPQASSSMTACGLARDAPRKQPGGQSSTASAGPPS*

Fig. 115

SEQ ID No. 115
MEDGVYEPPDLTPEERMELENIRRRKQELLVEIQRLREELSEAMSEVEGLEANEGSKTLQ
RNRKMAMGRKKFNMDPKKGIQFLVENELLQNTPEEIARFLYKGEGLNKTAIGDYLGEREE
LNLAVLHAFVDLHEFTDLNLVQALRQFLWSFRLPGEAQKIDRMMEAFAQRYCLCNPGVFQ
STDTCYVLSFAVIMLNTSLHNPNVRDKPGLERFVAMNRGINEGGDLPEELLRNLYDSIRN
EPFKIPEDDGNDLTHTFFNPDREGWLLKLGRGRVKTWKRRWFILTDNCLYYFEYTTDKEP
RGIIPLENLSIREVDDPRKPNCFELYIPNNKGQLIKACKTEADGRVVEGNHMVYRISAPT
QEEKDEWIKSIQAAVSVDPFYEMLAARKKRISVKKKQEQP*

Fig. 116

SEQ ID No. 116
MEDGVYEPPDLTPEERMELENIRRRKQELLVEIQRLREELSEAMSEVEGLEANEGSKTLQ
RNRKMAMGRKKFNMDPKKGIQFLVENELLQNTPEEIARFLYKGEGLNKTAIGDYLGEREE
LNLAVLHAFVDLHEFTDLNLVQALRQFLWSFRLPGEAQKIDRMMEAFAQRYCLCNPGVFQ
STDTCYVLSFAVIMLNTSLHNPNVRDKPGLERFVAMNRGINEGGDLPEELLRNLYDSIRN
EPFKIPEDDGNDLTHTFFNPDREGWLLKLGGRVKTWKRRWFILTDNCLYYFEYTTDKEPR
GIIPLENLSIREVDDPRKPNCFELYIPNNKGQLIKACKTEADGRVVEGNHMVYRISAPTQ
EEKDEWIKSIQAAVSVDPFYEMLAARKKRISVKKKQEQP*

Fig. 117

SEQ ID No. 117
MVNPTVFFDIAVDGEPLGRVSFELFADKVPKTAENFRALSTGEKGFGYKGSCFHRIIPGF
MCQGGDFTRHNGTGGKSIYGEKFEDENFILKHTGPGILSMANAGPNTNGSQFFICTAKTE
WLDGKHVVFGKVKEGMNIVEAMERFGSRNGKTSKKITIADCGQLE*

Fig. 118

SEQ ID No. 118
TAEEEASSEACAGPATRSPGWGDPGISHRDCCRRKAEWGTAESR*

Fig. 119

SEQ ID No. 119
EAELPDRGGAAVQVSSPKHCGLCWLLCSERLLLPGVRLPAQRLPGGPSPLPDPGLPTSLL
ASATGHPSGYSPGNSVSTSGQPQPHPWRHQEFQRPSG*

Fig. 120

SEQ ID 120
LRGLAPPSPPPVIVRRGPRGVAAQIPPASKLKHGGHPLQRLARGHPRLLPAPPGFHFQQQ
LLQQYRVPRGSHSPPPRSPQG*

Fig. 121

SEQ ID No. 121
APWPSAPVPATRDRAPRPARGRRPDPTSQQAKAWRPSPPAARSWPPTTTTGAAWVPLPAT
APAAVPSAPGKPFPTPQVSPRLTRVIGGPASFSGSPPSRSWPRCWSPQSTRNLPRPPAA*

Fig. 122

SEQ ID No. 122
WTCSPHPTPTTRRSTTSRSASWSARCAST*

BIOMARKER FOR THE PREDICTION OF RESPONSIVENESS TO AN ANTI-TUMOUR NECROSIS FACTOR ALPHA (TNF) TREATMENT

The invention refers to a method for diagnosing an individual who is to be subjected to or is being subjected to an anti-tumour necrosis factor alpha (TNFα or TNF) treatment to assess the responsiveness to an anti-TNF treatment which comprises the detection of immunoglobulin(s) against one or more biomarker proteins in a bodily fluid or an excrement of said patient, and sorting the individual into one of two categories based on detection of said immunoglobulin(s), wherein individuals are classified as NON-responder or responder. The invention refers to diagnostic kits comprising said one or more biomarker proteins and the use of these kits for assessing the responsiveness to an anti-TNF treatment of an individual who is to be subjected to or is being subjected to an anti-TNFα treatment.

BACKGROUND

Rheumatic diseases are the most common chronic inflammatory disorders. In Germany alone, one million patients suffer from immunologically mediated rheumatic diseases including rheumatoid arthritis (RA), spondyloarthropathies (SpA) and systemic autoimmune diseases like systemic lupus erythematosus (SLE), while additional five million individuals have osteoarthritis (OA), a primarily degenerative joint disease, which, however, in its active phases is also dominated by inflammatory processes. Rheumatoid arthritis leads to severe pain, loss of function and serious impairment of the quality of life. Besides these deleterious consequences for the individual patient, there is a striking socio-economic impact leading to direct and indirect costs of about 20 billion Euros in Germany per year. The demographic development clearly indicates that rheumatic diseases will dramatically increase over the next decades and will be equal in importance to cardiovascular diseases and cancer. Already now, rheumatic disorders dominate the number of patient visits in the General Practitioner's office and are the leading cause of absence from work and premature invalidity. In recognition of the tremendous impact of arthritic and bone diseases, the World Health Organization has announced the current decade as the "Decade of Bone and Joint Diseases".

A range of therapies for rheumatoid arthritis is available based on standard disease-modifying antirheumatic drugs (DMARDs), such as Methotrexate (MTX) and on biologicals, such as TNF inhibitors/antagonists. Chronically elevated levels of TNF have been implicated as a pathogenic component in rheumatoid arthritis. TNF inhibitors are biologicals which bind to soluble and cell membrane-associated form of TNFα and neutralise the proinflammatory effect of TNFα by preventing the binding of TNFα to the TNF-RI/II cell-surface receptors. TNFa-inhibiting biological agents comprise e.g. therapeutic antibodies (Adalimumab® & Infliximab®) and soluble receptor constructs (Etanercept®). These biologicals are currently used to treat active rheumatoid arthritis, all of which effectively reduce the signs and symptoms of the disease and inhibit radiographic joint damage progression. Currently ~10% of patients in Germany, but up to 30% in Scandinavian countries are treated with TNF-α inhibitors and the numbers are continuously growing. Anti-TNF-α antibodies (Adalimumab®; Humira) account for 90% of all biologicals in current use of rheumatoid arthritis therapy.

However, only 70% of rheumatoid arthritis patients benefit from a treatment with anti-TNFα, while 30% (~10.000 patients in Germany in 2006) remain non-responders. An anti-TNFα therapy costs currently ~20.000 € in Germany and hence, the costs of unsuccessful therapies account for 200 Mia € /year in Germany alone.

Next to rheumatoid arthritis, chronically elevated levels of TNF have been implicated as a pathogenic component in a number of other disease states—primarily autoimmune conditions—such as psoriasis, psoriatic arthritis, ankylosing spondylitis, Crohn's disease, ulcerative colitis, etc.

Currently, there are no biomarkers available, which can predict the outcome of a treatment with anti-TNF agents (e.g. TNF antagonists/inhibitors) prior treatment. Only reduction of all isotype levels of rheumatoid factors during and after treatment is associated with a positive response and outcome of the treatment (van Laar J M. Nat Clin Pract Rheumatol. 2007 October; 3(10):544-5. PMID: 17726429). However, high level of IgA rheumatoid factor in sera of patients with rheumatoid arthritis has been suggested to identify a subgroup of patients at risk of a poor clinical response to treatment with anti-TNFα antibodies (Bobbio-Pallavicini F. et al. Ann Rheum Dis. 2007 March; 66(3):302-7. PMID: 17079248; Bobbio-Pallavicini F. et al. Ann NY Acad Sci. 2007 August; 1109:287-95. PMID: 17785317; van Laar J M. Nat Clin Pract Rheumatol. 2007 October; 3(10):544-5. PMID: 17726429). The nature of anti-CCP antibodies suggested as a predictor for therapy efficacy is controversial (Braun-Moscovici Y et al. J Rheumatol. 2006 March; 33(3): 497-500. PMID: 16511906; Bobbio-Pallavicini F et al. Ann NY Acad Sci. 2007 August; 1109:287-95. PMID: 17785317; van Laar J M. Nat Clin Pract Rheumatol. 2007 October; 3(10):544-5. PMID: 17726429).

Thus, there is a need in the art for markers, which can predict the outcome of an anti-TNFα therapy prior to and during treatment. There is a need for stratification of patients who are to be subjected to or are being subjected to an anti-TNFα treatment and distinguishing between anti-TNFα treatment responder and Non-responder patients.

Subject of the present invention is a method for diagnosing an individual who is to be subjected to or is being subjected to an anti-TNFα treatment to assess the responsiveness to an anti-TNF treatment prior, during and/or after anti-TNFα treatment which comprises:

a. Detection of immunoglobulin(s) against one or more biomarker proteins in a bodily fluid or excrement of said patient, wherein the one or more biomarker is indicative for the responsiveness to an anti-TNF treatment prior, during and after anti-TNFα treatment.
b. Sorting the individual into responder or NON-responder based on detection of said immunoglobulin(s).

Thus, the invention provides for the first time marker which can predict the outcome of an anti-TNFα treatment prior to treatment in addition to during and/or after treatment. Anti-TNFalpha treatment may be conducted by administration of TNF inhibitors, e.g. TNF antagonists. These markers are not related to IgA rheumatoid factor. The marker according to the present invention can either be indicative of responder or of NON-responder as will be outlined below in detail. It is preferred that the responsiveness is assessed prior to treatment.

Subject of the present invention is a method for diagnosing an individual who is to be subjected to or is being subjected to an anti-TNFα treatment to assess the responsiveness to an anti-TNF treatment which comprises:

Detection of immunoglobulin(s) against one or more biomarker proteins in a bodily fluid or an excrement of

said patient, wherein a biomarker protein is an expression product encoded by a gene selected from the group comprising RAB11B, PPP2R1A, KPNB1, COG4 and FDFT1, wherein an individual positive for at least one of said immunoglobulin(s) is classified as NON-responder.

In a preferred embodiment of the above-identified method the individual is sorted into one of two categories based on detection of said immunoglobulin(s), wherein an individual positive for at least one of said immunoglobulin(s) is classified as NON-responder and, wherein an individual negative for any of said detected immunoglobulin(s) is classified as responder.

In a preferred embodiment of the inventive method at least two of the biomarker proteins of the protein marker group are detected wherein a biomarker protein is an expression product encoded by a gene selected from the group comprising RAB11B, PPP2R1A, KPNB1, COG4 and FDFT1 (Protein Set 1=RAB11B, PPP2R1A, KPNB1, COG4 and FDFT1). In another preferred embodiment of the inventive method at least expression products encoded by genes RAB11B, PPP2R1A, KPNB1, COG4 and FDFT1 are detected. In another preferred embodiment only expression products encoded by genes RAB11B, PPP2R1A, KPNB1, COG4 and FDFT1 are detected. In another preferred embodiment each and only the expression products encoded by genes RAB11B, PPP2R1A, KPNB1, COG4 and FDFT1 are detected.

In another preferred embodiment of the method for diagnosing an individual who is to be subjected to or is being subjected to an anti-TNFα treatment according to the invention the biomarker protein group additionally comprises at least one other expression product encoded by a gene selected from the group comprising PECI, CTNND2, NSMCE1, KTELC1, HS6ST1, ARMC6, TH1L, PSME1, GPC1, EDC4 (Protein Set 2) and at least one of the proteins of the entire group 1 and 2 (Protein Set 1 and 2) is detected. In a preferred embodiment of the invention at least one protein from Protein Set 1 is detected and additionally at least one of Protein Set 2 is detected. In another preferred embodiment at least two of the proteins of Protein Set 1 and additionally at least one of Protein Set 2 are detected. In another preferred embodiment Protein Set 1 and Protein Set 2 are detected.

In another preferred embodiment additionally to the above cited combinations of marker proteins a protein of Protein Set 3 is detected: the Protein Set 3 comprises the expression products encoded by genes PRC1, NAT6, EEF1AL3, NP_612480.1, PLXNA2, ELMO2 and NDUFS2.

In another preferred embodiment of the invention at least two marker proteins are selected from the group comprising the marker from protein sets 1, 2 and 3 for the method for diagnosing an individual who is to be subjected to or is being subjected to an anti-TNFα treatment to assess the responsiveness to an anti-TNF treatment prior, during and/or after anti-TNFα treatment. This means in this embodiment at least two marker are selected from the group comprising RAB11B, PPP2R1A, KPNB1, COG4, FDFT1, PECI, CTNND2, NSMCE1, KTELC1, HS6ST1, ARMC6, TH1L, PSME1, GPC1, EDC4, PRC1, NAT6, EEF1AL3, NP_612480.1, PLXNA2, ELMO2 and NDUFS2.

In another preferred embodiment at least three marker proteins are selected, more preferably four or five protein marker.

According to the present invention biomarker proteins of the present invention may be peptides, protein fragments, full length or splice variants or synthetically modified derivatives or post-translationally modified versions of the proteins encoded by aforementioned genes. Preferably, said protein fragments have a length of more than nine amino acids, more preferably at least n twelve or more than twelve amino acids. Modification of proteins may be but are not limited to deimination, deamidation and/or transglutamination. Additionally, they can be artificial polypeptides being expression products derived from incorrect reading frames within the gene. An examples for such an expression product derived from incorrect reading frames within the gene is shown in FIG. **122** which is a protein sequence derived from an incorrect reading frame of the gene HS6SP1. Another example is shown in FIG. **121** which is a protein sequence derived from an incorrect reading frame of the gene C20orfl149. Yet another example is shown in FIG. **120** which is a protein sequence derived from an incorrect reading frame of the gene IRAK1.

This means when for example IRAK1 is mentioned in the context of the present application it may concern the peptides, protein fragments, full length or splice variants or synthetically modified derivatives and/or post-translationally modified versions of IRAK1 and/or a protein sequence derived from an incorrect reading frame of the gene IRAK1.

A biomarker protein encompasses also variants thereof, such as peptides, protein fragments, artificial polypeptides, full length or splice variants, synthetically modified derivatives or post-translationally modified versions of the proteins encoded by aforementioned genes which are characterized in that these variants exhibit essentially the same ability to be recognized by the respective immunoglobulin as the biomarker proteins that are subject of the invention.

In particular, according to the present inventions biomarker proteins are encompassed wherein the sequences involved in binding to the respective immunoglobulin exhibit at least 80%, preferred at least 90%, more preferred at least 95% degree of sequence identity on the amino acid level to the sequences involved in binding of the biomarker proteins defined in SEQ ID No.s 59-122 as well as peptides, protein fragments, full length or splice variants, synthetically modified derivatives or post-translationally modified versions thereof exhibiting the same ability.

In context of the present invention a DNA sequence of a gene is defined by comprising all exons of a gene necessary to represent the protein coding sequence (CDS) or all splice variants thereof, as well as the exons representing the 5' untranslated region (UTR) and the 3' UTR.

According to the present invention all DNA sequences are encompassed which encode the before-mentioned biomarker proteins.

In particular, according to the present inventions furthermore DNA sequences are encompassed which exhibit referred to the sequence encoding a stretch which is involved in the binding region at least 80%, preferred at least 90%, more preferred at least 95% degree of sequence identity on the nucleic acid level to the DNA sequences encoding a stretch which is involved in the binding region defined in SEQ ID No.s 1-58 as well as fragments thereof encoding the biomarkers according to the present invention.

The before mentioned definitions for biomarker proteins and for genes encoding said biomarker proteins apply to every single embodiment of this inventions, any specific method, kit etc.

The determination of percent identity between two sequences is accomplished using the mathematical algorithm of Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90: 5873-5877. Such an algorithm is incorporated into the BLASTN and BLASTP programs of Altschul et al. (1990) J. Mol. Biol. 215: 403-410. BLAST nucleotide searches may be performed with the BLASTN program, score=100, word length=12, to obtain nucleotide sequences homologous to variant polypeptide encoding nucleic acids. BLAST protein

searches are performed with the BLASTP program, score=50, wordlength=3, to obtain amino acid sequences homologous to the variant polypeptide, respectively. To obtain gapped alignments for comparative purposes, Gapped BLAST is utilized as described in Altschul et al. (1997) Nucleic Acids Res. 25: 3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs are used.

The immunoglobulin(s) to be detected may be selected from IgA, IgD, IgG and IgM. In a preferred embodiment the immunoglobulin(s) to be detected is IgA or IgG. In the most preferred embodiment the immunoglobulin is IgA. The immunoglobulin(s) to be detected is not related to IgA rheumatoid factor.

In another preferred embodiment subsets of biomarker proteins may be used to assess the responsiveness to an anti-TNF treatment prior, during and/or after anti-TNFα treatment.

The respective set of proteins can not only predict responsiveness before, but also during treatment. Thus, a diagnostic assay based on one or more protein of the set will help the clinician in treatment decisions and the identification of anti-TNF therapy responders and non-responders a priory.

The bodily fluid and/or excrement from the individual to be assessed may be selected from a group comprising: blood, saliva, tears, synovial and spinal fluid, plasma, urine and stool.

An individual who is to be subjected to or is being subjected to an anti-TNFα treatment may suffer autoimmune conditions such as Crohn's disease, ulcerative colitis, psoriasis, psoriatic arthritis, ankylosing spondylitis, spondyloarthropathies, rheumatoid arthritis etc.

The method of the invention is especially suited for individuals suffering from rheumatoid arthritis.

Subject of the present invention is furthermore a kit for diagnosing an individual who is to be subjected to or is being subjected to an anti-TNFα treatment to assess the responsiveness to an anti-TNF treatment which comprises one or more biomarker proteins, wherein a biomarker protein is an expression product encoded by a gene selected from the group comprising RAB11B, PPP2R1A, KPNB1, COG4 and FDFT1. In a preferred embodiment the kit comprises at least those proteins encoded by a gene selected from the group comprising RAB11B, PPP2R1A, KPNB1, COG4 and FDFT1.

In a preferred embodiment of the inventive kit at least two of the biomarker proteins of the protein marker group are detected wherein a biomarker protein is an expression product encoded by a gene selected from the group comprising RAB11B, PPP2R1A, KPNB1, COG4 and FDFT1 (Protein Set 1=RAB11B, PPP2R1A, KPNB1, COG4 and FDFT1). In another preferred embodiment of the inventive kit at least one expression product encoded by genes RAB11B, PPP2R1A, KPNB1, COG4 and FDFT1 are detected. In another preferred embodiment only expression products encoded by genes RAB11B, PPP2R1A, KPNB1, COG4 and FDFT1 are detected. In another preferred embodiment each and only the expression products encoded by genes RAB11B, PPP2R1A, KPNB1, COG4 and FDFT1 are detected.

In another preferred embodiment of the kit for diagnosing an individual who is to be subjected to or is being subjected to an anti-TNFα treatment according to the invention the biomarker protein group additionally comprises at least one other expression product encoded by a gene selected from the group comprising PECI, CTNND2, NSMCE1, KTELC1, HS6ST1, ARMC6, TH1L, PSME1, GPC1, EDC4 (Protein Set 2) and at least one of the proteins of the entire group 1 and 2 (Protein Set 1 and 2) is detected. In a preferred embodiment of the invention at least one protein from Protein Set 1 is detected and additionally at least one of Protein Set 2 is detected. In another preferred embodiment at least two of the proteins of Protein Set 1 and additionally at least one of Protein Set 2 are detected. In another preferred embodiment Protein Set 1 and Protein Set 2 are detected.

In another preferred embodiment additionally to the above cited combinations of marker proteins a protein of Protein Set 3 is detected: the Protein Set 3 comprises the expression products encoded by genes PRC1, NAT6, EEF1AL3, NP_612480.1, PLXNA2, ELMO2 and NDUFS2.

In another preferred embodiment of the kit the biomarker protein group additionally comprises at least one expression product encoded by genes PECI, CTNND2, NSMCE1, KTELC1, HS6ST1, ARMC6, TH1L, PSME1, GPC1, EDC4, PRC1, NAT6, EEF1AL3, NP_612480.1, PLXNA2, ELMO2 and NDUFS2.

Another preferred embodiment of the invention is a kit for diagnosing an individual who is to be subjected to or is being subjected to an anti-TNFα treatment to assess the responsiveness to an anti-TNF treatment which comprises at least two biomarker proteins, wherein a biomarker protein is an expression product encoded by a gene selected from the group comprising RAB11B, PPP2R1A, KPNB1, COG4, FDFT1, PECI, CTNND2, NSMCE1, KTELC1, HS6ST1, ARMC6, TH1L, PSME1, GPC1, EDC4, PRC1, NAT6, EEF1AL3, NP_612480.1, PLXNA2, ELMO2 and NDUFS2.

As outlined above subject of the present invention is a method, wherein markers are detected and used to identify non-responder. A further embodiment of the present invention is the provision of marker(s), wherein the detection of those marker(s) is indicative for responder.

Thus, subject of the present invention is further a method for diagnosing an individual who is to be subjected to or is being subjected to an anti-TNFα treatment to assess the responsiveness to an anti-TNF treatment which comprises:

Detection of immunoglobulin(s) against one or more biomarker proteins in a bodily fluid or excrement of said patient, wherein a biomarker protein is an artificial peptides deduced from an expression product in an incorrect reading frame of a gene selected from the group comprising IRAK1 and C20orf149, wherein an individual positive for at least one of said immunoglobulin(s) is classified as responder.

In a preferred embodiment of the above-identified method the individual is sorted into one of two categories based on detection of said immunoglobulin(s), wherein an individual positive for at least one of said immunoglobulin(s) is classified as responder and, wherein an individual negative for any of said detected immunoglobulin(s) is classified as NON-responder.

In a preferred embodiment of the present invention the method for diagnosing an individual who is to be subjected to or is being subjected to an anti-TNFα treatment the biomarker protein group additionally comprises at least one other expression product encoded by a gene selected from a group comprising PSCD2L and PPIA.

In another preferred embodiment all members of the biomarker group are detected, the group comprising either artificial peptides deduced from an expression product in an incorrect reading frame of a gene or the expression products encoded by the following genes IRAK1 and C20orf149 as well as PSCD2L and PPIA.

The immunoglobulin(s) to be detected may be selected from IgA, IgD, IgG and IgM. In a preferred embodiment the immunoglobulin(s) to be detected is IgA or IgG. In the most

preferred embodiment the immunoglobulin is IgG. The immunoglobulin(s) to be detected is not related to IgA rheumatoid factor.

Subject of the method of the present invention is a method for diagnosing an individual who is to be subjected to or is being subjected to an anti-TNFα treatment, wherein the immunoglobulin(s) is IgA and/or IgG. IgG is especially preferred in the context of a method for diagnosing an individual who is to be subjected to or is being subjected to an anti-TNFα treatment to assess the responsiveness to an anti-TNF treatment, wherein an individual positive for at least one of before said immunoglobulin(s) is classified as responder.

The respective set of proteins can not only predict responsiveness before, but also during treatment. Thus, a diagnostic assay based on one or more protein of the set will help the clinician in treatment decisions and the identification of anti-TNF therapy responders and non-responders a priory.

The bodily fluid and/or excrement from the individual to be assessed may be selected from a group comprising: blood, saliva, tears, synovial and spinal fluid, plasma, urine and stool.

An individual who is to be subjected to or is being subjected to an anti-TNFα treatment may suffer autoimmune conditions such as Crohn's disease, ulcerative colitis, psoriasis, psoriatic arthritis, ankylosing spondylitis, spondyloarthropathies, rheumatoid arthritis etc.

The method of the invention is especially suited for individuals suffering from rheumatoid arthritis.

Subject of the present invention is also a kit for diagnosing an individual who is to be subjected to or is being subjected to an anti-TNFα treatment to assess the responsiveness to an anti-TNF treatment which comprises one or more biomarker proteins, wherein a biomarker protein is an artificial peptides deduced from an expression product in an incorrect reading frame of a gene selected from the group comprising IRAK1 and C20orf149.

In a preferred embodiment of the present invention the kit for diagnosing an individual who is to be subjected to or is being subjected to an anti-TNFα treatment the biomarker protein group additionally comprises at least one other expression product encoded by a gene selected from a group comprising PSCD2L and PPIA.

In another preferred embodiment all members of the biomarker group are detected, the group to comprising either artificial peptides deduced from an expression product in an incorrect reading frame of a gene or the expression products encoded by the following genes IRAK1 and C20orf149 as well as PSCD2L and PPIA.

In another embodiment of the invention the kit and the method according to the present invention is may additionally comprise one or more known diagnostic markers e.g. for autoimmune disorders. In a preferred embodiment the kit may also comprise other known diagnostic markers for rheumatoid arthritis.

The proteins, protein sets/kits may be conducted in different assay types known to a person skilled in the art.

The immunoglobulins to be detected are in or isolated from body fluids and excrements, such as blood, saliva, tears, synovial and spinal fluid, plasma, urine and stool, etc.

The diagnostic assay can be of any type applied in the field of diagnostics, including but not restricted to assays methods based on

enzymatic reactions
luminescence
fluorescence
radiochemicals

The preferred detection methods comprise strip tests, radioimmunoassay, chemiluminescence- and fluorescence-immunoassay, Immunoblot assay, Enzyme-linked immunoassay (ELISA), Luminex-based bead arrays, and protein microarray assay.

The assay types can further be microliter plate-based, chip-based, bead-based, wherein the biomarker proteins can be attached to the surface or in solution.

The assays can be homogenous or heterogeneous assays, sandwich assays, competitive and non-competitive assays (The Immunoassay Handbook, Ed. David Wild, Elsevier LTD, Oxford; 3rd ed. (May 2005), ISBN-13: 978-0080445267; Hultschig C et al., Curr Opin Chem Biol. 2006 February; 10(1):4-10. PMID: 16376134).

TNFα treatment is conducted by administration of a TNF inhibitor to an individual in need thereof. TNF inhibitors are biologicals which bind to soluble and cell membrane-associated form of TNFα and neutralise the proinflammatory effect of TNF by preventing the binding of TNFα to the TNF-RI/II cell-surface receptors. The TNF inhibitors can be anti-TNFα antibodies or receptor molecules but also of other types. The essential of a TNF inhibitor according to the present invention is the ability to capture TNF before it binds to the TNF receptor on the cells.

Subject to the present invention is also the use of the biomarker proteins and/or protein sets and the kits comprising these biomarker proteins and/or protein sets according to the present invention for assessing the responsiveness to an anti-TNFα treatment of an individual who is to be subjected to or is being subjected to an anti-TNFα treatment.

FIGURE DESCRIPTION

FIG. **1** shows SEQ ID No. 1 which is a DNA sequence of the gene RAB11B (Table 1, No. 1)

FIG. **2** shows SEQ ID No. 2 which is a DNA sequence of the gene PPP2R1A (Table 1, No. 2)

FIG. **3** shows SEQ ID No. 3 which is a DNA sequence of the gene PPP2R1A (Table 1, No. 2)

FIG. **4** shows SEQ ID No. 4 which is a DNA sequence of the gene KPNB1 (Table 1, No. 3)

FIG. **5** shows SEQ ID No. 5 which is a DNA sequence of the gene COG4 (Table 1, No. 4)

FIG. **6** shows SEQ ID No. 6 which is a DNA sequence of the gene COG4 (Table 1, No. 4)

FIG. **7** shows SEQ ID No. 7 which is a DNA sequence of the gene COG4 (Table 1, No. 4)

FIG. **8** shows SEQ ID No. 8 which is a DNA sequence of the gene COG4 (Table 1, No. 4)

FIG. **9** shows SEQ ID No. 9 which is a DNA sequence of the gene FDFT1 (Table 1, No. 5)

FIG. **10** shows SEQ ID No. 10 which is a DNA sequence of the gene PECI (Table 1, No. 6)

FIG. **11** shows SEQ ID No. 11 which is a DNA sequence of the gene PECI (Table 1, No. 6)

FIG. **12** shows SEQ ID No. 12 which is a DNA sequence of the gene PECI (Table 1, No. 6)

FIG. **13** shows SEQ ID No. 13 which is a DNA sequence of the gene PECI (Table 1, No. 6)

FIG. **14** shows SEQ ID No. 14 which is a DNA sequence of the gene PECI (Table 1, No. 6)

FIG. **15** shows SEQ ID No. 15 which is a DNA sequence of the gene CTNND2 (Table 1, No. 7)

FIG. **16** shows SEQ ID No. 16 which is a DNA sequence of the gene CTNND2 (Table 1, No. 7)

FIG. **17** shows SEQ ID No. 17 which is a DNA sequence of the gene NSMCE1 (Table 1, No. 8)

FIG. **18** shows SEQ ID No. 18 which is a DNA sequence of the gene NSMCE1 (Table 1, No. 8)

FIG. **19** shows SEQ ID No. 19 which is a DNA sequence of the gene NSMCE1 (Table 1, No. 8)

FIG. **20** shows SEQ ID No. 20 which is a DNA sequence of the gene KTELC1 (Table 1, No. 9)

FIG. **21** shows SEQ ID No. 21 which is a DNA sequence of the gene HS6ST1 (Table 1, No. 10)

FIG. **22** shows SEQ ID No. 22 which is a DNA sequence of the gene ARMC6 (Table 1, No. 11)

FIG. **23** shows SEQ ID No. 23 which is a DNA sequence of the gene ARMC6 (Table 1, No. 11)

FIG. **24** shows SEQ ID No. 24 which is a DNA sequence of the gene ARMC6 (Table 1, No. 11)

FIG. **25** shows SEQ ID No. 25 which is a DNA sequence of the gene ARMC6 (Table 1, No. 11)

FIG. **26** shows SEQ ID No. 26 which is a DNA sequence of the gene TH1L (Table 1, No. 12)

FIG. **27** shows SEQ ID No. 27 which is a DNA sequence of the gene PSME1 (Table 1, No. 13)

FIG. **28** shows SEQ ID No. 28 which is a DNA sequence of the gene PSME1 (Table 1, No. 13)

FIG. **29** shows SEQ ID No. 29 which is a DNA sequence of the gene GPC1 (Table 1, No. 14)

FIG. **30** shows SEQ ID No. 30 which is a DNA sequence of the gene EDC4 (Table 1, No. 15)

FIG. **31** shows SEQ ID No. 31 which is a DNA sequence of the gene EDC4 (Table 1, No. 15)

FIG. **32** shows SEQ ID No. 32 which is a DNA sequence of the gene PRC1 (Table 1, No. 16)

FIG. **33** shows SEQ ID No. 33 which is a DNA sequence of the gene PRC1 (Table 1, No. 16)

FIG. **34** shows SEQ ID No. 34 which is a DNA sequence of the gene PRC1 (Table 1, No. 16)

FIG. **35** shows SEQ ID No. 35 which is a DNA sequence of the gene NAT6 (Table 1, No. 17)

FIG. **36** shows SEQ ID No. 36 which is a DNA sequence of the gene NAT6 (Table 1, No. 17)

FIG. **37** shows SEQ ID No. 37 which is a DNA sequence of the gene NAT6 (Table 1, No. 17)

FIG. **38** shows SEQ ID No. 38 which is a DNA sequence of the gene EEF1AL3 (Table 1, No. 18)

FIG. **39** shows SEQ ID No. 39 which is a DNA sequence of the gene NP_612480.1 (Table 1, No. 19)

FIG. **40** shows SEQ ID No. 40 which is a DNA sequence of the gene PLXNA2 (Table 1, No. 20)

FIG. **41** shows SEQ ID No. 41 which is a DNA sequence of the gene PLXNA2 (Table 1, No. 20)

FIG. **42** shows SEQ ID No. 42 which is a DNA sequence of the gene ELMO2 (Table 1, No. 21)

FIG. **43** shows SEQ ID No. 43 which is a DNA sequence of the gene ELMO2 (Table 1, No. 21)

FIG. **44** shows SEQ ID No. 44 which is a DNA sequence of the gene ELMO2 (Table 1, No. 21)

FIG. **45** shows SEQ ID No. 45 which is a DNA sequence of the gene ELMO2 (Table 1, No. 21)

FIG. **46** shows SEQ ID No. 46 which is a DNA sequence of the gene NDUFS2 (Table 1, No. 22)

FIG. **47** shows SEQ ID No. 47 which is a DNA sequence of the gene NDUFS2 (Table 1, No. 22)

FIG. **48** shows SEQ ID No. 48 which is a DNA sequence of the gene IRAK1 (Table 1, No. 23)

FIG. **49** shows SEQ ID No. 49 which is a DNA sequence of the gene IRAK1 (Table 1, No. 23)

FIG. **50** shows SEQ ID No. 50 which is a DNA sequence of the gene IRAK1 (Table 1, No. 23)

FIG. **51** shows SEQ ID No. 51 which is a DNA sequence of the gene IRAK1 (Table 1, No. 23)

FIG. **52** shows SEQ ID No. 52 which is a DNA sequence of the gene IRAK1 (Table 1, No. 23)

FIG. **53** shows SEQ ID No. 53 which is a DNA sequence of the gene C20orf149 (Table 1, No. 24)

FIG. **54** shows SEQ ID No. 54 which is a DNA sequence of the gene C20orf149 (Table 1, No. 24)

FIG. **55** shows SEQ ID No. 55 which is a DNA sequence of the gene C20orf149 (Table 1, No. 24)

FIG. **56** shows SEQ ID No. 56 which is a DNA sequence of the gene PCSD2L (Table 1, No. 25)

FIG. **57** shows SEQ ID No. 57 which is a DNA sequence of the gene PCSD2L (Table 1, No. 25)

FIG. **58** shows SEQ ID No. 58 which is a DNA sequence of the gene PPIA (Table 1, No. 26)

FIG. **59** shows SEQ ID No. 59 which is a Protein sequence of the gene RAB11B (Table 1, No. 1)

FIG. **60** shows SEQ ID No. 60 which is a Protein sequence of the gene PPP2R1A (Table 1, No. 2)

FIG. **61** shows SEQ ID No. 61 which is a Protein sequence of the gene PPP2R1A (Table 1, No. 2)

FIG. **62** shows SEQ ID No. 62 which is a Protein sequence of the gene KPNB1 (Table 1, No. 3)

FIG. **64** shows SEQ ID No. 64 which is a Protein sequence of the gene COG4 (Table 1, No. 4)

FIG. **65** shows SEQ ID No. 65 which is a Protein sequence of the gene COG4 (Table 1, No. 4)

FIG. **66** shows SEQ ID No. 66 which is a Protein sequence of the gene COG4 (Table 1, No. 4)

FIG. **67** shows SEQ ID No. 67 which is a Protein sequence of the gene COG4 (Table 1, No. 4)

FIG. **68** shows SEQ ID No. 68 which is a Protein sequence of the gene FDFT1 (Table 1, No. 5)

FIG. **69** shows SEQ ID No. 69 which is a Protein sequence of the gene PECI (Table 1, No. 6)

FIG. **70** shows SEQ ID No. 70 which is a Protein sequence of the gene PECI (Table 1, No. 6)

FIG. **71** shows SEQ ID No. 71 which is a Protein sequence of the gene PECI (Table 1, No. 6)

FIG. **72** shows SEQ ID No. 72 which is a Protein sequence of the gene PECI (Table 1, No. 6)

FIG. **73** shows SEQ ID No. 73 which is a Protein sequence of the gene PECI (Table 1, No. 6)

FIG. **74** shows SEQ ID No. 74 which is a Protein sequence of the gene CTNND2 (Table 1, No. 7)

FIG. **75** shows SEQ ID No. 75 which is a Protein sequence of the gene CTNND2 (Table 1, No. 7)

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FIG. **77** shows SEQ ID No. 77 which is a Protein sequence of the gene NSMCE1 (Table 1, No. 8)

FIG. **78** shows SEQ ID No. 78 which is a Protein sequence of the gene NSMCE1 (Table 1, No. 8)

FIG. **79** shows SEQ ID No. 79 which is a Protein sequence of the gene KTELC1 (Table 1, No. 9)

FIG. **80** shows SEQ ID No. 80 which is a Protein sequence of the gene HS6ST1 (Table 1, No. 10)

FIG. **81** shows SEQ ID No. 81 which is a Protein sequence of the gene ARMC6 (Table 1, No. 11)

FIG. **82** shows SEQ ID No. 82 which is a Protein sequence of the gene ARMC6 (Table 1, No. 11)

FIG. **83** shows SEQ ID No. 83 which is a Protein sequence of the gene ARMC6 (Table 1, No. 11)

FIG. **84** shows SEQ ID No. 84 which is a Protein sequence of the gene ARMC6 (Table 1, No. 11)

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FIG. **87** shows SEQ ID No. 87 which is a Protein sequence of the gene PSME1 (Table 1, No. 13)

FIG. **88** shows SEQ ID No. 88 which is a Protein sequence of the gene GPC1 (Table 1, No. 14)

FIG. **89** shows SEQ ID No. 89 which is a Protein sequence of the gene EDC4 (Table 1, No. 15)

FIG. **90** shows SEQ ID No. 90 which is a Protein sequence of the gene EDC4 (Table 1, No. 15)

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FIG. **92** shows SEQ ID No. 92 which is a Protein sequence of the gene PRC1 (Table 1, No. 16)

FIG. **93** shows SEQ ID No. 93 which is a Protein sequence of the gene PRC1 (Table 1, No. 16)

FIG. **94** shows SEQ ID No. 94 which is a Protein sequence of the gene NAT6 (Table 1, No. 17)

FIG. **95** shows SEQ ID No. 95 which is a Protein sequence of the gene NAT6 (Table 1, No. 17)

FIG. **96** shows SEQ ID No. 96 which is a Protein sequence of the gene NAT6 (Table 1, No. 17)

FIG. **97** shows SEQ ID No. 97 which is a Protein sequence of the gene EEF1AL3 (Table 1, No. 18)

FIG. **98** shows SEQ ID No. 98 which is a Protein sequence of the gene NP_612480.1 (Table 1, No. 19)

FIG. **99** shows SEQ ID No. 99 which is a Protein sequence of the gene PLXNA2 (Table 1, No. 20)

FIG. **100** shows SEQ ID No. 100 which is a Protein sequence of the gene PLXNA2 (Table 1, No. 20)

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FIG. **102** shows SEQ ID No. 102 which is a Protein sequence of the gene ELMO2 (Table 1, No. 21)

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FIG. **104** shows SEQ ID No. 104 which is a Protein sequence of the gene ELMO2 (Table 1, No. 21)

FIG. **105** shows SEQ ID No. 105 which is a Protein sequence of the gene NDUFS2 (Table 1, No. 22)

FIG. **106** shows SEQ ID No. 106 which is a Protein sequence of the gene NDUFS2 (Table 1, No. 22)

FIG. **107** shows SEQ ID No. 107 which is a Protein sequence of the gene IRAK1 (Table 1, No. 23)

FIG. **108** shows SEQ ID No. 108 which is a Protein sequence of the gene IRAK1 (Table 1, No. 23)

FIG. **109** shows SEQ ID No. 109 which is a Protein sequence of the gene IRAK1 (Table 1, No. 23)

FIG. **110** shows SEQ ID No. 110 which is a Protein sequence of the gene IRAK1 (Table 1, No. 23)

FIG. **111** shows SEQ ID No. 111 which is a Protein sequence of the gene IRAK1 (Table 1, No. 23)

FIG. **112** shows SEQ ID No. 112 which is a Protein sequence of the gene C20orf149 (Table 1, No. 24)

FIG. **113** shows SEQ ID No. 113 which is a Protein sequence of the gene C20orf149 (Table 1, No. 24)

FIG. **114** shows SEQ ID No. 114 which is a Protein sequence of the gene C20orf149 (Table 1, No. 24)

FIG. **115** shows SEQ ID No. 115 which is a Protein sequence of the gene PCSD2L (Table 1, No. 25)

FIG. **116** shows SEQ ID No. 116 which is a Protein sequence of the gene PCSD2L (Table 1, No. 25)

FIG. **117** shows SEQ ID No. 117 which is a Protein sequence of the gene PPIA (Table 1, No. 26)

FIG. **118** shows SEQ ID No. 118 which is a Protein sequence derived from an incorrect reading frame of the gene HS6ST1 (Table 1, No. 10)

FIG. **119** shows SEQ ID No. 119 which is a Protein sequence derived from an incorrect reading frame of the gene IRAK1 (Table 1, No. 23)

FIG. **120** shows SEQ ID No. 120 which is a Protein sequence derived from an incorrect reading frame of the gene C20orf149 (Table 1, No. 24)

FIG. **121** shows SEQ ID No. 121 which is a Protein sequence derived from an incorrect reading frame of the gene C20orf149 (Table 1, No. 24)

FIG. **122** shows SEQ ID No. 122 which is a Protein sequence derived from an incorrect reading frame of the gene HS6SP1 (Table 1, No. 10)

EXAMPLES

The set of proteins which are subject of the present invention have been found by conducting serum screening experiments on protein macroarrays. The protein macroarrays consist of >38.000 individual *E. coli* clones expressing human gene fragments cloned from a foetal brain cDNA library. These fragments can be full length proteins and fragments thereof, as well as artificial peptides resulting from translation products in the incorrect reading frame. The technology for screening was developed at the MPI for Molecular Genetics and constitutes prior art; Büssow K, et al. Nucleic Acids Res. 1998 Nov. 1; 26(20:5007-8. PMID: 9776767; Büssow K, et al. Genomics 2000 Apr. 1; 65(1):1-8. PMID: 10777659) and has been applied since then in multiple scientific publications (e.g. Horn S, et al. Proteomics. 2006 January; 6(2):605-13. PMID: 16419013; Lueking A, et al. Mol Cell Proteomics. 2005 September; 4(9):1382-90. PMID: 15939964). The only amendment to the method described in the original paper is the incubation with patient serum and the use of specific secondary antibodies directed against different immunoglobulin isotypes such as IgG, IgA, IgM and IgD as described beneath:

Patient serum was diluted 1:40 in blocking buffer (3% Milk powder/TBST) and incubated overnight at room temperature, kept in slow motion on an orbital shaker. After incubation filters are washed 3×20 min. in TBST, followed by a second incubation for 1 h at room temperature with anti human IgG or anti human IgA secondary antibody (mouse) conjugated with alkaline phosphatase, 1:1000 in blocking buffer. Positive signals on the macroarray (PVDF filter) were recorded as described and correlated to the original *E. coli* clones stored in 384-well microtitre plates. *E. coli* clones corresponding with the signals on the macroarray were sequenced to obtain information of the insert, and hence the gene fragment of which the translation product is recognised by the patient sera. These fragments can be full length proteins and fragments thereof, as well as artificial peptides resulting from out-of frame-translation products.

The protein macroarrays were screened with pools of anti-TNFα treatment (Adalimumab®; Humira) responder and non-responder patient sera before and after therapy. Responder and non-responder patients were categorised according to the clinical response evaluated after 1 year (or at drop-out) in accordance with the European League Against Rheumatism criteria using the modified disease activity score that includes 28 joints (DAS 28). The DAS28 score and the European League Against Rheumatism (EULAR) response criteria are widely used to record disease activity and

therapeutic response in patients with RA (Van Gestel A M et al. Arthritis Rheum 1996; 39:34-40. PMID:

The DAS28 was developed and validated for patients with RA, and in addition to disease activity it also reflects the patient's satisfaction with reasonable accuracy. This composite index comprises 4 items, namely, swollen joint count (SJC), tender joint count (TJC), a visual analog scale (VAS) of the patient's assessment of general health (GH), and erythrocyte sedimentation rate (ESR; first hour), which are also part of the American College of Rheumatology (ACR) response criteria.

Description of the Used Patient Sera:

DAS28 values from 2 RA patient cohorts comprising 3 patients each were compared and sera of these patients before and after therapy were used for screening the protein macroarrays. RA cohort 1 (RA1) consisted of therapy responder patients and the RA cohort 2 (RA2) consisted of of age- and sex-matched patients seen during the same period who were therapy non-responders. Item weighting, factor loading, and internal consistency were assessed by factor analysis, principal component analysis, and calculation of Cronbach's alpha. The range of DAS 28 scores in the responder group initially before treatment was from 4.4-6 with a mean value of 4.83 and in the non responder group 4.1-8.6 with a mean value 6.2. Responder had a mean change of 2.36 during therapy while there was no mean change in the DAS28 in the non responder group.

Table 1 (consisting of Table 1 A and Table 1 B) shows a summary list of genes of which the expression products represent biomarker proteins and artificial peptides resulting from translation products in the incorrect reading frame found to be predictive for responsiveness to anti-TNFα antibody treatment (Adalimumab; Humira) of the patient groups described above having been subjected to an anti-TNFα treatment.

TABLE 1 A

List of candidate genes encoding a biomarker set detected by immunoglobulins of TNF inhibitor therapy NON-RESPONDER patients

No.	Importance	frame offset	ENSEMBL gene identifier	HGNC gene symbol	gene description and alternative identifiers
1	1: High	0	ENSG00000185236	RAB11B	Ras-related protein Rab-11B (GTP-binding protein YPT3). [Source: Uniprot/SWISSPROT; Acc: Q15907]
2	1: High	0	ENSG00000105568	PPP2R1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform (PP2A, subunit A, PR65-alpha isoform) (PP2A, subunit A, R1-alpha isoform) (Medium tumor antigen-associated 61 kDa protein). [Source: Uniprot/SWISSPROT; Acc: P30153]
3	1: High	0	ENSG00000108424	KPNB1	Importin beta-1 subunit (Karyopherin beta-1 subunit) (Nuclear factor P97) (Importin 90). [Source: Uniprot/SWISSPROT; Acc: Q14974]
4	1: High	0	ENSG00000103051	COG4	Conserved oligomeric Golgi complex component 4. [Source: Uniprot/SWISSPROT; Acc: Q9H9E3]
5	1: High	0	ENSG00000079459	FDFT1	Squalene synthetase (EC 2.5.1.21) (SQS) (SS) (Farnesyl-diphosphate farnesyltransferase) (FPP:FPP farnesyltransferase). [Source: Uniprot/SWISSPROT; Acc: P37268]
6	2: Medium	0	ENSG00000198721	PECI	Peroxisomal 3,2-trans-enoyl-CoA isomerase (EC 5.3.3.8) (Dodecenoyl-CoA isomerase) (Delta(3),delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase) (DBI-related protein 1) (DRS-1) (Hepatocellular carcinoma-associated antigen 88) (Renal carcinoma antige
7	2: Medium	0	ENSG00000169862	CTNND2	Catenin delta-2 (Delta-catenin) (Neural plakophilin-related ARM-repeat protein) (NPRAP) (Neurojungin) (GT24). [Source: Uniprot/SWISSPROT; Acc: Q9UQB3] chromosome NCBI36:5:11024952-11957110:-1
8	2: Medium	0	ENSG00000169189	NSMCE1	non-SMC element 1 homolog [Source: RefSeq_peptide; Acc: NP_659547] chromosome_NCBI36:16:27143817-27187586:-1
9	2: Medium	0	ENSG00000163389	KTELC1	KTEL motif-containing protein 1 precursor (CAP10-like 46 kDa protein) (Myelodysplastic syndromes relative protein). [Source: Uniprot/SWISSPROT; Acc: Q8NBL1]
10	2: Medium	−1	ENSG00000136720	HS6ST1	Heparan-sulfate 6-O-sulfotransferase 1 (EC 2.8.2.—) (HS6ST-1). [Source: Uniprot/SWISSPROT; Acc: O60243]
11	2: Medium	0	ENSG00000105676	ARMC6	Armadillo repeat-containing protein 6. [Source: Uniprot/SWISSPROT; Acc: Q6NXE6]chromosome_NCBI36:19:19005538-19029985:1
12	2: Medium	0	ENSG00000101158	TH1L	Negative elongation factor C/D (NELF-C/D) (TH1-like protein). [Source: Uniprot/SWISSPROT; Acc: Q8IXH7]
13	2: Medium	0	ENSG00000092010	PSME1	Proteasome activator complex subunit 1 (Proteasome activator 28-alpha subunit) (PA28alpha) (PA28a) (Activator of multicatalytic protease subunit 1) (11S regulator complex subunit alpha) (REG-alpha) (Interferon gamma up-regulated I-5111 protein) (IGUP I-51
14	2: Medium	0	ENSG00000063660	GPC1	Glypican-1 precursor. [Source: Uniprot/SWISSPROT; Acc: P35052]
15	2: Medium	0	ENSG00000038358	EDC4	autoantigen RCD8 [Source: RefSeq_peptide; Acc: NP_055144] chromosome_NCBI36:16:66464500-66475906:1
16	3: Low	0	ENSG00000198901	PRC1	Protein regulator of cytokinesis 1. [Source: Uniprot/SWISSPROT; Acc: O43663] chromosome_NCBI36:15:89310279-89338808:-1
17	3: Low	0	ENSG00000186792	NAT6	Hyaluronidase-3 precursor (EC 3.2.1.35) (Hyal-3) (Hyaluronoglucosaminidase-3) (LUCA-3). [Source: Uniprot/SWISSPROT; Acc: O43820] chromosome_NCBI36:3:50300178-50311903:-1
18	3: Low	0	ENSG00000185637	EEF1AL3	Eukaryotic translation elongation factor 1 alpha 1 (Fragment). [Source: Uniprot/SPTREMBL; Acc: Q5JR01] chromosome_NCBI36:9:134884631-134886374:1
19	3: Low	0	ENSG00000168005	NP_612480.1	chromosome_NCBI36:11:63337436-63351727:1
20	3: Low	0	ENSG00000076356	PLXNA2	Plexin-A2 precursor (Semaphorin receptor OCT). [Source: Uniprot/SWISSPROT; Acc: O75051] chromosome_NCBI36:1:206262210-206484288:-1

TABLE 1 A-continued

List of candidate genes encoding a biomarker set detected by immunoglobulins of TNF inhibitor therapy NON-RESPONDER patients

No.	Importance	frame offset	ENSEMBL gene identifier	HGNC gene symbol	gene description and alternative identifiers
21	3: Low	0	ENSG00000062598	ELMO2	Engulfment and cell motility protein 2 (CED-12 homolog A) (hCED-12A). [Source: Uniprot/SWISSPROT; Acc: Q96JJ3] chromosome_NCBI36:20:44428096-44468678:-1
22	3: Low	0	ENSG00000158864	NDUFS2	NADH-ubiquinone oxidoreductase 49 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-49 KD) (CI-49 KD). [Source: Uniprot/SWISSPROT; Acc: O75306]

TABLE 1 B

List of candidate genes encoding a biomarker set detected by immunoglobulins of TNF inhibitor therapy RESPONDER patients

No.	Importance	frame offset	ENSEMBL identifier	HGNC gene symbol	gene description and alternative identifiers
23	1: High	−1	ENSG00000184216	IRAK1	Interleukin-1 receptor-associated kinase 1 (EC 2.7.11.1) (IRAK-1). [Source: Uniprot/SWISSPROT; Acc: P51617]
24	1: High	−1	ENSG00000125534	C20orf149	UPF0362 protein C20orf149. [Source: Uniprot/SWISSPROT; Acc: Q9H3Y8]
25	2: Medium	0	ENSG00000105443	PSCD2L	Cytohesin-2 (ARF nucleotide-binding site opener) (ARNO protein) (ARF exchange factor). [Source: Uniprot/SWISSPROT; Acc: Q99418] chromosome_NCBI36:19:53664424-53674457:1
26	3: Low	0	ENSG00000198618	PPIA	Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPlase A) (Rotamase A) (Cyclophilin A) (Cyclosporin A-binding protein). [Source: Uniprot/SWISSPROT; Acc: P62937] chromosome_NCBI36:21:19151917-19152651:1

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<211> LENGTH: 2370
<212> TYPE: DNA
<213> ORGANISM: Human

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<211> LENGTH: 1014
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 6

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<210> SEQ ID NO 7
<211> LENGTH: 2358
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 7

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aagaggctgc gcctgtag 2358

<210> SEQ ID NO 8
<211> LENGTH: 2088
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 8

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cccaattccg gcccattgac gtggcgcctc acccctgctg aagtgcgcca ggtgctggcc 2040

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<210> SEQ ID NO 9
<211> LENGTH: 1254
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 9

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<210> SEQ ID NO 10
<211> LENGTH: 1080
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 10

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<210> SEQ ID NO 11
<211> LENGTH: 684
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 11

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aaagaagtct ggaccaggct gaaggcattt gcaaagcttc ccccaaatgc cttgagaatt 540

tcaaaagagg taatcaggaa aagagagaga gaaaaactac acgctgttaa tgctgaagaa 600

tgcaatgtcc ttcagggaag atggctatca gatgaatgca caaatgctgt ggtgaacttc 660

ttatccagaa aatcaaaact gtga 684

<210> SEQ ID NO 12
<211> LENGTH: 1185
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 12

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gtcactagtt tcccggtagt tcagctgcac atgaatagaa cagcaatgag agccagtcag 120

aaggactttg aaaattcaat gaatcaagtg aaactcttga aaaaggatcc aggaaacgaa 180

gtgaagctaa aactctacgc gctatataag caggccactg aaggaccttg taacatgccc 240

aaaccaggtg tatttgactt gatcaacaag gccaaatggg acgcatggaa tgcccttggc 300

agcctgccca aggaagctgc caggcagaac tatgtggatt tggtgtccag tttgagtcct 360

tcattggaat cctctagtca ggtggagcct ggaacagaca ggaaatcaac tgggtttgaa 420

actctggtgg tgacctccga agatggcatc acaaagatca tgttcaaccg gcccaaaaag 480

aaaaatgcca taaacactga gatgtatcat gaaattatgc gtgcacttaa agctgccagc 540

aaggatgact caatcatcac tgttttaaca ggaaatggtg actattacag tagtgggaat 600

gatctgacta acttcactga tattcccccc ggtggagtag aggagaaagc taaaaataat 660

gccgttttac tgagggaatt tgtgggctgt tttatagatt ttcctaagcc tctgattgca 720

gtggtcaatg gtccagctgt gggcatctcc gtcaccctcc ttgggctatt cgatgccgtg 780

tatgcatctg acagggcaac atttcataca ccatttagtc acctaggcca aagtccggaa 840

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atttttggaa agaagttaac agcgggagag gcatgtgctc aaggacttgt tactgaagtt 960

ttccctgata gcacttttca gaaagaagtc tggaccaggc tgaaggcatt tgcaaagctt 1020

cccccaaatg ccttgagaat ttcaaaagag gtaatcagga aaagagagag agaaaaacta 1080

cacgctgtta atgctgaaga atgcaatgtc cttcagggaa gatggctatc agatgaatgc 1140

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<210> SEQ ID NO 13
<211> LENGTH: 1095
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 13

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caggccactg aaggaccttg taacatgccc aaaccaggtg tatttgactt gatcaacaag 180

gccaaatggg acgcatggaa tgcccttggc agcctgccca aggaagctgc caggcagaac 240

tatgtggatt tggtgtccag tttgagtcct tcattggaat cctctagtca ggtggagcct 300

ggaacagaca ggaaatcaac tgggtttgaa actctggtgg tgacctccga agatggcatc 360

acaaagatca tgttcaaccg gcccaaaaag aaaaatgcca taaacactga gatgtatcat 420

gaaattatgc gtgcacttaa agctgccagc aaggatgact caatcatcac tgttttaaca 480

ggaaatggtg actattacag tagtgggaat gatctgacta acttcactga tattcccccc 540

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ggtggagtag aggagaaagc taaaaataat gccgttttac tgagggaatt tgtgggctgt 600

tttatagatt ttcctaagcc tctgattgca gtggtcaatg gtccagctgt gggcatctcc 660

gtcaccctcc ttgggctatt cgatgccgtg tatgcatctg acagggcaac atttcataca 720

ccatttagtc acctaggcca aagtccggaa ggatgctcct cttacacttt tccgaagata 780

atgagcccag ccaaggcaac agagatgctt atttttggaa agaagttaac agcgggagag 840

gcatgtgctc aaggacttgt tactgaagtt ttccctgata gcacttttca gaaagaagtc 900

tggaccaggc tgaaggcatt tgcaaagctt cccccaaatg ccttgagaat ttcaaaagag 960

gtaatcagga aaagagagag agaaaaacta cacgctgtta atgctgaaga atgcaatgtc 1020

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aaatcaaaac tgtga 1095

<210> SEQ ID NO 14
<211> LENGTH: 726
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 14

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cgtgcactta aagctgccag caaggatgac tcaatcatca ctgttttaac aggaaatggt 120

gactattaca gtagtgggaa tgatctgact aacttcactg atattccccc tggtggagta 180

gaggagaaag ctaaaaataa tgccgtttta ctgagggaat ttgtgggctg ttttatagat 240

tttcctaagc ctctgattgc agtggtcaat ggtccagctg tgggcatctc cgtcaccctc 300

cttgggctat tcgatgccgt gtatgcatct gacagggcaa catttcatac accatttagt 360

cacctaggcc aaagtccgga aggatgctcc tcttacactt ttccgaagat aatgagccca 420

gccaaggcaa cagagatgct tatttttgga aagaagttaa cagcgggaga ggcatgtgct 480

caaggacttg ttactgaagt tttccctgat agcacttttc agaaagaagt ctggaccagg 540

ctgaaggcat ttgcaaagct tcccccaaat gccttgagaa tttcaaaaga ggtaatcagg 600

aaaagagaga gagaaaaact acacgctgtt aatgctgaag aatgcaatgt ccttcaggga 660

agatggctat cagatgaatg cacaaatgct gtggtgaact tcttatccag aaaatcaaaa 720

ctgtga 726

<210> SEQ ID NO 15
<211> LENGTH: 3504
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 15

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gatggctctg aaacagaaac cacctctgcc atcctcgcct cagtcaaaga acaggaatta 180

cagtttgaaa ggctgacccg agagctggag gctgaacggc agatcgtagc cagccagctg 240

gagcgatgca agctcggatc cgagactggc agcatgagca gcatgagttc agcagaagag 300

cagtttcagt ggcagtcaca agatggtcaa aaagatatcg aagatgagct tacaacaggt 360

ctcgagctgg tggactcctg tattaggtca ctacaggaat caggaatact tgacccacag 420

gattattcta caggtgaaag gcccagcctg ctctcccaga gtgcacttca gctcaattcc 480

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aaacctgaag ggtctttcca gtatccggcc agctaccata gcaaccagac cctggccctg 540

ggggaaacca ccccttcaca gctcccggcc cgaggcacac aagcccgagc tacgggccag 600

agcttcagcc agggcacgac cagccgcgcc ggccacctgg cggggcccga gcccgcgccg 660

ccgccgccgc cgccgccgcg ggagccgttc gcgcccagcc tgggcagcgc cttccacctg 720

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caggggggacc ctctgccgcc agcacacacc ggcacctacc gcacgagcac agccccatct 1380

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tatgggaagg ccaacgatga taacaaaatt gccctgaaaa actgtggtgg catcccagca 1920

ctggtgaggt tactccgcaa gacgactgac ctggagatcc gggagctggt cacaggagtc 1980

ctttggaacc tctcctcatg cgatgcactc aaaatgccaa tcatccagga tgccctagca 2040

gtactgacca acgcggtgat tatcccccac tcaggctggg aaaattcgcc tcttcaggat 2100

gatcggaaaa tacagctgca ttcatcacag gtgctgcgta acgccaccgg gtgcctaagg 2160

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aaggatgctg agagctctgg gtgctggggc aagaagaaga agaaaaagaa atcccaagat 2460

cagtggtcag tatatatccg agccgctgtc cgaaaagaga aaggcctgcc catcctcgtg 2520

gagctgctcc gaatagacaa tgaccgtgtg gtgtgcgcgg tggccactgc gctgcggaac 2580

atggccttgg acgtcagaaa taaggagctc atcggcaaat acgccatgcg agacctagtc 2640

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acagtgacag ctgtctgctg cacactgcac gaagtgatta ccaagaacat ggagaacgcc 2760

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gataaacact ctccaaaagt ggtcaaggct gcatctcagg tcctcaacag catgtggcag 2880

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gaaatgatca gcctcaaaga aaggaaaaca gactacgagt gcaccggcag caacgccacc 3120

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caggtttcag cacagccagt cccacaggag cccagcagaa aagattacga gacctaccag 3300

ccatttcaga attccacaag aaattacgat gagtccttct tcgaggacca ggtccaccat 3360

cgccctcccg ccagcgagta caccatgcac ctgggtctca agtccaccgg caactacgtt 3420

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gcctcccccg actcctgggt gtga 3504

<210> SEQ ID NO 16
<211> LENGTH: 3678
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 16

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gatggctctg aaacagaaac cacctctgcc atcctcgcct cagtcaaaga acaggaatta 180

cagtttgaaa ggctgacccg agagctggag gctgaacggc agatcgtagc cagccagctg 240

gagcgatgca agctcggatc cgagactggc agcatgagca gcatgagttc agcagaagag 300

cagtttcagt ggcagtcaca agatggtcaa aaagatatcg aagatgagct tacaacaggt 360

ctcgagctgg tggactcctg tattaggtca ctacaggaat caggaatact tgacccacag 420

gattattcta caggtgaaag gcccagcctg ctctcccaga gtgcacttca gctcaattcc 480

aaacctgaag ggtctttcca gtatccggcc agctaccata gcaaccagac cctggccctg 540

ggggaaacca ccccttcaca gctcccggcc cgaggcacac aagcccgagc tacgggccag 600

agcttcagcc agggcacgac cagccgcgcc ggccacctgg cggggcccga gcccgcgccg 660

ccgccgccgc cgccgccgcg ggagccgttc gcgcccagcc tgggcagcgc cttccacctg 720

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cctgctctcc cgcctgaagg caccttggcc aggtccccgt ccattgatag cattcagaaa 1620

gatcccagag aatttggatg gagagacccg gaactgccgg aagtgattca gatgttgcag 1680

caccagtttc cctcggtcca gtctaacgcg gcagcctact tgcaacacct ctgttttgga 1740

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gatcggaaaa tacagctgca ttcatcacag gtgctgcgta acgccaccgg gtgcctaagg 2160

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cccgactcct gggtgtga 3678

<210> SEQ ID NO 17
<211> LENGTH: 438

<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 17

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acccatggcg tgctagagga atgggacgtg aagcgcttgc agacgcactg ctacaaggtc 180

catgaccgca atgccaccgt agataagttg gaggacttca tcaacaacat taacagtgtc 240

ttggagtcct tgtatattga gataaagaga ggagtcacgg aagatgatgg gagacccatt 300

tatgcgttgg tgaatcttgc tacaacttca atttccaaaa tggctacgga ttttgcagag 360

aatgaactgg atttgtttag aaaggctctg gaactgatta ttgactcaga aaccttgcgt 420

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<210> SEQ ID NO 18
<211> LENGTH: 801
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 18

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tacaaggtcc atgaccgcaa tgccaccgta gataagttgg aggacttcat caacaacatt 180

aacagtgtct tggagtcctt gtatattgag ataaagagag gagtcacgga agatgatggg 240

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gagaaggaag gggagttcac cctgcacggc cgggccatcc tggagatgga gcaatacatc 540

cgggagacgt accccgacgc ggtgaagatc tgcaatatct gtcacagcct cctcatccag 600

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ctgcggtcca ggcagcatta g 801

<210> SEQ ID NO 19
<211> LENGTH: 540
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 19

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ctccagttgc tgatgaccca tggcgtgcta gaggaatggg acgtgaagcg cttgcagacg 180

cactgctaca aggtccatga ccgcaatgcc accgtagata agttggagga cttcatcaac 240

aacattaaca gtgtcttgga gtccttgtat attgagataa agagaggagt cacggaagat 300

gatgggagac ccatttatgc gttggtgaat cttgctacaa cttcaatttc caaaatggct 360

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aagaagatga ggaagaagga agcgaggtgc tgcagaagtt tgttcaaaac aagtggctga 540

<210> SEQ ID NO 20
<211> LENGTH: 1179
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 20

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aggtctttgg agaattacga accatgttca agtcaaaact gcagctgcta ccatggtgtc 180

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gatcactgca aatacaagta tctgtttaat tttcgaggcg tagctgcaag tttccggttt 840

aaacacctct tcctgtgtgg ctcacttgtt ttccatgttg gtgatgagtg gctagaattc 900

ttctatccac agctgaagcc atgggttcac tatatcccag tcaaaacaga tctctccaat 960

gtccaagagc tgttacaatt tgtaaaagca aatgatgatg tagctcaaga gattgctgaa 1020

aggggaagcc agtttattag gaaccatttg cagatggatg acatcacctg ttactgggag 1080

aacctcttga gtgaatactc taaattcctg tcttataatg taacgagaag gaaaggttat 1140

gatcaaatta ttcccaaaat gttgaaaact gaactatag 1179

<210> SEQ ID NO 21
<211> LENGTH: 1236
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 21

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agcctgggcg cgcccggcgg ccgcgcgccg cccgacgacc tggacctgtt ccccacaccc 180

gacccccact acgagaagaa gtactacttc ccggtccgcg agctggagcg ctcgctgcgc 240

ttcgacatga agggcgacga cgtgatcgtc ttcctgcaca tccagaagac gggcggcacc 300

accttcggcc gccacctcgt gcagaacgta cgcctcgagg tgccgtgcga ctgccggccc 360

ggccagaaga agtgcacctg ctaccggccc aaccgccgcg agacttggct cttctcccgc 420

ttctccaccg gctggagctg cgggctgcac gccgactgga ccgagctcac caactgcgtg 480

cccggcgtgc tggaccgccg cgactccgcc gcgctgcgca cgcccaggaa gttctactac 540

atcaccctgc tacgagaccc cgtgtcccgc tacctgagcg agtggcggca tgtgcagagg 600

ggtgccacgt ggaagacgtc gttgcatatg tgtgatgggc gcacgcccac gcctgaggag 660

ctgccgccct gctacgaggg cacggactgg tcgggctgca cgctacagga gttcatggac 720

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tacaagcggc agctggagcg cagggagcag cgcctgagga gccgcgagga gcgtctgctg 1140

caccgggcca aggaggcact gccgcgggag gatgccgacg agccgggccg cgtgcccacc 1200

gaggactaca tgagccacat cattgagaag tggtag 1236

<210> SEQ ID NO 22
<211> LENGTH: 1395
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 22

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ctcgcggccc agaaggggggc ctaccccatc atcttcactg cctggaagct ggccactgca 180

ggtgaccagg gccttctgct ccagtccctc aatgccctgt cggtgctgac tgatggacag 240

ccagacctcc tggatgccca gggcctgcag ctcctagtgg ccacgctgac ccagaatgct 300

gatgaggctg acctgacctg ctctgggatc cgctgtgtgc gtcacgcttg cctgaaacat 360

gaacagaatc ggcaagacct ggtgaaagct ggcgtgctgc ctctgctgac tggtgccatc 420

acccatcatg gccaccacac tgacgtggtc agggaagcct gctgggccct gcgtgtcatg 480

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tgccaggagg tcgtcgacct cgggggcctg agcattctgg tgtccctgct agccgactgc 720

aatgaccacc agatgaggga ccagagcggc gttcaggagc tcgtgaagca agtgctgagc 780

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gagggtggcg gggctgtggc agcactgcag gccatgaagg cacacccgca gaaggccggc 1020

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ccatcctgga cctgggggct gaggcactca tcatgcaggc ccgatctgcc caccgtgact 1140

gtgaggacgt ggccaaggcc gccctgcggg acctgggttg tcatgtcgag ctccgagagc 1200

tgtggacagg ccagaggggc aacctggcgc catgacccca ggcccagtct ggtgactctg 1260

ggtgagtcgt gtgactcagg aatgggggta gatccatgtc ctccactgtc ccccattagt 1320

tctgtcccct tcacaatgag aagtgttttc tggcaggccc taggtaaagg gtcgggggag 1380

gggggagcct tgtag 1395

<210> SEQ ID NO 23
<211> LENGTH: 1431
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 23

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ggggttgatc tgagcaacat tgtaaagacg gcacctaaag tctctgcaga cggatcccag 180

gagcccacac atgacatcct gcagatgctc agtgacctcc aggagtctgt ggccagctct 240

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caggccttct cgaagcccat cctggacctg ggggctgagg cactcatcat gcaggcccga 1320

tctgcccacc gtgactgtga ggacgtggcc aaggccgccc tgcgggacct gggttgtcat 1380

gtcgagctcc gagagctgtg gacaggccag aggggcaacc tggcgccatg a 1431

<210> SEQ ID NO 24
<211> LENGTH: 1506
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 24

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tcaacacagg cgaagatggt ctccaagcgc attgcccagg agacctttga tgcagctgtg 120

cgcgagaaca tcgaggagtt tgcgatgggg ccagaggagg cagtgaaaga ggccgtggag 180

cagtttgaat cgcaaggggt tgatctgagc aacattgtaa agacggcacc taaagtctct 240

gcagacggat cccaggagcc cacacatgac atcctgcaga tgctcagtga cctccaggag 300

tctgtggcca gctctcgccc ccaggaggtg tcagcatacc tcacccgctt ctgcgaccag 360

tgcaaacagg acaaggcctg ccgcttcctc gcggcccaga agggggccta ccccatcatc 420

ttcactgcct ggaagctggc cactgcaggt gaccagggcc ttctgctcca gtccctcaat 480

gccctgtcgg tgctgactga tggacagcca gacctcctgg atgcccaggg cctgcagctc 540

ctagtggcca cgctgaccca gaatgctgat gaggctgacc tgacctgctc tgggatccgc 600

tgtgtgcgtc acgcttgcct gaaacatgaa cagaatcggc aagacctggt gaaagctggc 660

gtgctgcctc tgctgactgg tgccatcacc catcatggcc accacactga cgtggtcagg 720

gaagcctgct gggccctgcg tgtcatgacc ttcgatgacg acatccgtgt gcccctttggc 780

catgcccaca accatgccaa gatgattgtg caggagaaca aaggcttgaa ggtgctcatc 840

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tcccgcctgg ccattcgcaa cgagttctgc caggaggtcg tcgacctcgg gggcctgagc 960

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gacctgggtt gtcatgtcga gctccgagag ctgtggacag gccagagggg caacctggcg 1500

ccatga 1506

<210> SEQ ID NO 25
<211> LENGTH: 1431
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 25

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gagtttgcga tggggccaga ggaggcagtg aaagaggccg tggagcagtt tgaatcgcaa 120

ggggttgatc tgagcaacat tgtaaagacg gcacctaaag tctctgcaga cggatcccag 180

gagcccacac atgacatcct gcagatgctc agtgacctcc aggagtctgt ggccagctct 240

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acccagaatg ctgatgaggc tgacctgacc tgctctggga tccgctgtgt gcgtcacgct 540

tgcctgaaac atgaacagaa tcggcaagac ctggtgaaag ctggcgtgct gcctctgctg 600

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cagaaggccg gcgtgcagaa acaggcttgc atgctgatcc gaaacctggt ggcccacggc 1260

caggccttct cgaagcccat cctggacctg ggggctgagg cactcatcat gcaggcccga 1320

tctgcccacc gtgactgtga ggacgtggcc aaggccgccc tgcgggacct gggttgtcat 1380

gtcgagctcc gagagctgtg gacaggccag aggggcaacc tggcgccatg a 1431

<210> SEQ ID NO 26
<211> LENGTH: 1773
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 26

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gcggaggttc agcaagaatg cctgcataaa ttttccaccc gggattatat catggaaccc 180

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cagctcttat ctgaaaacta caccgctgtg gcccagactg tgaacctgct ggccgagtgg 300

ctcattcaga caggtgttga gccagtgcag gttcaggaaa ctgtggaaaa tcacttgaag 360

agtttgctga tcaaacattt tgacccccgc aaagcagatt ctatttttac tgaagaagga 420

gagaccccag cgtggctgga acagatgatt gcacatacca cgtggcggga ccttttttat 480

aaactggctg aagcccatcc agactgtttg atgctgaact tcaccgttaa gcttatttct 540

gacgcagggt accaggggga gatcaccagt gtgtccacag catgccagca gctagaagtg 600

ttctcgagag tgctccggac ctctctagct acaattttag atggaggaga agaaaacctt 660

gaaaaaaatc tccctgagtt tgccaagatg gtgtgccacg gggagcacac gtacctgttt 720

gcccaggcca tgatgtccgt gctggcccag gaggagcagg ggggctccgc tgtgcgcagg 780

atcgcccagg aagtgcagcg ctttgcccag gagaaaggtc atgacgccag tcagatcaca 840

ctagccttgg gcacagctgc ctcctacccc agggcctgcc aggctctcgg ggccatgctg 900

tccaaaggag ccctgaaccc tgctgacatc accgtcctgt tcaagatgtt cacaagcatg 960

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gcgtacgcag caagcgtggt tgagacctgg aagaagaaca agcgagtgag catcaataaa 1140

gatgagctga agtcaacgtc aaaagctgtc gaaaccgttc acaatttgtg ttgcaacgag 1200

aacaaagggg cctctgaact agtggcagaa ttgagcacac tttatcagtg tattaggttt 1260

ccagtggtag caatgggtgt gctgaagtgg gtggattgga ctgtatcaga accaaggtac 1320

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attgctcctc cttatacctc tgacttcgtg caacttttcc tccccatcct ggagaatgac 1680

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cactgcaaat ctaacttcat catggtgaac taa 1773

<210> SEQ ID NO 27
<211> LENGTH: 753
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 27

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ctctgtacca agacagagaa cctgctcggg agctatttcc ccaagaagat ttctgagctg 120

gatgcatttt taaaggagcc agctctcaat gaagccaact tgagcaatct gaaggcccca 180

ttggacatcc cagtgcctga tccagtcaag gagaaagaga aagaggagcg gaagaaacag 240

caggagaagg aagacaagga tgaaaagaag aaggggggagg atgaagacaa aggtcctccc 300

tgtggcccag tgaactgcaa tgaaaagatc gtggtccttc tgcagcgctt gaagcctgag 360

atcaaggatg tcattgagca gctcaacctg gtcaccacct ggttgcagct gcagatacct 420

cggattgagg atggtaacaa ttttggagtg gctgtccagg agaaggtgtt tgagctgatg 480

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gtgcacgagc tggatgaggc agagtaccgg gacatccggc tgatggtcat ggagatccgc 660

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acccactccc tgaccctgca ggctaggggt taa 753

<210> SEQ ID NO 28
<211> LENGTH: 750
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 28

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gatgcatttt taaaggagcc agctctcaat gaagccaact tgagcaatct gaaggcccca 180

ttggacatcc cagtgcctga tccagtcaag gagaaagaga aagaggagcg gaagaaacag 240

caggagaagg aagacaagga tgaaaagaag aaggggggagg atgaagacaa aggtcctccc 300

tgtggcccag tgaactgcaa tgaaaagatc gtggtccttc tgcagcgctt gaagcctgag 360

atcaaggatg tcattgagca gctcaacctg gtcaccacct ggttgcagct gcagatacct 420

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aatgcttatg ctgtgttata tgacatcatc ctgaagaact tcgagaagct caagaagccc 720

aggggagaaa caaagggaat gatctattga 750

<210> SEQ ID NO 29
<211> LENGTH: 1677
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 29

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cagggctgcg ggaaccccaa ggtcaacccc cagggccccg ggcctgagga gaagcggcgc 1080

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ctgtcagagc aggaaggaca gaagacctcg gctgccagct gcccccagcc cccgaccttc 1620

ctcctgcccc tcctcctctt cctggccctt acagtagcca ggccccggtg gcggtaa 1677

<210> SEQ ID NO 30
<211> LENGTH: 3645
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 30

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cagcctgtcg ccaagtatga ctgggaacag aagtactact atggcaacct gattgctgtg 420

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<211> LENGTH: 4206
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 31

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<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 32

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<211> LENGTH: 2025
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 33

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<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 34

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<211> LENGTH: 1164
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 35

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<210> SEQ ID NO 36
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<212> TYPE: DNA
<213> ORGANISM: Human

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<211> LENGTH: 1254
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 37

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<210> SEQ ID NO 38
<211> LENGTH: 1389
<212> TYPE: DNA
<213> ORGANISM: Human

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gataaactga aagctgagcg tgaacgtggt atcaccattg atatctcctt gtggaaattt 240

gagaccagca agtactatgt gactatcatt gatgccccag gacacagaga cttcatcaaa 300

aacatgatta cagggacatc tcaggctgac tgtgctgtcc tgattgttgc tgctggtgtt 360

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<210> SEQ ID NO 39
<211> LENGTH: 1146
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 39

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<211> LENGTH: 5730
<212> TYPE: DNA
<213> ORGANISM: Human

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<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 41

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<210> SEQ ID NO 42
<211> LENGTH: 2163
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 42

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<210> SEQ ID NO 43
<211> LENGTH: 2163
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 43

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tga 2163

<210> SEQ ID NO 44
<211> LENGTH: 1899
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 44

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<210> SEQ ID NO 45
<211> LENGTH: 2157
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 45

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<210> SEQ ID NO 46
<211> LENGTH: 1392
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 46

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gtggaatggg cacagcagtt tgggggagct gttatgtacc caagcaaaga aacagcccac 180

tggaagcctc caccttggaa tgatgtggac cctccaaagg acacaattgt gaagaacatt 240

accctgaact ttgggcccca acacccagca gcgcatggtg tcctgcgact agtgatggaa 300

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gagaagctca ttgaatacaa gacctatctt caggcccttc catactttga ccggctagac 420

tatgtgtcca tgatgtgtaa cgaacaggcc tattctctag ctgtggagaa gttgctaaac 480

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cgaatgcatg ctgcttatat ccggccagga ggagtgcacc aggacctacc ccttgggctt 720

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cgatgcaaga tcaaggctcc tggttttgcc catctggctg gtttggacaa gatgtctaag 1320

ggacacatgt tggcagatgt cgttgccatc ataggtaccc aagatattgt atttggagaa 1380

gtagatcggt ga 1392

<210> SEQ ID NO 47
<211> LENGTH: 1392
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 47

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gtggaatggg cacagcagtt tgggggagct gttatgtacc caagcaaaga aacagcccac 180

tggaagcctc caccttggaa tgatgtggac cctccaaagg acacaattgt gaagaacatt 240

accctgaact ttgggcccca acacccagca gcgcatggtg tcctgcgact agtgatggaa 300

ttgagtgggg agatggtgcg gaagtgtgat cctcacatcg ggctcctgca ccgaggcact 360

gagaagctca ttgaatacaa gacctatctt caggcccttc catactttga ccggctagac 420

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ttgaaccaca tcatggctgt gaccacacat gccctggacc ttggggccat gacccctttc 600

ttctggctgt ttgaagaaag ggagaagatg tttgagttct acgagcgagt gtctggagcc 660

cgaatgcatg ctgcttatat ccggccagga ggagtgcacc aggacctacc ccttgggctt 720

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cgatgcaaga tcaaggctcc tggttttgcc catctggctg gtttggacaa gatgtctaag 1320

ggacacatgt tggcagatgt cgttgccatc ataggtaccc aagatattgt atttggagaa 1380

gtagatcggt ga 1392

<210> SEQ ID NO 48
<211> LENGTH: 2139
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 48

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gactggtgcc agttcgccgc cctgatcgtg cgcgaccaga ccgagctgcg gctgtgcgag 180

cgctccgggc agcgcacggc cagcgtcctg tggccctgga tcaaccgcaa cgcccgtgtg 240

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gcctggcacc ctcccgcccc gcttccgtcc ccaggcacca ctgccccgag gcccagcagc 360

atccctgcac ccgccgaggc cgaggcctgg agccccccgga agttgccatc ctcagcctcc 420

accttcctct ccccagcttt tccaggctcc cagacccatt cagggcctga gctcggcctg 480

gtcccaagcc ctgcttccct gtggcctcca ccgccatctc cagccccttc ttctaccaag 540

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cccctctgtg agatttcccg gggcacccac aacttctcgg aggagctcaa gatcggggag 660

ggtggctttg ggtgcgtgta ccgggcggtg atgaggaaca cggtgtatgc tgtgaagagg 720

ctgaaggaga acgctgacct ggagtggact gcagtgaagc agagcttcct gaccgaggtg 780

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aggcaggggc ccgaagaaag tgatgaattt cagagctga 2139

<210> SEQ ID NO 49
<211> LENGTH: 2127
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 49

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gactggtgcc agttcggtgg gtggcggcgg gctgccgggg ggcgggaggc gcgcgggctc 180

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gagctgcggc tgtgcgagcg ctccgggcag cgcacggcca gcgtcctgtg gccctggatc 300

aaccgcaacg cccgtgtggc cgacctcgtg cacatcctca cgcacctgca gctgctccgt 360

gcgcgggaca tcatcacagc ctggcaccct cccgccccgc ttccgtcccc aggcaccact 420

gccccgaggc ccagcagcat ccctgcaccc gccgaggccg aggcctggag cccccggaag 480

ttgccatcct cagcctccac cttcctctcc ccagcttttc caggctccca gacccattca 540

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gagctcaaga tcggggaggg tggctttggg tgcgtgtacc gggcggtgat gaggaacacg 780

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tccctggagg accgtctcca ctgccagacc caggcctgcc cacctctctc ctggcctcag 1020

cgactggaca tccttctggg tacagcccgg gcaattcagt ttctacatca ggacagcccc 1080

agcctcatcc atggagacat caagagttcc aacgtccttc tggatgagag gctgacaccc 1140

aagctgggag actttggcct ggcccggttc agccgctttg ccgggtccag ccccagccag 1200

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tacatcaaga cgggaaggct ggctgtggac acggacacct tcagctttgg ggtggtagtg 1320

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aaagacctgg tggaagagga ggctgaggag gctggagtgg ctttgagaag cacccagagc 1440

acactgcaag caggtctggc tgcagatgcc tgggctgctc ccatcgccat gcagatctac 1500

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acggcaggag aatcgagctg ggggagtggc ccaggatccc ggcccacagc cgtggaagga 1920

ctggcccttg gcagctctgc atcatcgtcg tcagagccac cgcagattat catcaaccct 1980

gcccgacaga agatggtcca gaagctggcc ctgtacgagg atggggccct ggacagcctg 2040

cagctgctgt cgtccagctc cctcccaggc ttgggcctgg aacaggacag gcaggggccc 2100

gaagaaagtg atgaatttca gagctga 2127

<210> SEQ ID NO 50
<211> LENGTH: 1902
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 50

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gaggtgccgc cctgggtcat gtgccgcttc tacaaagtga tggacgccct ggagcccgcc 120

gactggtgcc agttcgccgc cctgatcgtg cgcgaccaga ccgagctgcg gctgtgcgag 180

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ccaggcccag agagctcagt gtccctcctg cagggagccc gccccctttcc gttttgctgg 600

cccctctgtg agatttcccg gggcacccac aacttctcgg aggagctcaa gatcggggag 660

ggtggctttg ggtgcgtgta ccgggcggtg atgaggaaca cggtgtatgc tgtgaagagg 720

ctgaaggaga acgctgacct ggagtggact gcagtgaagc agagcttcct gaccgaggtg 780

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agaggcccca accagcccgt ggagagtgac gagagcctag gcggcctctc tgctgccctg 1560

cgctcctggc acttgactcc aagctgccct ctggacccag cacccctcag ggaggccggc 1620

tgtcctcagg gggacacggc aggagaatcg agctgggggа gtggcccagg atcccggccc 1680

acagccgtgg aaggactggc ccttggcagc tctgcatcat cgtcgtcaga gccaccgcag 1740

attatcatca accctgcccg acagaagatg gtccagaagc tggccctgta cgaggatggg 1800

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gacaggcagg ggcccgaaga aagtgatgaa tttcagagct ga 1902

<210> SEQ ID NO 51
<211> LENGTH: 2082
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 51

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cgactggaca tccttctggg tacagcccgg gcaattcagt ttctacatca ggacagcccc 1080

agcctcatcc atggagacat caagagttcc aacgtccttc tggatgagag gctgacaccc 1140

aagctgggag actttggcct ggcccggttc agccgctttg ccgggtccag ccccagccag 1200

agcagcatgg tggcccggac acagacagtg cggggcaccc tggcctacct gcccgaggag 1260

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ctagagacct tggctggtca gagggctgtg aagacgcacg gtgccaggac caagtatctg 1380

aaagacctgg tggaagagga ggctgaggag gctggagtgg ctttgagaag cacccagagc 1440

acactgcaag caggtctggc tgcagatgcc tgggctgctc ccatcgccat gcagatctac 1500

aagaagcacc tgggccagct ggcctgctgc tgcctgcacc gccgggccaa aaggaggcct 1560

cctatgaccc aggagaactc ctacgtgtcc agcactggca gagcccacag tggggctgct 1620

ccatggcagc ccctggcagc gccatcagga gccagtgccc aggcagcaga gcagctgcag 1680

agaggcccca accagcccgt ggagagtgac gagagcctag gcggcctctc tgctgccctg 1740

cgctcctggc acttgactcc aagctgccct ctggacccag cacccctcag ggaggccggc 1800

tgtcctcagg gggacacggc aggagaatcg agctgggggа gtggcccagg atcccggccc 1860

acagccgtgg aaggactggc ccttggcagc tctgcatcat cgtcgtcaga gccaccgcag 1920

attatcatca accctgcccg acagaagatg gtccagaagc tggccctgta cgaggatggg 1980

gccctggaca gcctgcagct gctgtcgtcc agctccctcc caggcttggg cctggaacag 2040

gacaggcagg ggcccgaaga aagtgatgaa tttcagagct ga 2082

<210> SEQ ID NO 52
<211> LENGTH: 2049
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 52

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cccctctgtg agatttcccg gggcacccac aacttctcgg aggagctcaa gatcggggag 660

ggtggctttg ggtgcgtgta ccgggcggtg atgaggaaca cggtgtatgc tgtgaagagg 720

ctgaaggaga acgctgacct ggagtggact gcagtgaagc agagcttcct gaccgaggtg 780

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tccctcccag gcttgggcct ggaacaggac aggcaggggc ccgaagaaag tgatgaattt 2040

cagagctga 2049

<210> SEQ ID NO 53
<211> LENGTH: 423
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 53

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ctgggttcca cttccagcaa cagctcctgc agcagtaccg agtgccccgg ggaagccatt 120

ccccaccccc caggtgagtg caggatcgcc cctttctccc cccgctcctc caggagctgg 180

cagcatcaag accccacttc gcttctctca ggtctcccca aggctgaccc gggtcattgg 240

tgggccagct tctttttcgg gaagtccacc ctcccgttca tggccacggt gttggagtcc 300

gcagagcact cggaacctcc ccaggcctcc agcagcatga ccgcctgtgg cctggctcgg 360

gacgccccga ggaagcagcc cggcggtcag tccagcacag ccagcgctgg gcccccgtcc 420

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tga 423

<210> SEQ ID NO 54
<211> LENGTH: 213
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 54

atggcggcca tcccctccag cggctcgctc gtggccaccc acgactacta ccggcgccgc 60

ctgggttcca cttccagcaa cagctcctgc agcagtaccg agtgccccgg ggaagccatt 120

ccccaccccc caggtctccc caaggctgac ccgggtcatt ggtgggccag cttctttttc 180

gggaagtcca ccctcccacc ccccaccctg taa 213

<210> SEQ ID NO 55
<211> LENGTH: 345
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 55

atggcggcca tcccctccag cggctcgctc gtggccaccc acgactacta ccggcgccgc 60

ctgggttcca cttccagcaa cagctcctgc agcagtaccg agtgccccgg ggaagccatt 120

ccccaccccc caggtctccc caaggctgac ccgggtcatt ggtgggccag cttctttttc 180

gggaagtcca ccctcccgtt catggccacg gtgttggagt ccgcagagca ctcggaacct 240

ccccaggcct ccagcagcat gaccgcctgt ggcctggctc gggacgcccc gaggaagcag 300

cccggcggtc agtccagcac agccagcgct gggcccccgt cctga 345

<210> SEQ ID NO 56
<211> LENGTH: 1203
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 56

atggaggacg gcgtctatga acccccagac ctgactccgg aggagcggat ggagctggag 60

aacatccggc ggcggaagca ggagctgctg gtggagattc agcgcctgcg ggaggagctc 120

agtgaagcca tgagcgaggt ggaggggctg gaggccaatg agggcagtaa gaccttgcaa 180

cggaaccgga agatggcaat gggcaggaag aagttcaaca tggaccccaa gaaggggatc 240

cagttcttgg tggagaatga actgctgcag aacacacccg aggagatcgc ccgcttcctg 300

tacaagggcg aggggctgaa caagacagcc atcggggact acctgggggа gagggaagaa 360

ctgaacctgg cagtgctcca tgcttttgtg gatctgcatg agttcaccga cctcaatctg 420

gtgcaggccc tcaggcagtt tctatggagc tttcgcctac ccggagaggc ccagaaaatt 480

gaccggatga tggaggcctt cgcccagcga tactgcctgt gcaaccctgg ggttttccag 540

tccacagaca cgtgctatgt gctgtccttc gccgtcatca tgctcaacac cagtctccac 600

aatcccaatg tccgggacaa gccgggcctg gagcgctttg tggccatgaa ccggggcatc 660

aacgagggcg gggacctgcc tgaggagctg ctcaggaacc tgtacgacag catccgaaat 720

gagcccttca agattcctga ggatgacggg aatgacctga cccacacctt cttcaacccg 780

gaccgggagg gctggctcct gaagctgggt aggggccggg tgaagacgtg gaagcggcgc 840

tggtttatcc tcacagacaa ctgcctctac tactttgagt acaccacgga caaggagccc 900

cgaggaatca tccccctgga gaatctgagc atccgagagg tggacgaccc ccggaaaccg 960

aactgctttg aactttacat ccccaacaac aaggggcagc tcatcaaagc ctgcaaaact 1020

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gaggcggacg gccgagtggt ggagggaaac cacatggtgt accggatctc ggcccccacg 1080

caggaggaga aggacgagtg gatcaagtcc atccaggcgg ctgtgagtgt ggacccttc 1140

tatgagatgc tggcagcgag aaagaagcgg atttcagtca agaagaagca ggagcagccc 1200

tga 1203

<210> SEQ ID NO 57
<211> LENGTH: 1200
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 57

atggaggacg gcgtctatga acccccagac ctgactccgg aggagcggat ggagctggag 60

aacatccggc ggcggaagca ggagctgctg gtggagattc agcgcctgcg ggaggagctc 120

agtgaagcca tgagcgaggt ggaggggctg gaggccaatg agggcagtaa gaccttgcaa 180

cggaaccgga agatggcaat gggcaggaag aagttcaaca tggaccccaa gaaggggatc 240

cagttcttgg tggagaatga actgctgcag aacacacccg aggagatcgc ccgcttcctg 300

tacaagggcg aggggctgaa caagacagcc atcggggact acctgggggga gagggaagaa 360

ctgaacctgg cagtgctcca tgcttttgtg gatctgcatg agttcaccga cctcaatctg 420

gtgcaggccc tcaggcagtt tctatggagc tttcgcctac ccggagaggc ccagaaaatt 480

gaccggatga tggaggcctt cgcccagcga tactgcctgt gcaaccctgg ggttttccag 540

tccacagaca cgtgctatgt gctgtccttc gccgtcatca tgctcaacac cagtctccac 600

aatcccaatg tccgggacaa gccgggcctg gagcgctttg tggccatgaa ccggggcatc 660

aacgagggcg gggacctgcc tgaggagctg ctcaggaacc tgtacgacag catccgaaat 720

gagcccttca agattcctga ggatgacggg aatgacctga cccacacctt cttcaacccg 780

gaccgggagg gctggctcct gaagctgggg ggccgggtga agacgtggaa gcggcgctgg 840

tttatcctca cagacaactg cctctactac tttgagtaca ccacggacaa ggagccccga 900

ggaatcatcc ccctggagaa tctgagcatc cgagaggtgg acgacccccg gaaaccgaac 960

tgctttgaac tttacatccc caacaacaag gggcagctca tcaaagcctg caaaactgag 1020

gcggacggcc gagtggtgga gggaaaccac atggtgtacc ggatctcggc ccccacgcag 1080

gaggagaagg acgagtggat caagtccatc caggcggctg tgagtgtgga ccccttctat 1140

gagatgctgg cagcgagaaa gaagcggatt tcagtcaaga agaagcagga gcagccctga 1200

<210> SEQ ID NO 58
<211> LENGTH: 498
<212> TYPE: DNA
<213> ORGANISM: Human

<400> SEQUENCE: 58

atggtcaacc ccaccgtgtt cttcgacatt gccgtcgacg gcgagccctt gggccgcgtc 60

tcctttgagc tgtttgcaga caaggtccca aagacagcag aaaattttcg tgctctgagc 120

actggagaga aaggatttgg ttataagggt tcctgctttc acagaattat tccagggttt 180

atgtgtcagg gtggtgactt cacacgccat aatggcactg gtggcaagtc catctatggg 240

gagaaatttg aagatgagaa cttcatccta aagcatacag gtcctggcat cttgtccatg 300

gcaaatgctg gacccaacac aaatggatcc cagtttttca tctgcactgc caagactgag 360

tggttggatg gcaagcatgt ggtgtttggc aaagtgaaag aaggcatgaa tattgtggag 420

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gccatggagc gctttgggtc caggaatggc aagaccagca agaagatcac cattgctgac 480

tgtggacaac tcgaataa 498

<210> SEQ ID NO 59
<211> LENGTH: 218
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 59

Met Gly Thr Arg Asp Asp Glu Tyr Asp Tyr Leu Phe Lys Val Val Leu
1 5 10 15

Ile Gly Asp Ser Gly Val Gly Lys Ser Asn Leu Leu Ser Arg Phe Thr
20 25 30

Arg Asn Glu Phe Asn Leu Glu Ser Lys Ser Thr Ile Gly Val Glu Phe
35 40 45

Ala Thr Arg Ser Ile Gln Val Asp Gly Lys Thr Ile Lys Ala Gln Ile
50 55 60

Trp Asp Thr Ala Gly Gln Glu Arg Tyr Arg Ala Ile Thr Ser Ala Tyr
65 70 75 80

Tyr Arg Gly Ala Val Gly Ala Leu Leu Val Tyr Asp Ile Ala Lys His
85 90 95

Leu Thr Tyr Glu Asn Val Glu Arg Trp Leu Lys Glu Leu Arg Asp His
100 105 110

Ala Asp Ser Asn Ile Val Ile Met Leu Val Gly Asn Lys Ser Asp Leu
115 120 125

Arg His Leu Arg Ala Val Pro Thr Asp Glu Ala Arg Ala Phe Ala Glu
130 135 140

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

Val Glu Glu Ala Phe Lys Asn Ile Leu Thr Glu Ile Tyr Arg Ile Val
165 170 175

Ser Gln Lys Gln Ile Ala Asp Arg Ala Ala His Asp Glu Ser Pro Gly
180 185 190

Asn Asn Val Val Asp Ile Ser Val Pro Pro Thr Thr Asp Gly Gln Lys
195 200 205

Pro Asn Lys Leu Gln Cys Cys Gln Asn Leu
210 215

<210> SEQ ID NO 60
<211> LENGTH: 589
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 60

Met Ala Ala Ala Asp Gly Asp Asp Ser Leu Tyr Pro Ile Ala Val Leu
1 5 10 15

Ile Asp Glu Leu Arg Asn Glu Asp Val Gln Leu Arg Leu Asn Ser Ile
20 25 30

Lys Lys Leu Ser Thr Ile Ala Leu Ala Leu Gly Val Glu Arg Thr Arg
35 40 45

Ser Glu Leu Leu Pro Phe Leu Thr Asp Thr Ile Tyr Asp Glu Asp Glu
50 55 60

Val Leu Leu Ala Leu Ala Glu Gln Leu Gly Thr Phe Thr Thr Leu Val
65 70 75 80

Gly Gly Pro Glu Tyr Val His Cys Leu Leu Pro Pro Leu Glu Ser Leu
85 90 95

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Ala Thr Val Glu Glu Thr Val Val Arg Asp Lys Ala Val Glu Ser Leu
            100                 105                 110

Arg Ala Ile Ser His Glu His Ser Pro Ser Asp Leu Glu Ala His Phe
        115                 120                 125

Val Pro Leu Val Lys Arg Leu Ala Gly Gly Asp Trp Phe Thr Ser Arg
    130                 135                 140

Thr Ser Ala Cys Gly Leu Phe Ser Val Cys Tyr Pro Arg Val Ser Ser
145                 150                 155                 160

Ala Val Lys Ala Glu Leu Arg Gln Tyr Phe Arg Asn Leu Cys Ser Asp
                165                 170                 175

Asp Thr Pro Met Val Arg Arg Ala Ala Ala Ser Lys Leu Gly Glu Phe
            180                 185                 190

Ala Lys Val Leu Glu Leu Asp Asn Val Lys Ser Glu Ile Ile Pro Met
        195                 200                 205

Phe Ser Asn Leu Ala Ser Asp Glu Gln Asp Ser Val Arg Leu Leu Ala
    210                 215                 220

Val Glu Ala Cys Val Asn Ile Ala Gln Leu Leu Pro Gln Glu Asp Leu
225                 230                 235                 240

Glu Ala Leu Val Met Pro Thr Leu Arg Gln Ala Ala Glu Asp Lys Ser
                245                 250                 255

Trp Arg Val Arg Tyr Met Val Ala Asp Lys Phe Thr Glu Leu Gln Lys
            260                 265                 270

Ala Val Gly Pro Glu Ile Thr Lys Thr Asp Leu Val Pro Ala Phe Gln
        275                 280                 285

Asn Leu Met Lys Asp Cys Glu Ala Glu Val Arg Ala Ala Ala Ser His
    290                 295                 300

Lys Val Lys Glu Phe Cys Glu Asn Leu Ser Ala Asp Cys Arg Glu Asn
305                 310                 315                 320

Val Ile Met Ser Gln Ile Leu Pro Cys Ile Lys Glu Leu Val Ser Asp
                325                 330                 335

Ala Asn Gln His Val Lys Ser Ala Leu Ala Ser Val Ile Met Gly Leu
            340                 345                 350

Ser Pro Ile Leu Gly Lys Asp Asn Thr Ile Glu His Leu Leu Pro Leu
        355                 360                 365

Phe Leu Ala Gln Leu Lys Asp Glu Cys Pro Glu Val Arg Leu Asn Ile
    370                 375                 380

Ile Ser Asn Leu Asp Cys Val Asn Glu Val Ile Gly Ile Arg Gln Leu
385                 390                 395                 400

Ser Gln Ser Leu Leu Pro Ala Ile Val Glu Leu Ala Glu Asp Ala Lys
                405                 410                 415

Trp Arg Val Arg Leu Ala Ile Ile Glu Tyr Met Pro Leu Leu Ala Gly
            420                 425                 430

Gln Leu Gly Val Glu Phe Phe Asp Glu Lys Leu Asn Ser Leu Cys Met
        435                 440                 445

Ala Trp Leu Val Asp His Val Tyr Ala Ile Arg Glu Ala Ala Thr Ser
    450                 455                 460

Asn Leu Lys Lys Leu Val Glu Lys Phe Gly Lys Glu Trp Ala His Ala
465                 470                 475                 480

Thr Ile Ile Pro Lys Val Leu Ala Met Ser Gly Asp Pro Asn Tyr Leu
                485                 490                 495

His Arg Met Thr Thr Leu Phe Cys Ile Asn Val Leu Ser Glu Val Cys
            500                 505                 510
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Gly Gln Asp Ile Thr Thr Lys His Met Leu Pro Thr Val Leu Arg Met
        515                 520                 525

Ala Gly Asp Pro Val Ala Asn Val Arg Phe Asn Val Ala Lys Ser Leu
    530                 535                 540

Gln Lys Ile Gly Pro Ile Leu Asp Asn Ser Thr Leu Gln Ser Glu Val
545                 550                 555                 560

Lys Pro Ile Leu Glu Lys Leu Thr Gln Asp Gln Asp Val Asp Val Lys
                565                 570                 575

Tyr Phe Ala Gln Glu Ala Leu Thr Val Leu Ser Leu Ala
            580                 585


<210> SEQ ID NO 61
<211> LENGTH: 509
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 61

Met Arg Thr Phe Ser Phe Ala Ser Thr Ala Ser Arg Ser Cys Pro Pro
1               5                   10                  15

Ser Pro Trp Pro Leu Gly Leu Lys Gly Pro Glu Val Ser Phe Cys Leu
            20                  25                  30

Ser Leu Gln Ile Pro Ser Met Met Lys Met Arg Ser Ser Trp Pro Trp
        35                  40                  45

Gln Asn Ser Trp Glu Pro Ser Leu Pro Trp Trp Glu Ala Gln Ser Thr
    50                  55                  60

Cys Thr Ala Cys Cys Leu Phe Ser Val Cys Tyr Pro Arg Val Ser Ser
65                  70                  75                  80

Ala Val Lys Ala Glu Leu Arg Gln Tyr Phe Arg Asn Leu Cys Ser Asp
                85                  90                  95

Asp Thr Pro Met Val Arg Arg Ala Ala Ala Ser Lys Leu Gly Glu Phe
            100                 105                 110

Ala Lys Val Leu Glu Leu Asp Asn Val Lys Ser Glu Ile Ile Pro Met
        115                 120                 125

Phe Ser Asn Leu Ala Ser Asp Glu Gln Asp Ser Val Arg Leu Leu Ala
    130                 135                 140

Val Glu Ala Cys Val Asn Ile Ala Gln Leu Leu Pro Gln Glu Asp Leu
145                 150                 155                 160

Glu Ala Leu Val Met Pro Thr Leu Arg Gln Ala Ala Glu Asp Lys Ser
                165                 170                 175

Trp Arg Val Arg Tyr Met Val Ala Asp Lys Phe Thr Glu Leu Gln Lys
            180                 185                 190

Ala Val Gly Pro Glu Ile Thr Lys Thr Asp Leu Val Pro Ala Phe Gln
        195                 200                 205

Asn Leu Met Lys Asp Cys Glu Ala Glu Val Arg Ala Ala Ala Ser His
    210                 215                 220

Lys Val Lys Glu Phe Cys Glu Asn Leu Ser Ala Asp Cys Arg Glu Asn
225                 230                 235                 240

Val Ile Met Ser Gln Ile Leu Pro Cys Ile Lys Glu Leu Val Ser Asp
                245                 250                 255

Ala Asn Gln His Val Lys Ser Ala Leu Ala Ser Val Ile Met Gly Leu
            260                 265                 270

Ser Pro Ile Leu Gly Lys Asp Asn Thr Ile Glu His Leu Leu Pro Leu
        275                 280                 285

Phe Leu Ala Gln Leu Lys Asp Glu Cys Pro Glu Val Arg Leu Asn Ile
    290                 295                 300
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Ile Ser Asn Leu Asp Cys Val Asn Glu Val Ile Gly Ile Arg Gln Leu
305                 310                 315                 320

Ser Gln Ser Leu Leu Pro Ala Ile Val Glu Leu Ala Glu Asp Ala Lys
                325                 330                 335

Trp Arg Val Arg Leu Ala Ile Ile Glu Tyr Met Pro Leu Leu Ala Gly
            340                 345                 350

Gln Leu Gly Val Glu Phe Phe Asp Glu Lys Leu Asn Ser Leu Cys Met
        355                 360                 365

Ala Trp Leu Val Asp His Val Tyr Ala Ile Arg Glu Ala Ala Thr Ser
    370                 375                 380

Asn Leu Lys Lys Leu Val Glu Lys Phe Gly Lys Glu Trp Ala His Ala
385                 390                 395                 400

Thr Ile Ile Pro Lys Val Leu Ala Met Ser Gly Asp Pro Asn Tyr Leu
                405                 410                 415

His Arg Met Thr Thr Leu Phe Cys Ile Asn Val Leu Ser Glu Val Cys
            420                 425                 430

Gly Gln Asp Ile Thr Thr Lys His Met Leu Pro Thr Val Leu Arg Met
        435                 440                 445

Ala Gly Asp Pro Val Ala Asn Val Arg Phe Asn Val Ala Lys Ser Leu
    450                 455                 460

Gln Lys Ile Gly Pro Ile Leu Asp Asn Ser Thr Leu Gln Ser Glu Val
465                 470                 475                 480

Lys Pro Ile Leu Glu Lys Leu Thr Gln Asp Gln Asp Val Asp Val Lys
                485                 490                 495

Tyr Phe Ala Gln Glu Ala Leu Thr Val Leu Ser Leu Ala
            500                 505


<210> SEQ ID NO 62
<211> LENGTH: 876
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 62

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

Glu Leu Glu Ala Ala Gln Lys Phe Leu Glu Arg Ala Ala Val Glu Asn
            20                  25                  30

Leu Pro Thr Phe Leu Val Glu Leu Ser Arg Val Leu Ala Asn Pro Gly
        35                  40                  45

Asn Ser Gln Val Ala Arg Val Ala Ala Gly Leu Gln Ile Lys Asn Ser
    50                  55                  60

Leu Thr Ser Lys Asp Pro Asp Ile Lys Ala Gln Tyr Gln Gln Arg Trp
65                  70                  75                  80

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

Gln Thr Leu Gly Thr Glu Thr Tyr Arg Pro Ser Ser Ala Ser Gln Cys
            100                 105                 110

Val Ala Gly Ile Ala Cys Ala Glu Ile Pro Val Asn Gln Trp Pro Glu
        115                 120                 125

Leu Ile Pro Gln Leu Val Ala Asn Val Thr Asn Pro Asn Ser Thr Glu
    130                 135                 140

His Met Lys Glu Ser Thr Leu Glu Ala Ile Gly Tyr Ile Cys Gln Asp
145                 150                 155                 160

Ile Asp Pro Glu Gln Leu Gln Asp Lys Ser Asn Glu Ile Leu Thr Ala
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               165                 170                 175

Ile Ile Gln Gly Met Arg Lys Glu Glu Pro Ser Asn Asn Val Lys Leu
            180                 185                 190

Ala Ala Thr Asn Ala Leu Leu Asn Ser Leu Glu Phe Thr Lys Ala Asn
        195                 200                 205

Phe Asp Lys Glu Ser Glu Arg His Phe Ile Met Gln Val Val Cys Glu
    210                 215                 220

Ala Thr Gln Cys Pro Asp Thr Arg Val Arg Val Ala Ala Leu Gln Asn
225                 230                 235                 240

Leu Val Lys Ile Met Ser Leu Tyr Tyr Gln Tyr Met Glu Thr Tyr Met
                245                 250                 255

Gly Pro Ala Leu Phe Ala Ile Thr Ile Glu Ala Met Lys Ser Asp Ile
            260                 265                 270

Asp Glu Val Ala Leu Gln Gly Ile Glu Phe Trp Ser Asn Val Cys Asp
        275                 280                 285

Glu Glu Met Asp Leu Ala Ile Glu Ala Ser Glu Ala Ala Glu Gln Gly
    290                 295                 300

Arg Pro Pro Glu His Thr Ser Lys Phe Tyr Ala Lys Gly Ala Leu Gln
305                 310                 315                 320

Tyr Leu Val Pro Ile Leu Thr Gln Thr Leu Thr Lys Gln Asp Glu Asn
                325                 330                 335

Asp Asp Asp Asp Asp Trp Asn Pro Cys Lys Ala Ala Gly Val Cys Leu
            340                 345                 350

Met Leu Leu Ala Thr Cys Cys Glu Asp Asp Ile Val Pro His Val Leu
        355                 360                 365

Pro Phe Ile Lys Glu His Ile Lys Asn Pro Asp Trp Arg Tyr Arg Asp
    370                 375                 380

Ala Ala Val Met Ala Phe Gly Cys Ile Leu Glu Gly Pro Glu Pro Ser
385                 390                 395                 400

Gln Leu Lys Pro Leu Val Ile Gln Ala Met Pro Thr Leu Ile Glu Leu
                405                 410                 415

Met Lys Asp Pro Ser Val Val Val Arg Asp Thr Ala Ala Trp Thr Val
            420                 425                 430

Gly Arg Ile Cys Glu Leu Leu Pro Glu Ala Ala Ile Asn Asp Val Tyr
        435                 440                 445

Leu Ala Pro Leu Leu Gln Cys Leu Ile Glu Gly Leu Ser Ala Glu Pro
    450                 455                 460

Arg Val Ala Ser Asn Val Cys Trp Ala Phe Ser Ser Leu Ala Glu Ala
465                 470                 475                 480

Ala Tyr Glu Ala Ala Asp Val Ala Asp Asp Gln Glu Glu Pro Ala Thr
                485                 490                 495

Tyr Cys Leu Ser Ser Ser Phe Glu Leu Ile Val Gln Lys Leu Leu Glu
            500                 505                 510

Thr Thr Asp Arg Pro Asp Gly His Gln Asn Asn Leu Arg Ser Ser Ala
        515                 520                 525

Tyr Glu Ser Leu Met Glu Ile Val Lys Asn Ser Ala Lys Asp Cys Tyr
    530                 535                 540

Pro Ala Val Gln Lys Thr Thr Leu Val Ile Met Glu Arg Leu Gln Gln
545                 550                 555                 560

Val Leu Gln Met Glu Ser His Ile Gln Ser Thr Ser Asp Arg Ile Gln
                565                 570                 575

Phe Asn Asp Leu Gln Ser Leu Leu Cys Ala Thr Leu Gln Asn Val Leu
            580                 585                 590
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Arg Lys Val Gln His Gln Asp Ala Leu Gln Ile Ser Asp Val Val Met
        595                 600                 605

Ala Ser Leu Leu Arg Met Phe Gln Ser Thr Ala Gly Ser Gly Gly Val
    610                 615                 620

Gln Glu Asp Ala Leu Met Ala Val Ser Thr Leu Val Glu Val Leu Gly
625                 630                 635                 640

Gly Glu Phe Leu Lys Tyr Met Glu Ala Phe Lys Pro Phe Leu Gly Ile
                645                 650                 655

Gly Leu Lys Asn Tyr Ala Glu Tyr Gln Val Cys Leu Ala Ala Val Gly
            660                 665                 670

Leu Val Gly Asp Leu Cys Arg Ala Leu Gln Ser Asn Ile Ile Pro Phe
        675                 680                 685

Cys Asp Glu Val Met Gln Leu Leu Leu Glu Asn Leu Gly Asn Glu Asn
    690                 695                 700

Val His Arg Ser Val Lys Pro Gln Ile Leu Ser Val Phe Gly Asp Ile
705                 710                 715                 720

Ala Leu Ala Ile Gly Gly Glu Phe Lys Lys Tyr Leu Glu Val Val Leu
                725                 730                 735

Asn Thr Leu Gln Gln Ala Ser Gln Ala Gln Val Asp Lys Ser Asp Tyr
            740                 745                 750

Asp Met Val Asp Tyr Leu Asn Glu Leu Arg Glu Ser Cys Leu Glu Ala
        755                 760                 765

Tyr Thr Gly Ile Val Gln Gly Leu Lys Gly Asp Gln Glu Asn Val His
    770                 775                 780

Pro Asp Val Met Leu Val Gln Pro Arg Val Glu Phe Ile Leu Ser Phe
785                 790                 795                 800

Ile Asp His Ile Ala Gly Asp Glu Asp His Thr Asp Gly Val Val Ala
                805                 810                 815

Cys Ala Ala Gly Leu Ile Gly Asp Leu Cys Thr Ala Phe Gly Lys Asp
            820                 825                 830

Val Leu Lys Leu Val Glu Ala Arg Pro Met Ile His Glu Leu Leu Thr
        835                 840                 845

Glu Gly Arg Arg Ser Lys Thr Asn Lys Ala Lys Thr Leu Ala Thr Trp
    850                 855                 860

Ala Thr Lys Glu Leu Arg Lys Leu Lys Asn Gln Ala
865                 870                 875


<210> SEQ ID NO 63

<400> SEQUENCE: 63

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<210> SEQ ID NO 64
<211> LENGTH: 789
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 64

Met Gly Thr Lys Met Ala Asp Leu Asp Ser Pro Pro Lys Leu Ser Gly
1               5                   10                  15

Val Gln Gln Pro Ser Glu Gly Val Gly Gly Gly Arg Cys Ser Glu Ile
            20                  25                  30

Ser Ala Glu Leu Ile Arg Ser Leu Thr Glu Leu Gln Glu Leu Glu Ala
        35                  40                  45
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Val Tyr Glu Arg Leu Cys Gly Glu Glu Lys Val Val Glu Arg Glu Leu
    50                  55                  60

Asp Ala Leu Leu Glu Gln Gln Asn Thr Ile Glu Ser Lys Met Val Thr
65                  70                  75                  80

Leu His Arg Met Gly Pro Asn Leu Gln Leu Ile Glu Gly Asp Ala Lys
                85                  90                  95

Gln Leu Ala Gly Met Ile Thr Phe Thr Cys Asn Leu Ala Glu Asn Val
            100                 105                 110

Ser Ser Lys Val Arg Gln Leu Asp Leu Ala Lys Asn Arg Leu Tyr Gln
        115                 120                 125

Ala Ile Gln Arg Ala Asp Asp Ile Leu Asp Leu Lys Phe Cys Met Asp
    130                 135                 140

Gly Val Gln Thr Ala Leu Arg Ser Glu Asp Tyr Glu Gln Ala Ala Ala
145                 150                 155                 160

His Thr His Arg Tyr Leu Cys Leu Asp Lys Ser Val Ile Glu Leu Ser
                165                 170                 175

Arg Gln Gly Lys Glu Gly Ser Met Ile Asp Ala Asn Leu Lys Leu Leu
            180                 185                 190

Gln Glu Ala Glu Gln Arg Leu Lys Ala Ile Val Ala Glu Lys Phe Ala
        195                 200                 205

Ile Ala Thr Lys Glu Gly Asp Leu Pro Gln Val Glu Arg Phe Phe Lys
    210                 215                 220

Ile Phe Pro Leu Leu Gly Leu His Glu Glu Gly Leu Arg Lys Phe Ser
225                 230                 235                 240

Glu Tyr Leu Cys Lys Gln Val Ala Ser Lys Ala Glu Glu Asn Leu Leu
                245                 250                 255

Met Val Leu Gly Thr Asp Met Ser Asp Arg Arg Ala Ala Val Ile Phe
            260                 265                 270

Ala Asp Thr Leu Thr Leu Leu Phe Glu Gly Ile Ala Arg Ile Val Glu
        275                 280                 285

Thr His Gln Pro Ile Val Glu Thr Tyr Tyr Gly Pro Gly Arg Leu Tyr
    290                 295                 300

Thr Leu Ile Lys Tyr Leu Gln Val Glu Cys Asp Arg Gln Val Glu Lys
305                 310                 315                 320

Val Val Asp Lys Phe Ile Lys Gln Arg Asp Tyr His Gln Gln Phe Arg
                325                 330                 335

His Val Gln Asn Asn Leu Met Arg Asn Ser Thr Thr Glu Lys Ile Glu
            340                 345                 350

Pro Arg Glu Leu Asp Pro Ile Leu Thr Glu Val Thr Leu Met Asn Ala
        355                 360                 365

Arg Ser Glu Leu Tyr Leu Arg Phe Leu Lys Lys Arg Ile Ser Ser Asp
    370                 375                 380

Phe Glu Val Gly Asp Ser Met Ala Ser Glu Glu Val Lys Gln Glu His
385                 390                 395                 400

Gln Lys Cys Leu Asp Lys Leu Leu Asn Asn Cys Leu Leu Ser Cys Thr
                405                 410                 415

Met Gln Glu Leu Ile Gly Leu Tyr Val Thr Met Glu Glu Tyr Phe Met
            420                 425                 430

Arg Glu Thr Val Asn Lys Ala Val Ala Leu Asp Thr Tyr Glu Lys Gly
        435                 440                 445

Gln Leu Thr Ser Ser Met Val Asp Asp Val Phe Tyr Ile Val Lys Lys
    450                 455                 460

Cys Ile Gly Arg Ala Leu Ser Ser Ser Ser Ile Asp Cys Leu Cys Ala
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465                 470                 475                 480

Met Ile Asn Leu Ala Thr Thr Glu Leu Glu Ser Asp Phe Arg Asp Val
                485                 490                 495

Leu Cys Asn Lys Leu Arg Met Gly Phe Pro Ala Thr Thr Phe Gln Asp
            500                 505                 510

Ile Gln Arg Gly Val Thr Ser Ala Val Asn Ile Met His Ser Ser Leu
        515                 520                 525

Gln Gln Gly Lys Phe Asp Thr Lys Gly Ile Glu Ser Thr Asp Glu Ala
    530                 535                 540

Lys Met Ser Phe Leu Val Thr Leu Asn Asn Val Glu Val Cys Ser Glu
545                 550                 555                 560

Asn Ile Ser Thr Leu Lys Lys Thr Leu Glu Ser Asp Cys Thr Lys Leu
                565                 570                 575

Phe Ser Gln Gly Ile Gly Gly Glu Gln Ala Gln Ala Lys Phe Asp Ser
            580                 585                 590

Cys Leu Ser Asp Leu Ala Ala Val Ser Asn Lys Phe Arg Asp Leu Leu
        595                 600                 605

Gln Glu Gly Leu Thr Glu Leu Asn Ser Thr Ala Ile Lys Pro Gln Val
    610                 615                 620

Gln Pro Trp Ile Asn Ser Phe Phe Ser Val Ser His Asn Ile Glu Glu
625                 630                 635                 640

Glu Glu Phe Asn Asp Tyr Glu Ala Asn Asp Pro Trp Val Gln Gln Phe
                645                 650                 655

Ile Leu Asn Leu Glu Gln Gln Met Ala Glu Phe Lys Ala Ser Leu Ser
            660                 665                 670

Pro Val Ile Tyr Asp Ser Leu Thr Gly Leu Met Thr Ser Leu Val Ala
        675                 680                 685

Val Glu Leu Glu Lys Val Val Leu Lys Ser Thr Phe Asn Arg Leu Gly
    690                 695                 700

Gly Leu Gln Phe Asp Lys Glu Leu Arg Ser Leu Ile Ala Tyr Leu Thr
705                 710                 715                 720

Thr Val Thr Thr Trp Thr Ile Arg Asp Lys Phe Ala Arg Leu Ser Gln
                725                 730                 735

Met Ala Thr Ile Leu Asn Leu Glu Arg Val Thr Glu Ile Leu Asp Tyr
            740                 745                 750

Trp Gly Pro Asn Ser Gly Pro Leu Thr Trp Arg Leu Thr Pro Ala Glu
        755                 760                 765

Val Arg Gln Val Leu Ala Leu Arg Ile Asp Phe Arg Ser Glu Asp Ile
    770                 775                 780

Lys Arg Leu Arg Leu
785
```

<210> SEQ ID NO 65
<211> LENGTH: 785
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 65

```
Met Ala Asp Leu Asp Ser Pro Pro Lys Leu Ser Gly Val Gln Gln Pro
1               5                   10                  15

Ser Glu Gly Val Gly Gly Gly Arg Cys Ser Glu Ile Ser Ala Glu Leu
            20                  25                  30

Ile Arg Ser Leu Thr Glu Leu Gln Glu Leu Glu Ala Val Tyr Glu Arg
        35                  40                  45
```

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```
Leu Cys Gly Glu Glu Lys Val Val Glu Arg Glu Leu Asp Ala Leu Leu
    50                  55                  60

Glu Gln Gln Asn Thr Ile Glu Ser Lys Met Val Thr Leu His Arg Met
65                  70                  75                  80

Gly Pro Asn Leu Gln Leu Ile Glu Gly Asp Ala Lys Gln Leu Ala Gly
                85                  90                  95

Met Ile Thr Phe Thr Cys Asn Leu Ala Glu Asn Val Ser Ser Lys Val
            100                 105                 110

Arg Gln Leu Asp Leu Ala Lys Asn Arg Leu Tyr Gln Ala Ile Gln Arg
        115                 120                 125

Ala Asp Asp Ile Leu Asp Leu Lys Phe Cys Met Asp Gly Val Gln Thr
    130                 135                 140

Ala Leu Arg Ser Glu Asp Tyr Glu Gln Ala Ala Ala His Thr His Arg
145                 150                 155                 160

Tyr Leu Cys Leu Asp Lys Ser Val Ile Glu Leu Ser Arg Gln Gly Lys
                165                 170                 175

Glu Gly Ser Met Ile Asp Ala Asn Leu Lys Leu Leu Gln Glu Ala Glu
            180                 185                 190

Gln Arg Leu Lys Ala Ile Val Ala Glu Lys Phe Ala Ile Ala Thr Lys
        195                 200                 205

Glu Gly Asp Leu Pro Gln Val Glu Arg Phe Phe Lys Ile Phe Pro Leu
    210                 215                 220

Leu Gly Leu His Glu Glu Gly Leu Arg Lys Phe Ser Glu Tyr Leu Cys
225                 230                 235                 240

Lys Gln Val Ala Ser Lys Ala Glu Glu Asn Leu Leu Met Val Leu Gly
                245                 250                 255

Thr Asp Met Ser Asp Arg Arg Ala Ala Val Ile Phe Ala Asp Thr Leu
            260                 265                 270

Thr Leu Leu Phe Glu Gly Ile Ala Arg Ile Val Glu Thr His Gln Pro
        275                 280                 285

Ile Val Glu Thr Tyr Tyr Gly Pro Gly Arg Leu Tyr Thr Leu Ile Lys
    290                 295                 300

Tyr Leu Gln Val Glu Cys Asp Arg Gln Val Glu Lys Val Val Asp Lys
305                 310                 315                 320

Phe Ile Lys Gln Arg Asp Tyr His Gln Gln Phe Arg His Val Gln Asn
                325                 330                 335

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

Asp Pro Ile Leu Thr Glu Val Thr Leu Met Asn Ala Arg Ser Glu Leu
        355                 360                 365

Tyr Leu Arg Phe Leu Lys Lys Arg Ile Ser Ser Asp Phe Glu Val Gly
    370                 375                 380

Asp Ser Met Ala Ser Glu Glu Val Lys Gln Glu His Gln Lys Cys Leu
385                 390                 395                 400

Asp Lys Leu Leu Asn Asn Cys Leu Leu Ser Cys Thr Met Gln Glu Leu
                405                 410                 415

Ile Gly Leu Tyr Val Thr Met Glu Glu Tyr Phe Met Arg Glu Thr Val
            420                 425                 430

Asn Lys Ala Val Ala Leu Asp Thr Tyr Glu Lys Gly Gln Leu Thr Ser
        435                 440                 445

Ser Met Val Asp Asp Val Phe Tyr Ile Val Lys Lys Cys Ile Gly Arg
    450                 455                 460

Ala Leu Ser Ser Ser Ser Ile Asp Cys Leu Cys Ala Met Ile Asn Leu
```

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```
465                 470                 475                 480

Ala Thr Thr Glu Leu Glu Ser Asp Phe Arg Asp Val Leu Cys Asn Lys
                485                 490                 495

Leu Arg Met Gly Phe Pro Ala Thr Thr Phe Gln Asp Ile Gln Arg Gly
            500                 505                 510

Val Thr Ser Ala Val Asn Ile Met His Ser Ser Leu Gln Gln Gly Lys
        515                 520                 525

Phe Asp Thr Lys Gly Ile Glu Ser Thr Asp Glu Ala Lys Met Ser Phe
    530                 535                 540

Leu Val Thr Leu Asn Asn Val Glu Val Cys Ser Glu Asn Ile Ser Thr
545                 550                 555                 560

Leu Lys Lys Thr Leu Glu Ser Asp Cys Thr Lys Leu Phe Ser Gln Gly
                565                 570                 575

Ile Gly Gly Glu Gln Ala Gln Ala Lys Phe Asp Ser Cys Leu Ser Asp
            580                 585                 590

Leu Ala Ala Val Ser Asn Lys Phe Arg Asp Leu Leu Gln Glu Gly Leu
        595                 600                 605

Thr Glu Leu Asn Ser Thr Ala Ile Lys Pro Gln Val Gln Pro Trp Ile
    610                 615                 620

Asn Ser Phe Phe Ser Val Ser His Asn Ile Glu Glu Glu Glu Phe Asn
625                 630                 635                 640

Asp Tyr Glu Ala Asn Asp Pro Trp Val Gln Gln Phe Ile Leu Asn Leu
                645                 650                 655

Glu Gln Gln Met Ala Glu Phe Lys Ala Ser Leu Ser Pro Val Ile Tyr
            660                 665                 670

Asp Ser Leu Thr Gly Leu Met Thr Ser Leu Val Ala Val Glu Leu Glu
        675                 680                 685

Lys Val Val Leu Lys Ser Thr Phe Asn Arg Leu Gly Gly Leu Gln Phe
    690                 695                 700

Asp Lys Glu Leu Arg Ser Leu Ile Ala Tyr Leu Thr Thr Val Thr Thr
705                 710                 715                 720

Trp Thr Ile Arg Asp Lys Phe Ala Arg Leu Ser Gln Met Ala Thr Ile
                725                 730                 735

Leu Asn Leu Glu Arg Val Thr Glu Ile Leu Asp Tyr Trp Gly Pro Asn
            740                 745                 750

Ser Gly Pro Leu Thr Trp Arg Leu Thr Pro Ala Glu Val Arg Gln Val
        755                 760                 765

Leu Ala Leu Arg Ile Asp Phe Arg Ser Glu Asp Ile Lys Arg Leu Arg
    770                 775                 780

Leu
785


<210> SEQ ID NO 66
<211> LENGTH: 337
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 66

Met Ala Asp Leu Asp Ser Pro Pro Lys Leu Ser Gly Val Gln Gln Pro
1               5                   10                  15

Ser Glu Gly Val Gly Gly Gly Arg Cys Ser Glu Ile Ser Ala Glu Leu
            20                  25                  30

Ile Arg Ser Leu Thr Glu Leu Gln Glu Leu Glu Ala Val Tyr Glu Arg
        35                  40                  45
```

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```
Leu Cys Gly Glu Glu Lys Val Val Glu Arg Glu Leu Asp Ala Leu Leu
    50                  55                  60

Glu Gln Gln Asn Thr Ile Glu Ser Lys Met Val Thr Leu His Arg Met
65                  70                  75                  80

Gly Pro Asn Leu Gln Leu Ile Glu Gly Asp Ala Lys Gln Leu Ala Gly
                85                  90                  95

Met Ile Thr Phe Thr Cys Asn Leu Ala Glu Asn Val Ser Ser Lys Val
            100                 105                 110

Arg Gln Leu Asp Leu Ala Lys Asn Arg Leu Tyr Gln Ala Ile Gln Arg
        115                 120                 125

Ala Asp Asp Ile Leu Asp Leu Lys Phe Cys Met Asp Gly Val Gln Thr
    130                 135                 140

Ala Leu Arg Ser Glu Asp Tyr Glu Gln Ala Ala Ala His Thr His Arg
145                 150                 155                 160

Tyr Leu Cys Leu Asp Lys Ser Val Ile Glu Leu Ser Arg Gln Gly Lys
                165                 170                 175

Glu Gly Ser Met Ile Asp Ala Asn Leu Lys Leu Leu Gln Glu Ala Glu
            180                 185                 190

Gln Arg Leu Lys Ala Ile Val Ala Glu Lys Phe Ala Ile Ala Thr Lys
        195                 200                 205

Glu Gly Asp Leu Pro Gln Val Glu Arg Phe Phe Lys Ile Phe Pro Leu
    210                 215                 220

Leu Gly Leu His Glu Glu Gly Leu Arg Lys Phe Ser Glu Tyr Leu Cys
225                 230                 235                 240

Lys Gln Val Ala Ser Lys Ala Glu Glu Asn Leu Leu Met Val Leu Gly
                245                 250                 255

Thr Asp Met Ser Asp Arg Arg Ala Ala Val Ile Phe Ala Asp Thr Leu
            260                 265                 270

Thr Leu Leu Phe Glu Gly Ile Ala Arg Ile Val Glu Thr His Gln Pro
        275                 280                 285

Ile Val Glu Thr Tyr Tyr Gly Pro Gly Arg Leu Tyr Thr Leu Ile Lys
    290                 295                 300

Tyr Leu Gln Val Glu Cys Asp Arg Gln Val Glu Lys Val Val Asp Lys
305                 310                 315                 320

Phe Ile Lys Gln Arg Asp Tyr His Gln Gln Asn Phe Val Phe Ser Phe
                325                 330                 335

Phe
```

<210> SEQ ID NO 67
<211> LENGTH: 695
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 67

```
Met Gly Thr Lys Met Ala Asp Leu Asp Ser Pro Pro Lys Leu Ser Gly
1               5                   10                  15

Val Gln Gln Pro Ser Glu Gly Val Gly Gly Gly Arg Cys Ser Glu Ile
            20                  25                  30

Ser Ala Glu Leu Ile Arg Ser Leu Thr Glu Leu Gln Glu Leu Glu Ala
        35                  40                  45

Val Tyr Glu Arg Leu Cys Gly Glu Glu Lys Val Val Glu Arg Glu Leu
    50                  55                  60

Asp Ala Leu Leu Glu Gln Gln Asn Thr Ile Glu Ser Lys Met Val Thr
65                  70                  75                  80
```

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```
Leu His Arg Met Gly Pro Asn Leu Gln Leu Ile Glu Ala Asn Leu Lys
                85                  90                  95

Leu Leu Gln Glu Ala Glu Gln Arg Leu Lys Ala Ile Val Ala Glu Lys
            100                 105                 110

Phe Ala Ile Ala Thr Lys Glu Gly Asp Leu Pro Gln Val Glu Arg Phe
        115                 120                 125

Phe Lys Ile Phe Pro Leu Leu Gly Leu His Glu Glu Gly Leu Arg Lys
    130                 135                 140

Phe Ser Glu Tyr Leu Cys Lys Gln Val Ala Ser Lys Ala Glu Glu Asn
145                 150                 155                 160

Leu Leu Met Val Leu Gly Thr Asp Met Ser Asp Arg Arg Ala Ala Val
                165                 170                 175

Ile Phe Ala Asp Thr Leu Thr Leu Leu Phe Glu Gly Ile Ala Arg Ile
            180                 185                 190

Val Glu Thr His Gln Pro Ile Val Glu Thr Tyr Tyr Gly Pro Gly Arg
        195                 200                 205

Leu Tyr Thr Leu Ile Lys Tyr Leu Gln Val Glu Cys Asp Arg Gln Val
    210                 215                 220

Glu Lys Val Val Asp Lys Phe Ile Lys Gln Arg Asp Tyr His Gln Gln
225                 230                 235                 240

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

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

Asn Ala Arg Ser Glu Leu Tyr Leu Arg Phe Leu Lys Lys Arg Ile Ser
        275                 280                 285

Ser Asp Phe Glu Val Gly Asp Ser Met Ala Ser Glu Glu Val Lys Gln
    290                 295                 300

Glu His Gln Lys Cys Leu Asp Lys Leu Leu Asn Asn Cys Leu Leu Ser
305                 310                 315                 320

Cys Thr Met Gln Glu Leu Ile Gly Leu Tyr Val Thr Met Glu Glu Tyr
                325                 330                 335

Phe Met Arg Glu Thr Val Asn Lys Ala Val Ala Leu Asp Thr Tyr Glu
            340                 345                 350

Lys Gly Gln Leu Thr Ser Ser Met Val Asp Asp Val Phe Tyr Ile Val
        355                 360                 365

Lys Lys Cys Ile Gly Arg Ala Leu Ser Ser Ser Ser Ile Asp Cys Leu
    370                 375                 380

Cys Ala Met Ile Asn Leu Ala Thr Thr Glu Leu Glu Ser Asp Phe Arg
385                 390                 395                 400

Asp Val Leu Cys Asn Lys Leu Arg Met Gly Phe Pro Ala Thr Thr Phe
                405                 410                 415

Gln Asp Ile Gln Arg Gly Val Thr Ser Ala Val Asn Ile Met His Ser
            420                 425                 430

Ser Leu Gln Gln Gly Lys Phe Asp Thr Lys Gly Ile Glu Ser Thr Asp
        435                 440                 445

Glu Ala Lys Met Ser Phe Leu Val Thr Leu Asn Asn Val Glu Val Cys
    450                 455                 460

Ser Glu Asn Ile Ser Thr Leu Lys Lys Thr Leu Glu Ser Asp Cys Thr
465                 470                 475                 480

Lys Leu Phe Ser Gln Gly Ile Gly Gly Glu Gln Ala Gln Ala Lys Phe
                485                 490                 495

Asp Ser Cys Leu Ser Asp Leu Ala Ala Val Ser Asn Lys Phe Arg Asp
```

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```
            500                 505                 510

Leu Leu Gln Glu Gly Leu Thr Glu Leu Asn Ser Thr Ala Ile Lys Pro
        515                 520                 525

Gln Val Gln Pro Trp Ile Asn Ser Phe Phe Ser Val Ser His Asn Ile
    530                 535                 540

Glu Glu Glu Glu Phe Asn Asp Tyr Glu Ala Asn Asp Pro Trp Val Gln
545                 550                 555                 560

Gln Phe Ile Leu Asn Leu Glu Gln Gln Met Ala Glu Phe Lys Ala Ser
                565                 570                 575

Leu Ser Pro Val Ile Tyr Asp Ser Leu Thr Gly Leu Met Thr Ser Leu
            580                 585                 590

Val Ala Val Glu Leu Glu Lys Val Val Leu Lys Ser Thr Phe Asn Arg
        595                 600                 605

Leu Gly Gly Leu Gln Phe Asp Lys Glu Leu Arg Ser Leu Ile Ala Tyr
    610                 615                 620

Leu Thr Thr Val Thr Thr Trp Thr Ile Arg Asp Lys Phe Ala Arg Leu
625                 630                 635                 640

Ser Gln Met Ala Thr Ile Leu Asn Leu Glu Arg Val Thr Glu Ile Leu
                645                 650                 655

Asp Tyr Trp Gly Pro Asn Ser Gly Pro Leu Thr Trp Arg Leu Thr Pro
            660                 665                 670

Ala Glu Val Arg Gln Val Leu Ala Leu Arg Ile Asp Phe Arg Ser Glu
        675                 680                 685

Asp Ile Lys Arg Leu Arg Leu
    690                 695


<210> SEQ ID NO 68
<211> LENGTH: 417
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 68

Met Glu Phe Val Lys Cys Leu Gly His Pro Glu Glu Phe Tyr Asn Leu
1               5                   10                  15

Val Arg Phe Arg Ile Gly Gly Lys Arg Lys Val Met Pro Lys Met Asp
            20                  25                  30

Gln Asp Ser Leu Ser Ser Ser Leu Lys Thr Cys Tyr Lys Tyr Leu Asn
        35                  40                  45

Gln Thr Ser Arg Ser Phe Ala Ala Val Ile Gln Ala Leu Asp Gly Glu
    50                  55                  60

Met Arg Asn Ala Val Cys Ile Phe Tyr Leu Val Leu Arg Ala Leu Asp
65                  70                  75                  80

Thr Leu Glu Asp Asp Met Thr Ile Ser Val Glu Lys Lys Val Pro Leu
                85                  90                  95

Leu His Asn Phe His Ser Phe Leu Tyr Gln Pro Asp Trp Arg Phe Met
            100                 105                 110

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

Ser Leu Glu Phe Arg Asn Leu Ala Glu Lys Tyr Gln Thr Val Ile Ala
    130                 135                 140

Asp Ile Cys Arg Arg Met Gly Ile Gly Met Ala Glu Phe Leu Asp Lys
145                 150                 155                 160

His Val Thr Ser Glu Gln Glu Trp Asp Lys Tyr Cys His Tyr Val Ala
                165                 170                 175
```

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```
Gly Leu Val Gly Ile Gly Leu Ser Arg Leu Phe Ser Ala Ser Glu Phe
            180                 185                 190

Glu Asp Pro Leu Val Gly Glu Asp Thr Glu Arg Ala Asn Ser Met Gly
        195                 200                 205

Leu Phe Leu Gln Lys Thr Asn Ile Ile Arg Asp Tyr Leu Glu Asp Gln
    210                 215                 220

Gln Gly Gly Arg Glu Phe Trp Pro Gln Glu Val Trp Ser Arg Tyr Val
225                 230                 235                 240

Lys Lys Leu Gly Asp Phe Ala Lys Pro Glu Asn Ile Asp Leu Ala Val
                245                 250                 255

Gln Cys Leu Asn Glu Leu Ile Thr Asn Ala Leu His His Ile Pro Asp
            260                 265                 270

Val Ile Thr Tyr Leu Ser Arg Leu Arg Asn Gln Ser Val Phe Asn Phe
        275                 280                 285

Cys Ala Ile Pro Gln Val Met Ala Ile Ala Thr Leu Ala Ala Cys Tyr
    290                 295                 300

Asn Asn Gln Gln Val Phe Lys Gly Ala Val Lys Ile Arg Lys Gly Gln
305                 310                 315                 320

Ala Val Thr Leu Met Met Asp Ala Thr Asn Met Pro Ala Val Lys Ala
                325                 330                 335

Ile Ile Tyr Gln Tyr Met Glu Glu Ile Tyr His Arg Ile Pro Asp Ser
            340                 345                 350

Asp Pro Ser Ser Ser Lys Thr Arg Gln Ile Ile Ser Thr Ile Arg Thr
        355                 360                 365

Gln Asn Leu Pro Asn Cys Gln Leu Ile Ser Arg Ser His Tyr Ser Pro
    370                 375                 380

Ile Tyr Leu Ser Phe Val Met Leu Leu Ala Ala Leu Ser Trp Gln Tyr
385                 390                 395                 400

Leu Thr Thr Leu Ser Gln Val Thr Glu Asp Tyr Val Gln Thr Gly Glu
                405                 410                 415

His


<210> SEQ ID NO 69
<211> LENGTH: 359
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 69

Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser Met Asn Gln Val Lys
1               5                   10                  15

Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys Leu Lys Leu Tyr Ala
            20                  25                  30

Leu Tyr Lys Gln Ala Thr Glu Gly Pro Cys Asn Met Pro Lys Pro Gly
        35                  40                  45

Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp Ala Trp Asn Ala Leu
    50                  55                  60

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

Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser Gln Val Glu Pro Gly
                85                  90                  95

Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu Val Val Thr Ser Glu
            100                 105                 110

Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro Lys Lys Lys Asn Ala
        115                 120                 125
```

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```
Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg Ala Leu Lys Ala Ala
    130                 135                 140

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

Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr Asp Ile Pro Pro Gly
                165                 170                 175

Gly Val Glu Glu Lys Ala Lys Asn Asn Ala Val Leu Leu Arg Glu Phe
            180                 185                 190

Val Gly Cys Phe Ile Asp Phe Pro Lys Pro Leu Ile Ala Val Val Asn
        195                 200                 205

Gly Pro Ala Val Gly Ile Ser Val Thr Leu Leu Gly Leu Phe Asp Ala
    210                 215                 220

Val Tyr Ala Ser Asp Arg Ala Thr Phe His Thr Pro Phe Ser His Leu
225                 230                 235                 240

Gly Gln Ser Pro Glu Gly Cys Ser Ser Tyr Thr Phe Pro Lys Ile Met
                245                 250                 255

Ser Pro Ala Lys Ala Thr Glu Met Leu Ile Phe Gly Lys Lys Leu Thr
            260                 265                 270

Ala Gly Glu Ala Cys Ala Gln Gly Leu Val Thr Glu Val Phe Pro Asp
        275                 280                 285

Ser Thr Phe Gln Lys Glu Val Trp Thr Arg Leu Lys Ala Phe Ala Lys
    290                 295                 300

Leu Pro Pro Asn Ala Leu Arg Ile Ser Lys Glu Val Ile Arg Lys Arg
305                 310                 315                 320

Glu Arg Glu Lys Leu His Ala Val Asn Ala Glu Glu Cys Asn Val Leu
                325                 330                 335

Gln Gly Arg Trp Leu Ser Asp Glu Cys Thr Asn Ala Val Val Asn Phe
            340                 345                 350

Leu Ser Arg Lys Ser Lys Leu
        355


<210> SEQ ID NO 70
<211> LENGTH: 227
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 70

Met Tyr His Glu Ile Met Arg Ala Leu Lys Ala Ala Ser Lys Asp Asp
1               5                   10                  15

Ser Ile Ile Thr Val Leu Thr Gly Asn Gly Asp Tyr Tyr Ser Ser Gly
            20                  25                  30

Asn Asp Leu Thr Asn Phe Thr Asp Ile Pro Pro Gly Gly Val Glu Glu
        35                  40                  45

Lys Ala Lys Asn Asn Ala Val Leu Leu Arg Glu Phe Val Gly Cys Phe
    50                  55                  60

Ile Asp Phe Pro Lys Pro Leu Ile Ala Val Val Asn Gly Pro Ala Val
65                  70                  75                  80

Gly Ile Ser Val Thr Leu Leu Gly Leu Phe Asp Ala Val Tyr Ala Ser
                85                  90                  95

Asp Arg Ala Thr Phe His Thr Pro Phe Ser His Leu Gly Gln Ser Pro
            100                 105                 110

Glu Gly Cys Ser Ser Tyr Thr Phe Pro Lys Ile Met Ser Pro Ala Lys
        115                 120                 125

Ala Thr Glu Met Leu Ile Phe Gly Lys Lys Leu Thr Ala Gly Glu Ala
    130                 135                 140
```

```
Cys Ala Gln Gly Leu Val Thr Glu Val Phe Pro Asp Ser Thr Phe Gln
145                 150                 155                 160

Lys Glu Val Trp Thr Arg Leu Lys Ala Phe Ala Lys Leu Pro Pro Asn
                165                 170                 175

Ala Leu Arg Ile Ser Lys Glu Val Ile Arg Lys Arg Glu Arg Glu Lys
            180                 185                 190

Leu His Ala Val Asn Ala Glu Glu Cys Asn Val Leu Gln Gly Arg Trp
        195                 200                 205

Leu Ser Asp Glu Cys Thr Asn Ala Val Val Asn Phe Leu Ser Arg Lys
    210                 215                 220

Ser Lys Leu
225


<210> SEQ ID NO 71
<211> LENGTH: 394
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 71

Met Ala Met Ala Tyr Leu Ala Trp Arg Leu Ala Arg Arg Ser Cys Pro
1               5                   10                  15

Ser Ser Leu Gln Val Thr Ser Phe Pro Val Val Gln Leu His Met Asn
            20                  25                  30

Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser Met Asn
        35                  40                  45

Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys Leu Lys
    50                  55                  60

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

Lys Pro Gly Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp Ala Trp
                85                  90                  95

Asn Ala Leu Gly Ser Leu Pro Lys Glu Ala Ala Arg Gln Asn Tyr Val
            100                 105                 110

Asp Leu Val Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser Gln Val
        115                 120                 125

Glu Pro Gly Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu Val Val
    130                 135                 140

Thr Ser Glu Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro Lys Lys
145                 150                 155                 160

Lys Asn Ala Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg Ala Leu
                165                 170                 175

Lys Ala Ala Ser Lys Asp Asp Ser Ile Ile Thr Val Leu Thr Gly Asn
            180                 185                 190

Gly Asp Tyr Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr Asp Ile
        195                 200                 205

Pro Pro Gly Gly Val Glu Glu Lys Ala Lys Asn Asn Ala Val Leu Leu
    210                 215                 220

Arg Glu Phe Val Gly Cys Phe Ile Asp Phe Pro Lys Pro Leu Ile Ala
225                 230                 235                 240

Val Val Asn Gly Pro Ala Val Gly Ile Ser Val Thr Leu Leu Gly Leu
                245                 250                 255

Phe Asp Ala Val Tyr Ala Ser Asp Arg Ala Thr Phe His Thr Pro Phe
            260                 265                 270

Ser His Leu Gly Gln Ser Pro Glu Gly Cys Ser Ser Tyr Thr Phe Pro
```

-continued

```
        275                 280                 285

Lys Ile Met Ser Pro Ala Lys Ala Thr Glu Met Leu Ile Phe Gly Lys
    290                 295                 300

Lys Leu Thr Ala Gly Glu Ala Cys Ala Gln Gly Leu Val Thr Glu Val
305                 310                 315                 320

Phe Pro Asp Ser Thr Phe Gln Lys Glu Val Trp Thr Arg Leu Lys Ala
                325                 330                 335

Phe Ala Lys Leu Pro Pro Asn Ala Leu Arg Ile Ser Lys Glu Val Ile
            340                 345                 350

Arg Lys Arg Glu Arg Glu Lys Leu His Ala Val Asn Ala Glu Glu Cys
        355                 360                 365

Asn Val Leu Gln Gly Arg Trp Leu Ser Asp Glu Cys Thr Asn Ala Val
    370                 375                 380

Val Asn Phe Leu Ser Arg Lys Ser Lys Leu
385                 390


<210> SEQ ID NO 72
<211> LENGTH: 364
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 72

Met Asn Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser
1               5                   10                  15

Met Asn Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys
            20                  25                  30

Leu Lys Leu Tyr Ala Leu Tyr Lys Gln Ala Thr Glu Gly Pro Cys Asn
        35                  40                  45

Met Pro Lys Pro Gly Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp
    50                  55                  60

Ala Trp Asn Ala Leu Gly Ser Leu Pro Lys Glu Ala Ala Arg Gln Asn
65                  70                  75                  80

Tyr Val Asp Leu Val Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser
                85                  90                  95

Gln Val Glu Pro Gly Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu
            100                 105                 110

Val Val Thr Ser Glu Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro
        115                 120                 125

Lys Lys Lys Asn Ala Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg
    130                 135                 140

Ala Leu Lys Ala Ala Ser Lys Asp Asp Ser Ile Ile Thr Val Leu Thr
145                 150                 155                 160

Gly Asn Gly Asp Tyr Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr
                165                 170                 175

Asp Ile Pro Pro Gly Gly Val Glu Glu Lys Ala Lys Asn Asn Ala Val
            180                 185                 190

Leu Leu Arg Glu Phe Val Gly Cys Phe Ile Asp Phe Pro Lys Pro Leu
        195                 200                 205

Ile Ala Val Val Asn Gly Pro Ala Val Gly Ile Ser Val Thr Leu Leu
    210                 215                 220

Gly Leu Phe Asp Ala Val Tyr Ala Ser Asp Arg Ala Thr Phe His Thr
225                 230                 235                 240

Pro Phe Ser His Leu Gly Gln Ser Pro Glu Gly Cys Ser Ser Tyr Thr
                245                 250                 255
```

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```
Phe Pro Lys Ile Met Ser Pro Ala Lys Ala Thr Glu Met Leu Ile Phe
            260                 265                 270

Gly Lys Lys Leu Thr Ala Gly Glu Ala Cys Ala Gln Gly Leu Val Thr
        275                 280                 285

Glu Val Phe Pro Asp Ser Thr Phe Gln Lys Glu Val Trp Thr Arg Leu
    290                 295                 300

Lys Ala Phe Ala Lys Leu Pro Pro Asn Ala Leu Arg Ile Ser Lys Glu
305                 310                 315                 320

Val Ile Arg Lys Arg Glu Arg Glu Lys Leu His Ala Val Asn Ala Glu
                325                 330                 335

Glu Cys Asn Val Leu Gln Gly Arg Trp Leu Ser Asp Glu Cys Thr Asn
            340                 345                 350

Ala Val Val Asn Phe Leu Ser Arg Lys Ser Lys Leu
        355                 360


<210> SEQ ID NO 73
<211> LENGTH: 241
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 73

Met Phe Asn Arg Pro Lys Lys Lys Asn Ala Ile Asn Thr Glu Met Tyr
1               5                   10                  15

His Glu Ile Met Arg Ala Leu Lys Ala Ala Ser Lys Asp Asp Ser Ile
            20                  25                  30

Ile Thr Val Leu Thr Gly Asn Gly Asp Tyr Tyr Ser Ser Gly Asn Asp
        35                  40                  45

Leu Thr Asn Phe Thr Asp Ile Pro Pro Gly Gly Val Glu Glu Lys Ala
    50                  55                  60

Lys Asn Asn Ala Val Leu Leu Arg Glu Phe Val Gly Cys Phe Ile Asp
65                  70                  75                  80

Phe Pro Lys Pro Leu Ile Ala Val Val Asn Gly Pro Ala Val Gly Ile
                85                  90                  95

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

Ala Thr Phe His Thr Pro Phe Ser His Leu Gly Gln Ser Pro Glu Gly
        115                 120                 125

Cys Ser Ser Tyr Thr Phe Pro Lys Ile Met Ser Pro Ala Lys Ala Thr
    130                 135                 140

Glu Met Leu Ile Phe Gly Lys Lys Leu Thr Ala Gly Glu Ala Cys Ala
145                 150                 155                 160

Gln Gly Leu Val Thr Glu Val Phe Pro Asp Ser Thr Phe Gln Lys Glu
                165                 170                 175

Val Trp Thr Arg Leu Lys Ala Phe Ala Lys Leu Pro Pro Asn Ala Leu
            180                 185                 190

Arg Ile Ser Lys Glu Val Ile Arg Lys Arg Glu Arg Glu Lys Leu His
        195                 200                 205

Ala Val Asn Ala Glu Glu Cys Asn Val Leu Gln Gly Arg Trp Leu Ser
    210                 215                 220

Asp Glu Cys Thr Asn Ala Val Val Asn Phe Leu Ser Arg Lys Ser Lys
225                 230                 235                 240

Leu


<210> SEQ ID NO 74
<211> LENGTH: 1225
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<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 74

Met Phe Ala Arg Lys Pro Pro Gly Ala Ala Pro Leu Gly Ala Met Pro
1 5 10 15

Val Pro Asp Gln Pro Ser Ser Ala Ser Glu Lys Thr Ser Ser Leu Ser
20 25 30

Pro Gly Leu Asn Thr Ser Asn Gly Asp Gly Ser Glu Thr Glu Thr Thr
35 40 45

Ser Ala Ile Leu Ala Ser Val Lys Glu Gln Glu Leu Gln Phe Glu Arg
50 55 60

Leu Thr Arg Glu Leu Glu Ala Glu Arg Gln Ile Val Ala Ser Gln Leu
65 70 75 80

Glu Arg Cys Lys Leu Gly Ser Glu Thr Gly Ser Met Ser Ser Met Ser
85 90 95

Ser Ala Glu Glu Gln Phe Gln Trp Gln Ser Gln Asp Gly Gln Lys Asp
100 105 110

Ile Glu Asp Glu Leu Thr Thr Gly Leu Glu Leu Val Asp Ser Cys Ile
115 120 125

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

Gly Glu Arg Pro Ser Leu Leu Ser Gln Ser Ala Leu Gln Leu Asn Ser
145 150 155 160

Lys Pro Glu Gly Ser Phe Gln Tyr Pro Ala Ser Tyr His Ser Asn Gln
165 170 175

Thr Leu Ala Leu Gly Glu Thr Thr Pro Ser Gln Leu Pro Ala Arg Gly
180 185 190

Thr Gln Ala Arg Ala Thr Gly Gln Ser Phe Ser Gln Gly Thr Thr Ser
195 200 205

Arg Ala Gly His Leu Ala Gly Pro Glu Pro Ala Pro Pro Pro Pro Pro
210 215 220

Pro Pro Arg Glu Pro Phe Ala Pro Ser Leu Gly Ser Ala Phe His Leu
225 230 235 240

Pro Asp Ala Pro Pro Ala Ala Ala Ala Ala Ala Leu Tyr Tyr Ser Ser
245 250 255

Ser Thr Leu Pro Ala Pro Pro Arg Gly Gly Ser Pro Leu Ala Ala Pro
260 265 270

Gln Gly Gly Ser Pro Thr Lys Leu Gln Arg Gly Gly Ser Ala Pro Glu
275 280 285

Gly Ala Thr Tyr Ala Ala Pro Arg Gly Ser Ser Pro Lys Gln Ser Pro
290 295 300

Ser Arg Leu Ala Lys Ser Tyr Ser Thr Ser Ser Pro Ile Asn Ile Val
305 310 315 320

Val Ser Ser Ala Gly Leu Ser Pro Ile Arg Val Thr Ser Pro Pro Thr
325 330 335

Val Gln Ser Thr Ile Ser Ser Ser Pro Ile His Gln Leu Ser Ser Thr
340 345 350

Ile Gly Thr Tyr Ala Thr Leu Ser Pro Thr Lys Arg Leu Val His Ala
355 360 365

Ser Glu Gln Tyr Ser Lys His Ser Gln Glu Leu Tyr Ala Thr Ala Thr
370 375 380

Leu Gln Arg Pro Gly Ser Leu Ala Ala Gly Ser Arg Ala Ser Tyr Ser
385 390 395 400

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Ser Gln His Gly His Leu Gly Pro Glu Leu Arg Ala Leu Gln Ser Pro
               405                 410                 415

Glu His His Ile Asp Pro Ile Tyr Glu Asp Arg Val Tyr Gln Lys Pro
           420                 425                 430

Pro Met Arg Ser Leu Ser Gln Ser Gln Gly Asp Pro Leu Pro Pro Ala
       435                 440                 445

His Thr Gly Thr Tyr Arg Thr Ser Thr Ala Pro Ser Ser Pro Gly Val
   450                 455                 460

Asp Ser Val Pro Leu Gln Arg Thr Gly Ser Gln His Gly Pro Gln Asn
465                 470                 475                 480

Ala Ala Ala Ala Thr Phe Gln Arg Ala Ser Tyr Ala Ala Gly Pro Ala
               485                 490                 495

Ser Asn Tyr Ala Asp Pro Tyr Arg Gln Leu Gln Tyr Cys Pro Ser Val
           500                 505                 510

Glu Ser Pro Tyr Ser Lys Ser Gly Pro Ala Leu Pro Pro Glu Gly Thr
       515                 520                 525

Leu Ala Arg Ser Pro Ser Ile Asp Ser Ile Gln Lys Asp Pro Arg Glu
   530                 535                 540

Phe Gly Trp Arg Asp Pro Glu Leu Pro Glu Val Ile Gln Met Leu Gln
545                 550                 555                 560

His Gln Phe Pro Ser Val Gln Ser Asn Ala Ala Ala Tyr Leu Gln His
               565                 570                 575

Leu Cys Phe Gly Asp Asn Lys Ile Lys Ala Glu Ile Arg Arg Gln Gly
           580                 585                 590

Gly Ile Gln Leu Leu Val Asp Leu Leu Asp His Arg Met Thr Glu Val
       595                 600                 605

His Arg Ser Ala Cys Gly Ala Leu Arg Asn Leu Val Tyr Gly Lys Ala
   610                 615                 620

Asn Asp Asp Asn Lys Ile Ala Leu Lys Asn Cys Gly Gly Ile Pro Ala
625                 630                 635                 640

Leu Val Arg Leu Leu Arg Lys Thr Thr Asp Leu Glu Ile Arg Glu Leu
               645                 650                 655

Val Thr Gly Val Leu Trp Asn Leu Ser Ser Cys Asp Ala Leu Lys Met
           660                 665                 670

Pro Ile Ile Gln Asp Ala Leu Ala Val Leu Thr Asn Ala Val Ile Ile
       675                 680                 685

Pro His Ser Gly Trp Glu Asn Ser Pro Leu Gln Asp Asp Arg Lys Ile
   690                 695                 700

Gln Leu His Ser Ser Gln Val Leu Arg Asn Ala Thr Gly Cys Leu Arg
705                 710                 715                 720

Asn Val Ser Ser Ala Gly Glu Glu Ala Arg Arg Arg Met Arg Glu Cys
               725                 730                 735

Asp Gly Leu Thr Asp Ala Leu Leu Tyr Val Ile Gln Ser Ala Leu Gly
           740                 745                 750

Ser Ser Glu Ile Asp Ser Lys Thr Val Glu Asn Cys Val Cys Ile Leu
       755                 760                 765

Arg Asn Leu Ser Tyr Arg Leu Ala Ala Glu Thr Ser Gln Gly Gln His
   770                 775                 780

Met Gly Thr Asp Glu Leu Asp Gly Leu Leu Cys Gly Glu Ala Asn Gly
785                 790                 795                 800

Lys Asp Ala Glu Ser Ser Gly Cys Trp Gly Lys Lys Lys Lys Lys Lys
               805                 810                 815
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Lys Ser Gln Asp Gln Trp Asp Gly Val Gly Pro Leu Pro Asp Cys Ala
            820                 825                 830

Glu Pro Pro Lys Gly Ile Gln Met Leu Trp His Pro Ser Ile Val Lys
        835                 840                 845

Pro Tyr Leu Thr Leu Leu Ser Glu Cys Ser Asn Pro Asp Thr Leu Glu
    850                 855                 860

Gly Ala Ala Gly Ala Leu Gln Asn Leu Ala Ala Gly Ser Trp Lys Trp
865                 870                 875                 880

Ser Val Tyr Ile Arg Ala Ala Val Arg Lys Glu Lys Gly Leu Pro Ile
                885                 890                 895

Leu Val Glu Leu Leu Arg Ile Asp Asn Asp Arg Val Val Cys Ala Val
            900                 905                 910

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

Ile Gly Lys Tyr Ala Met Arg Asp Leu Val His Arg Leu Pro Gly Gly
    930                 935                 940

Asn Asn Ser Asn Asn Thr Ala Ser Lys Ala Met Ser Asp Asp Thr Val
945                 950                 955                 960

Thr Ala Val Cys Cys Thr Leu His Glu Val Ile Thr Lys Asn Met Glu
                965                 970                 975

Asn Ala Lys Ala Leu Arg Asp Ala Gly Gly Ile Glu Lys Leu Val Gly
            980                 985                 990

Ile Ser Lys Ser Lys Gly Asp Lys  His Ser Pro Lys Val  Val Lys Ala
        995                 1000                1005

Ala Ser  Gln Val Leu Asn Ser  Met Trp Gln Tyr Arg  Asp Leu Arg
    1010                1015                1020

Ser Leu  Tyr Lys Lys Asp Gly  Trp Ser Gln Tyr His  Phe Val Ala
    1025                1030                1035

Ser Ser  Ser Thr Ile Glu Arg  Asp Arg Gln Arg Pro  Tyr Ser Ser
    1040                1045                1050

Ser Arg  Thr Pro Ser Ile Ser  Pro Val Arg Val Ser  Pro Asn Asn
    1055                1060                1065

Arg Ser  Ala Ser Ala Pro Ala  Ser Pro Arg Glu Met  Ile Ser Leu
    1070                1075                1080

Lys Glu  Arg Lys Thr Asp Tyr  Glu Cys Thr Gly Ser  Asn Ala Thr
    1085                1090                1095

Tyr His  Gly Ala Lys Gly Glu  His Thr Ser Arg Lys  Asp Ala Met
    1100                1105                1110

Thr Ala  Gln Asn Thr Gly Ile  Ser Thr Leu Tyr Arg  Asn Ser Tyr
    1115                1120                1125

Gly Ala  Pro Ala Glu Asp Ile  Lys His Asn Gln Val  Ser Ala Gln
    1130                1135                1140

Pro Val  Pro Gln Glu Pro Ser  Arg Lys Asp Tyr Glu  Thr Tyr Gln
    1145                1150                1155

Pro Phe  Gln Asn Ser Thr Arg  Asn Tyr Asp Glu Ser  Phe Phe Glu
    1160                1165                1170

Asp Gln  Val His His Arg Pro  Pro Ala Ser Glu Tyr  Thr Met His
    1175                1180                1185

Leu Gly  Leu Lys Ser Thr Gly  Asn Tyr Val Asp Phe  Tyr Ser Ala
    1190                1195                1200

Ala Arg  Pro Tyr Ser Glu Leu  Asn Tyr Glu Thr Ser  His Tyr Pro
    1205                1210                1215

Ala Ser  Pro Asp Ser Trp Val
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1220 1225

<210> SEQ ID NO 75
<211> LENGTH: 1167
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 75

Met Phe Ala Arg Lys Pro Pro Gly Ala Ala Pro Leu Gly Ala Met Pro
1 5 10 15

Val Pro Asp Gln Pro Ser Ser Ala Ser Glu Lys Thr Ser Ser Leu Ser
20 25 30

Pro Gly Leu Asn Thr Ser Asn Gly Asp Gly Ser Glu Thr Glu Thr Thr
35 40 45

Ser Ala Ile Leu Ala Ser Val Lys Glu Gln Glu Leu Gln Phe Glu Arg
50 55 60

Leu Thr Arg Glu Leu Glu Ala Glu Arg Gln Ile Val Ala Ser Gln Leu
65 70 75 80

Glu Arg Cys Lys Leu Gly Ser Glu Thr Gly Ser Met Ser Ser Met Ser
85 90 95

Ser Ala Glu Glu Gln Phe Gln Trp Gln Ser Gln Asp Gly Gln Lys Asp
100 105 110

Ile Glu Asp Glu Leu Thr Thr Gly Leu Glu Leu Val Asp Ser Cys Ile
115 120 125

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

Gly Glu Arg Pro Ser Leu Leu Ser Gln Ser Ala Leu Gln Leu Asn Ser
145 150 155 160

Lys Pro Glu Gly Ser Phe Gln Tyr Pro Ala Ser Tyr His Ser Asn Gln
165 170 175

Thr Leu Ala Leu Gly Glu Thr Thr Pro Ser Gln Leu Pro Ala Arg Gly
180 185 190

Thr Gln Ala Arg Ala Thr Gly Gln Ser Phe Ser Gln Gly Thr Thr Ser
195 200 205

Arg Ala Gly His Leu Ala Gly Pro Glu Pro Ala Pro Pro Pro Pro Pro
210 215 220

Pro Pro Arg Glu Pro Phe Ala Pro Ser Leu Gly Ser Ala Phe His Leu
225 230 235 240

Pro Asp Ala Pro Pro Ala Ala Ala Ala Ala Ala Leu Tyr Tyr Ser Ser
245 250 255

Ser Thr Leu Pro Ala Pro Pro Arg Gly Gly Ser Pro Leu Ala Ala Pro
260 265 270

Gln Gly Gly Ser Pro Thr Lys Leu Gln Arg Gly Gly Ser Ala Pro Glu
275 280 285

Gly Ala Thr Tyr Ala Ala Pro Arg Gly Ser Ser Pro Lys Gln Ser Pro
290 295 300

Ser Arg Leu Ala Lys Ser Tyr Ser Thr Ser Ser Pro Ile Asn Ile Val
305 310 315 320

Val Ser Ser Ala Gly Leu Ser Pro Ile Arg Val Thr Ser Pro Pro Thr
325 330 335

Val Gln Ser Thr Ile Ser Ser Ser Pro Ile His Gln Leu Ser Ser Thr
340 345 350

Ile Gly Thr Tyr Ala Thr Leu Ser Pro Thr Lys Arg Leu Val His Ala
355 360 365

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Ser Glu Gln Tyr Ser Lys His Ser Gln Glu Leu Tyr Ala Thr Ala Thr
    370                 375                 380

Leu Gln Arg Pro Gly Ser Leu Ala Ala Gly Ser Arg Ala Ser Tyr Ser
385                 390                 395                 400

Ser Gln His Gly His Leu Gly Pro Glu Leu Arg Ala Leu Gln Ser Pro
                405                 410                 415

Glu His His Ile Asp Pro Ile Tyr Glu Asp Arg Val Tyr Gln Lys Pro
            420                 425                 430

Pro Met Arg Ser Leu Ser Gln Ser Gln Gly Asp Pro Leu Pro Pro Ala
        435                 440                 445

His Thr Gly Thr Tyr Arg Thr Ser Thr Ala Pro Ser Ser Pro Gly Val
    450                 455                 460

Asp Ser Val Pro Leu Gln Arg Thr Gly Ser Gln His Gly Pro Gln Asn
465                 470                 475                 480

Ala Ala Ala Ala Thr Phe Gln Arg Ala Ser Tyr Ala Ala Gly Pro Ala
                485                 490                 495

Ser Asn Tyr Ala Asp Pro Tyr Arg Gln Leu Gln Tyr Cys Pro Ser Val
            500                 505                 510

Glu Ser Pro Tyr Ser Lys Ser Gly Pro Ala Leu Pro Pro Glu Gly Thr
        515                 520                 525

Leu Ala Arg Ser Pro Ser Ile Asp Ser Ile Gln Lys Asp Pro Arg Glu
    530                 535                 540

Phe Gly Trp Arg Asp Pro Glu Leu Pro Glu Val Ile Gln Met Leu Gln
545                 550                 555                 560

His Gln Phe Pro Ser Val Gln Ser Asn Ala Ala Ala Tyr Leu Gln His
                565                 570                 575

Leu Cys Phe Gly Asp Asn Lys Ile Lys Ala Glu Ile Arg Arg Gln Gly
            580                 585                 590

Gly Ile Gln Leu Leu Val Asp Leu Leu Asp His Arg Met Thr Glu Val
        595                 600                 605

His Arg Ser Ala Cys Gly Ala Leu Arg Asn Leu Val Tyr Gly Lys Ala
    610                 615                 620

Asn Asp Asp Asn Lys Ile Ala Leu Lys Asn Cys Gly Gly Ile Pro Ala
625                 630                 635                 640

Leu Val Arg Leu Leu Arg Lys Thr Thr Asp Leu Glu Ile Arg Glu Leu
                645                 650                 655

Val Thr Gly Val Leu Trp Asn Leu Ser Ser Cys Asp Ala Leu Lys Met
            660                 665                 670

Pro Ile Ile Gln Asp Ala Leu Ala Val Leu Thr Asn Ala Val Ile Ile
        675                 680                 685

Pro His Ser Gly Trp Glu Asn Ser Pro Leu Gln Asp Asp Arg Lys Ile
    690                 695                 700

Gln Leu His Ser Ser Gln Val Leu Arg Asn Ala Thr Gly Cys Leu Arg
705                 710                 715                 720

Asn Val Ser Ser Ala Gly Glu Glu Ala Arg Arg Arg Met Arg Glu Cys
                725                 730                 735

Asp Gly Leu Thr Asp Ala Leu Leu Tyr Val Ile Gln Ser Ala Leu Gly
            740                 745                 750

Ser Ser Glu Ile Asp Ser Lys Thr Val Glu Asn Cys Val Cys Ile Leu
        755                 760                 765

Arg Asn Leu Ser Tyr Arg Leu Ala Ala Glu Thr Ser Gln Gly Gln His
    770                 775                 780

Met Gly Thr Asp Glu Leu Asp Gly Leu Leu Cys Gly Glu Ala Asn Gly
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785                 790                 795                 800

Lys Asp Ala Glu Ser Ser Gly Cys Trp Gly Lys Lys Lys Lys Lys Lys
                805                 810                 815

Lys Ser Gln Asp Gln Trp Ser Val Tyr Ile Arg Ala Ala Val Arg Lys
            820                 825                 830

Glu Lys Gly Leu Pro Ile Leu Val Glu Leu Leu Arg Ile Asp Asn Asp
        835                 840                 845

Arg Val Val Cys Ala Val Ala Thr Ala Leu Arg Asn Met Ala Leu Asp
    850                 855                 860

Val Arg Asn Lys Glu Leu Ile Gly Lys Tyr Ala Met Arg Asp Leu Val
865                 870                 875                 880

His Arg Leu Pro Gly Gly Asn Asn Ser Asn Asn Thr Ala Ser Lys Ala
                885                 890                 895

Met Ser Asp Asp Thr Val Thr Ala Val Cys Cys Thr Leu His Glu Val
            900                 905                 910

Ile Thr Lys Asn Met Glu Asn Ala Lys Ala Leu Arg Asp Ala Gly Gly
        915                 920                 925

Ile Glu Lys Leu Val Gly Ile Ser Lys Ser Lys Gly Asp Lys His Ser
    930                 935                 940

Pro Lys Val Val Lys Ala Ala Ser Gln Val Leu Asn Ser Met Trp Gln
945                 950                 955                 960

Tyr Arg Asp Leu Arg Ser Leu Tyr Lys Lys Asp Gly Trp Ser Gln Tyr
                965                 970                 975

His Phe Val Ala Ser Ser Ser Thr Ile Glu Arg Asp Arg Gln Arg Pro
            980                 985                 990

Tyr Ser Ser Ser Arg Thr Pro Ser  Ile Ser Pro Val Arg  Val Ser Pro
        995                 1000                1005

Asn Asn  Arg Ser Ala Ser Ala  Pro Ala Ser Pro Arg  Glu Met Ile
    1010                1015                1020

Ser Leu  Lys Glu Arg Lys Thr  Asp Tyr Glu Cys Thr  Gly Ser Asn
    1025                1030                1035

Ala Thr  Tyr His Gly Ala Lys  Gly Glu His Thr Ser  Arg Lys Asp
    1040                1045                1050

Ala Met  Thr Ala Gln Asn Thr  Gly Ile Ser Thr Leu  Tyr Arg Asn
    1055                1060                1065

Ser Tyr  Gly Ala Pro Ala Glu  Asp Ile Lys His Asn  Gln Val Ser
    1070                1075                1080

Ala Gln  Pro Val Pro Gln Glu  Pro Ser Arg Lys Asp  Tyr Glu Thr
    1085                1090                1095

Tyr Gln  Pro Phe Gln Asn Ser  Thr Arg Asn Tyr Asp  Glu Ser Phe
    1100                1105                1110

Phe Glu  Asp Gln Val His His  Arg Pro Pro Ala Ser  Glu Tyr Thr
    1115                1120                1125

Met His  Leu Gly Leu Lys Ser  Thr Gly Asn Tyr Val  Asp Phe Tyr
    1130                1135                1140

Ser Ala  Ala Arg Pro Tyr Ser  Glu Leu Asn Tyr Glu  Thr Ser His
    1145                1150                1155

Tyr Pro  Ala Ser Pro Asp Ser  Trp Val
    1160                1165


<210> SEQ ID NO 76
<211> LENGTH: 266
<212> TYPE: PRT
<213> ORGANISM: Human
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<400> SEQUENCE: 76

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

Arg Phe Leu Gln Leu Leu Met Thr His Gly Val Leu Glu Glu Trp Asp
20 25 30

Val Lys Arg Leu Gln Thr His Cys Tyr Lys Val His Asp Arg Asn Ala
35 40 45

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

Glu Ser Leu Tyr Ile Glu Ile Lys Arg Gly Val Thr Glu Asp Asp Gly
65 70 75 80

Arg Pro Ile Tyr Ala Leu Val Asn Leu Ala Thr Thr Ser Ile Ser Lys
85 90 95

Met Ala Thr Asp Phe Ala Glu Asn Glu Leu Asp Leu Phe Arg Lys Ala
100 105 110

Leu Glu Leu Ile Ile Asp Ser Glu Thr Gly Phe Ala Ser Ser Thr Asn
115 120 125

Ile Leu Asn Leu Val Asp Gln Leu Lys Gly Lys Lys Met Arg Lys Lys
130 135 140

Glu Ala Glu Gln Val Leu Gln Lys Phe Val Gln Asn Lys Trp Leu Ile
145 150 155 160

Glu Lys Glu Gly Glu Phe Thr Leu His Gly Arg Ala Ile Leu Glu Met
165 170 175

Glu Gln Tyr Ile Arg Glu Thr Tyr Pro Asp Ala Val Lys Ile Cys Asn
180 185 190

Ile Cys His Ser Leu Leu Ile Gln Gly Gln Ser Cys Glu Thr Cys Gly
195 200 205

Ile Arg Met His Leu Pro Cys Val Ala Lys Tyr Phe Gln Ser Asn Ala
210 215 220

Glu Pro Arg Cys Pro His Cys Asn Asp Tyr Trp Pro His Glu Ile Pro
225 230 235 240

Lys Val Phe Asp Pro Glu Lys Glu Arg Glu Ser Gly Val Leu Lys Ser
245 250 255

Asn Lys Lys Ser Leu Arg Ser Arg Gln His
260 265

<210> SEQ ID NO 77
<211> LENGTH: 145
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 77

Pro Tyr Pro Leu Ala Arg Trp Asp Ala Leu Gly Leu Pro Val Arg Ser
1 5 10 15

His Met Gln Gly Ser Thr Arg Arg Met Gly Val Met Thr Asp Val His
20 25 30

Arg Arg Phe Leu Gln Leu Leu Met Thr His Gly Val Leu Glu Glu Trp
35 40 45

Asp Val Lys Arg Leu Gln Thr His Cys Tyr Lys Val His Asp Arg Asn
50 55 60

Ala Thr Val Asp Lys Leu Glu Asp Phe Ile Asn Asn Ile Asn Ser Val
65 70 75 80

Leu Glu Ser Leu Tyr Ile Glu Ile Lys Arg Gly Val Thr Glu Asp Asp
85 90 95

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Gly Arg Pro Ile Tyr Ala Leu Val Asn Leu Ala Thr Thr Ser Ile Ser
            100                 105                 110

Lys Met Ala Thr Asp Phe Ala Glu Asn Glu Leu Asp Leu Phe Arg Lys
        115                 120                 125

Ala Leu Glu Leu Ile Ile Asp Ser Glu Thr Leu Arg Leu Pro Gln Thr
    130                 135                 140

Tyr
145


<210> SEQ ID NO 78
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 78

Val His Leu Ala Thr Val Ser Ala Ser Ala Ala Trp Asp Ala Leu Gly
1               5                   10                  15

Leu Pro Val Arg Ser His Met Gln Gly Ser Thr Arg Arg Met Gly Val
            20                  25                  30

Met Thr Asp Val His Arg Arg Phe Leu Gln Leu Leu Met Thr His Gly
        35                  40                  45

Val Leu Glu Glu Trp Asp Val Lys Arg Leu Gln Thr His Cys Tyr Lys
    50                  55                  60

Val His Asp Arg Asn Ala Thr Val Asp Lys Leu Glu Asp Phe Ile Asn
65                  70                  75                  80

Asn Ile Asn Ser Val Leu Glu Ser Leu Tyr Ile Glu Ile Lys Arg Gly
                85                  90                  95

Val Thr Glu Asp Asp Gly Arg Pro Ile Tyr Ala Leu Val Asn Leu Ala
            100                 105                 110

Thr Thr Ser Ile Ser Lys Met Ala Thr Asp Phe Ala Glu Asn Glu Leu
        115                 120                 125

Asp Leu Phe Arg Lys Ala Leu Glu Leu Ile Ile Asp Ser Glu Thr Gly
    130                 135                 140

Phe Ala Ser Ser Thr Asn Ile Leu Asn Leu Val Asp Gln Leu Lys Gly
145                 150                 155                 160

Lys Lys Met Arg Lys Lys Glu Ala Arg Cys Cys Arg Ser Leu Phe Lys
                165                 170                 175

Thr Ser Gly


<210> SEQ ID NO 79
<211> LENGTH: 392
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 79

Met Glu Trp Trp Ala Ser Ser Pro Leu Arg Leu Trp Leu Leu Leu Phe
1               5                   10                  15

Leu Leu Pro Ser Ala Gln Gly Arg Gln Lys Glu Ser Gly Ser Lys Trp
            20                  25                  30

Lys Val Phe Ile Asp Gln Ile Asn Arg Ser Leu Glu Asn Tyr Glu Pro
        35                  40                  45

Cys Ser Ser Gln Asn Cys Ser Cys Tyr His Gly Val Ile Glu Glu Asp
    50                  55                  60

Leu Thr Pro Phe Arg Gly Gly Ile Ser Arg Lys Met Met Ala Glu Val
65                  70                  75                  80
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Val Arg Arg Lys Leu Gly Thr His Tyr Gln Ile Thr Lys Asn Arg Leu
                85                  90                  95

Tyr Arg Glu Asn Asp Cys Met Phe Pro Ser Arg Cys Ser Gly Val Glu
            100                 105                 110

His Phe Ile Leu Glu Val Ile Gly Arg Leu Pro Asp Met Glu Met Val
        115                 120                 125

Ile Asn Val Arg Asp Tyr Pro Gln Val Pro Lys Trp Met Glu Pro Ala
    130                 135                 140

Ile Pro Val Phe Ser Phe Ser Lys Thr Ser Glu Tyr His Asp Ile Met
145                 150                 155                 160

Tyr Pro Ala Trp Thr Phe Trp Glu Gly Gly Pro Ala Val Trp Pro Ile
                165                 170                 175

Tyr Pro Thr Gly Leu Gly Arg Trp Asp Leu Phe Arg Glu Asp Leu Val
            180                 185                 190

Arg Ser Ala Ala Gln Trp Pro Trp Lys Lys Lys Asn Ser Thr Ala Tyr
        195                 200                 205

Phe Arg Gly Ser Arg Thr Ser Pro Glu Arg Asp Pro Leu Ile Leu Leu
    210                 215                 220

Ser Arg Lys Asn Pro Lys Leu Val Asp Ala Glu Tyr Thr Lys Asn Gln
225                 230                 235                 240

Ala Trp Lys Ser Met Lys Asp Thr Leu Gly Lys Pro Ala Ala Lys Asp
                245                 250                 255

Val His Leu Val Asp His Cys Lys Tyr Lys Tyr Leu Phe Asn Phe Arg
            260                 265                 270

Gly Val Ala Ala Ser Phe Arg Phe Lys His Leu Phe Leu Cys Gly Ser
        275                 280                 285

Leu Val Phe His Val Gly Asp Glu Trp Leu Glu Phe Phe Tyr Pro Gln
    290                 295                 300

Leu Lys Pro Trp Val His Tyr Ile Pro Val Lys Thr Asp Leu Ser Asn
305                 310                 315                 320

Val Gln Glu Leu Leu Gln Phe Val Lys Ala Asn Asp Asp Val Ala Gln
                325                 330                 335

Glu Ile Ala Glu Arg Gly Ser Gln Phe Ile Arg Asn His Leu Gln Met
            340                 345                 350

Asp Asp Ile Thr Cys Tyr Trp Glu Asn Leu Leu Ser Glu Tyr Ser Lys
        355                 360                 365

Phe Leu Ser Tyr Asn Val Thr Arg Arg Lys Gly Tyr Asp Gln Ile Ile
    370                 375                 380

Pro Lys Met Leu Lys Thr Glu Leu
385                 390


<210> SEQ ID NO 80
<211> LENGTH: 411
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 80

Met Arg Arg Arg Arg Ala Gly Gly Arg Thr Met Val Glu Arg Ala Ser
1               5                   10                  15

Lys Phe Val Leu Val Val Ala Gly Ser Val Cys Phe Met Leu Ile Leu
            20                  25                  30

Tyr Gln Tyr Ala Gly Pro Gly Leu Ser Leu Gly Ala Pro Gly Gly Arg
        35                  40                  45

Ala Pro Pro Asp Asp Leu Asp Leu Phe Pro Thr Pro Asp Pro His Tyr
    50                  55                  60
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Glu Lys Lys Tyr Tyr Phe Pro Val Arg Glu Leu Glu Arg Ser Leu Arg
65                  70                  75                  80

Phe Asp Met Lys Gly Asp Asp Val Ile Val Phe Leu His Ile Gln Lys
                85                  90                  95

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

Glu Val Pro Cys Asp Cys Arg Pro Gly Gln Lys Lys Cys Thr Cys Tyr
        115                 120                 125

Arg Pro Asn Arg Arg Glu Thr Trp Leu Phe Ser Arg Phe Ser Thr Gly
    130                 135                 140

Trp Ser Cys Gly Leu His Ala Asp Trp Thr Glu Leu Thr Asn Cys Val
145                 150                 155                 160

Pro Gly Val Leu Asp Arg Arg Asp Ser Ala Ala Leu Arg Thr Pro Arg
                165                 170                 175

Lys Phe Tyr Tyr Ile Thr Leu Leu Arg Asp Pro Val Ser Arg Tyr Leu
            180                 185                 190

Ser Glu Trp Arg His Val Gln Arg Gly Ala Thr Trp Lys Thr Ser Leu
        195                 200                 205

His Met Cys Asp Gly Arg Thr Pro Thr Pro Glu Glu Leu Pro Pro Cys
    210                 215                 220

Tyr Glu Gly Thr Asp Trp Ser Gly Cys Thr Leu Gln Glu Phe Met Asp
225                 230                 235                 240

Cys Pro Tyr Asn Leu Ala Asn Asn Arg Gln Val Arg Met Leu Ala Asp
                245                 250                 255

Leu Ser Leu Val Gly Cys Tyr Asn Leu Ser Phe Ile Pro Glu Gly Lys
            260                 265                 270

Arg Ala Gln Leu Leu Leu Glu Ser Ala Lys Lys Asn Leu Arg Gly Met
        275                 280                 285

Ala Phe Phe Gly Leu Thr Glu Phe Gln Arg Lys Thr Gln Tyr Leu Phe
    290                 295                 300

Glu Arg Thr Phe Asn Leu Lys Phe Ile Arg Pro Phe Met Gln Tyr Asn
305                 310                 315                 320

Ser Thr Arg Ala Gly Gly Val Glu Val Asp Glu Asp Thr Ile Arg Arg
                325                 330                 335

Ile Glu Glu Leu Asn Asp Leu Asp Met Gln Leu Tyr Asp Tyr Ala Lys
            340                 345                 350

Asp Leu Phe Gln Gln Arg Tyr Gln Tyr Lys Arg Gln Leu Glu Arg Arg
        355                 360                 365

Glu Gln Arg Leu Arg Ser Arg Glu Glu Arg Leu Leu His Arg Ala Lys
    370                 375                 380

Glu Ala Leu Pro Arg Glu Asp Ala Asp Glu Pro Gly Arg Val Pro Thr
385                 390                 395                 400

Glu Asp Tyr Met Ser His Ile Ile Glu Lys Trp
                405                 410


<210> SEQ ID NO 81
<211> LENGTH: 464
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 81

Met Thr Ser Cys Arg Cys Ser Val Thr Ser Arg Ser Leu Trp Pro Ala
1               5                   10                  15

Leu Ala Pro Arg Arg Cys Gln His Thr Ser Pro Ala Ser Ala Gln Cys
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           20                  25                  30

Lys Gln Asp Lys Ala Cys Arg Phe Leu Ala Ala Gln Lys Gly Ala Tyr
        35                  40                  45

Pro Ile Ile Phe Thr Ala Trp Lys Leu Ala Thr Ala Gly Asp Gln Gly
    50                  55                  60

Leu Leu Leu Gln Ser Leu Asn Ala Leu Ser Val Leu Thr Asp Gly Gln
65                  70                  75                  80

Pro Asp Leu Leu Asp Ala Gln Gly Leu Gln Leu Leu Val Ala Thr Leu
                85                  90                  95

Thr Gln Asn Ala Asp Glu Ala Asp Leu Thr Cys Ser Gly Ile Arg Cys
            100                 105                 110

Val Arg His Ala Cys Leu Lys His Glu Gln Asn Arg Gln Asp Leu Val
        115                 120                 125

Lys Ala Gly Val Leu Pro Leu Leu Thr Gly Ala Ile Thr His His Gly
    130                 135                 140

His His Thr Asp Val Val Arg Glu Ala Cys Trp Ala Leu Arg Val Met
145                 150                 155                 160

Thr Phe Asp Asp Asp Ile Arg Val Pro Phe Gly His Ala His Asn His
                165                 170                 175

Ala Lys Met Ile Val Gln Glu Asn Lys Gly Leu Lys Val Leu Ile Glu
            180                 185                 190

Ala Thr Lys Ala Phe Leu Asp Asn Pro Gly Ile Leu Ser Glu Leu Cys
        195                 200                 205

Gly Thr Leu Ser Arg Leu Ala Ile Arg Asn Glu Phe Cys Gln Glu Val
    210                 215                 220

Val Asp Leu Gly Gly Leu Ser Ile Leu Val Ser Leu Leu Ala Asp Cys
225                 230                 235                 240

Asn Asp His Gln Met Arg Asp Gln Ser Gly Val Gln Glu Leu Val Lys
                245                 250                 255

Gln Val Leu Ser Thr Leu Arg Ala Ile Ala Gly Asn Asp Asp Val Lys
            260                 265                 270

Asp Ala Ile Val Arg Ala Gly Gly Thr Glu Ser Ile Val Ala Ala Met
        275                 280                 285

Thr Gln His Leu Thr Ser Pro Gln Val Cys Glu Gln Ser Cys Ala Ala
    290                 295                 300

Leu Cys Phe Leu Ala Leu Arg Lys Pro Asp Asn Ser Arg Ile Ile Val
305                 310                 315                 320

Glu Gly Gly Gly Ala Val Ala Ala Leu Gln Ala Met Lys Ala His Pro
                325                 330                 335

Gln Lys Ala Gly Val Gln Lys Gln Ala Cys Met Leu Ile Arg Asn Leu
            340                 345                 350

Val Ala His Arg Pro Ser Arg Ser Pro Ser Trp Thr Trp Gly Leu Arg
        355                 360                 365

His Ser Ser Cys Arg Pro Asp Leu Pro Thr Val Thr Val Arg Thr Trp
    370                 375                 380

Pro Arg Pro Pro Cys Gly Thr Trp Val Val Met Ser Ser Ser Glu Ser
385                 390                 395                 400

Cys Gly Gln Ala Arg Gly Ala Thr Trp Arg His Asp Pro Arg Pro Ser
                405                 410                 415

Leu Val Thr Leu Gly Glu Ser Cys Asp Ser Gly Met Gly Val Asp Pro
            420                 425                 430

Cys Pro Pro Leu Ser Pro Ile Ser Ser Val Pro Phe Thr Met Arg Ser
        435                 440                 445
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Val Phe Trp Gln Ala Leu Gly Lys Gly Ser Gly Glu Gly Gly Ala Leu
    450                 455                 460


<210> SEQ ID NO 82
<211> LENGTH: 501
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 82

Met Ser Glu Arg Cys Cys Ser Arg Tyr Ser Ser Gly Ala Ser Ile Gly
1               5                   10                  15

Cys Thr Pro Thr Ser Thr Gln Ala Lys Met Val Ser Lys Arg Ile Ala
            20                  25                  30

Gln Glu Thr Phe Asp Ala Ala Val Arg Glu Asn Ile Glu Glu Phe Ala
        35                  40                  45

Met Gly Pro Glu Glu Ala Val Lys Glu Ala Val Glu Gln Phe Glu Ser
    50                  55                  60

Gln Gly Val Asp Leu Ser Asn Ile Val Lys Thr Ala Pro Lys Val Ser
65                  70                  75                  80

Ala Asp Gly Ser Gln Glu Pro Thr His Asp Ile Leu Gln Met Leu Ser
                85                  90                  95

Asp Leu Gln Glu Ser Val Ala Ser Ser Arg Pro Gln Glu Val Ser Ala
            100                 105                 110

Tyr Leu Thr Arg Phe Cys Asp Gln Cys Lys Gln Asp Lys Ala Cys Arg
        115                 120                 125

Phe Leu Ala Ala Gln Lys Gly Ala Tyr Pro Ile Ile Phe Thr Ala Trp
    130                 135                 140

Lys Leu Ala Thr Ala Gly Asp Gln Gly Leu Leu Leu Gln Ser Leu Asn
145                 150                 155                 160

Ala Leu Ser Val Leu Thr Asp Gly Gln Pro Asp Leu Leu Asp Ala Gln
                165                 170                 175

Gly Leu Gln Leu Leu Val Ala Thr Leu Thr Gln Asn Ala Asp Glu Ala
            180                 185                 190

Asp Leu Thr Cys Ser Gly Ile Arg Cys Val Arg His Ala Cys Leu Lys
        195                 200                 205

His Glu Gln Asn Arg Gln Asp Leu Val Lys Ala Gly Val Leu Pro Leu
    210                 215                 220

Leu Thr Gly Ala Ile Thr His His Gly His His Thr Asp Val Val Arg
225                 230                 235                 240

Glu Ala Cys Trp Ala Leu Arg Val Met Thr Phe Asp Asp Asp Ile Arg
                245                 250                 255

Val Pro Phe Gly His Ala His Asn His Ala Lys Met Ile Val Gln Glu
            260                 265                 270

Asn Lys Gly Leu Lys Val Leu Ile Glu Ala Thr Lys Ala Phe Leu Asp
        275                 280                 285

Asn Pro Gly Ile Leu Ser Glu Leu Cys Gly Thr Leu Ser Arg Leu Ala
    290                 295                 300

Ile Arg Asn Glu Phe Cys Gln Glu Val Val Asp Leu Gly Gly Leu Ser
305                 310                 315                 320

Ile Leu Val Ser Leu Leu Ala Asp Cys Asn Asp His Gln Met Arg Asp
                325                 330                 335

Gln Ser Gly Val Gln Glu Leu Val Lys Gln Val Leu Ser Thr Leu Arg
            340                 345                 350

Ala Ile Ala Gly Asn Asp Asp Val Lys Asp Ala Ile Val Arg Ala Gly
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        355                 360                 365

Gly Thr Glu Ser Ile Val Ala Ala Met Thr Gln His Leu Thr Ser Pro
    370                 375                 380

Gln Val Cys Glu Gln Ser Cys Ala Ala Leu Cys Phe Leu Ala Leu Arg
385                 390                 395                 400

Lys Pro Asp Asn Ser Arg Ile Ile Val Glu Gly Gly Gly Ala Val Ala
                405                 410                 415

Ala Leu Gln Ala Met Lys Ala His Pro Gln Lys Ala Gly Val Gln Lys
            420                 425                 430

Gln Ala Cys Met Leu Ile Arg Asn Leu Val Ala His Gly Gln Ala Phe
        435                 440                 445

Ser Lys Pro Ile Leu Asp Leu Gly Ala Glu Ala Leu Ile Met Gln Ala
    450                 455                 460

Arg Ser Ala His Arg Asp Cys Glu Asp Val Ala Lys Ala Ala Leu Arg
465                 470                 475                 480

Asp Leu Gly Cys His Val Glu Leu Arg Glu Leu Trp Thr Gly Gln Arg
                485                 490                 495

Gly Asn Leu Ala Pro
            500


<210> SEQ ID NO 83
<211> LENGTH: 476
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 83

Met Val Ser Lys Arg Ile Ala Gln Glu Thr Phe Asp Ala Ala Val Arg
1               5                   10                  15

Glu Asn Ile Glu Glu Phe Ala Met Gly Pro Glu Glu Ala Val Lys Glu
            20                  25                  30

Ala Val Glu Gln Phe Glu Ser Gln Gly Val Asp Leu Ser Asn Ile Val
        35                  40                  45

Lys Thr Ala Pro Lys Val Ser Ala Asp Gly Ser Gln Glu Pro Thr His
    50                  55                  60

Asp Ile Leu Gln Met Leu Ser Asp Leu Gln Glu Ser Val Ala Ser Ser
65                  70                  75                  80

Arg Pro Gln Glu Val Ser Ala Tyr Leu Thr Arg Phe Cys Asp Gln Cys
                85                  90                  95

Lys Gln Asp Lys Ala Cys Arg Phe Leu Ala Ala Gln Lys Gly Ala Tyr
            100                 105                 110

Pro Ile Ile Phe Thr Ala Trp Lys Leu Ala Thr Ala Gly Asp Gln Gly
        115                 120                 125

Leu Leu Leu Gln Ser Leu Asn Ala Leu Ser Val Leu Thr Asp Gly Gln
    130                 135                 140

Pro Asp Leu Leu Asp Ala Gln Gly Leu Gln Leu Leu Val Ala Thr Leu
145                 150                 155                 160

Thr Gln Asn Ala Asp Glu Ala Asp Leu Thr Cys Ser Gly Ile Arg Cys
                165                 170                 175

Val Arg His Ala Cys Leu Lys His Glu Gln Asn Arg Gln Asp Leu Val
            180                 185                 190

Lys Ala Gly Val Leu Pro Leu Leu Thr Gly Ala Ile Thr His His Gly
        195                 200                 205

His His Thr Asp Val Val Arg Glu Ala Cys Trp Ala Leu Arg Val Met
    210                 215                 220
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Thr Phe Asp Asp Asp Ile Arg Val Pro Phe Gly His Ala His Asn His
225                 230                 235                 240

Ala Lys Met Ile Val Gln Glu Asn Lys Gly Leu Lys Val Leu Ile Glu
                245                 250                 255

Ala Thr Lys Ala Phe Leu Asp Asn Pro Gly Ile Leu Ser Glu Leu Cys
            260                 265                 270

Gly Thr Leu Ser Arg Leu Ala Ile Arg Asn Glu Phe Cys Gln Glu Val
        275                 280                 285

Val Asp Leu Gly Gly Leu Ser Ile Leu Val Ser Leu Leu Ala Asp Cys
    290                 295                 300

Asn Asp His Gln Met Arg Asp Gln Ser Gly Val Gln Glu Leu Val Lys
305                 310                 315                 320

Gln Val Leu Ser Thr Leu Arg Ala Ile Ala Gly Asn Asp Asp Val Lys
                325                 330                 335

Asp Ala Ile Val Arg Ala Gly Gly Thr Glu Ser Ile Val Ala Ala Met
            340                 345                 350

Thr Gln His Leu Thr Ser Pro Gln Val Cys Glu Gln Ser Cys Ala Ala
        355                 360                 365

Leu Cys Phe Leu Ala Leu Arg Lys Pro Asp Asn Ser Arg Ile Ile Val
    370                 375                 380

Glu Gly Gly Gly Ala Val Ala Ala Leu Gln Ala Met Lys Ala His Pro
385                 390                 395                 400

Gln Lys Ala Gly Val Gln Lys Gln Ala Cys Met Leu Ile Arg Asn Leu
                405                 410                 415

Val Ala His Gly Gln Ala Phe Ser Lys Pro Ile Leu Asp Leu Gly Ala
            420                 425                 430

Glu Ala Leu Ile Met Gln Ala Arg Ser Ala His Arg Asp Cys Glu Asp
        435                 440                 445

Val Ala Lys Ala Ala Leu Arg Asp Leu Gly Cys His Val Glu Leu Arg
    450                 455                 460

Glu Leu Trp Thr Gly Gln Arg Gly Asn Leu Ala Pro
465                 470                 475


<210> SEQ ID NO 84
<211> LENGTH: 476
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 84

Met Val Ser Lys Arg Ile Ala Gln Glu Thr Phe Asp Ala Ala Val Arg
1               5                   10                  15

Glu Asn Ile Glu Glu Phe Ala Met Gly Pro Glu Glu Ala Val Lys Glu
            20                  25                  30

Ala Val Glu Gln Phe Glu Ser Gln Gly Val Asp Leu Ser Asn Ile Val
        35                  40                  45

Lys Thr Ala Pro Lys Val Ser Ala Asp Gly Ser Gln Glu Pro Thr His
    50                  55                  60

Asp Ile Leu Gln Met Leu Ser Asp Leu Gln Glu Ser Val Ala Ser Ser
65                  70                  75                  80

Arg Pro Gln Glu Val Ser Ala Tyr Leu Thr Arg Phe Cys Asp Gln Cys
                85                  90                  95

Lys Gln Asp Lys Ala Cys Arg Phe Leu Ala Ala Gln Lys Gly Ala Tyr
            100                 105                 110

Pro Ile Ile Phe Thr Ala Trp Lys Leu Ala Thr Ala Gly Asp Gln Gly
        115                 120                 125
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Leu Leu Leu Gln Ser Leu Asn Ala Leu Ser Val Leu Thr Asp Gly Gln
    130                 135                 140

Pro Asp Leu Leu Asp Ala Gln Gly Leu Gln Leu Leu Val Ala Thr Leu
145                 150                 155                 160

Thr Gln Asn Ala Asp Glu Ala Asp Leu Thr Cys Ser Gly Ile Arg Cys
                165                 170                 175

Val Arg His Ala Cys Leu Lys His Glu Gln Asn Arg Gln Asp Leu Val
            180                 185                 190

Lys Ala Gly Val Leu Pro Leu Leu Thr Gly Ala Ile Thr His His Gly
        195                 200                 205

His His Thr Asp Val Val Arg Glu Ala Cys Trp Ala Leu Arg Val Met
    210                 215                 220

Thr Phe Asp Asp Asp Ile Arg Val Pro Phe Gly His Ala His Asn His
225                 230                 235                 240

Ala Lys Met Ile Val Gln Glu Asn Lys Gly Leu Lys Val Leu Ile Glu
                245                 250                 255

Ala Thr Lys Ala Phe Leu Asp Asn Pro Gly Ile Leu Ser Glu Leu Cys
            260                 265                 270

Gly Thr Leu Ser Arg Leu Ala Ile Arg Asn Glu Phe Cys Gln Glu Val
        275                 280                 285

Val Asp Leu Gly Gly Leu Ser Ile Leu Val Ser Leu Leu Ala Asp Cys
    290                 295                 300

Asn Asp His Gln Met Arg Asp Gln Ser Gly Val Gln Glu Leu Val Lys
305                 310                 315                 320

Gln Val Leu Ser Thr Leu Arg Ala Ile Ala Gly Asn Asp Asp Val Lys
                325                 330                 335

Asp Ala Ile Val Arg Ala Gly Gly Thr Glu Ser Ile Val Ala Ala Met
            340                 345                 350

Thr Gln His Leu Thr Ser Pro Gln Val Cys Glu Gln Ser Cys Ala Ala
        355                 360                 365

Leu Cys Phe Leu Ala Leu Arg Lys Pro Asp Asn Ser Arg Ile Ile Val
    370                 375                 380

Glu Gly Gly Gly Ala Val Ala Ala Leu Gln Ala Met Lys Ala His Pro
385                 390                 395                 400

Gln Lys Ala Gly Val Gln Lys Gln Ala Cys Met Leu Ile Arg Asn Leu
                405                 410                 415

Val Ala His Gly Gln Ala Phe Ser Lys Pro Ile Leu Asp Leu Gly Ala
            420                 425                 430

Glu Ala Leu Ile Met Gln Ala Arg Ser Ala His Arg Asp Cys Glu Asp
        435                 440                 445

Val Ala Lys Ala Ala Leu Arg Asp Leu Gly Cys His Val Glu Leu Arg
    450                 455                 460

Glu Leu Trp Thr Gly Gln Arg Gly Asn Leu Ala Pro
465                 470                 475


<210> SEQ ID NO 85
<211> LENGTH: 590
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 85

Met Ala Gly Ala Val Pro Gly Ala Ile Met Asp Glu Asp Tyr Tyr Gly
1               5                   10                  15

Ser Ala Ala Glu Trp Gly Asp Glu Ala Asp Gly Gly Gln Gln Glu Asp
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           20                  25                  30

Asp Ser Gly Glu Gly Glu Asp Asp Ala Glu Val Gln Gln Glu Cys Leu
        35                  40                  45

His Lys Phe Ser Thr Arg Asp Tyr Ile Met Glu Pro Ser Ile Phe Asn
    50                  55                  60

Thr Leu Lys Arg Tyr Phe Gln Ala Gly Gly Ser Pro Glu Asn Val Ile
65                  70                  75                  80

Gln Leu Leu Ser Glu Asn Tyr Thr Ala Val Ala Gln Thr Val Asn Leu
                85                  90                  95

Leu Ala Glu Trp Leu Ile Gln Thr Gly Val Glu Pro Val Gln Val Gln
            100                 105                 110

Glu Thr Val Glu Asn His Leu Lys Ser Leu Leu Ile Lys His Phe Asp
        115                 120                 125

Pro Arg Lys Ala Asp Ser Ile Phe Thr Glu Glu Gly Glu Thr Pro Ala
    130                 135                 140

Trp Leu Glu Gln Met Ile Ala His Thr Thr Trp Arg Asp Leu Phe Tyr
145                 150                 155                 160

Lys Leu Ala Glu Ala His Pro Asp Cys Leu Met Leu Asn Phe Thr Val
                165                 170                 175

Lys Leu Ile Ser Asp Ala Gly Tyr Gln Gly Glu Ile Thr Ser Val Ser
            180                 185                 190

Thr Ala Cys Gln Gln Leu Glu Val Phe Ser Arg Val Leu Arg Thr Ser
        195                 200                 205

Leu Ala Thr Ile Leu Asp Gly Gly Glu Glu Asn Leu Glu Lys Asn Leu
    210                 215                 220

Pro Glu Phe Ala Lys Met Val Cys His Gly Glu His Thr Tyr Leu Phe
225                 230                 235                 240

Ala Gln Ala Met Met Ser Val Leu Ala Gln Glu Glu Gln Gly Gly Ser
                245                 250                 255

Ala Val Arg Arg Ile Ala Gln Glu Val Gln Arg Phe Ala Gln Glu Lys
            260                 265                 270

Gly His Asp Ala Ser Gln Ile Thr Leu Ala Leu Gly Thr Ala Ala Ser
        275                 280                 285

Tyr Pro Arg Ala Cys Gln Ala Leu Gly Ala Met Leu Ser Lys Gly Ala
    290                 295                 300

Leu Asn Pro Ala Asp Ile Thr Val Leu Phe Lys Met Phe Thr Ser Met
305                 310                 315                 320

Asp Pro Pro Pro Val Glu Leu Ile Arg Val Pro Ala Phe Leu Asp Leu
                325                 330                 335

Phe Met Gln Ser Leu Phe Lys Pro Gly Ala Arg Ile Asn Gln Asp His
            340                 345                 350

Lys His Lys Tyr Ile His Ile Leu Ala Tyr Ala Ala Ser Val Val Glu
        355                 360                 365

Thr Trp Lys Lys Asn Lys Arg Val Ser Ile Asn Lys Asp Glu Leu Lys
    370                 375                 380

Ser Thr Ser Lys Ala Val Glu Thr Val His Asn Leu Cys Cys Asn Glu
385                 390                 395                 400

Asn Lys Gly Ala Ser Glu Leu Val Ala Glu Leu Ser Thr Leu Tyr Gln
                405                 410                 415

Cys Ile Arg Phe Pro Val Val Ala Met Gly Val Leu Lys Trp Val Asp
            420                 425                 430

Trp Thr Val Ser Glu Pro Arg Tyr Phe Gln Leu Gln Thr Asp His Thr
        435                 440                 445
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Pro Val His Leu Ala Leu Leu Asp Glu Ile Ser Thr Cys His Gln Leu
    450                 455                 460

Leu His Pro Gln Val Leu Gln Leu Leu Val Lys Leu Phe Glu Thr Glu
465                 470                 475                 480

His Ser Gln Leu Asp Val Met Glu Gln Leu Glu Leu Lys Lys Thr Leu
                485                 490                 495

Leu Asp Arg Met Val His Leu Leu Ser Arg Gly Tyr Val Leu Pro Val
            500                 505                 510

Val Ser Tyr Ile Arg Lys Cys Leu Glu Lys Leu Asp Thr Asp Ile Ser
        515                 520                 525

Leu Ile Arg Tyr Phe Val Thr Glu Val Leu Asp Val Ile Ala Pro Pro
    530                 535                 540

Tyr Thr Ser Asp Phe Val Gln Leu Phe Leu Pro Ile Leu Glu Asn Asp
545                 550                 555                 560

Ser Ile Ala Gly Thr Ile Lys Thr Glu Gly Glu His Asp Pro Val Thr
                565                 570                 575

Glu Phe Ile Ala His Cys Lys Ser Asn Phe Ile Met Val Asn
            580                 585                 590


<210> SEQ ID NO 86
<211> LENGTH: 250
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 86

Met Ala Met Leu Arg Val Gln Pro Glu Ala Gln Ala Lys Val Asp Val
1               5                   10                  15

Phe Arg Glu Asp Leu Cys Thr Lys Thr Glu Asn Leu Leu Gly Ser Tyr
            20                  25                  30

Phe Pro Lys Lys Ile Ser Glu Leu Asp Ala Phe Leu Lys Glu Pro Ala
        35                  40                  45

Leu Asn Glu Ala Asn Leu Ser Asn Leu Lys Ala Pro Leu Asp Ile Pro
    50                  55                  60

Val Pro Asp Pro Val Lys Glu Lys Glu Lys Glu Glu Arg Lys Lys Gln
65                  70                  75                  80

Gln Glu Lys Glu Asp Lys Asp Glu Lys Lys Lys Gly Glu Asp Glu Asp
                85                  90                  95

Lys Gly Pro Pro Cys Gly Pro Val Asn Cys Asn Glu Lys Ile Val Val
            100                 105                 110

Leu Leu Gln Arg Leu Lys Pro Glu Ile Lys Asp Val Ile Glu Gln Leu
        115                 120                 125

Asn Leu Val Thr Thr Trp Leu Gln Leu Gln Ile Pro Arg Ile Glu Asp
    130                 135                 140

Gly Asn Asn Phe Gly Val Ala Val Gln Glu Lys Val Phe Glu Leu Met
145                 150                 155                 160

Thr Ser Leu His Thr Lys Leu Glu Gly Phe His Thr Gln Ile Ser Lys
                165                 170                 175

Tyr Phe Ser Glu Arg Gly Asp Ala Val Thr Lys Ala Ala Lys Gln Pro
            180                 185                 190

His Val Gly Asp Tyr Arg Gln Leu Val His Glu Leu Asp Glu Ala Glu
        195                 200                 205

Tyr Arg Asp Ile Arg Leu Met Val Met Glu Ile Arg Asn Ala Tyr Val
    210                 215                 220

Arg Arg Gln Gly Gln Gly Arg Gly Gly Gln Arg Gln Leu Ser Gln Ala
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225                 230                 235                 240

Thr His Ser Leu Thr Leu Gln Ala Arg Gly
                245                 250


<210> SEQ ID NO 87
<211> LENGTH: 249
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 87

Met Ala Met Leu Arg Val Gln Pro Glu Ala Gln Ala Lys Val Asp Val
1               5                   10                  15

Phe Arg Glu Asp Leu Cys Thr Lys Thr Glu Asn Leu Leu Gly Ser Tyr
            20                  25                  30

Phe Pro Lys Lys Ile Ser Glu Leu Asp Ala Phe Leu Lys Glu Pro Ala
        35                  40                  45

Leu Asn Glu Ala Asn Leu Ser Asn Leu Lys Ala Pro Leu Asp Ile Pro
    50                  55                  60

Val Pro Asp Pro Val Lys Glu Lys Glu Lys Glu Glu Arg Lys Lys Gln
65                  70                  75                  80

Gln Glu Lys Glu Asp Lys Asp Glu Lys Lys Lys Gly Glu Asp Glu Asp
                85                  90                  95

Lys Gly Pro Pro Cys Gly Pro Val Asn Cys Asn Glu Lys Ile Val Val
            100                 105                 110

Leu Leu Gln Arg Leu Lys Pro Glu Ile Lys Asp Val Ile Glu Gln Leu
        115                 120                 125

Asn Leu Val Thr Thr Trp Leu Gln Leu Gln Ile Pro Arg Ile Glu Asp
    130                 135                 140

Gly Asn Asn Phe Gly Val Ala Val Gln Glu Lys Val Phe Glu Leu Met
145                 150                 155                 160

Thr Ser Leu His Thr Lys Leu Glu Gly Phe His Thr Gln Ile Ser Lys
                165                 170                 175

Tyr Phe Ser Glu Arg Gly Asp Ala Val Thr Lys Ala Ala Lys Gln Pro
            180                 185                 190

His Val Gly Asp Tyr Arg Gln Leu Val His Glu Leu Asp Glu Ala Glu
        195                 200                 205

Tyr Arg Asp Ile Arg Leu Met Val Met Glu Ile Arg Asn Ala Tyr Ala
    210                 215                 220

Val Leu Tyr Asp Ile Ile Leu Lys Asn Phe Glu Lys Leu Lys Lys Pro
225                 230                 235                 240

Arg Gly Glu Thr Lys Gly Met Ile Tyr
                245


<210> SEQ ID NO 88
<211> LENGTH: 558
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 88

Met Glu Leu Arg Ala Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala Ala
1               5                   10                  15

Leu Val Ala Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys
            20                  25                  30

Gly Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp
        35                  40                  45

Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln
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    50                  55                  60

Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn Arg
65                  70                  75                  80

Ser His Ala Glu Leu Glu Thr Ala Leu Arg Asp Ser Ser Arg Val Leu
                85                  90                  95

Gln Ala Met Leu Ala Thr Gln Leu Arg Ser Phe Asp Asp His Phe Gln
            100                 105                 110

His Leu Leu Asn Asp Ser Glu Arg Thr Leu Gln Ala Thr Phe Pro Gly
        115                 120                 125

Ala Phe Gly Glu Leu Tyr Thr Gln Asn Ala Arg Ala Phe Arg Asp Leu
    130                 135                 140

Tyr Ser Glu Leu Arg Leu Tyr Tyr Arg Gly Ala Asn Leu His Leu Glu
145                 150                 155                 160

Glu Thr Leu Ala Glu Phe Trp Ala Arg Leu Leu Glu Arg Leu Phe Lys
                165                 170                 175

Gln Leu His Pro Gln Leu Leu Leu Pro Asp Asp Tyr Leu Asp Cys Leu
            180                 185                 190

Gly Lys Gln Ala Glu Ala Leu Arg Pro Phe Gly Glu Ala Pro Arg Glu
        195                 200                 205

Leu Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala Arg Ser Phe Val
    210                 215                 220

Gln Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val
225                 230                 235                 240

Pro Leu Gly Pro Glu Cys Ser Arg Ala Val Met Lys Leu Val Tyr Cys
                245                 250                 255

Ala His Cys Leu Gly Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys
            260                 265                 270

Arg Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala
        275                 280                 285

Glu Trp Arg Asn Leu Leu Asp Ser Met Val Leu Ile Thr Asp Lys Phe
    290                 295                 300

Trp Gly Thr Ser Gly Val Glu Ser Val Ile Gly Ser Val His Thr Trp
305                 310                 315                 320

Leu Ala Glu Ala Ile Asn Ala Leu Gln Asp Asn Arg Asp Thr Leu Thr
                325                 330                 335

Ala Lys Val Ile Gln Gly Cys Gly Asn Pro Lys Val Asn Pro Gln Gly
            340                 345                 350

Pro Gly Pro Glu Glu Lys Arg Arg Arg Gly Lys Leu Ala Pro Arg Glu
        355                 360                 365

Arg Pro Pro Ser Gly Thr Leu Glu Lys Leu Val Ser Glu Ala Lys Ala
    370                 375                 380

Gln Leu Arg Asp Val Gln Asp Phe Trp Ile Ser Leu Pro Gly Thr Leu
385                 390                 395                 400

Cys Ser Glu Lys Met Ala Leu Ser Thr Ala Ser Asp Asp Arg Cys Trp
                405                 410                 415

Asn Gly Met Ala Arg Gly Arg Tyr Leu Pro Glu Val Met Gly Asp Gly
            420                 425                 430

Leu Ala Asn Gln Ile Asn Asn Pro Glu Val Glu Val Asp Ile Thr Lys
        435                 440                 445

Pro Asp Met Thr Ile Arg Gln Gln Ile Met Gln Leu Lys Ile Met Thr
    450                 455                 460

Asn Arg Leu Arg Ser Ala Tyr Asn Gly Asn Asp Val Asp Phe Gln Asp
465                 470                 475                 480
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Ala Ser Asp Asp Gly Ser Gly Ser Gly Ser Gly Asp Gly Cys Leu Asp
                485                 490                 495

Asp Leu Cys Ser Arg Lys Val Ser Arg Lys Ser Ser Ser Ser Arg Thr
            500                 505                 510

Pro Leu Thr His Ala Leu Pro Gly Leu Ser Glu Gln Glu Gly Gln Lys
        515                 520                 525

Thr Ser Ala Ala Ser Cys Pro Gln Pro Pro Thr Phe Leu Leu Pro Leu
    530                 535                 540

Leu Leu Phe Leu Ala Leu Thr Val Ala Arg Pro Arg Trp Arg
545                 550                 555


<210> SEQ ID NO 89
<211> LENGTH: 1214
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 89

Met Ala Ser Cys Ala Ser Ile Asp Ile Glu Asp Ala Thr Gln His Leu
1               5                   10                  15

Arg Asp Ile Leu Lys Leu Asp Arg Pro Ala Gly Gly Pro Ser Ala Glu
            20                  25                  30

Ser Pro Arg Pro Ser Ser Ala Tyr Asn Gly Asp Leu Asn Gly Leu Leu
        35                  40                  45

Val Pro Asp Pro Leu Cys Ser Gly Asp Ser Thr Ser Ala Asn Lys Thr
    50                  55                  60

Gly Leu Arg Thr Met Pro Pro Ile Asn Leu Gln Glu Lys Gln Val Ile
65                  70                  75                  80

Cys Leu Ser Gly Asp Asp Ser Ser Thr Cys Ile Gly Ile Leu Ala Lys
                85                  90                  95

Glu Val Glu Ile Val Ala Ser Ser Asp Ser Ser Ile Ser Ser Lys Ala
            100                 105                 110

Arg Gly Ser Asn Lys Val Lys Ile Gln Pro Val Ala Lys Tyr Asp Trp
        115                 120                 125

Glu Gln Lys Tyr Tyr Tyr Gly Asn Leu Ile Ala Val Ser Asn Ser Phe
    130                 135                 140

Leu Ala Tyr Ala Ile Arg Ala Ala Asn Asn Gly Ser Ala Met Val Arg
145                 150                 155                 160

Val Ile Ser Val Ser Thr Ser Glu Arg Thr Leu Leu Lys Gly Phe Thr
                165                 170                 175

Gly Ser Val Ala Asp Leu Ala Phe Ala His Leu Asn Ser Pro Gln Leu
            180                 185                 190

Ala Cys Leu Asp Glu Ala Gly Asn Leu Phe Val Trp Arg Leu Ala Leu
        195                 200                 205

Val Asn Gly Lys Ile Gln Glu Glu Ile Leu Val His Ile Arg Gln Pro
    210                 215                 220

Glu Gly Thr Pro Leu Asn His Phe Arg Arg Ile Ile Trp Cys Pro Phe
225                 230                 235                 240

Ile Pro Glu Glu Ser Glu Asp Cys Cys Glu Glu Ser Ser Pro Thr Val
                245                 250                 255

Ala Leu Leu His Glu Asp Arg Ala Glu Val Trp Asp Leu Asp Met Leu
            260                 265                 270

Arg Ser Ser His Ser Thr Trp Pro Val Asp Val Ser Gln Ile Lys Gln
        275                 280                 285

Gly Phe Ile Val Val Lys Gly His Ser Thr Cys Leu Ser Glu Gly Ala
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    290                 295                 300

Leu Ser Pro Asp Gly Thr Val Leu Ala Thr Ala Ser His Asp Gly Tyr
305                 310                 315                 320

Val Lys Phe Trp Gln Ile Tyr Ile Glu Gly Gln Asp Glu Pro Arg Cys
                325                 330                 335

Leu His Glu Trp Lys Pro His Asp Gly Arg Pro Leu Ser Cys Leu Leu
            340                 345                 350

Phe Cys Asp Asn His Lys Lys Gln Asp Pro Asp Val Pro Phe Trp Arg
        355                 360                 365

Phe Leu Ile Thr Gly Ala Asp Gln Asn Arg Glu Leu Lys Met Trp Cys
    370                 375                 380

Thr Val Ser Trp Thr Cys Leu Gln Thr Ile Arg Phe Ser Pro Asp Ile
385                 390                 395                 400

Phe Ser Ser Val Ser Val Pro Pro Ser Leu Lys Val Cys Leu Asp Leu
                405                 410                 415

Ser Ala Glu Tyr Leu Ile Leu Ser Asp Val Gln Arg Lys Val Leu Tyr
            420                 425                 430

Val Met Glu Leu Leu Gln Asn Gln Glu Glu Gly His Ala Cys Phe Ser
        435                 440                 445

Ser Ile Ser Glu Phe Leu Leu Thr His Pro Val Leu Ser Phe Gly Ile
    450                 455                 460

Gln Val Val Ser Arg Cys Arg Leu Arg His Thr Glu Val Leu Pro Ala
465                 470                 475                 480

Glu Glu Glu Asn Asp Ser Leu Gly Ala Asp Gly Thr His Gly Ala Gly
                485                 490                 495

Ala Met Glu Ser Ala Ala Gly Val Leu Ile Lys Leu Phe Cys Val His
            500                 505                 510

Thr Lys Ala Leu Gln Asp Val Gln Ile Arg Phe Gln Pro Gln Leu Asn
        515                 520                 525

Pro Asp Val Val Ala Pro Leu Pro Thr His Thr Ala His Glu Asp Phe
    530                 535                 540

Thr Phe Gly Glu Ser Arg Pro Glu Leu Gly Ser Glu Gly Leu Gly Ser
545                 550                 555                 560

Ala Ala His Gly Ser Gln Pro Asp Leu Arg Arg Ile Val Glu Leu Pro
                565                 570                 575

Ala Pro Ala Asp Phe Leu Ser Leu Ser Ser Glu Thr Lys Pro Lys Leu
            580                 585                 590

Met Thr Pro Asp Ala Phe Met Thr Pro Ser Ala Ser Leu Gln Gln Ile
        595                 600                 605

Thr Ala Ser Pro Ser Ser Ser Ser Ser Gly Ser Ser Ser Ser Ser Ser
    610                 615                 620

Ser Ser Ser Ser Ser Leu Thr Ala Val Ser Ala Met Ser Ser Thr Ser
625                 630                 635                 640

Ala Val Asp Pro Ser Leu Thr Arg Pro Pro Glu Glu Leu Thr Leu Ser
                645                 650                 655

Pro Lys Leu Gln Leu Asp Gly Ser Leu Thr Met Ser Ser Ser Gly Ser
            660                 665                 670

Leu Gln Ala Ser Pro Arg Gly Leu Leu Pro Gly Leu Leu Pro Ala Pro
        675                 680                 685

Ala Asp Lys Leu Thr Pro Lys Gly Pro Gly Gln Val Pro Thr Ala Thr
    690                 695                 700

Ser Ala Leu Ser Leu Glu Leu Gln Glu Val Glu Pro Leu Gly Leu Pro
705                 710                 715                 720
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Gln Ala Ser Pro Ser Arg Thr Arg Ser Pro Asp Val Ile Ser Ser Ala
               725                 730                 735

Ser Thr Ala Leu Ser Gln Asp Ile Pro Glu Ile Ala Ser Glu Ala Leu
           740                 745                 750

Ser Arg Gly Phe Gly Ser Ser Ala Pro Glu Gly Leu Glu Pro Asp Ser
        755                 760                 765

Met Ala Ser Ala Ala Ser Ala Leu His Leu Leu Ser Pro Arg Pro Arg
    770                 775                 780

Pro Gly Pro Glu Leu Gly Pro Gln Leu Gly Leu Asp Gly Gly Pro Gly
785                 790                 795                 800

Asp Gly Asp Arg His Asn Thr Pro Ser Leu Leu Glu Ala Ala Leu Thr
               805                 810                 815

Gln Glu Ala Ser Thr Pro Asp Ser Gln Val Trp Pro Thr Ala Pro Asp
           820                 825                 830

Ile Thr Arg Glu Thr Cys Ser Thr Leu Ala Glu Ser Pro Arg Asn Gly
        835                 840                 845

Leu Gln Glu Lys His Lys Ser Leu Ala Phe His Arg Pro Pro Tyr His
    850                 855                 860

Leu Leu Gln Gln Arg Asp Ser Gln Asp Ala Ser Ala Glu Gln Ser Asp
865                 870                 875                 880

His Asp Asp Glu Val Ala Ser Leu Ala Ser Ala Ser Gly Gly Phe Gly
               885                 890                 895

Thr Lys Val Pro Ala Pro Arg Leu Pro Ala Lys Asp Trp Lys Thr Lys
           900                 905                 910

Gly Ser Pro Arg Thr Ser Pro Lys Leu Lys Arg Lys Ser Lys Lys Asp
        915                 920                 925

Asp Gly Asp Ala Ala Met Gly Ser Arg Leu Thr Glu His Gln Val Ala
    930                 935                 940

Glu Pro Pro Glu Asp Trp Pro Ala Leu Ile Trp Gln Gln Gln Arg Glu
945                 950                 955                 960

Leu Ala Glu Leu Arg His Ser Gln Glu Glu Leu Leu Gln Arg Leu Cys
               965                 970                 975

Thr Gln Leu Glu Gly Leu Gln Ser Thr Val Thr Gly His Val Glu Arg
           980                 985                 990

Ala Leu Glu Thr Arg His Glu Gln  Glu Gln Arg Arg Leu  Glu Arg Ala
        995                 1000                1005

Leu Ala  Glu Gly Gln Gln Arg  Gly Gly Gln Leu Gln  Glu Gln Leu
    1010                1015                1020

Thr Gln  Gln Leu Ser Gln Ala  Leu Ser Ser Ala Val  Ala Gly Arg
    1025                1030                1035

Leu Glu  Arg Ser Ile Arg Asp  Glu Ile Lys Lys Thr  Val Pro Pro
    1040                1045                1050

Cys Val  Ser Arg Ser Leu Glu  Pro Met Ala Gly Gln  Leu Ser Asn
    1055                1060                1065

Ser Val  Ala Thr Lys Leu Thr  Ala Val Glu Gly Ser  Met Lys Glu
    1070                1075                1080

Asn Ile  Ser Lys Leu Leu Lys  Ser Lys Asn Leu Thr  Asp Ala Ile
    1085                1090                1095

Ala Arg  Ala Ala Ala Asp Thr  Leu Gln Gly Pro Met  Gln Ala Ala
    1100                1105                1110

Tyr Arg  Glu Ala Phe Gln Ser  Val Val Leu Pro Ala  Phe Glu Lys
    1115                1120                1125
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Ser Cys  Gln Ala Met Phe Gln  Gln Ile Asn Asp Ser  Phe Arg Leu
    1130                1135                1140

Gly Thr  Gln Glu Tyr Leu Gln  Gln Leu Glu Ser His  Met Lys Ser
    1145                1150                1155

Arg Lys  Ala Arg Glu Gln Glu  Ala Arg Glu Pro Val  Leu Ala Gln
    1160                1165                1170

Leu Arg  Gly Leu Val Ser Thr  Leu Gln Ser Ala Thr  Glu Gln Met
    1175                1180                1185

Pro Pro  Trp Pro Ala Val Phe  Val Leu Arg Cys Ser  Thr Ser Cys
    1190                1195                1200

Met Trp  Leu Trp Ala Ala Cys  Arg Ser Pro Phe
    1205                1210


<210> SEQ ID NO 90
<211> LENGTH: 1401
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 90

Met Ala Ser Cys Ala Ser Ile Asp Ile Glu Asp Ala Thr Gln His Leu
1               5                   10                  15

Arg Asp Ile Leu Lys Leu Asp Arg Pro Ala Gly Gly Pro Ser Ala Glu
            20                  25                  30

Ser Pro Arg Pro Ser Ser Ala Tyr Asn Gly Asp Leu Asn Gly Leu Leu
        35                  40                  45

Val Pro Asp Pro Leu Cys Ser Gly Asp Ser Thr Ser Ala Asn Lys Thr
    50                  55                  60

Gly Leu Arg Thr Met Pro Pro Ile Asn Leu Gln Glu Lys Gln Val Ile
65                  70                  75                  80

Cys Leu Ser Gly Asp Asp Ser Ser Thr Cys Ile Gly Ile Leu Ala Lys
                85                  90                  95

Glu Val Glu Ile Val Ala Ser Ser Asp Ser Ser Ile Ser Ser Lys Ala
            100                 105                 110

Arg Gly Ser Asn Lys Val Lys Ile Gln Pro Val Ala Lys Tyr Asp Trp
        115                 120                 125

Glu Gln Lys Tyr Tyr Tyr Gly Asn Leu Ile Ala Val Ser Asn Ser Phe
    130                 135                 140

Leu Ala Tyr Ala Ile Arg Ala Ala Asn Asn Gly Ser Ala Met Val Arg
145                 150                 155                 160

Val Ile Ser Val Ser Thr Ser Glu Arg Thr Leu Leu Lys Gly Phe Thr
                165                 170                 175

Gly Ser Val Ala Asp Leu Ala Phe Ala His Leu Asn Ser Pro Gln Leu
            180                 185                 190

Ala Cys Leu Asp Glu Ala Gly Asn Leu Phe Val Trp Arg Leu Ala Leu
        195                 200                 205

Val Asn Gly Lys Ile Gln Glu Glu Ile Leu Val His Ile Arg Gln Pro
    210                 215                 220

Glu Gly Thr Pro Leu Asn His Phe Arg Arg Ile Ile Trp Cys Pro Phe
225                 230                 235                 240

Ile Pro Glu Glu Ser Glu Asp Cys Cys Glu Glu Ser Ser Pro Thr Val
                245                 250                 255

Ala Leu Leu His Glu Asp Arg Ala Glu Val Trp Asp Leu Asp Met Leu
            260                 265                 270

Arg Ser Ser His Ser Thr Trp Pro Val Asp Val Ser Gln Ile Lys Gln
        275                 280                 285
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```
Gly Phe Ile Val Val Lys Gly His Ser Thr Cys Leu Ser Glu Gly Ala
    290                 295                 300

Leu Ser Pro Asp Gly Thr Val Leu Ala Thr Ala Ser His Asp Gly Tyr
305                 310                 315                 320

Val Lys Phe Trp Gln Ile Tyr Ile Glu Gly Gln Asp Glu Pro Arg Cys
                325                 330                 335

Leu His Glu Trp Lys Pro His Asp Gly Arg Pro Leu Ser Cys Leu Leu
            340                 345                 350

Phe Cys Asp Asn His Lys Lys Gln Asp Pro Asp Val Pro Phe Trp Arg
        355                 360                 365

Phe Leu Ile Thr Gly Ala Asp Gln Asn Arg Glu Leu Lys Met Trp Cys
    370                 375                 380

Thr Val Ser Trp Thr Cys Leu Gln Thr Ile Arg Phe Ser Pro Asp Ile
385                 390                 395                 400

Phe Ser Ser Val Ser Val Pro Pro Ser Leu Lys Val Cys Leu Asp Leu
                405                 410                 415

Ser Ala Glu Tyr Leu Ile Leu Ser Asp Val Gln Arg Lys Val Leu Tyr
            420                 425                 430

Val Met Glu Leu Leu Gln Asn Gln Glu Glu Gly His Ala Cys Phe Ser
        435                 440                 445

Ser Ile Ser Glu Phe Leu Leu Thr His Pro Val Leu Ser Phe Gly Ile
    450                 455                 460

Gln Val Val Ser Arg Cys Arg Leu Arg His Thr Glu Val Leu Pro Ala
465                 470                 475                 480

Glu Glu Glu Asn Asp Ser Leu Gly Ala Asp Gly Thr His Gly Ala Gly
                485                 490                 495

Ala Met Glu Ser Ala Ala Gly Val Leu Ile Lys Leu Phe Cys Val His
            500                 505                 510

Thr Lys Ala Leu Gln Asp Val Gln Ile Arg Phe Gln Pro Gln Leu Asn
        515                 520                 525

Pro Asp Val Val Ala Pro Leu Pro Thr His Thr Ala His Glu Asp Phe
    530                 535                 540

Thr Phe Gly Glu Ser Arg Pro Glu Leu Gly Ser Glu Gly Leu Gly Ser
545                 550                 555                 560

Ala Ala His Gly Ser Gln Pro Asp Leu Arg Arg Ile Val Glu Leu Pro
                565                 570                 575

Ala Pro Ala Asp Phe Leu Ser Leu Ser Ser Glu Thr Lys Pro Lys Leu
            580                 585                 590

Met Thr Pro Asp Ala Phe Met Thr Pro Ser Ala Ser Leu Gln Gln Ile
        595                 600                 605

Thr Ala Ser Pro Ser Ser Ser Ser Ser Gly Ser Ser Ser Ser Ser Ser
    610                 615                 620

Ser Ser Ser Ser Ser Leu Thr Ala Val Ser Ala Met Ser Ser Thr Ser
625                 630                 635                 640

Ala Val Asp Pro Ser Leu Thr Arg Pro Pro Glu Glu Leu Thr Leu Ser
                645                 650                 655

Pro Lys Leu Gln Leu Asp Gly Ser Leu Thr Met Ser Ser Ser Gly Ser
            660                 665                 670

Leu Gln Ala Ser Pro Arg Gly Leu Leu Pro Gly Leu Leu Pro Ala Pro
        675                 680                 685

Ala Asp Lys Leu Thr Pro Lys Gly Pro Gly Gln Val Pro Thr Ala Thr
    690                 695                 700
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Ser Ala Leu Ser Leu Glu Leu Gln Glu Val Glu Pro Leu Gly Leu Pro
705                 710                 715                 720

Gln Ala Ser Pro Ser Arg Thr Arg Ser Pro Asp Val Ile Ser Ser Ala
                725                 730                 735

Ser Thr Ala Leu Ser Gln Asp Ile Pro Glu Ile Ala Ser Glu Ala Leu
            740                 745                 750

Ser Arg Gly Phe Gly Ser Ser Ala Pro Glu Gly Leu Glu Pro Asp Ser
        755                 760                 765

Met Ala Ser Ala Ala Ser Ala Leu His Leu Leu Ser Pro Arg Pro Arg
    770                 775                 780

Pro Gly Pro Glu Leu Gly Pro Gln Leu Gly Leu Asp Gly Gly Pro Gly
785                 790                 795                 800

Asp Gly Asp Arg His Asn Thr Pro Ser Leu Leu Glu Ala Ala Leu Thr
                805                 810                 815

Gln Glu Ala Ser Thr Pro Asp Ser Gln Val Trp Pro Thr Ala Pro Asp
            820                 825                 830

Ile Thr Arg Glu Thr Cys Ser Thr Leu Ala Glu Ser Pro Arg Asn Gly
        835                 840                 845

Leu Gln Glu Lys His Lys Ser Leu Ala Phe His Arg Pro Pro Tyr His
    850                 855                 860

Leu Leu Gln Gln Arg Asp Ser Gln Asp Ala Ser Ala Glu Gln Ser Asp
865                 870                 875                 880

His Asp Asp Glu Val Ala Ser Leu Ala Ser Ala Ser Gly Gly Phe Gly
                885                 890                 895

Thr Lys Val Pro Ala Pro Arg Leu Pro Ala Lys Asp Trp Lys Thr Lys
            900                 905                 910

Gly Ser Pro Arg Thr Ser Pro Lys Leu Lys Arg Lys Ser Lys Lys Asp
        915                 920                 925

Asp Gly Asp Ala Ala Met Gly Ser Arg Leu Thr Glu His Gln Val Ala
    930                 935                 940

Glu Pro Pro Glu Asp Trp Pro Ala Leu Ile Trp Gln Gln Gln Arg Glu
945                 950                 955                 960

Leu Ala Glu Leu Arg His Ser Gln Glu Glu Leu Leu Gln Arg Leu Cys
                965                 970                 975

Thr Gln Leu Glu Gly Leu Gln Ser Thr Val Thr Gly His Val Glu Arg
            980                 985                 990

Ala Leu Glu Thr Arg His Glu Gln  Glu Gln Arg Arg Leu  Glu Arg Ala
        995                 1000                1005

Leu Ala  Glu Gly Gln Gln Arg  Gly Gly Gln Leu Gln  Glu Gln Leu
    1010                1015                1020

Thr Gln  Gln Leu Ser Gln Ala  Leu Ser Ser Ala Val  Ala Gly Arg
    1025                1030                1035

Leu Glu  Arg Ser Ile Arg Asp  Glu Ile Lys Lys Thr  Val Pro Pro
    1040                1045                1050

Cys Val  Ser Arg Ser Leu Glu  Pro Met Ala Gly Gln  Leu Ser Asn
    1055                1060                1065

Ser Val  Ala Thr Lys Leu Thr  Ala Val Glu Gly Ser  Met Lys Glu
    1070                1075                1080

Asn Ile  Ser Lys Leu Leu Lys  Ser Lys Asn Leu Thr  Asp Ala Ile
    1085                1090                1095

Ala Arg  Ala Ala Ala Asp Thr  Leu Gln Gly Pro Met  Gln Ala Ala
    1100                1105                1110

Tyr Arg  Glu Ala Phe Gln Ser  Val Val Leu Pro Ala  Phe Glu Lys
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    1115                1120                1125

Ser Cys  Gln Ala Met Phe Gln  Gln Ile Asn Asp Ser  Phe Arg Leu
    1130                1135                1140

Gly Thr  Gln Glu Tyr Leu Gln  Gln Leu Glu Ser His  Met Lys Ser
    1145                1150                1155

Arg Lys  Ala Arg Glu Gln Glu  Ala Arg Glu Pro Val  Leu Ala Gln
    1160                1165                1170

Leu Arg  Gly Leu Val Ser Thr  Leu Gln Ser Ala Thr  Glu Gln Met
    1175                1180                1185

Ala Ala  Thr Val Ala Gly Ser  Val Arg Ala Glu Val  Gln His Gln
    1190                1195                1200

Leu His  Val Ala Val Gly Ser  Leu Gln Glu Ser Ile  Leu Ala Gln
    1205                1210                1215

Val Gln  Arg Ile Val Lys Gly  Glu Val Ser Val Ala  Leu Lys Glu
    1220                1225                1230

Gln Gln  Ala Ala Val Thr Ser  Ser Ile Met Gln Ala  Met Arg Ser
    1235                1240                1245

Ala Ala  Gly Thr Pro Val Pro  Ser Ala His Leu Asp  Cys Gln Ala
    1250                1255                1260

Gln Gln  Ala His Ile Leu Gln  Leu Leu Gln Gln Gly  His Leu Asn
    1265                1270                1275

Gln Ala  Phe Gln Gln Ala Leu  Thr Ala Ala Asp Leu  Asn Leu Val
    1280                1285                1290

Leu Tyr  Val Cys Glu Thr Val  Asp Pro Ala Gln Val  Phe Gly Gln
    1295                1300                1305

Pro Pro  Cys Pro Leu Ser Gln  Pro Val Leu Leu Ser  Leu Ile Gln
    1310                1315                1320

Gln Leu  Ala Ser Asp Leu Gly  Thr Arg Thr Asp Leu  Lys Leu Ser
    1325                1330                1335

Tyr Leu  Glu Glu Ala Val Met  His Leu Asp His Ser  Asp Pro Ile
    1340                1345                1350

Thr Arg  Asp His Met Gly Ser  Val Met Ala Gln Val  Arg Gln Lys
    1355                1360                1365

Leu Phe  Gln Phe Leu Gln Ala  Glu Pro His Asn Ser  Leu Gly Lys
    1370                1375                1380

Ala Ala  Arg Arg Leu Ser Leu  Met Leu His Gly Leu  Val Thr Pro
    1385                1390                1395

Ser Leu  Pro
    1400


<210> SEQ ID NO 91
<211> LENGTH: 620
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 91

Met Arg Arg Ser Glu Val Leu Ala Glu Glu Ser Ile Val Cys Leu Gln
1               5                  10                  15

Lys Ala Leu Asn His Leu Arg Glu Ile Trp Glu Leu Ile Gly Ile Pro
            20                  25                  30

Glu Asp Gln Arg Leu Gln Arg Thr Glu Val Val Lys Lys His Ile Lys
        35                  40                  45

Glu Leu Leu Asp Met Met Ile Ala Glu Glu Glu Ser Leu Lys Glu Arg
    50                  55                  60
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Leu Ile Lys Ser Ile Ser Val Cys Gln Lys Glu Leu Asn Thr Leu Cys
65                  70                  75                  80

Ser Glu Leu His Val Glu Pro Phe Gln Glu Glu Gly Glu Thr Thr Ile
                85                  90                  95

Leu Gln Leu Glu Lys Asp Leu Arg Thr Gln Val Glu Leu Met Arg Lys
            100                 105                 110

Gln Lys Lys Glu Arg Lys Gln Glu Leu Lys Leu Leu Gln Glu Gln Asp
        115                 120                 125

Gln Glu Leu Cys Glu Ile Leu Cys Met Pro His Tyr Asp Ile Asp Ser
    130                 135                 140

Ala Ser Val Pro Ser Leu Glu Glu Leu Asn Gln Phe Arg Gln His Val
145                 150                 155                 160

Thr Thr Leu Arg Glu Thr Lys Ala Ser Arg Arg Glu Glu Phe Val Ser
                165                 170                 175

Ile Lys Arg Gln Ile Ile Leu Cys Met Glu Ala Leu Asp His Thr Pro
            180                 185                 190

Asp Thr Ser Phe Glu Arg Asp Val Val Cys Glu Asp Glu Asp Ala Phe
        195                 200                 205

Cys Leu Ser Leu Glu Asn Ile Ala Thr Leu Gln Lys Leu Leu Arg Gln
    210                 215                 220

Leu Glu Met Gln Lys Ser Gln Asn Glu Ala Val Cys Glu Gly Leu Arg
225                 230                 235                 240

Thr Gln Ile Arg Glu Leu Trp Asp Arg Leu Gln Ile Pro Glu Glu Glu
                245                 250                 255

Arg Glu Ala Val Ala Thr Ile Met Ser Gly Ser Lys Ala Lys Val Arg
            260                 265                 270

Lys Ala Leu Gln Leu Glu Val Asp Arg Leu Glu Glu Leu Lys Met Gln
        275                 280                 285

Asn Met Lys Lys Val Ile Glu Ala Ile Arg Val Glu Leu Val Gln Tyr
    290                 295                 300

Trp Asp Gln Cys Phe Tyr Ser Gln Glu Gln Arg Gln Ala Phe Ala Pro
305                 310                 315                 320

Phe Cys Ala Glu Asp Tyr Thr Glu Ser Leu Leu Gln Leu His Asp Ala
                325                 330                 335

Glu Ile Val Arg Leu Lys Asn Tyr Tyr Glu Val His Lys Glu Leu Phe
            340                 345                 350

Glu Gly Val Gln Lys Trp Glu Glu Thr Trp Arg Leu Phe Leu Glu Phe
        355                 360                 365

Glu Arg Lys Ala Ser Asp Pro Asn Arg Phe Thr Asn Arg Gly Gly Asn
    370                 375                 380

Leu Leu Lys Glu Glu Lys Gln Arg Ala Lys Leu Gln Lys Met Leu Pro
385                 390                 395                 400

Lys Leu Glu Glu Glu Leu Lys Ala Arg Ile Glu Leu Trp Glu Gln Glu
                405                 410                 415

His Ser Lys Ala Phe Met Val Asn Gly Gln Lys Phe Met Glu Tyr Val
            420                 425                 430

Ala Glu Gln Trp Glu Met His Arg Leu Glu Lys Glu Arg Ala Lys Gln
        435                 440                 445

Glu Arg Gln Leu Lys Asn Lys Lys Gln Thr Glu Thr Glu Met Leu Tyr
    450                 455                 460

Gly Ser Ala Pro Arg Thr Pro Ser Lys Arg Arg Gly Leu Ala Pro Asn
465                 470                 475                 480

Thr Pro Gly Lys Ala Arg Lys Leu Asn Thr Thr Thr Met Ser Asn Ala
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                485                 490                 495

Thr Ala Asn Ser Ser Ile Arg Pro Ile Phe Gly Gly Thr Val Tyr His
            500                 505                 510

Ser Pro Val Ser Arg Leu Pro Pro Ser Gly Ser Lys Pro Val Ala Ala
        515                 520                 525

Ser Thr Cys Ser Gly Lys Lys Thr Pro Arg Thr Gly Arg His Gly Ala
    530                 535                 540

Asn Lys Glu Asn Leu Glu Leu Asn Gly Ser Ile Leu Ser Gly Gly Tyr
545                 550                 555                 560

Pro Gly Ser Ala Pro Leu Gln Arg Asn Phe Ser Ile Asn Ser Val Ala
                565                 570                 575

Ser Thr Tyr Ser Glu Phe Ala Lys Asp Pro Ser Leu Ser Asp Ser Ser
            580                 585                 590

Thr Val Gly Leu Gln Arg Glu Leu Ser Lys Ala Ser Lys Ser Asp Ala
        595                 600                 605

Thr Ser Gly Ile Leu Asn Ser Thr Asn Ile Gln Ser
    610                 615                 620


<210> SEQ ID NO 92
<211> LENGTH: 674
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 92

Thr Arg Leu Arg Pro Val Ala Arg Phe Glu Ile Leu Arg Gly Ser Thr
1               5                   10                  15

Ala Arg Gly Ala Ala Thr Arg Ser Asp Ile Ala Gly Val Cys Gly Trp
            20                  25                  30

Leu Leu Leu Ser Gly Pro Cys Gly Val Gly Leu Asp Leu Asp Ser Arg
        35                  40                  45

Leu Leu Gly Ala Ser Ala Met Arg Arg Ser Glu Val Leu Ala Glu Glu
    50                  55                  60

Ser Ile Val Cys Leu Gln Lys Ala Leu Asn His Leu Arg Glu Ile Trp
65                  70                  75                  80

Glu Leu Ile Gly Ile Pro Glu Asp Gln Arg Leu Gln Arg Thr Glu Val
                85                  90                  95

Val Lys Lys His Ile Lys Glu Leu Leu Asp Met Met Ile Ala Glu Glu
            100                 105                 110

Glu Ser Leu Lys Glu Arg Leu Ile Lys Ser Ile Ser Val Cys Gln Lys
        115                 120                 125

Glu Leu Asn Thr Leu Cys Ser Glu Leu His Val Glu Pro Phe Gln Glu
    130                 135                 140

Glu Gly Glu Thr Thr Ile Leu Gln Leu Glu Lys Asp Leu Arg Thr Gln
145                 150                 155                 160

Val Glu Leu Met Arg Lys Gln Lys Lys Glu Arg Lys Gln Glu Leu Lys
                165                 170                 175

Leu Leu Gln Glu Gln Asp Gln Glu Leu Cys Glu Ile Leu Cys Met Pro
            180                 185                 190

His Tyr Asp Ile Asp Ser Ala Ser Val Pro Ser Leu Glu Glu Leu Asn
        195                 200                 205

Gln Phe Arg Gln His Val Thr Thr Leu Arg Glu Thr Lys Ala Ser Arg
    210                 215                 220

Arg Glu Glu Phe Val Ser Ile Lys Arg Gln Ile Ile Leu Cys Met Glu
225                 230                 235                 240
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Ala Leu Asp His Thr Pro Asp Thr Ser Phe Glu Arg Asp Val Val Cys
                245                 250                 255

Glu Asp Glu Asp Ala Phe Cys Leu Ser Leu Glu Asn Ile Ala Thr Leu
            260                 265                 270

Gln Lys Leu Leu Arg Gln Leu Glu Met Gln Lys Ser Gln Asn Glu Ala
        275                 280                 285

Val Cys Glu Gly Leu Arg Thr Gln Ile Arg Glu Leu Trp Asp Arg Leu
    290                 295                 300

Gln Ile Pro Glu Glu Glu Arg Glu Ala Val Ala Thr Ile Met Ser Gly
305                 310                 315                 320

Ser Lys Ala Lys Val Arg Lys Ala Leu Gln Leu Glu Val Asp Arg Leu
                325                 330                 335

Glu Glu Leu Lys Met Gln Asn Met Lys Lys Val Ile Glu Ala Ile Arg
            340                 345                 350

Val Glu Leu Val Gln Tyr Trp Asp Gln Cys Phe Tyr Ser Gln Glu Gln
        355                 360                 365

Arg Gln Ala Phe Ala Pro Phe Cys Ala Glu Asp Tyr Thr Glu Ser Leu
    370                 375                 380

Leu Gln Leu His Asp Ala Glu Ile Val Arg Leu Lys Asn Tyr Tyr Glu
385                 390                 395                 400

Val His Lys Glu Leu Phe Glu Gly Val Gln Lys Trp Glu Glu Thr Trp
                405                 410                 415

Arg Leu Phe Leu Glu Phe Glu Arg Lys Ala Ser Asp Pro Asn Arg Phe
            420                 425                 430

Thr Asn Arg Gly Gly Asn Leu Leu Lys Glu Glu Lys Gln Arg Ala Lys
        435                 440                 445

Leu Gln Lys Met Leu Pro Lys Leu Glu Glu Glu Leu Lys Ala Arg Ile
    450                 455                 460

Glu Leu Trp Glu Gln Glu His Ser Lys Ala Phe Met Val Asn Gly Gln
465                 470                 475                 480

Lys Phe Met Glu Tyr Val Ala Glu Gln Trp Glu Met His Arg Leu Glu
                485                 490                 495

Lys Glu Arg Ala Lys Gln Glu Arg Gln Leu Lys Asn Lys Lys Gln Thr
            500                 505                 510

Glu Thr Glu Met Leu Tyr Gly Ser Ala Pro Arg Thr Pro Ser Lys Arg
        515                 520                 525

Arg Gly Leu Ala Pro Asn Thr Pro Gly Lys Ala Arg Lys Leu Asn Thr
    530                 535                 540

Thr Thr Met Ser Asn Ala Thr Ala Asn Ser Ser Ile Arg Pro Ile Phe
545                 550                 555                 560

Gly Gly Thr Val Tyr His Ser Pro Val Ser Arg Leu Pro Pro Ser Gly
                565                 570                 575

Ser Lys Pro Val Ala Ala Ser Thr Cys Ser Gly Lys Lys Thr Pro Arg
            580                 585                 590

Thr Gly Arg His Gly Ala Asn Lys Glu Asn Leu Glu Leu Asn Gly Ser
        595                 600                 605

Ile Leu Ser Gly Gly Tyr Pro Gly Ser Ala Pro Leu Gln Arg Asn Phe
    610                 615                 620

Ser Ile Asn Ser Val Ala Ser Thr Tyr Ser Glu Phe Ala Lys Asp Pro
625                 630                 635                 640

Ser Leu Ser Asp Ser Ser Thr Val Gly Leu Gln Arg Glu Leu Ser Lys
                645                 650                 655

Ala Ser Lys Ser Asp Ala Thr Ser Gly Ile Leu Asn Ser Thr Asn Ile
```

660 665 670

Gln Ser

<210> SEQ ID NO 93
<211> LENGTH: 660
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 93

Thr Arg Leu Arg Pro Val Ala Arg Phe Glu Ile Leu Arg Gly Ser Thr
1 5 10 15

Ala Arg Gly Ala Ala Thr Arg Ser Asp Ile Ala Gly Val Cys Gly Trp
20 25 30

Leu Leu Leu Ser Gly Pro Cys Gly Val Gly Leu Asp Leu Asp Ser Arg
35 40 45

Leu Leu Gly Ala Ser Ala Met Arg Arg Ser Glu Val Leu Ala Glu Glu
50 55 60

Ser Ile Val Cys Leu Gln Lys Ala Leu Asn His Leu Arg Glu Ile Trp
65 70 75 80

Glu Leu Ile Gly Ile Pro Glu Asp Gln Arg Leu Gln Arg Thr Glu Val
85 90 95

Val Lys Lys His Ile Lys Glu Leu Leu Asp Met Met Ile Ala Glu Glu
100 105 110

Glu Ser Leu Lys Glu Arg Leu Ile Lys Ser Ile Ser Val Cys Gln Lys
115 120 125

Glu Leu Asn Thr Leu Cys Ser Glu Leu His Val Glu Pro Phe Gln Glu
130 135 140

Glu Gly Glu Thr Thr Ile Leu Gln Leu Glu Lys Asp Leu Arg Thr Gln
145 150 155 160

Val Glu Leu Met Arg Lys Gln Lys Lys Glu Arg Lys Gln Glu Leu Lys
165 170 175

Leu Leu Gln Glu Gln Asp Gln Glu Leu Cys Glu Ile Leu Cys Met Pro
180 185 190

His Tyr Asp Ile Asp Ser Ala Ser Val Pro Ser Leu Glu Glu Leu Asn
195 200 205

Gln Phe Arg Gln His Val Thr Thr Leu Arg Glu Thr Lys Ala Ser Arg
210 215 220

Arg Glu Glu Phe Val Ser Ile Lys Arg Gln Ile Ile Leu Cys Met Glu
225 230 235 240

Ala Leu Asp His Thr Pro Asp Thr Ser Phe Glu Arg Asp Val Val Cys
245 250 255

Glu Asp Glu Asp Ala Phe Cys Leu Ser Leu Glu Asn Ile Ala Thr Leu
260 265 270

Gln Lys Leu Leu Arg Gln Leu Glu Met Gln Lys Ser Gln Asn Glu Ala
275 280 285

Val Cys Glu Gly Leu Arg Thr Gln Ile Arg Glu Leu Trp Asp Arg Leu
290 295 300

Gln Ile Pro Glu Glu Glu Arg Glu Ala Val Ala Thr Ile Met Ser Gly
305 310 315 320

Ser Lys Ala Lys Val Arg Lys Ala Leu Gln Leu Glu Val Asp Arg Leu
325 330 335

Glu Glu Leu Lys Met Gln Asn Met Lys Lys Val Ile Glu Ala Ile Arg
340 345 350

Val Glu Leu Val Gln Tyr Trp Asp Gln Cys Phe Tyr Ser Gln Glu Gln

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        355                 360                 365

Arg Gln Ala Phe Ala Pro Phe Cys Ala Glu Asp Tyr Thr Glu Ser Leu
    370                 375                 380

Leu Gln Leu His Asp Ala Glu Ile Val Arg Leu Lys Asn Tyr Tyr Glu
385                 390                 395                 400

Val His Lys Glu Leu Phe Glu Gly Val Gln Lys Trp Glu Glu Thr Trp
                405                 410                 415

Arg Leu Phe Leu Glu Phe Glu Arg Lys Ala Ser Asp Pro Asn Arg Phe
            420                 425                 430

Thr Asn Arg Gly Gly Asn Leu Leu Lys Glu Glu Lys Gln Arg Ala Lys
        435                 440                 445

Leu Gln Lys Met Leu Pro Lys Leu Glu Glu Glu Leu Lys Ala Arg Ile
    450                 455                 460

Glu Leu Trp Glu Gln Glu His Ser Lys Ala Phe Met Val Asn Gly Gln
465                 470                 475                 480

Lys Phe Met Glu Tyr Val Ala Glu Gln Trp Glu Met His Arg Leu Glu
                485                 490                 495

Lys Glu Arg Ala Lys Gln Glu Arg Gln Leu Lys Asn Lys Lys Gln Thr
            500                 505                 510

Glu Thr Glu Met Leu Tyr Gly Ser Ala Pro Arg Thr Pro Ser Lys Arg
        515                 520                 525

Arg Gly Leu Ala Pro Asn Thr Pro Gly Lys Ala Arg Lys Leu Asn Thr
    530                 535                 540

Thr Thr Met Ser Asn Ala Thr Ala Asn Ser Ser Ile Arg Pro Ile Phe
545                 550                 555                 560

Gly Gly Thr Val Tyr His Ser Pro Val Ser Arg Leu Pro Pro Ser Gly
                565                 570                 575

Ser Lys Pro Val Ala Ala Ser Thr Cys Ser Gly Lys Lys Thr Pro Arg
            580                 585                 590

Thr Gly Arg His Gly Ala Asn Lys Glu Asn Leu Glu Leu Asn Gly Ser
        595                 600                 605

Ile Leu Ser Gly Gly Tyr Pro Gly Ser Ala Pro Leu Gln Arg Asn Phe
    610                 615                 620

Ser Ile Asn Ser Val Ala Ser Thr Tyr Ser Glu Phe Ala Arg Glu Leu
625                 630                 635                 640

Ser Lys Ala Ser Lys Ser Asp Ala Thr Ser Gly Ile Leu Asn Ser Thr
                645                 650                 655

Asn Ile Gln Ser
            660


<210> SEQ ID NO 94
<211> LENGTH: 417
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 94

Met Thr Thr Gln Leu Gly Pro Ala Leu Val Leu Gly Val Ala Leu Cys
1               5                   10                  15

Leu Gly Cys Gly Gln Pro Leu Pro Gln Val Pro Glu Arg Pro Phe Ser
            20                  25                  30

Val Leu Trp Asn Val Pro Ser Ala His Cys Glu Ala Arg Phe Gly Val
        35                  40                  45

His Leu Pro Leu Asn Ala Leu Gly Ile Ile Ala Asn Arg Gly Gln His
    50                  55                  60
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Phe His Gly Gln Asn Met Thr Ile Phe Tyr Lys Asn Gln Leu Gly Leu
65                  70                  75                  80

Tyr Pro Tyr Phe Gly Pro Arg Gly Thr Ala His Asn Gly Gly Ile Pro
                85                  90                  95

Gln Ala Leu Pro Leu Asp Arg His Leu Ala Leu Ala Ala Tyr Gln Ile
            100                 105                 110

His His Ser Leu Arg Pro Gly Phe Ala Gly Pro Ala Val Leu Asp Trp
        115                 120                 125

Glu Glu Trp Cys Pro Leu Trp Ala Gly Asn Trp Gly Arg Arg Arg Ala
    130                 135                 140

Tyr Gln Ala Ala Ser Trp Ala Trp Ala Gln Gln Val Phe Pro Asp Leu
145                 150                 155                 160

Asp Pro Gln Glu Gln Leu Tyr Lys Ala Tyr Thr Gly Phe Glu Gln Ala
                165                 170                 175

Ala Arg Ala Leu Met Glu Asp Thr Leu Arg Val Ala Gln Ala Leu Arg
            180                 185                 190

Pro His Gly Leu Trp Gly Phe Tyr His Tyr Pro Ala Cys Gly Asn Gly
        195                 200                 205

Trp His Ser Met Ala Ser Asn Tyr Thr Gly Arg Cys His Ala Ala Thr
    210                 215                 220

Leu Ala Arg Asn Thr Gln Leu His Trp Leu Trp Ala Ala Ser Ser Ala
225                 230                 235                 240

Leu Phe Pro Ser Ile Tyr Leu Pro Pro Arg Leu Pro Pro Ala His His
                245                 250                 255

Gln Ala Phe Val Arg His Arg Leu Glu Glu Ala Phe Arg Val Ala Leu
            260                 265                 270

Val Gly His Arg His Pro Leu Pro Val Leu Ala Tyr Val Arg Leu Thr
        275                 280                 285

His Arg Arg Ser Gly Arg Phe Leu Ser Gln Asp Asp Leu Val Gln Ser
    290                 295                 300

Ile Gly Val Ser Ala Ala Leu Gly Ala Ala Gly Val Val Leu Trp Gly
305                 310                 315                 320

Asp Leu Ser Leu Ser Ser Ser Glu Glu Glu Cys Trp His Leu His Asp
                325                 330                 335

Tyr Leu Val Asp Thr Leu Gly Pro Tyr Val Ile Asn Val Thr Arg Ala
            340                 345                 350

Ala Met Ala Cys Ser His Gln Arg Cys His Gly His Gly Arg Cys Ala
        355                 360                 365

Arg Arg Asp Pro Gly Gln Met Glu Ala Phe Leu His Leu Trp Pro Asp
    370                 375                 380

Gly Ser Leu Gly Asp Trp Lys Ser Phe Ser Cys His Cys Tyr Trp Gly
385                 390                 395                 400

Trp Ala Gly Pro Thr Cys Gln Glu Pro Arg Pro Gly Pro Lys Glu Ala
                405                 410                 415

Val


<210> SEQ ID NO 95
<211> LENGTH: 462
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 95

Met Thr Thr Gln Leu Gly Pro Ala Leu Val Leu Gly Val Ala Leu Cys
1               5                   10                  15
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Leu Gly Cys Gly Gln Pro Leu Pro Gln Val Pro Glu Arg Pro Phe Ser
            20                  25                  30

Val Leu Trp Asn Val Pro Ser Ala His Cys Glu Ala Arg Phe Gly Val
        35                  40                  45

His Leu Pro Leu Asn Ala Leu Gly Ile Ile Ala Asn Arg Gly Gln His
    50                  55                  60

Phe His Gly Gln Asn Met Thr Ile Phe Tyr Lys Asn Gln Leu Gly Leu
65                  70                  75                  80

Tyr Pro Tyr Phe Gly Pro Arg Gly Thr Ala His Asn Gly Gly Ile Pro
                85                  90                  95

Gln Ala Leu Pro Leu Asp Arg His Leu Ala Leu Ala Ala Tyr Gln Ile
            100                 105                 110

His His Ser Leu Arg Pro Gly Phe Ala Gly Pro Ala Val Leu Asp Trp
        115                 120                 125

Glu Glu Trp Cys Pro Leu Trp Ala Gly Asn Trp Gly Arg Arg Arg Ala
    130                 135                 140

Tyr Gln Ala Ala Ser Trp Ala Trp Ala Gln Gln Val Phe Pro Asp Leu
145                 150                 155                 160

Asp Pro Gln Glu Gln Leu Tyr Lys Ala Tyr Thr Gly Phe Glu Gln Ala
                165                 170                 175

Ala Arg Ala Leu Met Glu Asp Thr Leu Arg Val Ala Gln Ala Leu Arg
            180                 185                 190

Pro His Gly Leu Trp Gly Phe Tyr His Tyr Pro Ala Cys Gly Asn Gly
        195                 200                 205

Trp His Ser Met Ala Ser Asn Tyr Thr Gly Arg Cys His Ala Ala Thr
    210                 215                 220

Leu Ala Arg Asn Thr Gln Leu His Trp Leu Trp Ala Ala Ser Ser Ala
225                 230                 235                 240

Leu Phe Pro Ser Ile Tyr Leu Pro Pro Arg Leu Pro Pro Ala His His
                245                 250                 255

Gln Ala Phe Val Arg His Arg Leu Glu Glu Ala Phe Arg Val Ala Leu
            260                 265                 270

Val Gly His Arg His Pro Leu Pro Val Leu Ala Tyr Val Arg Leu Thr
        275                 280                 285

His Arg Arg Ser Gly Arg Phe Leu Ser Gln Asp Asp Leu Val Gln Ser
    290                 295                 300

Ile Gly Val Ser Ala Ala Leu Gly Ala Ala Gly Val Val Leu Trp Gly
305                 310                 315                 320

Asp Leu Ser Leu Ser Ser Ser Glu Glu Glu Cys Trp His Leu His Asp
                325                 330                 335

Tyr Leu Val Asp Thr Leu Gly Pro Tyr Val Ile Asn Val Thr Arg Ala
            340                 345                 350

Ala Met Ala Cys Ser His Gln Arg Cys His Gly His Gly Arg Cys Ala
        355                 360                 365

Arg Arg Asp Pro Gly Gln Met Glu Ala Phe Leu His Leu Trp Pro Asp
    370                 375                 380

Gly Ser Leu Gly Asp Trp Lys Ser Phe Ser Cys His Cys Tyr Trp Gly
385                 390                 395                 400

Trp Ala Gly Pro Thr Cys Gln Glu Pro Leu Gly Leu Lys Lys Gln Tyr
                405                 410                 415

Lys Ala Arg Ala Pro Ala Thr Ala Ser Ser Phe Pro Cys Cys His Phe
            420                 425                 430

Ser Ser Pro Gly Thr Thr Leu Ser His Ser Cys Ser Ile Gln Phe Thr
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        435                 440                 445

Val Asn Pro Pro Lys His Thr Pro Arg Phe Pro Trp Asn Pro
    450                 455                 460


<210> SEQ ID NO 96
<211> LENGTH: 387
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 96

Met Thr Thr Gln Leu Gly Pro Ala Leu Val Leu Gly Val Ala Leu Cys
1               5                   10                  15

Leu Gly Cys Gly Gln Pro Leu Pro Gln Val Pro Glu Arg Pro Phe Ser
            20                  25                  30

Val Leu Trp Asn Val Pro Ser Ala His Cys Glu Ala Arg Phe Gly Val
        35                  40                  45

His Leu Pro Leu Asn Ala Leu Gly Ile Ile Ala Asn Arg Gly Gln His
    50                  55                  60

Phe His Gly Gln Asn Met Thr Ile Phe Tyr Lys Asn Gln Leu Gly Leu
65                  70                  75                  80

Tyr Pro Tyr Phe Gly Pro Arg Gly Thr Ala His Asn Gly Gly Ile Pro
                85                  90                  95

Gln Ala Leu Pro Leu Asp Arg His Leu Ala Leu Ala Ala Tyr Gln Ile
            100                 105                 110

His His Ser Leu Arg Pro Gly Phe Ala Gly Pro Ala Val Leu Asp Trp
        115                 120                 125

Glu Glu Trp Cys Pro Leu Trp Ala Gly Asn Trp Gly Arg Arg Arg Ala
    130                 135                 140

Tyr Gln Ala Ala Ser Trp Ala Trp Ala Gln Gln Val Phe Pro Asp Leu
145                 150                 155                 160

Asp Pro Gln Glu Gln Leu Tyr Lys Ala Tyr Thr Gly Phe Glu Gln Ala
                165                 170                 175

Ala Arg Ala Leu Met Glu Asp Thr Leu Arg Val Ala Gln Ala Leu Arg
            180                 185                 190

Pro His Gly Leu Trp Gly Phe Tyr His Tyr Pro Ala Cys Gly Asn Gly
        195                 200                 205

Trp His Ser Met Ala Ser Asn Tyr Thr Gly Arg Cys His Ala Ala Thr
    210                 215                 220

Leu Ala Arg Asn Thr Gln Leu His Trp Leu Trp Ala Ala Ser Ser Ala
225                 230                 235                 240

Leu Phe Pro Ser Ile Tyr Leu Pro Pro Arg Leu Pro Pro Ala His His
                245                 250                 255

Gln Ala Phe Val Arg His Arg Leu Glu Glu Ala Phe Arg Val Ala Leu
            260                 265                 270

Val Gly His Arg His Pro Leu Pro Val Leu Ala Tyr Val Arg Leu Thr
        275                 280                 285

His Arg Arg Ser Gly Arg Phe Leu Ser Gln Glu Glu Cys Trp His Leu
    290                 295                 300

His Asp Tyr Leu Val Asp Thr Leu Gly Pro Tyr Val Ile Asn Val Thr
305                 310                 315                 320

Arg Ala Ala Met Ala Cys Ser His Gln Arg Cys His Gly His Gly Arg
                325                 330                 335

Cys Ala Arg Arg Asp Pro Gly Gln Met Glu Ala Phe Leu His Leu Trp
            340                 345                 350
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Pro Asp Gly Ser Leu Gly Asp Trp Lys Ser Phe Ser Cys His Cys Tyr
        355                 360                 365

Trp Gly Trp Ala Gly Pro Thr Cys Gln Glu Pro Arg Pro Gly Pro Lys
    370                 375                 380

Glu Ala Val
385


<210> SEQ ID NO 97
<211> LENGTH: 462
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 97

Met Gly Lys Glu Lys Thr His Ile Asn Ile Val Val Ile Gly His Val
1               5                   10                  15

Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Cys Gly
            20                  25                  30

Gly Ile Asp Lys Arg Thr Ile Glu Lys Phe Glu Lys Glu Ala Ala Glu
        35                  40                  45

Met Gly Lys Gly Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
    50                  55                  60

Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ser Leu Trp Lys Phe
65                  70                  75                  80

Glu Thr Ser Lys Tyr Tyr Val Thr Ile Ile Asp Ala Pro Gly His Arg
                85                  90                  95

Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala
            100                 105                 110

Val Leu Ile Val Ala Ala Gly Val Gly Glu Phe Glu Ala Gly Ile Ser
        115                 120                 125

Lys Asn Gly Gln Thr Arg Glu His Ala Leu Leu Ala Tyr Thr Leu Gly
    130                 135                 140

Val Lys Gln Leu Ile Val Gly Val Asn Lys Met Asp Ser Thr Glu Pro
145                 150                 155                 160

Pro Tyr Ser Gln Lys Arg Tyr Glu Glu Ile Val Lys Glu Val Ser Thr
                165                 170                 175

Tyr Ile Lys Lys Ile Gly Tyr Asn Pro Asp Thr Val Ala Phe Val Pro
            180                 185                 190

Ile Ser Gly Trp Asn Gly Asp Asn Met Leu Glu Pro Ser Ala Asn Met
        195                 200                 205

Pro Trp Phe Lys Gly Trp Lys Val Thr Arg Lys Asp Gly Asn Ala Ser
    210                 215                 220

Gly Thr Thr Leu Leu Glu Ala Leu Asp Cys Ile Leu Pro Pro Thr Arg
225                 230                 235                 240

Pro Thr Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile
                245                 250                 255

Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Val Leu
            260                 265                 270

Lys Pro Gly Met Val Val Thr Phe Ala Pro Val Asn Val Thr Thr Glu
        275                 280                 285

Val Lys Ser Val Glu Met His His Glu Ala Leu Ser Glu Ala Leu Pro
    290                 295                 300

Gly Asp Asn Val Gly Phe Lys Val Lys Asn Val Ser Val Lys Asp Val
305                 310                 315                 320

Arg Arg Gly Asn Val Ala Gly Asp Ser Lys Asn Asp Pro Pro Met Glu
                325                 330                 335
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Ala Ala Gly Phe Thr Ala Gln Val Ile Ile Leu Asn His Pro Gly Gln
            340                 345                 350

Ile Ser Ala Gly Tyr Ala Pro Val Leu Asp Cys His Met Ala His Ile
        355                 360                 365

Ala Cys Lys Phe Ala Glu Leu Lys Glu Lys Ile Asp Arg Arg Ser Gly
    370                 375                 380

Lys Lys Leu Glu Asp Gly Pro Lys Phe Leu Lys Ser Gly Asp Ala Ala
385                 390                 395                 400

Ile Val Asp Met Val Pro Gly Lys Pro Met Cys Val Glu Ser Phe Ser
                405                 410                 415

Asp Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr
            420                 425                 430

Val Ala Val Gly Val Ile Lys Ala Val Asp Lys Lys Ala Ala Gly Ala
        435                 440                 445

Gly Lys Val Thr Lys Ser Ala Gln Lys Ala Gln Lys Ala Lys
    450                 455                 460


<210> SEQ ID NO 98
<211> LENGTH: 381
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 98

Met Ala Leu Lys Ala Glu Gly Ala Ala Leu Asp Cys Phe Glu Val Thr
1               5                   10                  15

Leu Lys Cys Glu Glu Gly Glu Asp Glu Glu Glu Ala Met Val Val Ala
            20                  25                  30

Val Ile Pro Arg Pro Glu Pro Met Leu Arg Val Thr Gln Gln Glu Lys
        35                  40                  45

Thr Pro Pro Pro Arg Pro Ser Pro Leu Glu Ala Gly Ser Asp Gly Cys
    50                  55                  60

Glu Glu Pro Lys Gln Gln Val Ser Trp Glu Gln Glu Phe Leu Val Gly
65                  70                  75                  80

Ser Ser Pro Gly Gly Ser Gly Arg Ala Leu Cys Met Val Cys Gly Ala
                85                  90                  95

Glu Ile Arg Ala Pro Ser Ala Asp Thr Ala Arg Ser His Ile Leu Glu
            100                 105                 110

Gln His Pro His Thr Leu Asp Leu Ser Pro Ser Glu Lys Ser Asn Ile
        115                 120                 125

Leu Glu Ala Trp Ser Glu Gly Val Ala Leu Leu Gln Asp Val Arg Ala
    130                 135                 140

Glu Gln Pro Ser Pro Pro Asn Ser Asp Ser Gly Gln Asp Ala His Pro
145                 150                 155                 160

Asp Pro Asp Ala Asn Pro Asp Ala Ala Arg Met Pro Ala Glu Ile Val
                165                 170                 175

Val Leu Leu Asp Ser Glu Asp Asn Pro Ser Leu Pro Lys Arg Ser Arg
            180                 185                 190

Pro Arg Gly Leu Arg Pro Leu Glu Leu Pro Ala Val Pro Ala Thr Glu
        195                 200                 205

Pro Gly Asn Lys Lys Pro Arg Gly Gln Arg Trp Lys Glu Pro Pro Gly
    210                 215                 220

Glu Glu Pro Val Arg Lys Lys Arg Gly Arg Pro Met Thr Lys Asn Leu
225                 230                 235                 240

Asp Pro Asp Pro Glu Pro Pro Ser Pro Asp Ser Pro Thr Glu Thr Phe
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               245                 250                 255

Ala Ala Pro Ala Glu Val Arg His Phe Thr Asp Gly Ser Phe Pro Ala
            260                 265                 270

Gly Phe Val Leu Gln Leu Phe Ser His Thr Gln Leu Arg Gly Pro Asp
        275                 280                 285

Ser Lys Asp Ser Pro Lys Asp Arg Glu Val Ala Glu Gly Gly Leu Pro
    290                 295                 300

Arg Ala Glu Ser Pro Ser Pro Ala Pro Pro Pro Gly Leu Arg Gly Thr
305                 310                 315                 320

Leu Asp Leu Gln Val Ile Arg Val Arg Met Glu Glu Pro Pro Ala Val
                325                 330                 335

Ser Leu Leu Gln Asp Trp Ser Arg His Pro Gln Gly Thr Lys Arg Val
            340                 345                 350

Gly Ala Gly Asp Thr Ser Asp Trp Pro Thr Val Leu Ser Glu Ser Ser
        355                 360                 365

Thr Thr Val Ala Gly Lys Pro Glu Lys Gly Asn Gly Val
    370                 375                 380


<210> SEQ ID NO 99
<211> LENGTH: 1909
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 99

Met Ser Thr His Arg Ser Arg Leu Leu Thr Ala Ala Pro Leu Ser Met
1               5                   10                  15

Glu Gln Arg Arg Pro Trp Pro Arg Ala Leu Glu Val Asp Ser Arg Ser
            20                  25                  30

Val Val Leu Leu Ser Val Val Trp Val Leu Leu Ala Pro Pro Ala Ala
        35                  40                  45

Gly Met Pro Gln Phe Ser Thr Phe His Ser Glu Asn Arg Asp Trp Thr
    50                  55                  60

Phe Asn His Leu Thr Val His Gln Gly Thr Gly Ala Val Tyr Val Gly
65                  70                  75                  80

Ala Ile Asn Arg Val Tyr Lys Leu Thr Gly Asn Leu Thr Ile Gln Val
                85                  90                  95

Ala His Lys Thr Gly Pro Glu Glu Asp Asn Lys Ser Cys Tyr Pro Pro
            100                 105                 110

Leu Ile Val Gln Pro Cys Ser Glu Val Leu Thr Leu Thr Asn Asn Val
        115                 120                 125

Asn Lys Leu Leu Ile Ile Asp Tyr Ser Glu Asn Arg Leu Leu Ala Cys
    130                 135                 140

Gly Ser Leu Tyr Gln Gly Val Cys Lys Leu Leu Arg Leu Asp Asp Leu
145                 150                 155                 160

Phe Ile Leu Val Glu Pro Ser His Lys Lys Glu His Tyr Leu Ser Ser
                165                 170                 175

Val Asn Lys Thr Gly Thr Met Tyr Gly Val Ile Val Arg Ser Glu Gly
            180                 185                 190

Glu Asp Gly Lys Leu Phe Ile Gly Thr Ala Val Asp Gly Lys Gln Asp
        195                 200                 205

Tyr Phe Pro Thr Leu Ser Ser Arg Lys Leu Pro Arg Asp Pro Glu Ser
    210                 215                 220

Ser Ala Met Leu Asp Tyr Glu Leu His Ser Asp Phe Val Ser Ser Leu
225                 230                 235                 240
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Ile Lys Ile Pro Ser Asp Thr Leu Ala Leu Val Ser His Phe Asp Ile
                245                 250                 255

Phe Tyr Ile Tyr Gly Phe Ala Ser Gly Gly Phe Val Tyr Phe Leu Thr
            260                 265                 270

Val Gln Pro Glu Thr Pro Glu Gly Val Ala Ile Asn Ser Ala Gly Asp
        275                 280                 285

Leu Phe Tyr Thr Ser Arg Ile Val Arg Leu Cys Lys Asp Asp Pro Lys
    290                 295                 300

Phe His Ser Tyr Val Ser Leu Pro Phe Gly Cys Thr Arg Ala Gly Val
305                 310                 315                 320

Glu Tyr Arg Leu Leu Gln Ala Ala Tyr Leu Ala Lys Pro Gly Asp Ser
                325                 330                 335

Leu Ala Gln Ala Phe Asn Ile Thr Ser Gln Asp Asp Val Leu Phe Ala
            340                 345                 350

Ile Phe Ser Lys Gly Gln Lys Gln Tyr His His Pro Pro Asp Asp Ser
        355                 360                 365

Ala Leu Cys Ala Phe Pro Ile Arg Ala Ile Asn Leu Gln Ile Lys Glu
    370                 375                 380

Arg Leu Gln Ser Cys Tyr Gln Gly Glu Gly Asn Leu Glu Leu Asn Trp
385                 390                 395                 400

Leu Leu Gly Lys Asp Val Gln Cys Thr Lys Ala Pro Val Pro Ile Asp
                405                 410                 415

Asp Asn Phe Cys Gly Leu Asp Ile Asn Gln Pro Leu Gly Gly Ser Thr
            420                 425                 430

Pro Val Glu Gly Leu Thr Leu Tyr Thr Thr Ser Arg Asp Arg Met Thr
        435                 440                 445

Ser Val Ala Ser Tyr Val Tyr Asn Gly Tyr Ser Val Val Phe Val Gly
    450                 455                 460

Thr Lys Ser Gly Lys Leu Lys Lys Ile Arg Ala Asp Gly Pro Pro His
465                 470                 475                 480

Gly Gly Val Gln Tyr Glu Met Val Ser Val Leu Lys Asp Gly Ser Pro
                485                 490                 495

Ile Leu Arg Asp Met Ala Phe Ser Ile Asp Gln Arg Tyr Leu Tyr Val
            500                 505                 510

Met Ser Glu Arg Gln Val Thr Arg Val Pro Val Glu Ser Cys Glu Gln
        515                 520                 525

Tyr Thr Thr Cys Gly Glu Cys Leu Ser Ser Gly Asp Pro His Cys Gly
    530                 535                 540

Trp Cys Ala Leu His Asn Met Cys Ser Arg Arg Asp Lys Cys Gln Gln
545                 550                 555                 560

Ala Trp Glu Pro Asn Arg Phe Ala Ala Ser Ile Ser Gln Cys Val Ser
                565                 570                 575

Leu Ala Val His Pro Ser Ser Ile Ser Val Ser Glu His Ser Arg Leu
            580                 585                 590

Leu Ser Leu Val Val Ser Asp Ala Pro Asp Leu Ser Ala Gly Ile Ala
        595                 600                 605

Cys Ala Phe Gly Asn Leu Thr Glu Val Glu Gly Gln Val Ser Gly Ser
    610                 615                 620

Gln Val Ile Cys Ile Ser Pro Gly Pro Lys Asp Val Pro Val Ile Pro
625                 630                 635                 640

Leu Asp Gln Asp Trp Phe Gly Leu Glu Leu Gln Leu Arg Ser Lys Glu
                645                 650                 655

Thr Gly Lys Ile Phe Val Ser Thr Glu Phe Lys Phe Tyr Asn Cys Ser
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           660                 665                 670

Ala His Gln Leu Cys Leu Ser Cys Val Asn Ser Ala Phe Arg Cys His
        675                 680                 685

Trp Cys Lys Tyr Arg Asn Leu Cys Thr His Asp Pro Thr Thr Cys Ser
    690                 695                 700

Phe Gln Glu Gly Arg Ile Asn Ile Ser Glu Asp Cys Pro Gln Leu Val
705                 710                 715                 720

Pro Thr Glu Glu Ile Leu Ile Pro Val Gly Glu Val Lys Pro Ile Thr
                725                 730                 735

Leu Lys Ala Arg Asn Leu Pro Gln Pro Gln Ser Gly Gln Arg Gly Tyr
            740                 745                 750

Glu Cys Val Leu Asn Ile Gln Gly Ala Ile His Arg Val Pro Ala Leu
        755                 760                 765

Arg Phe Asn Ser Ser Ser Val Gln Cys Gln Asn Ser Ser Tyr Gln Tyr
    770                 775                 780

Asp Gly Met Asp Ile Ser Asn Leu Ala Val Asp Phe Ala Val Val Trp
785                 790                 795                 800

Asn Gly Asn Phe Ile Ile Asp Asn Pro Gln Asp Leu Lys Val His Leu
                805                 810                 815

Tyr Lys Cys Ala Ala Gln Arg Glu Ser Cys Gly Leu Cys Leu Lys Ala
            820                 825                 830

Asp Arg Lys Phe Glu Cys Gly Trp Cys Ser Gly Glu Arg Arg Cys Thr
        835                 840                 845

Leu His Gln His Cys Thr Ser Pro Ser Ser Pro Trp Leu Asp Trp Ser
    850                 855                 860

Ser His Asn Val Lys Cys Ser Asn Pro Gln Ile Thr Glu Ile Leu Thr
865                 870                 875                 880

Val Ser Gly Pro Pro Glu Gly Gly Thr Arg Val Thr Ile His Gly Val
                885                 890                 895

Asn Leu Gly Leu Asp Phe Ser Glu Ile Ala His His Val Gln Val Ala
            900                 905                 910

Gly Val Pro Cys Thr Pro Leu Pro Gly Glu Tyr Ile Ile Ala Glu Gln
        915                 920                 925

Ile Val Cys Glu Met Gly His Ala Leu Val Gly Thr Thr Ser Gly Pro
    930                 935                 940

Val Arg Leu Cys Ile Gly Glu Cys Lys Pro Glu Phe Met Thr Lys Ser
945                 950                 955                 960

His Gln Gln Tyr Thr Phe Val Asn Pro Ser Val Leu Ser Leu Asn Pro
                965                 970                 975

Ile Arg Gly Pro Glu Ser Gly Gly Thr Met Val Thr Ile Thr Gly His
            980                 985                 990

Tyr Leu Gly Ala Gly Ser Ser Val  Ala Val Tyr Leu Gly  Asn Gln Thr
        995                 1000                1005

Cys Glu  Phe Tyr Gly Arg Ser  Met Ser Glu Ile Val  Cys Val Ser
    1010                1015                1020

Pro Pro  Ser Ser Asn Gly Leu  Gly Pro Val Pro Val  Ser Val Ser
    1025                1030                1035

Val Asp  Arg Ala His Val Asp  Ser Asn Leu Gln Phe  Glu Tyr Ile
    1040                1045                1050

Asp Asp  Pro Arg Val Gln Arg  Ile Glu Pro Glu Trp  Ser Ile Ala
    1055                1060                1065

Ser Gly  His Thr Pro Leu Thr  Ile Thr Gly Phe Asn  Leu Asp Val
    1070                1075                1080
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Ile Gln  Glu Pro Arg Ile Arg  Val Lys Phe Asn Gly  Lys Glu Ser
    1085                1090                1095

Val Asn  Val Cys Lys Val Val  Asn Thr Thr Thr Leu  Thr Cys Leu
    1100                1105                1110

Ala Pro  Ser Leu Thr Thr Asp  Tyr Arg Pro Gly Leu  Asp Thr Val
    1115                1120                1125

Glu Arg  Pro Asp Glu Phe Gly  Phe Val Phe Asn Asn  Val Gln Ser
    1130                1135                1140

Leu Leu  Ile Tyr Asn Asp Thr  Lys Phe Ile Tyr Tyr  Pro Asn Pro
    1145                1150                1155

Thr Phe  Glu Leu Leu Ser Pro  Thr Gly Val Leu Asp  Gln Lys Pro
    1160                1165                1170

Gly Ser  Pro Ile Ile Leu Lys  Gly Lys Asn Leu Cys  Pro Pro Ala
    1175                1180                1185

Ser Gly  Gly Ala Lys Leu Asn  Tyr Thr Val Leu Ile  Gly Glu Thr
    1190                1195                1200

Pro Cys  Ala Val Thr Val Ser  Glu Thr Gln Leu Leu  Cys Glu Pro
    1205                1210                1215

Pro Asn  Leu Thr Gly Gln His  Lys Val Met Val His  Val Gly Gly
    1220                1225                1230

Met Val  Phe Ser Pro Gly Ser  Val Ser Val Ile Ser  Asp Ser Leu
    1235                1240                1245

Leu Thr  Leu Pro Ala Ile Val  Ser Ile Ala Ala Gly  Gly Ser Leu
    1250                1255                1260

Leu Leu  Ile Ile Val Ile Ile  Val Leu Ile Ala Tyr  Lys Arg Lys
    1265                1270                1275

Ser Arg  Glu Asn Asp Leu Thr  Leu Lys Arg Leu Gln  Met Gln Met
    1280                1285                1290

Asp Asn  Leu Glu Ser Arg Val  Ala Leu Glu Cys Lys  Glu Ala Phe
    1295                1300                1305

Ala Glu  Leu Gln Thr Asp Ile  Asn Glu Leu Thr Ser  Asp Leu Asp
    1310                1315                1320

Arg Ser  Gly Ile Pro Tyr Leu  Asp Tyr Arg Thr Tyr  Ala Met Arg
    1325                1330                1335

Val Leu  Phe Pro Gly Ile Glu  Asp His Pro Val Leu  Arg Glu Leu
    1340                1345                1350

Glu Val  Gln Gly Asn Gly Gln  Gln His Val Glu Lys  Ala Leu Lys
    1355                1360                1365

Leu Phe  Ala Gln Leu Ile Asn  Asn Lys Val Phe Leu  Leu Thr Phe
    1370                1375                1380

Ile Arg  Thr Leu Glu Leu Gln  Arg Ser Phe Ser Met  Arg Asp Arg
    1385                1390                1395

Gly Asn  Val Ala Ser Leu Ile  Met Thr Gly Leu Gln  Gly Arg Leu
    1400                1405                1410

Glu Tyr  Ala Thr Asp Val Leu  Lys Gln Leu Leu Ser  Asp Leu Ile
    1415                1420                1425

Asp Lys  Asn Leu Glu Asn Lys  Asn His Pro Lys Leu  Leu Leu Arg
    1430                1435                1440

Arg Thr  Glu Ser Val Ala Glu  Lys Met Leu Thr Asn  Trp Phe Ala
    1445                1450                1455

Phe Leu  Leu His Lys Phe Leu  Lys Glu Cys Ala Gly  Glu Pro Leu
    1460                1465                1470
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Phe Met  Leu Tyr Cys Ala Ile  Lys Gln Gln Met Glu  Lys Gly Pro
    1475                1480                1485

Ile Asp  Ala Ile Thr Gly Glu  Ala Arg Tyr Ser Leu  Ser Glu Asp
    1490                1495                1500

Lys Leu  Ile Arg Gln Gln Ile  Glu Tyr Lys Thr Leu  Ile Leu Asn
    1505                1510                1515

Cys Val  Asn Pro Asp Asn Glu  Asn Ser Pro Glu Ile  Pro Val Lys
    1520                1525                1530

Val Leu  Asn Cys Asp Thr Ile  Thr Gln Val Lys Glu  Lys Ile Leu
    1535                1540                1545

Asp Ala  Val Tyr Lys Asn Val  Pro Tyr Ser Gln Arg  Pro Arg Ala
    1550                1555                1560

Val Asp  Met Asp Leu Glu Trp  Arg Gln Gly Arg Ile  Ala Arg Val
    1565                1570                1575

Val Leu  Gln Asp Glu Asp Ile  Thr Thr Lys Ile Glu  Gly Asp Trp
    1580                1585                1590

Lys Arg  Leu Asn Thr Leu Met  His Tyr Gln Val Ser  Asp Arg Ser
    1595                1600                1605

Val Val  Ala Leu Val Pro Lys  Gln Thr Ser Ser Tyr  Asn Ile Pro
    1610                1615                1620

Ala Ser  Ala Ser Ile Ser Arg  Thr Ser Ile Ser Arg  Tyr Asp Ser
    1625                1630                1635

Ser Phe  Arg Tyr Thr Gly Ser  Pro Asp Ser Leu Arg  Ser Arg Ala
    1640                1645                1650

Pro Met  Ile Thr Pro Asp Leu  Glu Ser Gly Val Lys  Val Trp His
    1655                1660                1665

Leu Val  Lys Asn His Asp His  Gly Asp Gln Lys Glu  Gly Asp Arg
    1670                1675                1680

Gly Ser  Lys Met Val Ser Glu  Ile Tyr Leu Thr Arg  Leu Leu Ala
    1685                1690                1695

Thr Lys  Gly Thr Leu Gln Lys  Phe Val Asp Asp Leu  Phe Glu Thr
    1700                1705                1710

Leu Phe  Ser Thr Val His Arg  Gly Ser Ala Leu Pro  Leu Ala Ile
    1715                1720                1725

Lys Tyr  Met Phe Asp Phe Leu  Asp Glu Gln Ala Asp  Arg His Ser
    1730                1735                1740

Ile His  Asp Thr Asp Val Arg  His Thr Trp Lys Ser  Asn Cys Leu
    1745                1750                1755

Pro Leu  Arg Phe Trp Val Asn  Val Ile Lys Asn Pro  Gln Phe Val
    1760                1765                1770

Phe Asp  Ile His Lys Gly Ser  Ile Thr Asp Ala Cys  Leu Ser Val
    1775                1780                1785

Val Ala  Gln Thr Phe Met Asp  Ser Cys Ser Thr Ser  Glu His Arg
    1790                1795                1800

Leu Gly  Lys Asp Ser Pro Ser  Asn Lys Leu Leu Tyr  Ala Lys Asp
    1805                1810                1815

Ile Pro  Ser Tyr Lys Ser Trp  Val Glu Arg Tyr Tyr  Ala Asp Ile
    1820                1825                1830

Ala Lys  Leu Pro Ala Ile Ser  Asp Gln Asp Met Asn  Ala Tyr Leu
    1835                1840                1845

Ala Glu  Gln Ser Arg Leu His  Ala Val Glu Phe Asn  Met Leu Ser
    1850                1855                1860

Ala Leu  Asn Glu Ile Tyr Ser  Tyr Val Ser Lys Tyr  Ser Glu Glu
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    1865                1870                1875

Leu Ile  Gly Ala Leu Glu Gln  Asp Glu Gln Ala Arg  Arg Gln Arg
    1880                1885                1890

Leu Ala  Tyr Lys Val Glu Gln  Leu Ile Asn Ala Met  Ser Ile Glu
    1895                1900                1905

Ser


<210> SEQ ID NO 100
<211> LENGTH: 1894
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 100

Met Glu Gln Arg Arg Pro Trp Pro Arg Ala Leu Glu Val Asp Ser Arg
1               5                   10                  15

Ser Val Val Leu Leu Ser Val Val Trp Val Leu Leu Ala Pro Pro Ala
            20                  25                  30

Ala Gly Met Pro Gln Phe Ser Thr Phe His Ser Glu Asn Arg Asp Trp
        35                  40                  45

Thr Phe Asn His Leu Thr Val His Gln Gly Thr Gly Ala Val Tyr Val
    50                  55                  60

Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr Gly Asn Leu Thr Ile Gln
65                  70                  75                  80

Val Ala His Lys Thr Gly Pro Glu Glu Asp Asn Lys Ser Cys Tyr Pro
                85                  90                  95

Pro Leu Ile Val Gln Pro Cys Ser Glu Val Leu Thr Leu Thr Asn Asn
            100                 105                 110

Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser Glu Asn Arg Leu Leu Ala
        115                 120                 125

Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys Leu Leu Arg Leu Asp Asp
    130                 135                 140

Leu Phe Ile Leu Val Glu Pro Ser His Lys Lys Glu His Tyr Leu Ser
145                 150                 155                 160

Ser Val Asn Lys Thr Gly Thr Met Tyr Gly Val Ile Val Arg Ser Glu
                165                 170                 175

Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr Ala Val Asp Gly Lys Gln
            180                 185                 190

Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys Leu Pro Arg Asp Pro Glu
        195                 200                 205

Ser Ser Ala Met Leu Asp Tyr Glu Leu His Ser Asp Phe Val Ser Ser
    210                 215                 220

Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala Leu Val Ser His Phe Asp
225                 230                 235                 240

Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly Gly Phe Val Tyr Phe Leu
                245                 250                 255

Thr Val Gln Pro Glu Thr Pro Glu Gly Val Ala Ile Asn Ser Ala Gly
            260                 265                 270

Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg Leu Cys Lys Asp Asp Pro
        275                 280                 285

Lys Phe His Ser Tyr Val Ser Leu Pro Phe Gly Cys Thr Arg Ala Gly
    290                 295                 300

Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr Leu Ala Lys Pro Gly Asp
305                 310                 315                 320

Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser Gln Asp Asp Val Leu Phe
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               325                 330                 335

Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr His His Pro Pro Asp Asp
            340                 345                 350

Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala Ile Asn Leu Gln Ile Lys
        355                 360                 365

Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu Gly Asn Leu Glu Leu Asn
    370                 375                 380

Trp Leu Leu Gly Lys Asp Val Gln Cys Thr Lys Ala Pro Val Pro Ile
385                 390                 395                 400

Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn Gln Pro Leu Gly Gly Ser
                405                 410                 415

Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr Thr Ser Arg Asp Arg Met
            420                 425                 430

Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly Tyr Ser Val Val Phe Val
        435                 440                 445

Gly Thr Lys Ser Gly Lys Leu Lys Lys Ile Arg Ala Asp Gly Pro Pro
    450                 455                 460

His Gly Gly Val Gln Tyr Glu Met Val Ser Val Leu Lys Asp Gly Ser
465                 470                 475                 480

Pro Ile Leu Arg Asp Met Ala Phe Ser Ile Asp Gln Arg Tyr Leu Tyr
                485                 490                 495

Val Met Ser Glu Arg Gln Val Thr Arg Val Pro Val Glu Ser Cys Glu
            500                 505                 510

Gln Tyr Thr Thr Cys Gly Glu Cys Leu Ser Ser Gly Asp Pro His Cys
        515                 520                 525

Gly Trp Cys Ala Leu His Asn Met Cys Ser Arg Arg Asp Lys Cys Gln
    530                 535                 540

Gln Ala Trp Glu Pro Asn Arg Phe Ala Ala Ser Ile Ser Gln Cys Val
545                 550                 555                 560

Ser Leu Ala Val His Pro Ser Ser Ile Ser Val Ser Glu His Ser Arg
                565                 570                 575

Leu Leu Ser Leu Val Val Ser Asp Ala Pro Asp Leu Ser Ala Gly Ile
            580                 585                 590

Ala Cys Ala Phe Gly Asn Leu Thr Glu Val Glu Gly Gln Val Ser Gly
        595                 600                 605

Ser Gln Val Ile Cys Ile Ser Pro Gly Pro Lys Asp Val Pro Val Ile
    610                 615                 620

Pro Leu Asp Gln Asp Trp Phe Gly Leu Glu Leu Gln Leu Arg Ser Lys
625                 630                 635                 640

Glu Thr Gly Lys Ile Phe Val Ser Thr Glu Phe Lys Phe Tyr Asn Cys
                645                 650                 655

Ser Ala His Gln Leu Cys Leu Ser Cys Val Asn Ser Ala Phe Arg Cys
            660                 665                 670

His Trp Cys Lys Tyr Arg Asn Leu Cys Thr His Asp Pro Thr Thr Cys
        675                 680                 685

Ser Phe Gln Glu Gly Arg Ile Asn Ile Ser Glu Asp Cys Pro Gln Leu
    690                 695                 700

Val Pro Thr Glu Glu Ile Leu Ile Pro Val Gly Glu Val Lys Pro Ile
705                 710                 715                 720

Thr Leu Lys Ala Arg Asn Leu Pro Gln Pro Gln Ser Gly Gln Arg Gly
                725                 730                 735

Tyr Glu Cys Val Leu Asn Ile Gln Gly Ala Ile His Arg Val Pro Ala
            740                 745                 750
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Leu Arg Phe Asn Ser Ser Ser Val Gln Cys Gln Asn Ser Ser Tyr Gln
        755                 760                 765

Tyr Asp Gly Met Asp Ile Ser Asn Leu Ala Val Asp Phe Ala Val Val
    770                 775                 780

Trp Asn Gly Asn Phe Ile Ile Asp Asn Pro Gln Asp Leu Lys Val His
785                 790                 795                 800

Leu Tyr Lys Cys Ala Ala Gln Arg Glu Ser Cys Gly Leu Cys Leu Lys
                805                 810                 815

Ala Asp Arg Lys Phe Glu Cys Gly Trp Cys Ser Gly Glu Arg Arg Cys
            820                 825                 830

Thr Leu His Gln His Cys Thr Ser Pro Ser Ser Pro Trp Leu Asp Trp
        835                 840                 845

Ser Ser His Asn Val Lys Cys Ser Asn Pro Gln Ile Thr Glu Ile Leu
    850                 855                 860

Thr Val Ser Gly Pro Pro Glu Gly Gly Thr Arg Val Thr Ile His Gly
865                 870                 875                 880

Val Asn Leu Gly Leu Asp Phe Ser Glu Ile Ala His His Val Gln Val
                885                 890                 895

Ala Gly Val Pro Cys Thr Pro Leu Pro Gly Glu Tyr Ile Ile Ala Glu
            900                 905                 910

Gln Ile Val Cys Glu Met Gly His Ala Leu Val Gly Thr Thr Ser Gly
        915                 920                 925

Pro Val Arg Leu Cys Ile Gly Glu Cys Lys Pro Glu Phe Met Thr Lys
    930                 935                 940

Ser His Gln Gln Tyr Thr Phe Val Asn Pro Ser Val Leu Ser Leu Asn
945                 950                 955                 960

Pro Ile Arg Gly Pro Glu Ser Gly Gly Thr Met Val Thr Ile Thr Gly
                965                 970                 975

His Tyr Leu Gly Ala Gly Ser Ser Val Ala Val Tyr Leu Gly Asn Gln
            980                 985                 990

Thr Cys Glu Phe Tyr Gly Arg Ser  Met Ser Glu Ile Val  Cys Val Ser
        995                 1000                1005

Pro Pro  Ser Ser Asn Gly Leu  Gly Pro Val Pro Val  Ser Val Ser
    1010                1015                1020

Val Asp  Arg Ala His Val Asp  Ser Asn Leu Gln Phe  Glu Tyr Ile
    1025                1030                1035

Asp Asp  Pro Arg Val Gln Arg  Ile Glu Pro Glu Trp  Ser Ile Ala
    1040                1045                1050

Ser Gly  His Thr Pro Leu Thr  Ile Thr Gly Phe Asn  Leu Asp Val
    1055                1060                1065

Ile Gln  Glu Pro Arg Ile Arg  Val Lys Phe Asn Gly  Lys Glu Ser
    1070                1075                1080

Val Asn  Val Cys Lys Val Val  Asn Thr Thr Thr Leu  Thr Cys Leu
    1085                1090                1095

Ala Pro  Ser Leu Thr Thr Asp  Tyr Arg Pro Gly Leu  Asp Thr Val
    1100                1105                1110

Glu Arg  Pro Asp Glu Phe Gly  Phe Val Phe Asn Asn  Val Gln Ser
    1115                1120                1125

Leu Leu  Ile Tyr Asn Asp Thr  Lys Phe Ile Tyr Tyr  Pro Asn Pro
    1130                1135                1140

Thr Phe  Glu Leu Leu Ser Pro  Thr Gly Val Leu Asp  Gln Lys Pro
    1145                1150                1155
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Gly Ser  Pro Ile Ile Leu Lys  Gly Lys Asn Leu Cys  Pro Pro Ala
    1160                1165                1170

Ser Gly  Gly Ala Lys Leu Asn  Tyr Thr Val Leu Ile  Gly Glu Thr
    1175                1180                1185

Pro Cys  Ala Val Thr Val Ser  Glu Thr Gln Leu Leu  Cys Glu Pro
    1190                1195                1200

Pro Asn  Leu Thr Gly Gln His  Lys Val Met Val His  Val Gly Gly
    1205                1210                1215

Met Val  Phe Ser Pro Gly Ser  Val Ser Val Ile Ser  Asp Ser Leu
    1220                1225                1230

Leu Thr  Leu Pro Ala Ile Val  Ser Ile Ala Ala Gly  Gly Ser Leu
    1235                1240                1245

Leu Leu  Ile Ile Val Ile Ile  Val Leu Ile Ala Tyr  Lys Arg Lys
    1250                1255                1260

Ser Arg  Glu Asn Asp Leu Thr  Leu Lys Arg Leu Gln  Met Gln Met
    1265                1270                1275

Asp Asn  Leu Glu Ser Arg Val  Ala Leu Glu Cys Lys  Glu Ala Phe
    1280                1285                1290

Ala Glu  Leu Gln Thr Asp Ile  Asn Glu Leu Thr Ser  Asp Leu Asp
    1295                1300                1305

Arg Ser  Gly Ile Pro Tyr Leu  Asp Tyr Arg Thr Tyr  Ala Met Arg
    1310                1315                1320

Val Leu  Phe Pro Gly Ile Glu  Asp His Pro Val Leu  Arg Glu Leu
    1325                1330                1335

Glu Val  Gln Gly Asn Gly Gln  Gln His Val Glu Lys  Ala Leu Lys
    1340                1345                1350

Leu Phe  Ala Gln Leu Ile Asn  Asn Lys Val Phe Leu  Leu Thr Phe
    1355                1360                1365

Ile Arg  Thr Leu Glu Leu Gln  Arg Ser Phe Ser Met  Arg Asp Arg
    1370                1375                1380

Gly Asn  Val Ala Ser Leu Ile  Met Thr Gly Leu Gln  Gly Arg Leu
    1385                1390                1395

Glu Tyr  Ala Thr Asp Val Leu  Lys Gln Leu Leu Ser  Asp Leu Ile
    1400                1405                1410

Asp Lys  Asn Leu Glu Asn Lys  Asn His Pro Lys Leu  Leu Leu Arg
    1415                1420                1425

Arg Thr  Glu Ser Val Ala Glu  Lys Met Leu Thr Asn  Trp Phe Ala
    1430                1435                1440

Phe Leu  Leu His Lys Phe Leu  Lys Glu Cys Ala Gly  Glu Pro Leu
    1445                1450                1455

Phe Met  Leu Tyr Cys Ala Ile  Lys Gln Gln Met Glu  Lys Gly Pro
    1460                1465                1470

Ile Asp  Ala Ile Thr Gly Glu  Ala Arg Tyr Ser Leu  Ser Glu Asp
    1475                1480                1485

Lys Leu  Ile Arg Gln Gln Ile  Glu Tyr Lys Thr Leu  Ile Leu Asn
    1490                1495                1500

Cys Val  Asn Pro Asp Asn Glu  Asn Ser Pro Glu Ile  Pro Val Lys
    1505                1510                1515

Val Leu  Asn Cys Asp Thr Ile  Thr Gln Val Lys Glu  Lys Ile Leu
    1520                1525                1530

Asp Ala  Val Tyr Lys Asn Val  Pro Tyr Ser Gln Arg  Pro Arg Ala
    1535                1540                1545

Val Asp  Met Asp Leu Glu Trp  Arg Gln Gly Arg Ile  Ala Arg Val
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    1550                1555                1560

Val Leu  Gln Asp Glu Asp Ile  Thr Thr Lys Ile Glu  Gly Asp Trp
    1565                1570                1575

Lys Arg  Leu Asn Thr Leu Met  His Tyr Gln Val Ser  Asp Arg Ser
    1580                1585                1590

Val Val  Ala Leu Val Pro Lys  Gln Thr Ser Ser Tyr  Asn Ile Pro
    1595                1600                1605

Ala Ser  Ala Ser Ile Ser Arg  Thr Ser Ile Ser Arg  Tyr Asp Ser
    1610                1615                1620

Ser Phe  Arg Tyr Thr Gly Ser  Pro Asp Ser Leu Arg  Ser Arg Ala
    1625                1630                1635

Pro Met  Ile Thr Pro Asp Leu  Glu Ser Gly Val Lys  Val Trp His
    1640                1645                1650

Leu Val  Lys Asn His Asp His  Gly Asp Gln Lys Glu  Gly Asp Arg
    1655                1660                1665

Gly Ser  Lys Met Val Ser Glu  Ile Tyr Leu Thr Arg  Leu Leu Ala
    1670                1675                1680

Thr Lys  Gly Thr Leu Gln Lys  Phe Val Asp Asp Leu  Phe Glu Thr
    1685                1690                1695

Leu Phe  Ser Thr Val His Arg  Gly Ser Ala Leu Pro  Leu Ala Ile
    1700                1705                1710

Lys Tyr  Met Phe Asp Phe Leu  Asp Glu Gln Ala Asp  Arg His Ser
    1715                1720                1725

Ile His  Asp Thr Asp Val Arg  His Thr Trp Lys Ser  Asn Cys Leu
    1730                1735                1740

Pro Leu  Arg Phe Trp Val Asn  Val Ile Lys Asn Pro  Gln Phe Val
    1745                1750                1755

Phe Asp  Ile His Lys Gly Ser  Ile Thr Asp Ala Cys  Leu Ser Val
    1760                1765                1770

Val Ala  Gln Thr Phe Met Asp  Ser Cys Ser Thr Ser  Glu His Arg
    1775                1780                1785

Leu Gly  Lys Asp Ser Pro Ser  Asn Lys Leu Leu Tyr  Ala Lys Asp
    1790                1795                1800

Ile Pro  Ser Tyr Lys Ser Trp  Val Glu Arg Tyr Tyr  Ala Asp Ile
    1805                1810                1815

Ala Lys  Leu Pro Ala Ile Ser  Asp Gln Asp Met Asn  Ala Tyr Leu
    1820                1825                1830

Ala Glu  Gln Ser Arg Leu His  Ala Val Glu Phe Asn  Met Leu Ser
    1835                1840                1845

Ala Leu  Asn Glu Ile Tyr Ser  Tyr Val Ser Lys Tyr  Ser Glu Glu
    1850                1855                1860

Leu Ile  Gly Ala Leu Glu Gln  Asp Glu Gln Ala Arg  Arg Gln Arg
    1865                1870                1875

Leu Ala  Tyr Lys Val Glu Gln  Leu Ile Asn Ala Met  Ser Ile Glu
    1880                1885                1890

Ser


<210> SEQ ID NO 101
<211> LENGTH: 720
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 101

Met Pro Pro Pro Ser Asp Ile Val Lys Val Ala Ile Glu Trp Pro Gly
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1               5                   10                  15

Ala Asn Ala Gln Leu Leu Glu Ile Asp Gln Lys Arg Pro Leu Ala Ser
            20                  25                  30

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

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

Thr Arg Ser Asp Ile Lys Asn Gly Thr Ile Leu Gln Leu Ala Ile Ser
65                  70                  75                  80

Pro Ser Arg Ala Ala Arg Gln Leu Met Glu Arg Thr Gln Ser Ser Asn
                85                  90                  95

Met Glu Thr Arg Leu Asp Ala Met Lys Glu Leu Ala Lys Leu Ser Ala
            100                 105                 110

Asp Val Thr Phe Ala Thr Glu Phe Ile Asn Met Asp Gly Ile Ile Val
        115                 120                 125

Leu Thr Arg Leu Val Glu Ser Gly Thr Lys Leu Leu Ser His Tyr Ser
    130                 135                 140

Glu Met Leu Ala Phe Thr Leu Thr Ala Phe Leu Glu Leu Met Asp His
145                 150                 155                 160

Gly Ile Val Ser Trp Asp Met Val Ser Ile Thr Phe Ile Lys Gln Ile
                165                 170                 175

Ala Gly Tyr Val Ser Gln Pro Met Val Asp Val Ser Ile Leu Gln Arg
            180                 185                 190

Ser Leu Ala Ile Leu Glu Ser Met Val Leu Asn Ser Gln Ser Leu Tyr
        195                 200                 205

Gln Lys Ile Ala Glu Glu Ile Thr Val Gly Gln Leu Ile Ser His Leu
    210                 215                 220

Gln Val Ser Asn Gln Glu Ile Gln Thr Tyr Ala Ile Ala Leu Ile Asn
225                 230                 235                 240

Ala Leu Phe Leu Lys Ala Pro Glu Asp Lys Arg Gln Asp Met Ala Asn
                245                 250                 255

Ala Phe Ala Gln Lys His Leu Arg Ser Ile Ile Leu Asn His Val Ile
            260                 265                 270

Arg Gly Asn Arg Pro Ile Lys Thr Glu Met Ala His Gln Leu Tyr Val
        275                 280                 285

Leu Gln Val Leu Thr Phe Asn Leu Leu Glu Glu Arg Met Met Thr Lys
    290                 295                 300

Met Asp Pro Asn Asp Gln Ala Gln Arg Asp Ile Ile Phe Glu Leu Arg
305                 310                 315                 320

Arg Ile Ala Phe Asp Ala Glu Ser Asp Pro Ser Asn Ala Pro Gly Ser
                325                 330                 335

Gly Thr Glu Lys Arg Lys Ala Met Tyr Thr Lys Asp Tyr Lys Met Leu
            340                 345                 350

Gly Phe Thr Asn His Ile Asn Pro Ala Met Asp Phe Thr Gln Thr Pro
        355                 360                 365

Pro Gly Met Leu Ala Leu Asp Asn Met Leu Tyr Leu Ala Lys Val His
    370                 375                 380

Gln Asp Thr Tyr Ile Arg Ile Val Leu Glu Asn Ser Ser Arg Glu Asp
385                 390                 395                 400

Lys His Glu Cys Pro Phe Gly Arg Ser Ala Ile Glu Leu Thr Lys Met
                405                 410                 415

Leu Cys Glu Ile Leu Gln Val Gly Glu Leu Pro Asn Glu Gly Arg Asn
            420                 425                 430
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Asp Tyr His Pro Met Phe Phe Thr His Asp Arg Ala Phe Glu Glu Leu
        435                 440                 445

Phe Gly Ile Cys Ile Gln Leu Leu Asn Lys Thr Trp Lys Glu Met Arg
    450                 455                 460

Ala Thr Ala Glu Asp Phe Asn Lys Val Met Gln Val Val Arg Glu Gln
465                 470                 475                 480

Ile Thr Arg Ala Leu Pro Ser Lys Pro Asn Ser Leu Asp Gln Phe Lys
                485                 490                 495

Ser Lys Leu Arg Ser Leu Ser Tyr Ser Glu Ile Leu Arg Leu Arg Gln
            500                 505                 510

Ser Glu Arg Met Ser Gln Asp Asp Phe Gln Ser Pro Pro Ile Val Glu
        515                 520                 525

Leu Arg Glu Lys Ile Gln Pro Glu Ile Leu Glu Leu Ile Lys Gln Gln
    530                 535                 540

Arg Leu Asn Arg Leu Cys Glu Gly Ser Ser Phe Arg Lys Ile Gly Asn
545                 550                 555                 560

Arg Arg Arg Gln Glu Arg Phe Trp Tyr Cys Arg Leu Ala Leu Asn His
                565                 570                 575

Lys Val Leu His Tyr Gly Asp Leu Asp Asp Asn Pro Gln Gly Glu Val
            580                 585                 590

Thr Phe Glu Ser Leu Gln Glu Lys Ile Pro Val Ala Asp Ile Lys Ala
        595                 600                 605

Ile Val Thr Gly Lys Asp Cys Pro His Met Lys Glu Lys Ser Ala Leu
    610                 615                 620

Lys Gln Asn Lys Glu Val Leu Glu Leu Ala Phe Ser Ile Leu Tyr Asp
625                 630                 635                 640

Pro Asp Glu Thr Leu Asn Phe Ile Ala Pro Asn Lys Tyr Glu Tyr Cys
                645                 650                 655

Ile Trp Ile Asp Gly Leu Ser Ala Leu Leu Gly Lys Asp Met Ser Ser
            660                 665                 670

Glu Leu Thr Lys Ser Asp Leu Asp Thr Leu Leu Ser Met Glu Met Lys
        675                 680                 685

Leu Arg Leu Leu Asp Leu Glu Asn Ile Gln Ile Pro Glu Ala Pro Pro
    690                 695                 700

Pro Ile Pro Lys Glu Pro Ser Ser Tyr Asp Phe Val Tyr His Tyr Gly
705                 710                 715                 720


<210> SEQ ID NO 102
<211> LENGTH: 720
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 102

Met Pro Pro Pro Ser Asp Ile Val Lys Val Ala Ile Glu Trp Pro Gly
1               5                   10                  15

Ala Asn Ala Gln Leu Leu Glu Ile Asp Gln Lys Arg Pro Leu Ala Ser
            20                  25                  30

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

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

Thr Arg Ser Asp Ile Lys Asn Gly Thr Ile Leu Gln Leu Ala Ile Ser
65                  70                  75                  80

Pro Ser Arg Ala Ala Arg Gln Leu Met Glu Arg Thr Gln Ser Ser Asn
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               85                  90                  95

Met Glu Thr Arg Leu Asp Ala Met Lys Glu Leu Ala Lys Leu Ser Ala
            100                 105                 110

Asp Val Thr Phe Ala Thr Glu Phe Ile Asn Met Asp Gly Ile Ile Val
        115                 120                 125

Leu Thr Arg Leu Val Glu Ser Gly Thr Lys Leu Leu Ser His Tyr Ser
    130                 135                 140

Glu Met Leu Ala Phe Thr Leu Thr Ala Phe Leu Glu Leu Met Asp His
145                 150                 155                 160

Gly Ile Val Ser Trp Asp Met Val Ser Ile Thr Phe Ile Lys Gln Ile
                165                 170                 175

Ala Gly Tyr Val Ser Gln Pro Met Val Asp Val Ser Ile Leu Gln Arg
            180                 185                 190

Ser Leu Ala Ile Leu Glu Ser Met Val Leu Asn Ser Gln Ser Leu Tyr
        195                 200                 205

Gln Lys Ile Ala Glu Glu Ile Thr Val Gly Gln Leu Ile Ser His Leu
    210                 215                 220

Gln Val Ser Asn Gln Glu Ile Gln Thr Tyr Ala Ile Ala Leu Ile Asn
225                 230                 235                 240

Ala Leu Phe Leu Lys Ala Pro Glu Asp Lys Arg Gln Asp Met Ala Asn
                245                 250                 255

Ala Phe Ala Gln Lys His Leu Arg Ser Ile Ile Leu Asn His Val Ile
            260                 265                 270

Arg Gly Asn Arg Pro Ile Lys Thr Glu Met Ala His Gln Leu Tyr Val
        275                 280                 285

Leu Gln Val Leu Thr Phe Asn Leu Leu Glu Glu Arg Met Met Thr Lys
    290                 295                 300

Met Asp Pro Asn Asp Gln Ala Gln Arg Asp Ile Ile Phe Glu Leu Arg
305                 310                 315                 320

Arg Ile Ala Phe Asp Ala Glu Ser Asp Pro Ser Asn Ala Pro Gly Ser
                325                 330                 335

Gly Thr Glu Lys Arg Lys Ala Met Tyr Thr Lys Asp Tyr Lys Met Leu
            340                 345                 350

Gly Phe Thr Asn His Ile Asn Pro Ala Met Asp Phe Thr Gln Thr Pro
        355                 360                 365

Pro Gly Met Leu Ala Leu Asp Asn Met Leu Tyr Leu Ala Lys Val His
    370                 375                 380

Gln Asp Thr Tyr Ile Arg Ile Val Leu Glu Asn Ser Ser Arg Glu Asp
385                 390                 395                 400

Lys His Glu Cys Pro Phe Gly Arg Ser Ala Ile Glu Leu Thr Lys Met
                405                 410                 415

Leu Cys Glu Ile Leu Gln Val Gly Glu Leu Pro Asn Glu Gly Arg Asn
            420                 425                 430

Asp Tyr His Pro Met Phe Phe Thr His Asp Arg Ala Phe Glu Glu Leu
        435                 440                 445

Phe Gly Ile Cys Ile Gln Leu Leu Asn Lys Thr Trp Lys Glu Met Arg
    450                 455                 460

Ala Thr Ala Glu Asp Phe Asn Lys Val Met Gln Val Val Arg Glu Gln
465                 470                 475                 480

Ile Thr Arg Ala Leu Pro Ser Lys Pro Asn Ser Leu Asp Gln Phe Lys
                485                 490                 495

Ser Lys Leu Arg Ser Leu Ser Tyr Ser Glu Ile Leu Arg Leu Arg Gln
            500                 505                 510
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Ser Glu Arg Met Ser Gln Asp Asp Phe Gln Ser Pro Pro Ile Val Glu
        515                 520                 525

Leu Arg Glu Lys Ile Gln Pro Glu Ile Leu Glu Leu Ile Lys Gln Gln
    530                 535                 540

Arg Leu Asn Arg Leu Cys Glu Gly Ser Ser Phe Arg Lys Ile Gly Asn
545                 550                 555                 560

Arg Arg Arg Gln Glu Arg Phe Trp Tyr Cys Arg Leu Ala Leu Asn His
                565                 570                 575

Lys Val Leu His Tyr Gly Asp Leu Asp Asp Asn Pro Gln Gly Glu Val
            580                 585                 590

Thr Phe Glu Ser Leu Gln Glu Lys Ile Pro Val Ala Asp Ile Lys Ala
        595                 600                 605

Ile Val Thr Gly Lys Asp Cys Pro His Met Lys Glu Lys Ser Ala Leu
    610                 615                 620

Lys Gln Asn Lys Glu Val Leu Glu Leu Ala Phe Ser Ile Leu Tyr Asp
625                 630                 635                 640

Pro Asp Glu Thr Leu Asn Phe Ile Ala Pro Asn Lys Tyr Glu Tyr Cys
                645                 650                 655

Ile Trp Ile Asp Gly Leu Ser Ala Leu Leu Gly Lys Asp Met Ser Ser
            660                 665                 670

Glu Leu Thr Lys Ser Asp Leu Asp Thr Leu Leu Ser Met Glu Met Lys
        675                 680                 685

Leu Arg Leu Leu Asp Leu Glu Asn Ile Gln Ile Pro Glu Ala Pro Pro
    690                 695                 700

Pro Ile Pro Lys Glu Pro Ser Ser Tyr Asp Phe Val Tyr His Tyr Gly
705                 710                 715                 720


<210> SEQ ID NO 103
<211> LENGTH: 718
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 103

Met Pro Pro Pro Ser Asp Ile Val Lys Val Ala Ile Glu Trp Pro Gly
1               5                   10                  15

Ala Asn Ala Gln Leu Leu Glu Ile Asp Gln Lys Arg Pro Leu Ala Ser
            20                  25                  30

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

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

Thr Arg Ser Asp Ile Lys Asn Gly Thr Ile Leu Gln Leu Ala Ile Ser
65                  70                  75                  80

Pro Ser Arg Ala Ala Arg Gln Leu Met Glu Arg Thr Gln Ser Ser Asn
                85                  90                  95

Met Glu Thr Arg Leu Asp Ala Met Lys Glu Leu Ala Lys Leu Ser Ala
            100                 105                 110

Asp Val Thr Phe Ala Thr Glu Phe Ile Asn Met Asp Gly Ile Ile Val
        115                 120                 125

Leu Thr Arg Leu Val Glu Ser Gly Thr Lys Leu Leu Ser His Glu Met
    130                 135                 140

Leu Ala Phe Thr Leu Thr Ala Phe Leu Glu Leu Met Asp His Gly Ile
145                 150                 155                 160

Val Ser Trp Asp Met Val Ser Ile Thr Phe Ile Lys Gln Ile Ala Gly
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               165                 170                 175

Tyr Val Ser Gln Pro Met Val Asp Val Ser Ile Leu Gln Arg Ser Leu
            180                 185                 190

Ala Ile Leu Glu Ser Met Val Leu Asn Ser Gln Ser Leu Tyr Gln Lys
        195                 200                 205

Ile Ala Glu Glu Ile Thr Val Gly Gln Leu Ile Ser His Leu Gln Val
    210                 215                 220

Ser Asn Gln Glu Ile Gln Thr Tyr Ala Ile Ala Leu Ile Asn Ala Leu
225                 230                 235                 240

Phe Leu Lys Ala Pro Glu Asp Lys Arg Gln Asp Met Ala Asn Ala Phe
                245                 250                 255

Ala Gln Lys His Leu Arg Ser Ile Ile Leu Asn His Val Ile Arg Gly
            260                 265                 270

Asn Arg Pro Ile Lys Thr Glu Met Ala His Gln Leu Tyr Val Leu Gln
        275                 280                 285

Val Leu Thr Phe Asn Leu Leu Glu Glu Arg Met Met Thr Lys Met Asp
    290                 295                 300

Pro Asn Asp Gln Ala Gln Arg Asp Ile Ile Phe Glu Leu Arg Arg Ile
305                 310                 315                 320

Ala Phe Asp Ala Glu Ser Asp Pro Ser Asn Ala Pro Gly Ser Gly Thr
                325                 330                 335

Glu Lys Arg Lys Ala Met Tyr Thr Lys Asp Tyr Lys Met Leu Gly Phe
            340                 345                 350

Thr Asn His Ile Asn Pro Ala Met Asp Phe Thr Gln Thr Pro Pro Gly
        355                 360                 365

Met Leu Ala Leu Asp Asn Met Leu Tyr Leu Ala Lys Val His Gln Asp
    370                 375                 380

Thr Tyr Ile Arg Ile Val Leu Glu Asn Ser Ser Arg Glu Asp Lys His
385                 390                 395                 400

Glu Cys Pro Phe Gly Arg Ser Ala Ile Glu Leu Thr Lys Met Leu Cys
                405                 410                 415

Glu Ile Leu Gln Val Gly Glu Leu Pro Asn Glu Gly Arg Asn Asp Tyr
            420                 425                 430

His Pro Met Phe Phe Thr His Asp Arg Ala Phe Glu Glu Leu Phe Gly
        435                 440                 445

Ile Cys Ile Gln Leu Leu Asn Lys Thr Trp Lys Glu Met Arg Ala Thr
    450                 455                 460

Ala Glu Asp Phe Asn Lys Val Met Gln Val Val Arg Glu Gln Ile Thr
465                 470                 475                 480

Arg Ala Leu Pro Ser Lys Pro Asn Ser Leu Asp Gln Phe Lys Ser Lys
                485                 490                 495

Leu Arg Ser Leu Ser Tyr Ser Glu Ile Leu Arg Leu Arg Gln Ser Glu
            500                 505                 510

Arg Met Ser Gln Asp Asp Phe Gln Ser Pro Pro Ile Val Glu Leu Arg
        515                 520                 525

Glu Lys Ile Gln Pro Glu Ile Leu Glu Leu Ile Lys Gln Gln Arg Leu
    530                 535                 540

Asn Arg Leu Cys Glu Gly Ser Ser Phe Arg Lys Ile Gly Asn Arg Arg
545                 550                 555                 560

Arg Gln Glu Arg Phe Trp Tyr Cys Arg Leu Ala Leu Asn His Lys Val
                565                 570                 575

Leu His Tyr Gly Asp Leu Asp Asp Asn Pro Gln Gly Glu Val Thr Phe
            580                 585                 590
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Glu Ser Leu Gln Glu Lys Ile Pro Val Ala Asp Ile Lys Ala Ile Val
        595                 600                 605

Thr Gly Lys Asp Cys Pro His Met Lys Glu Lys Ser Ala Leu Lys Gln
    610                 615                 620

Asn Lys Glu Val Leu Glu Leu Ala Phe Ser Ile Leu Tyr Asp Pro Asp
625                 630                 635                 640

Glu Thr Leu Asn Phe Ile Ala Pro Asn Lys Tyr Glu Tyr Cys Ile Trp
                645                 650                 655

Ile Asp Gly Leu Ser Ala Leu Leu Gly Lys Asp Met Ser Ser Glu Leu
            660                 665                 670

Thr Lys Ser Asp Leu Asp Thr Leu Leu Ser Met Glu Met Lys Leu Arg
        675                 680                 685

Leu Leu Asp Leu Glu Asn Ile Gln Ile Pro Glu Ala Pro Pro Pro Ile
    690                 695                 700

Pro Lys Glu Pro Ser Ser Tyr Asp Phe Val Tyr His Tyr Gly
705                 710                 715


<210> SEQ ID NO 104
<211> LENGTH: 632
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 104

Met Glu Arg Thr Gln Ser Ser Asn Met Glu Thr Arg Leu Asp Ala Met
1               5                   10                  15

Lys Glu Leu Ala Lys Leu Ser Ala Asp Val Thr Phe Ala Thr Glu Phe
            20                  25                  30

Ile Asn Met Asp Gly Ile Ile Val Leu Thr Arg Leu Val Glu Ser Gly
        35                  40                  45

Thr Lys Leu Leu Ser His Tyr Ser Glu Met Leu Ala Phe Thr Leu Thr
    50                  55                  60

Ala Phe Leu Glu Leu Met Asp His Gly Ile Val Ser Trp Asp Met Val
65                  70                  75                  80

Ser Ile Thr Phe Ile Lys Gln Ile Ala Gly Tyr Val Ser Gln Pro Met
                85                  90                  95

Val Asp Val Ser Ile Leu Gln Arg Ser Leu Ala Ile Leu Glu Ser Met
            100                 105                 110

Val Leu Asn Ser Gln Ser Leu Tyr Gln Lys Ile Ala Glu Glu Ile Thr
        115                 120                 125

Val Gly Gln Leu Ile Ser His Leu Gln Val Ser Asn Gln Glu Ile Gln
    130                 135                 140

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

Asp Lys Arg Gln Asp Met Ala Asn Ala Phe Ala Gln Lys His Leu Arg
                165                 170                 175

Ser Ile Ile Leu Asn His Val Ile Arg Gly Asn Arg Pro Ile Lys Thr
            180                 185                 190

Glu Met Ala His Gln Leu Tyr Val Leu Gln Val Leu Thr Phe Asn Leu
        195                 200                 205

Leu Glu Glu Arg Met Met Thr Lys Met Asp Pro Asn Asp Gln Ala Gln
    210                 215                 220

Arg Asp Ile Ile Phe Glu Leu Arg Arg Ile Ala Phe Asp Ala Glu Ser
225                 230                 235                 240

Asp Pro Ser Asn Ala Pro Gly Ser Gly Thr Glu Lys Arg Lys Ala Met
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               245                 250                 255

Tyr Thr Lys Asp Tyr Lys Met Leu Gly Phe Thr Asn His Ile Asn Pro
            260                 265                 270

Ala Met Asp Phe Thr Gln Thr Pro Pro Gly Met Leu Ala Leu Asp Asn
        275                 280                 285

Met Leu Tyr Leu Ala Lys Val His Gln Asp Thr Tyr Ile Arg Ile Val
    290                 295                 300

Leu Glu Asn Ser Ser Arg Glu Asp Lys His Glu Cys Pro Phe Gly Arg
305                 310                 315                 320

Ser Ala Ile Glu Leu Thr Lys Met Leu Cys Glu Ile Leu Gln Val Gly
                325                 330                 335

Glu Leu Pro Asn Glu Gly Arg Asn Asp Tyr His Pro Met Phe Phe Thr
            340                 345                 350

His Asp Arg Ala Phe Glu Glu Leu Phe Gly Ile Cys Ile Gln Leu Leu
        355                 360                 365

Asn Lys Thr Trp Lys Glu Met Arg Ala Thr Ala Glu Asp Phe Asn Lys
    370                 375                 380

Val Met Gln Val Val Arg Glu Gln Ile Thr Arg Ala Leu Pro Ser Lys
385                 390                 395                 400

Pro Asn Ser Leu Asp Gln Phe Lys Ser Lys Leu Arg Ser Leu Ser Tyr
                405                 410                 415

Ser Glu Ile Leu Arg Leu Arg Gln Ser Glu Arg Met Ser Gln Asp Asp
            420                 425                 430

Phe Gln Ser Pro Pro Ile Val Glu Leu Arg Glu Lys Ile Gln Pro Glu
        435                 440                 445

Ile Leu Glu Leu Ile Lys Gln Gln Arg Leu Asn Arg Leu Cys Glu Gly
    450                 455                 460

Ser Ser Phe Arg Lys Ile Gly Asn Arg Arg Arg Gln Glu Arg Phe Trp
465                 470                 475                 480

Tyr Cys Arg Leu Ala Leu Asn His Lys Val Leu His Tyr Gly Asp Leu
                485                 490                 495

Asp Asp Asn Pro Gln Gly Glu Val Thr Phe Glu Ser Leu Gln Glu Lys
            500                 505                 510

Ile Pro Val Ala Asp Ile Lys Ala Ile Val Thr Gly Lys Asp Cys Pro
        515                 520                 525

His Met Lys Glu Lys Ser Ala Leu Lys Gln Asn Lys Glu Val Leu Glu
    530                 535                 540

Leu Ala Phe Ser Ile Leu Tyr Asp Pro Asp Glu Thr Leu Asn Phe Ile
545                 550                 555                 560

Ala Pro Asn Lys Tyr Glu Tyr Cys Ile Trp Ile Asp Gly Leu Ser Ala
                565                 570                 575

Leu Leu Gly Lys Asp Met Ser Ser Glu Leu Thr Lys Ser Asp Leu Asp
            580                 585                 590

Thr Leu Leu Ser Met Glu Met Lys Leu Arg Leu Leu Asp Leu Glu Asn
        595                 600                 605

Ile Gln Ile Pro Glu Ala Pro Pro Pro Ile Pro Lys Glu Pro Ser Ser
    610                 615                 620

Tyr Asp Phe Val Tyr His Tyr Gly
625                 630


<210> SEQ ID NO 105
<211> LENGTH: 463
<212> TYPE: PRT
<213> ORGANISM: Human
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<400> SEQUENCE: 105

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Met Ala Ala Leu Arg Ala Leu Cys Gly Phe Arg Gly Val Ala Ala Gln
1               5                  10                  15

Val Leu Arg Pro Gly Ala Gly Val Arg Leu Pro Ile Gln Pro Ser Arg
            20                  25                  30

Gly Val Arg Gln Trp Gln Pro Asp Val Glu Trp Ala Gln Gln Phe Gly
        35                  40                  45

Gly Ala Val Met Tyr Pro Ser Lys Glu Thr Ala His Trp Lys Pro Pro
    50                  55                  60

Pro Trp Asn Asp Val Asp Pro Pro Lys Asp Thr Ile Val Lys Asn Ile
65                  70                  75                  80

Thr Leu Asn Phe Gly Pro Gln His Pro Ala Ala His Gly Val Leu Arg
                85                  90                  95

Leu Val Met Glu Leu Ser Gly Glu Met Val Arg Lys Cys Asp Pro His
            100                 105                 110

Ile Gly Leu Leu His Arg Gly Thr Glu Lys Leu Ile Glu Tyr Lys Thr
        115                 120                 125

Tyr Leu Gln Ala Leu Pro Tyr Phe Asp Arg Leu Asp Tyr Val Ser Met
    130                 135                 140

Met Cys Asn Glu Gln Ala Tyr Ser Leu Ala Val Glu Lys Leu Leu Asn
145                 150                 155                 160

Ile Arg Pro Pro Pro Arg Ala Gln Trp Ile Arg Val Leu Phe Gly Glu
                165                 170                 175

Ile Thr Arg Leu Leu Asn His Ile Met Ala Val Thr Thr His Ala Leu
            180                 185                 190

Asp Leu Gly Ala Met Thr Pro Phe Phe Trp Leu Phe Glu Glu Arg Glu
        195                 200                 205

Lys Met Phe Glu Phe Tyr Glu Arg Val Ser Gly Ala Arg Met His Ala
    210                 215                 220

Ala Tyr Ile Arg Pro Gly Gly Val His Gln Asp Leu Pro Leu Gly Leu
225                 230                 235                 240

Met Asp Asp Ile Tyr Gln Phe Ser Lys Asn Phe Ser Leu Arg Leu Asp
                245                 250                 255

Glu Leu Glu Glu Leu Leu Thr Asn Asn Arg Ile Trp Arg Asn Arg Thr
            260                 265                 270

Ile Asp Ile Gly Val Val Thr Ala Glu Glu Ala Leu Asn Tyr Gly Phe
        275                 280                 285

Ser Gly Val Met Leu Arg Gly Ser Gly Ile Gln Trp Asp Leu Arg Lys
    290                 295                 300

Thr Gln Pro Tyr Asp Val Tyr Asp Gln Val Glu Phe Asp Val Pro Val
305                 310                 315                 320

Gly Ser Arg Gly Asp Cys Tyr Asp Arg Tyr Leu Cys Arg Val Glu Glu
                325                 330                 335

Met Arg Gln Ser Leu Arg Ile Ile Ala Gln Cys Leu Asn Lys Met Pro
            340                 345                 350

Pro Gly Glu Ile Lys Val Asp Asp Ala Lys Val Ser Pro Pro Lys Arg
        355                 360                 365

Ala Glu Met Lys Thr Ser Met Glu Ser Leu Ile His His Phe Lys Leu
    370                 375                 380

Tyr Thr Glu Gly Tyr Gln Val Pro Pro Gly Ala Thr Tyr Thr Ala Ile
385                 390                 395                 400

Glu Ala Pro Lys Gly Glu Phe Gly Val Tyr Leu Val Ser Asp Gly Ser
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                405                 410                 415

Ser Arg Pro Tyr Arg Cys Lys Ile Lys Ala Pro Gly Phe Ala His Leu
            420                 425                 430

Ala Gly Leu Asp Lys Met Ser Lys Gly His Met Leu Ala Asp Val Val
        435                 440                 445

Ala Ile Ile Gly Thr Gln Asp Ile Val Phe Gly Glu Val Asp Arg
    450                 455                 460


<210> SEQ ID NO 106
<211> LENGTH: 463
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 106

Met Ala Ala Leu Arg Ala Leu Cys Gly Phe Arg Gly Val Ala Ala Gln
1               5                   10                  15

Val Leu Arg Pro Gly Ala Gly Val Arg Leu Pro Ile Gln Pro Ser Arg
            20                  25                  30

Gly Val Arg Gln Trp Gln Pro Asp Val Glu Trp Ala Gln Gln Phe Gly
        35                  40                  45

Gly Ala Val Met Tyr Pro Ser Lys Glu Thr Ala His Trp Lys Pro Pro
    50                  55                  60

Pro Trp Asn Asp Val Asp Pro Pro Lys Asp Thr Ile Val Lys Asn Ile
65                  70                  75                  80

Thr Leu Asn Phe Gly Pro Gln His Pro Ala Ala His Gly Val Leu Arg
                85                  90                  95

Leu Val Met Glu Leu Ser Gly Glu Met Val Arg Lys Cys Asp Pro His
            100                 105                 110

Ile Gly Leu Leu His Arg Gly Thr Glu Lys Leu Ile Glu Tyr Lys Thr
        115                 120                 125

Tyr Leu Gln Ala Leu Pro Tyr Phe Asp Arg Leu Asp Tyr Val Ser Met
    130                 135                 140

Met Cys Asn Glu Gln Ala Tyr Ser Leu Ala Val Glu Lys Leu Leu Asn
145                 150                 155                 160

Ile Arg Pro Pro Pro Arg Ala Gln Trp Ile Arg Val Leu Phe Gly Glu
                165                 170                 175

Ile Thr Arg Leu Leu Asn His Ile Met Ala Val Thr Thr His Ala Leu
            180                 185                 190

Asp Leu Gly Ala Met Thr Pro Phe Phe Trp Leu Phe Glu Glu Arg Glu
        195                 200                 205

Lys Met Phe Glu Phe Tyr Glu Arg Val Ser Gly Ala Arg Met His Ala
    210                 215                 220

Ala Tyr Ile Arg Pro Gly Gly Val His Gln Asp Leu Pro Leu Gly Leu
225                 230                 235                 240

Met Asp Asp Ile Tyr Gln Phe Ser Lys Asn Phe Ser Leu Arg Leu Asp
                245                 250                 255

Glu Leu Glu Glu Leu Leu Thr Asn Asn Arg Ile Trp Arg Asn Arg Thr
            260                 265                 270

Ile Asp Ile Gly Val Val Thr Ala Glu Glu Ala Leu Asn Tyr Gly Phe
        275                 280                 285

Ser Gly Val Met Leu Arg Gly Ser Gly Ile Gln Trp Asp Leu Arg Lys
    290                 295                 300

Thr Gln Pro Tyr Asp Val Tyr Asp Gln Val Glu Phe Asp Val Pro Val
305                 310                 315                 320
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Gly Ser Arg Gly Asp Cys Tyr Asp Arg Tyr Leu Cys Arg Val Glu Glu
                325                 330                 335

Met Arg Gln Ser Leu Arg Ile Ile Ala Gln Cys Leu Asn Lys Met Pro
            340                 345                 350

Pro Gly Glu Ile Lys Val Asp Asp Ala Lys Val Ser Pro Pro Lys Arg
        355                 360                 365

Ala Glu Met Lys Thr Ser Met Glu Ser Leu Ile His His Phe Lys Leu
    370                 375                 380

Tyr Thr Glu Gly Tyr Gln Val Pro Pro Gly Ala Thr Tyr Thr Ala Ile
385                 390                 395                 400

Glu Ala Pro Lys Gly Glu Phe Gly Val Tyr Leu Val Ser Asp Gly Ser
                405                 410                 415

Ser Arg Pro Tyr Arg Cys Lys Ile Lys Ala Pro Gly Phe Ala His Leu
            420                 425                 430

Ala Gly Leu Asp Lys Met Ser Lys Gly His Met Leu Ala Asp Val Val
        435                 440                 445

Ala Ile Ile Gly Thr Gln Asp Ile Val Phe Gly Glu Val Asp Arg
    450                 455                 460


<210> SEQ ID NO 107
<211> LENGTH: 693
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 107

Met Ala Gly Gly Pro Gly Pro Gly Glu Pro Ala Ala Pro Gly Ala Gln
1               5                   10                  15

His Phe Leu Tyr Glu Val Pro Pro Trp Val Met Cys Arg Phe Tyr Lys
            20                  25                  30

Val Met Asp Ala Leu Glu Pro Ala Asp Trp Cys Gln Phe Gly Gly Trp
        35                  40                  45

Arg Arg Ala Ala Gly Gly Arg Glu Ala Arg Gly Leu Leu Ala Pro Thr
    50                  55                  60

Pro Asp Ala Pro Arg Pro Ala Ala Ala Leu Ile Val Arg Asp Gln Thr
65                  70                  75                  80

Glu Leu Arg Leu Cys Glu Arg Ser Gly Gln Arg Thr Ala Ser Val Leu
                85                  90                  95

Trp Pro Trp Ile Asn Arg Asn Ala Arg Val Ala Asp Leu Val His Ile
            100                 105                 110

Leu Thr His Leu Gln Leu Leu Arg Ala Arg Asp Ile Ile Thr Ala Trp
        115                 120                 125

His Pro Pro Ala Pro Leu Pro Ser Pro Gly Thr Thr Ala Pro Arg Pro
    130                 135                 140

Ser Ser Ile Pro Ala Pro Ala Glu Ala Glu Ala Trp Ser Pro Arg Lys
145                 150                 155                 160

Leu Pro Ser Ser Ala Ser Thr Phe Leu Ser Pro Ala Phe Pro Gly Ser
                165                 170                 175

Gln Thr His Ser Gly Pro Glu Leu Gly Leu Val Pro Ser Pro Ala Ser
            180                 185                 190

Leu Trp Pro Pro Pro Pro Ser Pro Ala Pro Ser Ser Thr Lys Pro Gly
        195                 200                 205

Pro Glu Ser Ser Val Ser Leu Leu Gln Gly Ala Arg Pro Phe Pro Phe
    210                 215                 220

Cys Trp Pro Leu Cys Glu Ile Ser Arg Gly Thr His Asn Phe Ser Glu
225                 230                 235                 240
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Glu Leu Lys Ile Gly Glu Gly Gly Phe Gly Cys Val Tyr Arg Ala Val
               245                 250                 255

Met Arg Asn Thr Val Tyr Ala Val Lys Arg Leu Lys Glu Asn Ala Asp
           260                 265                 270

Leu Glu Trp Thr Ala Val Lys Gln Ser Phe Leu Thr Glu Val Glu Gln
       275                 280                 285

Leu Ser Arg Phe Arg His Pro Asn Ile Val Asp Phe Ala Gly Tyr Cys
   290                 295                 300

Ala Gln Asn Gly Phe Tyr Cys Leu Val Tyr Gly Phe Leu Pro Asn Gly
305                 310                 315                 320

Ser Leu Glu Asp Arg Leu His Cys Gln Thr Gln Ala Cys Pro Pro Leu
               325                 330                 335

Ser Trp Pro Gln Arg Leu Asp Ile Leu Leu Gly Thr Ala Arg Ala Ile
           340                 345                 350

Gln Phe Leu His Gln Asp Ser Pro Ser Leu Ile His Gly Asp Ile Lys
       355                 360                 365

Ser Ser Asn Val Leu Leu Asp Glu Arg Leu Thr Pro Lys Leu Gly Asp
   370                 375                 380

Phe Gly Leu Ala Arg Phe Ser Arg Phe Ala Gly Ser Ser Pro Ser Gln
385                 390                 395                 400

Ser Ser Met Val Ala Arg Thr Gln Thr Val Arg Gly Thr Leu Ala Tyr
               405                 410                 415

Leu Pro Glu Glu Tyr Ile Lys Thr Gly Arg Leu Ala Val Asp Thr Asp
           420                 425                 430

Thr Phe Ser Phe Gly Val Val Val Leu Glu Thr Leu Ala Gly Gln Arg
       435                 440                 445

Ala Val Lys Thr His Gly Ala Arg Thr Lys Tyr Leu Lys Asp Leu Val
   450                 455                 460

Glu Glu Glu Ala Glu Glu Ala Gly Val Ala Leu Arg Ser Thr Gln Ser
465                 470                 475                 480

Thr Leu Gln Ala Gly Leu Ala Ala Asp Ala Trp Ala Ala Pro Ile Ala
               485                 490                 495

Met Gln Ile Tyr Lys Lys His Leu Gly Gln Leu Ala Cys Cys Cys Leu
           500                 505                 510

His Arg Arg Ala Lys Arg Arg Pro Pro Met Thr Gln Glu Asn Ser Tyr
       515                 520                 525

Val Ser Ser Thr Gly Arg Ala His Ser Gly Ala Ala Pro Trp Gln Pro
   530                 535                 540

Leu Ala Ala Pro Ser Gly Ala Ser Ala Gln Ala Ala Glu Gln Leu Gln
545                 550                 555                 560

Arg Gly Pro Asn Gln Pro Val Glu Ser Asp Glu Ser Leu Gly Gly Leu
               565                 570                 575

Ser Ala Ala Leu Arg Ser Trp His Leu Thr Pro Ser Cys Pro Leu Asp
           580                 585                 590

Pro Ala Pro Leu Arg Glu Ala Gly Cys Pro Gln Gly Asp Thr Ala Gly
       595                 600                 605

Glu Ser Ser Trp Gly Ser Gly Pro Gly Ser Arg Pro Thr Ala Val Glu
   610                 615                 620

Gly Leu Ala Leu Gly Ser Ser Ala Ser Ser Ser Ser Glu Pro Pro Gln
625                 630                 635                 640

Ile Ile Ile Asn Pro Ala Arg Gln Lys Met Val Gln Lys Leu Ala Leu
               645                 650                 655
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Tyr Glu Asp Gly Ala Leu Asp Ser Leu Gln Leu Leu Ser Ser Ser Ser
            660                 665                 670

Leu Pro Gly Leu Gly Leu Glu Gln Asp Arg Gln Gly Pro Glu Glu Ser
        675                 680                 685

Asp Glu Phe Gln Ser
    690


<210> SEQ ID NO 108
<211> LENGTH: 712
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 108

Met Ala Gly Gly Pro Gly Pro Gly Glu Pro Ala Ala Pro Gly Ala Gln
1               5                   10                  15

His Phe Leu Tyr Glu Val Pro Pro Trp Val Met Cys Arg Phe Tyr Lys
            20                  25                  30

Val Met Asp Ala Leu Glu Pro Ala Asp Trp Cys Gln Phe Ala Ala Leu
        35                  40                  45

Ile Val Arg Asp Gln Thr Glu Leu Arg Leu Cys Glu Arg Ser Gly Gln
    50                  55                  60

Arg Thr Ala Ser Val Leu Trp Pro Trp Ile Asn Arg Asn Ala Arg Val
65                  70                  75                  80

Ala Asp Leu Val His Ile Leu Thr His Leu Gln Leu Leu Arg Ala Arg
                85                  90                  95

Asp Ile Ile Thr Ala Trp His Pro Pro Ala Pro Leu Pro Ser Pro Gly
            100                 105                 110

Thr Thr Ala Pro Arg Pro Ser Ser Ile Pro Ala Pro Ala Glu Ala Glu
        115                 120                 125

Ala Trp Ser Pro Arg Lys Leu Pro Ser Ser Ala Ser Thr Phe Leu Ser
    130                 135                 140

Pro Ala Phe Pro Gly Ser Gln Thr His Ser Gly Pro Glu Leu Gly Leu
145                 150                 155                 160

Val Pro Ser Pro Ala Ser Leu Trp Pro Pro Pro Pro Ser Pro Ala Pro
                165                 170                 175

Ser Ser Thr Lys Pro Gly Pro Glu Ser Ser Val Ser Leu Leu Gln Gly
            180                 185                 190

Ala Arg Pro Phe Pro Phe Cys Trp Pro Leu Cys Glu Ile Ser Arg Gly
        195                 200                 205

Thr His Asn Phe Ser Glu Glu Leu Lys Ile Gly Glu Gly Gly Phe Gly
    210                 215                 220

Cys Val Tyr Arg Ala Val Met Arg Asn Thr Val Tyr Ala Val Lys Arg
225                 230                 235                 240

Leu Lys Glu Asn Ala Asp Leu Glu Trp Thr Ala Val Lys Gln Ser Phe
                245                 250                 255

Leu Thr Glu Val Glu Gln Leu Ser Arg Phe Arg His Pro Asn Ile Val
            260                 265                 270

Asp Phe Ala Gly Tyr Cys Ala Gln Asn Gly Phe Tyr Cys Leu Val Tyr
        275                 280                 285

Gly Phe Leu Pro Asn Gly Ser Leu Glu Asp Arg Leu His Cys Gln Thr
    290                 295                 300

Gln Ala Cys Pro Pro Leu Ser Trp Pro Gln Arg Leu Asp Ile Leu Leu
305                 310                 315                 320

Gly Thr Ala Arg Ala Ile Gln Phe Leu His Gln Asp Ser Pro Ser Leu
                325                 330                 335
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Ile His Gly Asp Ile Lys Ser Ser Asn Val Leu Leu Asp Glu Arg Leu
            340                 345                 350

Thr Pro Lys Leu Gly Asp Phe Gly Leu Ala Arg Phe Ser Arg Phe Ala
        355                 360                 365

Gly Ser Ser Pro Ser Gln Ser Ser Met Val Ala Arg Thr Gln Thr Val
    370                 375                 380

Arg Gly Thr Leu Ala Tyr Leu Pro Glu Glu Tyr Ile Lys Thr Gly Arg
385                 390                 395                 400

Leu Ala Val Asp Thr Asp Thr Phe Ser Phe Gly Val Val Val Leu Glu
                405                 410                 415

Thr Leu Ala Gly Gln Arg Ala Val Lys Thr His Gly Ala Arg Thr Lys
            420                 425                 430

Tyr Leu Lys Asp Leu Val Glu Glu Glu Ala Glu Glu Ala Gly Val Ala
        435                 440                 445

Leu Arg Ser Thr Gln Ser Thr Leu Gln Ala Gly Leu Ala Ala Asp Ala
    450                 455                 460

Trp Ala Ala Pro Ile Ala Met Gln Ile Tyr Lys Lys His Leu Asp Pro
465                 470                 475                 480

Arg Pro Gly Pro Cys Pro Pro Glu Leu Gly Leu Gly Leu Gly Gln Leu
                485                 490                 495

Ala Cys Cys Cys Leu His Arg Arg Ala Lys Arg Arg Pro Pro Met Thr
            500                 505                 510

Gln Val Tyr Glu Arg Leu Glu Lys Leu Gln Ala Val Val Ala Gly Val
        515                 520                 525

Pro Gly His Ser Glu Ala Ala Ser Cys Ile Pro Pro Ser Pro Gln Glu
    530                 535                 540

Asn Ser Tyr Val Ser Ser Thr Gly Arg Ala His Ser Gly Ala Ala Pro
545                 550                 555                 560

Trp Gln Pro Leu Ala Ala Pro Ser Gly Ala Ser Ala Gln Ala Ala Glu
                565                 570                 575

Gln Leu Gln Arg Gly Pro Asn Gln Pro Val Glu Ser Asp Glu Ser Leu
            580                 585                 590

Gly Gly Leu Ser Ala Ala Leu Arg Ser Trp His Leu Thr Pro Ser Cys
        595                 600                 605

Pro Leu Asp Pro Ala Pro Leu Arg Glu Ala Gly Cys Pro Gln Gly Asp
    610                 615                 620

Thr Ala Gly Glu Ser Ser Trp Gly Ser Gly Pro Gly Ser Arg Pro Thr
625                 630                 635                 640

Ala Val Glu Gly Leu Ala Leu Gly Ser Ser Ala Ser Ser Ser Ser Glu
                645                 650                 655

Pro Pro Gln Ile Ile Ile Asn Pro Ala Arg Gln Lys Met Val Gln Lys
            660                 665                 670

Leu Ala Leu Tyr Glu Asp Gly Ala Leu Asp Ser Leu Gln Leu Leu Ser
        675                 680                 685

Ser Ser Ser Leu Pro Gly Leu Gly Leu Glu Gln Asp Arg Gln Gly Pro
    690                 695                 700

Glu Glu Ser Asp Glu Phe Gln Ser
705                 710


<210> SEQ ID NO 109
<211> LENGTH: 682
<212> TYPE: PRT
<213> ORGANISM: Human
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<400> SEQUENCE: 109

```
Met Ala Gly Gly Pro Gly Pro Gly Glu Pro Ala Ala Pro Gly Ala Gln
1               5                  10                  15

His Phe Leu Tyr Glu Val Pro Pro Trp Val Met Cys Arg Phe Tyr Lys
            20                  25                  30

Val Met Asp Ala Leu Glu Pro Ala Asp Trp Cys Gln Phe Ala Ala Leu
        35                  40                  45

Ile Val Arg Asp Gln Thr Glu Leu Arg Leu Cys Glu Arg Ser Gly Gln
    50                  55                  60

Arg Thr Ala Ser Val Leu Trp Pro Trp Ile Asn Arg Asn Ala Arg Val
65                  70                  75                  80

Ala Asp Leu Val His Ile Leu Thr His Leu Gln Leu Leu Arg Ala Arg
                85                  90                  95

Asp Ile Ile Thr Ala Trp His Pro Pro Ala Pro Leu Pro Ser Pro Gly
            100                 105                 110

Thr Thr Ala Pro Arg Pro Ser Ser Ile Pro Ala Pro Ala Glu Ala Glu
        115                 120                 125

Ala Trp Ser Pro Arg Lys Leu Pro Ser Ser Ala Ser Thr Phe Leu Ser
    130                 135                 140

Pro Ala Phe Pro Gly Ser Gln Thr His Ser Gly Pro Glu Leu Gly Leu
145                 150                 155                 160

Val Pro Ser Pro Ala Ser Leu Trp Pro Pro Pro Pro Ser Pro Ala Pro
                165                 170                 175

Ser Ser Thr Lys Pro Gly Pro Glu Ser Ser Val Ser Leu Leu Gln Gly
            180                 185                 190

Ala Arg Pro Phe Pro Phe Cys Trp Pro Leu Cys Glu Ile Ser Arg Gly
        195                 200                 205

Thr His Asn Phe Ser Glu Glu Leu Lys Ile Gly Glu Gly Gly Phe Gly
    210                 215                 220

Cys Val Tyr Arg Ala Val Met Arg Asn Thr Val Tyr Ala Val Lys Arg
225                 230                 235                 240

Leu Lys Glu Asn Ala Asp Leu Glu Trp Thr Ala Val Lys Gln Ser Phe
                245                 250                 255

Leu Thr Glu Val Glu Gln Leu Ser Arg Phe Arg His Pro Asn Ile Val
            260                 265                 270

Asp Phe Ala Gly Tyr Cys Ala Gln Asn Gly Phe Tyr Cys Leu Val Tyr
        275                 280                 285

Gly Phe Leu Pro Asn Gly Ser Leu Glu Asp Arg Leu His Cys Gln Thr
    290                 295                 300

Gln Ala Cys Pro Pro Leu Ser Trp Pro Gln Arg Leu Asp Ile Leu Leu
305                 310                 315                 320

Gly Thr Ala Arg Ala Ile Gln Phe Leu His Gln Asp Ser Pro Ser Leu
                325                 330                 335

Ile His Gly Asp Ile Lys Ser Ser Asn Val Leu Leu Asp Glu Arg Leu
            340                 345                 350

Thr Pro Lys Leu Gly Asp Phe Gly Leu Ala Arg Phe Ser Arg Phe Ala
        355                 360                 365

Gly Ser Ser Pro Ser Gln Ser Ser Met Val Ala Arg Thr Gln Thr Val
    370                 375                 380

Arg Gly Thr Leu Ala Tyr Leu Pro Glu Glu Tyr Ile Lys Thr Gly Arg
385                 390                 395                 400

Leu Ala Val Asp Thr Asp Thr Phe Ser Phe Gly Val Val Val Leu Glu
                405                 410                 415
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Thr Leu Ala Gly Gln Arg Ala Val Lys Thr His Gly Ala Arg Thr Lys
            420                 425                 430

Tyr Leu Lys Asp Leu Val Glu Glu Glu Ala Glu Glu Ala Gly Val Ala
        435                 440                 445

Leu Arg Ser Thr Gln Ser Thr Leu Gln Ala Gly Leu Ala Ala Asp Ala
    450                 455                 460

Trp Ala Ala Pro Ile Ala Met Gln Ile Tyr Lys Lys His Leu Asp Pro
465                 470                 475                 480

Arg Pro Gly Pro Cys Pro Pro Glu Leu Gly Leu Gly Leu Gly Gln Leu
                485                 490                 495

Ala Cys Cys Cys Leu His Arg Arg Ala Lys Arg Arg Pro Pro Met Thr
            500                 505                 510

Gln Glu Asn Ser Tyr Val Ser Ser Thr Gly Arg Ala His Ser Gly Ala
        515                 520                 525

Ala Pro Trp Gln Pro Leu Ala Ala Pro Ser Gly Ala Ser Ala Gln Ala
    530                 535                 540

Ala Glu Gln Leu Gln Arg Gly Pro Asn Gln Pro Val Glu Ser Asp Glu
545                 550                 555                 560

Ser Leu Gly Gly Leu Ser Ala Ala Leu Arg Ser Trp His Leu Thr Pro
                565                 570                 575

Ser Cys Pro Leu Asp Pro Ala Pro Leu Arg Glu Ala Gly Cys Pro Gln
            580                 585                 590

Gly Asp Thr Ala Gly Glu Ser Ser Trp Gly Ser Gly Pro Gly Ser Arg
        595                 600                 605

Pro Thr Ala Val Glu Gly Leu Ala Leu Gly Ser Ser Ala Ser Ser Ser
    610                 615                 620

Ser Glu Pro Pro Gln Ile Ile Ile Asn Pro Ala Arg Gln Lys Met Val
625                 630                 635                 640

Gln Lys Leu Ala Leu Tyr Glu Asp Gly Ala Leu Asp Ser Leu Gln Leu
                645                 650                 655

Leu Ser Ser Ser Ser Leu Pro Gly Leu Gly Leu Glu Gln Asp Arg Gln
            660                 665                 670

Gly Pro Glu Glu Ser Asp Glu Phe Gln Ser
        675                 680


<210> SEQ ID NO 110
<211> LENGTH: 633
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 110

Met Ala Gly Gly Pro Gly Pro Gly Glu Pro Ala Ala Pro Gly Ala Gln
1               5                   10                  15

His Phe Leu Tyr Glu Val Pro Pro Trp Val Met Cys Arg Phe Tyr Lys
            20                  25                  30

Val Met Asp Ala Leu Glu Pro Ala Asp Trp Cys Gln Phe Ala Ala Leu
        35                  40                  45

Ile Val Arg Asp Gln Thr Glu Leu Arg Leu Cys Glu Arg Ser Gly Gln
    50                  55                  60

Arg Thr Ala Ser Val Leu Trp Pro Trp Ile Asn Arg Asn Ala Arg Val
65                  70                  75                  80

Ala Asp Leu Val His Ile Leu Thr His Leu Gln Leu Leu Arg Ala Arg
                85                  90                  95

Asp Ile Ile Thr Ala Trp His Pro Pro Ala Pro Leu Pro Ser Pro Gly
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-continued

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           100                 105                 110

Thr Thr Ala Pro Arg Pro Ser Ser Ile Pro Ala Pro Ala Glu Ala Glu
        115                 120                 125

Ala Trp Ser Pro Arg Lys Leu Pro Ser Ser Ala Ser Thr Phe Leu Ser
    130                 135                 140

Pro Ala Phe Pro Gly Ser Gln Thr His Ser Gly Pro Glu Leu Gly Leu
145                 150                 155                 160

Val Pro Ser Pro Ala Ser Leu Trp Pro Pro Pro Pro Ser Pro Ala Pro
                165                 170                 175

Ser Ser Thr Lys Pro Gly Pro Glu Ser Ser Val Ser Leu Leu Gln Gly
            180                 185                 190

Ala Arg Pro Phe Pro Phe Cys Trp Pro Leu Cys Glu Ile Ser Arg Gly
        195                 200                 205

Thr His Asn Phe Ser Glu Glu Leu Lys Ile Gly Glu Gly Gly Phe Gly
    210                 215                 220

Cys Val Tyr Arg Ala Val Met Arg Asn Thr Val Tyr Ala Val Lys Arg
225                 230                 235                 240

Leu Lys Glu Asn Ala Asp Leu Glu Trp Thr Ala Val Lys Gln Ser Phe
                245                 250                 255

Leu Thr Glu Val Glu Gln Leu Ser Arg Phe Arg His Pro Asn Ile Val
            260                 265                 270

Asp Phe Ala Gly Tyr Cys Ala Gln Asn Gly Phe Tyr Cys Leu Val Tyr
        275                 280                 285

Gly Phe Leu Pro Asn Gly Ser Leu Glu Asp Arg Leu His Cys Gln Thr
    290                 295                 300

Gln Ala Cys Pro Pro Leu Ser Trp Pro Gln Arg Leu Asp Ile Leu Leu
305                 310                 315                 320

Gly Thr Ala Arg Ala Ile Gln Phe Leu His Gln Asp Ser Pro Ser Leu
                325                 330                 335

Ile His Gly Asp Ile Lys Ser Ser Asn Val Leu Leu Asp Glu Arg Leu
            340                 345                 350

Thr Pro Lys Leu Gly Asp Phe Gly Leu Ala Arg Phe Ser Arg Phe Ala
        355                 360                 365

Gly Ser Ser Pro Ser Gln Ser Ser Met Val Ala Arg Thr Gln Thr Val
    370                 375                 380

Arg Gly Thr Leu Ala Tyr Leu Pro Glu Glu Tyr Ile Lys Thr Gly Arg
385                 390                 395                 400

Leu Ala Val Asp Thr Asp Thr Phe Ser Phe Gly Val Val Val Leu Glu
                405                 410                 415

Thr Leu Ala Gly Gln Arg Ala Val Lys Thr His Gly Ala Arg Thr Lys
            420                 425                 430

Tyr Leu Val Tyr Glu Arg Leu Glu Lys Leu Gln Ala Val Val Ala Gly
        435                 440                 445

Val Pro Gly His Ser Glu Ala Ala Ser Cys Ile Pro Pro Ser Pro Gln
    450                 455                 460

Glu Asn Ser Tyr Val Ser Ser Thr Gly Arg Ala His Ser Gly Ala Ala
465                 470                 475                 480

Pro Trp Gln Pro Leu Ala Ala Pro Ser Gly Ala Ser Ala Gln Ala Ala
                485                 490                 495

Glu Gln Leu Gln Arg Gly Pro Asn Gln Pro Val Glu Ser Asp Glu Ser
            500                 505                 510

Leu Gly Gly Leu Ser Ala Ala Leu Arg Ser Trp His Leu Thr Pro Ser
        515                 520                 525
```

```
Cys Pro Leu Asp Pro Ala Pro Leu Arg Glu Ala Gly Cys Pro Gln Gly
    530                 535                 540

Asp Thr Ala Gly Glu Ser Ser Trp Gly Ser Gly Pro Gly Ser Arg Pro
545                 550                 555                 560

Thr Ala Val Glu Gly Leu Ala Leu Gly Ser Ser Ala Ser Ser Ser Ser
                565                 570                 575

Glu Pro Pro Gln Ile Ile Ile Asn Pro Ala Arg Gln Lys Met Val Gln
            580                 585                 590

Lys Leu Ala Leu Tyr Glu Asp Gly Ala Leu Asp Ser Leu Gln Leu Leu
        595                 600                 605

Ser Ser Ser Ser Leu Pro Gly Leu Gly Leu Glu Gln Asp Arg Gln Gly
    610                 615                 620

Pro Glu Glu Ser Asp Glu Phe Gln Ser
625                 630


<210> SEQ ID NO 111
<211> LENGTH: 708
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 111

Met Ala Gly Gly Pro Gly Pro Gly Glu Pro Ala Ala Pro Gly Ala Gln
1               5                   10                  15

His Phe Leu Tyr Glu Val Pro Pro Trp Val Met Cys Arg Phe Tyr Lys
            20                  25                  30

Val Met Asp Ala Leu Glu Pro Ala Asp Trp Cys Gln Phe Gly Gly Trp
        35                  40                  45

Arg Arg Ala Ala Gly Gly Arg Glu Ala Arg Gly Leu Leu Ala Pro Thr
    50                  55                  60

Pro Asp Ala Pro Arg Pro Ala Ala Ala Leu Ile Val Arg Asp Gln Thr
65                  70                  75                  80

Glu Leu Arg Leu Cys Glu Arg Ser Gly Gln Arg Thr Ala Ser Val Leu
                85                  90                  95

Trp Pro Trp Ile Asn Arg Asn Ala Arg Val Ala Asp Leu Val His Ile
            100                 105                 110

Leu Thr His Leu Gln Leu Leu Arg Ala Arg Asp Ile Ile Thr Ala Trp
        115                 120                 125

His Pro Pro Ala Pro Leu Pro Ser Pro Gly Thr Thr Ala Pro Arg Pro
    130                 135                 140

Ser Ser Ile Pro Ala Pro Ala Glu Ala Glu Ala Trp Ser Pro Arg Lys
145                 150                 155                 160

Leu Pro Ser Ser Ala Ser Thr Phe Leu Ser Pro Ala Phe Pro Gly Ser
                165                 170                 175

Gln Thr His Ser Gly Pro Glu Leu Gly Leu Val Pro Ser Pro Ala Ser
            180                 185                 190

Leu Trp Pro Pro Pro Pro Ser Pro Ala Pro Ser Ser Thr Lys Pro Gly
        195                 200                 205

Pro Glu Ser Ser Val Ser Leu Leu Gln Gly Ala Arg Pro Phe Pro Phe
    210                 215                 220

Cys Trp Pro Leu Cys Glu Ile Ser Arg Gly Thr His Asn Phe Ser Glu
225                 230                 235                 240

Glu Leu Lys Ile Gly Glu Gly Gly Phe Gly Cys Val Tyr Arg Ala Val
                245                 250                 255

Met Arg Asn Thr Val Tyr Ala Val Lys Arg Leu Lys Glu Asn Ala Asp
```

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           260                 265                 270

Leu Glu Trp Thr Ala Val Lys Gln Ser Phe Leu Thr Glu Val Glu Gln
        275                 280                 285

Leu Ser Arg Phe Arg His Pro Asn Ile Val Asp Phe Ala Gly Tyr Cys
    290                 295                 300

Ala Gln Asn Gly Phe Tyr Cys Leu Val Tyr Gly Phe Leu Pro Asn Gly
305                 310                 315                 320

Ser Leu Glu Asp Arg Leu His Cys Gln Thr Gln Ala Cys Pro Pro Leu
                325                 330                 335

Ser Trp Pro Gln Arg Leu Asp Ile Leu Leu Gly Thr Ala Arg Ala Ile
            340                 345                 350

Gln Phe Leu His Gln Asp Ser Pro Ser Leu Ile His Gly Asp Ile Lys
        355                 360                 365

Ser Ser Asn Val Leu Leu Asp Glu Arg Leu Thr Pro Lys Leu Gly Asp
    370                 375                 380

Phe Gly Leu Ala Arg Phe Ser Arg Phe Ala Gly Ser Ser Pro Ser Gln
385                 390                 395                 400

Ser Ser Met Val Ala Arg Thr Gln Thr Val Arg Gly Thr Leu Ala Tyr
                405                 410                 415

Leu Pro Glu Glu Tyr Ile Lys Thr Gly Arg Leu Ala Val Asp Thr Asp
            420                 425                 430

Thr Phe Ser Phe Gly Val Val Val Leu Glu Thr Leu Ala Gly Gln Arg
        435                 440                 445

Ala Val Lys Thr His Gly Ala Arg Thr Lys Tyr Leu Lys Asp Leu Val
    450                 455                 460

Glu Glu Glu Ala Glu Glu Ala Gly Val Ala Leu Arg Ser Thr Gln Ser
465                 470                 475                 480

Thr Leu Gln Ala Gly Leu Ala Ala Asp Ala Trp Ala Ala Pro Ile Ala
                485                 490                 495

Met Gln Ile Tyr Lys Lys His Leu Asp Pro Arg Pro Gly Pro Cys Pro
            500                 505                 510

Pro Glu Leu Gly Leu Gly Leu Gly Gln Leu Ala Cys Cys Cys Leu His
        515                 520                 525

Arg Arg Ala Lys Arg Arg Pro Pro Met Thr Gln Glu Asn Ser Tyr Val
    530                 535                 540

Ser Ser Thr Gly Arg Ala His Ser Gly Ala Ala Pro Trp Gln Pro Leu
545                 550                 555                 560

Ala Ala Pro Ser Gly Ala Ser Ala Gln Ala Ala Glu Gln Leu Gln Arg
                565                 570                 575

Gly Pro Asn Gln Pro Val Glu Ser Asp Glu Ser Leu Gly Gly Leu Ser
            580                 585                 590

Ala Ala Leu Arg Ser Trp His Leu Thr Pro Ser Cys Pro Leu Asp Pro
        595                 600                 605

Ala Pro Leu Arg Glu Ala Gly Cys Pro Gln Gly Asp Thr Ala Gly Glu
    610                 615                 620

Ser Ser Trp Gly Ser Gly Pro Gly Ser Arg Pro Thr Ala Val Glu Gly
625                 630                 635                 640

Leu Ala Leu Gly Ser Ser Ala Ser Ser Ser Ser Glu Pro Pro Gln Ile
                645                 650                 655

Ile Ile Asn Pro Ala Arg Gln Lys Met Val Gln Lys Leu Ala Leu Tyr
            660                 665                 670

Glu Asp Gly Ala Leu Asp Ser Leu Gln Leu Leu Ser Ser Ser Ser Leu
        675                 680                 685
```

Pro Gly Leu Gly Leu Glu Gln Asp Arg Gln Gly Pro Glu Glu Ser Asp
690 695 700

Glu Phe Gln Ser
705

<210> SEQ ID NO 112
<211> LENGTH: 140
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 112

Met Ala Ala Ile Pro Ser Ser Gly Ser Leu Val Ala Thr His Asp Tyr
1 5 10 15

Tyr Arg Arg Arg Leu Gly Ser Thr Ser Ser Asn Ser Ser Cys Ser Ser
20 25 30

Thr Glu Cys Pro Gly Glu Ala Ile Pro His Pro Pro Gly Glu Cys Arg
35 40 45

Ile Ala Pro Phe Ser Pro Arg Ser Ser Arg Ser Trp Gln His Gln Asp
50 55 60

Pro Thr Ser Leu Leu Ser Gly Leu Pro Lys Ala Asp Pro Gly His Trp
65 70 75 80

Trp Ala Ser Phe Phe Phe Gly Lys Ser Thr Leu Pro Phe Met Ala Thr
85 90 95

Val Leu Glu Ser Ala Glu His Ser Glu Pro Pro Gln Ala Ser Ser Ser
100 105 110

Met Thr Ala Cys Gly Leu Ala Arg Asp Ala Pro Arg Lys Gln Pro Gly
115 120 125

Gly Gln Ser Ser Thr Ala Ser Ala Gly Pro Pro Ser
130 135 140

<210> SEQ ID NO 113
<211> LENGTH: 70
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 113

Met Ala Ala Ile Pro Ser Ser Gly Ser Leu Val Ala Thr His Asp Tyr
1 5 10 15

Tyr Arg Arg Arg Leu Gly Ser Thr Ser Ser Asn Ser Ser Cys Ser Ser
20 25 30

Thr Glu Cys Pro Gly Glu Ala Ile Pro His Pro Pro Gly Leu Pro Lys
35 40 45

Ala Asp Pro Gly His Trp Trp Ala Ser Phe Phe Phe Gly Lys Ser Thr
50 55 60

Leu Pro Pro Pro Thr Leu
65 70

<210> SEQ ID NO 114
<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 114

Met Ala Ala Ile Pro Ser Ser Gly Ser Leu Val Ala Thr His Asp Tyr
1 5 10 15

Tyr Arg Arg Arg Leu Gly Ser Thr Ser Ser Asn Ser Ser Cys Ser Ser
20 25 30

```
Thr Glu Cys Pro Gly Glu Ala Ile Pro His Pro Pro Gly Leu Pro Lys
        35                  40                  45

Ala Asp Pro Gly His Trp Trp Ala Ser Phe Phe Phe Gly Lys Ser Thr
    50                  55                  60

Leu Pro Phe Met Ala Thr Val Leu Glu Ser Ala Glu His Ser Glu Pro
65                  70                  75                  80

Pro Gln Ala Ser Ser Ser Met Thr Ala Cys Gly Leu Ala Arg Asp Ala
                85                  90                  95

Pro Arg Lys Gln Pro Gly Gly Gln Ser Ser Thr Ala Ser Ala Gly Pro
            100                 105                 110

Pro Ser


<210> SEQ ID NO 115
<211> LENGTH: 400
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 115

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

Met Glu Leu Glu Asn Ile Arg Arg Arg Lys Gln Glu Leu Leu Val Glu
            20                  25                  30

Ile Gln Arg Leu Arg Glu Glu Leu Ser Glu Ala Met Ser Glu Val Glu
        35                  40                  45

Gly Leu Glu Ala Asn Glu Gly Ser Lys Thr Leu Gln Arg Asn Arg Lys
    50                  55                  60

Met Ala Met Gly Arg Lys Lys Phe Asn Met Asp Pro Lys Lys Gly Ile
65                  70                  75                  80

Gln Phe Leu Val Glu Asn Glu Leu Leu Gln Asn Thr Pro Glu Glu Ile
                85                  90                  95

Ala Arg Phe Leu Tyr Lys Gly Glu Gly Leu Asn Lys Thr Ala Ile Gly
            100                 105                 110

Asp Tyr Leu Gly Glu Arg Glu Glu Leu Asn Leu Ala Val Leu His Ala
        115                 120                 125

Phe Val Asp Leu His Glu Phe Thr Asp Leu Asn Leu Val Gln Ala Leu
    130                 135                 140

Arg Gln Phe Leu Trp Ser Phe Arg Leu Pro Gly Glu Ala Gln Lys Ile
145                 150                 155                 160

Asp Arg Met Met Glu Ala Phe Ala Gln Arg Tyr Cys Leu Cys Asn Pro
                165                 170                 175

Gly Val Phe Gln Ser Thr Asp Thr Cys Tyr Val Leu Ser Phe Ala Val
            180                 185                 190

Ile Met Leu Asn Thr Ser Leu His Asn Pro Asn Val Arg Asp Lys Pro
        195                 200                 205

Gly Leu Glu Arg Phe Val Ala Met Asn Arg Gly Ile Asn Glu Gly Gly
    210                 215                 220

Asp Leu Pro Glu Glu Leu Leu Arg Asn Leu Tyr Asp Ser Ile Arg Asn
225                 230                 235                 240

Glu Pro Phe Lys Ile Pro Glu Asp Asp Gly Asn Asp Leu Thr His Thr
                245                 250                 255

Phe Phe Asn Pro Asp Arg Glu Gly Trp Leu Leu Lys Leu Gly Arg Gly
            260                 265                 270

Arg Val Lys Thr Trp Lys Arg Arg Trp Phe Ile Leu Thr Asp Asn Cys
        275                 280                 285
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```
Leu Tyr Tyr Phe Glu Tyr Thr Thr Asp Lys Glu Pro Arg Gly Ile Ile
    290                 295                 300

Pro Leu Glu Asn Leu Ser Ile Arg Glu Val Asp Asp Pro Arg Lys Pro
305                 310                 315                 320

Asn Cys Phe Glu Leu Tyr Ile Pro Asn Asn Lys Gly Gln Leu Ile Lys
                325                 330                 335

Ala Cys Lys Thr Glu Ala Asp Gly Arg Val Val Glu Gly Asn His Met
            340                 345                 350

Val Tyr Arg Ile Ser Ala Pro Thr Gln Glu Glu Lys Asp Glu Trp Ile
        355                 360                 365

Lys Ser Ile Gln Ala Ala Val Ser Val Asp Pro Phe Tyr Glu Met Leu
    370                 375                 380

Ala Ala Arg Lys Lys Arg Ile Ser Val Lys Lys Lys Gln Glu Gln Pro
385                 390                 395                 400


<210> SEQ ID NO 116
<211> LENGTH: 399
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 116

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

Met Glu Leu Glu Asn Ile Arg Arg Arg Lys Gln Glu Leu Leu Val Glu
            20                  25                  30

Ile Gln Arg Leu Arg Glu Glu Leu Ser Glu Ala Met Ser Glu Val Glu
        35                  40                  45

Gly Leu Glu Ala Asn Glu Gly Ser Lys Thr Leu Gln Arg Asn Arg Lys
    50                  55                  60

Met Ala Met Gly Arg Lys Lys Phe Asn Met Asp Pro Lys Lys Gly Ile
65                  70                  75                  80

Gln Phe Leu Val Glu Asn Glu Leu Leu Gln Asn Thr Pro Glu Glu Ile
                85                  90                  95

Ala Arg Phe Leu Tyr Lys Gly Glu Gly Leu Asn Lys Thr Ala Ile Gly
            100                 105                 110

Asp Tyr Leu Gly Glu Arg Glu Glu Leu Asn Leu Ala Val Leu His Ala
        115                 120                 125

Phe Val Asp Leu His Glu Phe Thr Asp Leu Asn Leu Val Gln Ala Leu
    130                 135                 140

Arg Gln Phe Leu Trp Ser Phe Arg Leu Pro Gly Glu Ala Gln Lys Ile
145                 150                 155                 160

Asp Arg Met Met Glu Ala Phe Ala Gln Arg Tyr Cys Leu Cys Asn Pro
                165                 170                 175

Gly Val Phe Gln Ser Thr Asp Thr Cys Tyr Val Leu Ser Phe Ala Val
            180                 185                 190

Ile Met Leu Asn Thr Ser Leu His Asn Pro Asn Val Arg Asp Lys Pro
        195                 200                 205

Gly Leu Glu Arg Phe Val Ala Met Asn Arg Gly Ile Asn Glu Gly Gly
    210                 215                 220

Asp Leu Pro Glu Glu Leu Leu Arg Asn Leu Tyr Asp Ser Ile Arg Asn
225                 230                 235                 240

Glu Pro Phe Lys Ile Pro Glu Asp Asp Gly Asn Asp Leu Thr His Thr
                245                 250                 255

Phe Phe Asn Pro Asp Arg Glu Gly Trp Leu Leu Lys Leu Gly Gly Arg
            260                 265                 270
```

```
Val Lys Thr Trp Lys Arg Arg Trp Phe Ile Leu Thr Asp Asn Cys Leu
        275                 280                 285

Tyr Tyr Phe Glu Tyr Thr Thr Asp Lys Glu Pro Arg Gly Ile Ile Pro
    290                 295                 300

Leu Glu Asn Leu Ser Ile Arg Glu Val Asp Asp Pro Arg Lys Pro Asn
305                 310                 315                 320

Cys Phe Glu Leu Tyr Ile Pro Asn Asn Lys Gly Gln Leu Ile Lys Ala
                325                 330                 335

Cys Lys Thr Glu Ala Asp Gly Arg Val Val Glu Gly Asn His Met Val
            340                 345                 350

Tyr Arg Ile Ser Ala Pro Thr Gln Glu Glu Lys Asp Glu Trp Ile Lys
        355                 360                 365

Ser Ile Gln Ala Ala Val Ser Val Asp Pro Phe Tyr Glu Met Leu Ala
    370                 375                 380

Ala Arg Lys Lys Arg Ile Ser Val Lys Lys Lys Gln Glu Gln Pro
385                 390                 395


<210> SEQ ID NO 117
<211> LENGTH: 165
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 117

Met Val Asn Pro Thr Val Phe Phe Asp Ile Ala Val Asp Gly Glu Pro
1               5                   10                  15

Leu Gly Arg Val Ser Phe Glu Leu Phe Ala Asp Lys Val Pro Lys Thr
            20                  25                  30

Ala Glu Asn Phe Arg Ala Leu Ser Thr Gly Glu Lys Gly Phe Gly Tyr
        35                  40                  45

Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe Met Cys Gln Gly
    50                  55                  60

Gly Asp Phe Thr Arg His Asn Gly Thr Gly Gly Lys Ser Ile Tyr Gly
65                  70                  75                  80

Glu Lys Phe Glu Asp Glu Asn Phe Ile Leu Lys His Thr Gly Pro Gly
                85                  90                  95

Ile Leu Ser Met Ala Asn Ala Gly Pro Asn Thr Asn Gly Ser Gln Phe
            100                 105                 110

Phe Ile Cys Thr Ala Lys Thr Glu Trp Leu Asp Gly Lys His Val Val
        115                 120                 125

Phe Gly Lys Val Lys Glu Gly Met Asn Ile Val Glu Ala Met Glu Arg
    130                 135                 140

Phe Gly Ser Arg Asn Gly Lys Thr Ser Lys Lys Ile Thr Ile Ala Asp
145                 150                 155                 160

Cys Gly Gln Leu Glu
                165


<210> SEQ ID NO 118
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 118

Thr Ala Glu Glu Glu Ala Ser Ser Glu Ala Cys Ala Gly Pro Ala Thr
1               5                   10                  15

Arg Ser Pro Gly Trp Gly Asp Pro Gly Ile Ser His Arg Asp Cys Cys
            20                  25                  30
```

Arg Arg Lys Ala Glu Trp Gly Thr Ala Glu Ser Arg
35 40

<210> SEQ ID NO 119
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 119

Glu Ala Glu Leu Pro Asp Arg Gly Gly Ala Ala Val Gln Val Ser Ser
1 5 10 15

Pro Lys His Cys Gly Leu Cys Trp Leu Leu Cys Ser Glu Arg Leu Leu
20 25 30

Leu Pro Gly Val Arg Leu Pro Ala Gln Arg Leu Pro Gly Gly Pro Ser
35 40 45

Pro Leu Pro Asp Pro Gly Leu Pro Thr Ser Leu Leu Ala Ser Ala Thr
50 55 60

Gly His Pro Ser Gly Tyr Ser Pro Gly Asn Ser Val Ser Thr Ser Gly
65 70 75 80

Gln Pro Gln Pro His Pro Trp Arg His Gln Glu Phe Gln Arg Pro Ser
85 90 95

Gly

<210> SEQ ID NO 120
<211> LENGTH: 81
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 120

Leu Arg Gly Leu Ala Pro Pro Ser Pro Pro Pro Val Ile Val Arg Arg
1 5 10 15

Gly Pro Arg Gly Val Ala Ala Gln Ile Pro Pro Ala Ser Lys Leu Lys
20 25 30

His Gly Gly His Pro Leu Gln Arg Leu Ala Arg Gly His Pro Arg Leu
35 40 45

Leu Pro Ala Pro Pro Gly Phe His Phe Gln Gln Gln Leu Leu Gln Gln
50 55 60

Tyr Arg Val Pro Arg Gly Ser His Ser Pro Pro Pro Arg Ser Pro Gln
65 70 75 80

Gly

<210> SEQ ID NO 121
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 121

Ala Pro Trp Pro Ser Ala Pro Val Pro Ala Thr Arg Asp Arg Ala Pro
1 5 10 15

Arg Pro Ala Arg Gly Arg Arg Pro Asp Pro Thr Ser Gln Gln Ala Lys
20 25 30

Ala Trp Arg Pro Ser Pro Pro Ala Ala Arg Ser Trp Pro Pro Thr Thr
35 40 45

Thr Thr Gly Ala Ala Trp Val Pro Leu Pro Ala Thr Ala Pro Ala Ala
50 55 60

Val Pro Ser Ala Pro Gly Lys Pro Phe Pro Thr Pro Gln Val Ser Pro
65 70 75 80

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```
Arg Leu Thr Arg Val Ile Gly Gly Pro Ala Ser Phe Ser Gly Ser Pro
                85                  90                  95

Pro Ser Arg Ser Trp Pro Arg Cys Trp Ser Pro Gln Ser Thr Arg Asn
            100                 105                 110

Leu Pro Arg Pro Pro Ala Ala
        115


<210> SEQ ID NO 122
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Human

<400> SEQUENCE: 122

Trp Thr Cys Ser Pro His Pro Thr Pro Thr Thr Arg Arg Ser Thr Thr
1               5                   10                  15

Ser Arg Ser Ala Ser Trp Ser Ala Arg Cys Ala Ser Thr
            20                  25
```

The invention claimed is:

1. A method for diagnosing whether an individual suffering from rheumatoid arthritis will be non-responsive to anti-TNFα treatment, comprising:

(i) obtaining a biological sample from the individual;

(ii) providing a surface comprising one or more biomarker proteins, wherein the biomarker protein(s) comprises one or more sequences selected from the group consisting of SEQ ID NO. 59, SEQ ID NO. 60, SEQ ID NO. 61, SEQ ID NO. 62, SEQ ID NO. 63, SEQ ID NO. 64, SEQ ID NO. 65, SEQ ID NO. 66, SEQ ID NO. 67, and SEQ ID NO. 68 attached to said surface;

(iii) incubating said surface with said biological sample;

(iv) washing the product of step (iii), and incubating with an antibody that binds the IgA isotype;

(v) wherein the presence of IgA isotype immunoglobulin(s) that bind to one or more of said biomarker proteins classifies the individual as a NON-Responder to anti-TNFα treatment.

2. The method of claim **1**, wherein the biomarker protein group additionally comprises at least one other expression product encoded by a gene selected from the group comprising PECI, CTNND2, NSMCE1, KTELC1, HS6ST1, ARMC6, TH1L, PSME1, GPC1, EDC4, PRC1, NAT6, EEF1AL3, NP_612480.1, PLXNA2, ELMO2 and NDUFS2; wherein the biomarker protein comprises the sequence selected from the group consisting of SEQ ID NO. 69 to SEQ ID NO. 79, SEQ ID NO. 81 to SEQ ID NO. 106, and SEQ ID NO. 118.

3. The method of claim **1**, wherein the biological sample is selected from the group consisting of blood, saliva, tears, synovial fluid, spinal fluid, plasma, urine, and stool.

4. The method of claim **1**, further comprising treating an individual classified as a NON-responder with therapy that does not include anti-TNFα treatment.

5. The method of claim **1**, further comprising treating an individual not classified as a NON-responder with therapy that does include anti-TNFα treatment.

* * * * *

专利名称(译)	生物标志物用于预测对抗肿瘤坏死因子α（TNF）治疗的反应性		
公开(公告)号	US9052312	公开(公告)日	2015-06-09
申请号	US12/740166	申请日	2008-10-31
[标]申请(专利权)人(译)	马普科技促进协会		
申请(专利权)人(译)	马普GESELLSCHAFT ZUR FORDERUNG DER学问E.V.		
当前申请(专利权)人(译)	马普GESELLSCHAFT ZUR FORDERUNG DER学问E.V.		
[标]发明人	KONTHUR ZOLTAN LEHRACH HANS SKRINER KARL		
发明人	KONTHUR, ZOLTAN LEHRACH, HANS SKRINER, KARL		
IPC分类号	G01N33/53 G01N33/564 G01N33/68		
CPC分类号	G01N33/564 G01N33/6854 G01N33/6863 G01N2333/82 G01N2333/91171 G01N2333/9121 G01N2333/916 G01N2800/102 G01N2800/52 G01N2333/4703 G01N2333/705 G01N33/573 G01N33/68 G01N2333/47 G01N2333/91205 G01N2333/99 G01N2800/10		
代理机构(译)	FOLEY & Lardner的律师事务所		
优先权	2007119810 2007-10-31 EP		
其他公开文献	US20110045490A1		
外部链接	Espacenet USPTO		

摘要(译)

本发明涉及一种诊断接受或正在接受抗肿瘤坏死因子α（TNFα或TNF）治疗的个体以评估对抗TNF治疗的反应性的方法，所述抗TNF治疗包括检测免疫球蛋白。（s）针对体液或所述患者的排泄物中的一种或多种生物标志物蛋白质，并基于所述免疫球蛋白的检测将个体分类成两类中的一类，其中个体被分类为非应答者或应答者。本发明涉及包含所述一种或多种生物标志物蛋白的诊断试剂盒，以及这些试剂盒用于评估对经受抗TNFα治疗或正在进行抗TNFα治疗的个体的抗TNF治疗的反应性的用途。

Fig. 1

SEQ ID No. 1
RAB11B
>ENSG00000185236|19|protein_coding|ENST00000328024|ENSP00000333547
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