SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.

<120> Antigen-Binding Proteins that Activate
the Leptin Receptor

<130> 10178WO01

<150> 62/240,021
<151> 2015-10-12

<150> 62/359,757
<151> 2016-07-08

<150> 62/375,495
<151> 2016-08-16

<150> 62/393,143
<151> 2016-09-12

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

65 70 75 80
Leu Gln Met Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Ser Tyr Asn Trp Asn Tyr Trp Tyr Phe Asp Phe Trp Gly Arg Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
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<400> 22
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            20   25   30
Ala Met Tyr Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Val Leu Tyr Ser Asp Gly Ser Asn Lys Tyr Tyr Ile Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Thr Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Ser Ser Leu Arg Ala Asp Asp Ser Ala Leu Tyr Tyr Cys
                85   90   95
Ala Arg Leu Asn Trp Asp Tyr Trp Tyr Phe Asp Leu Trp Gly Arg Gly
            100   105   110
Thr Leu Val Thr Val Ser Ser
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Gly Phe Thr Phe Ser Thr Tyr Ala
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ccaggcaagg ggctggagtg ggtgtcagtt atatatcatg atggaagtta taaatactat 180
gaagactccg tgaagggccg attcaccatc gccagagaca attccaagaa cacgctttat 240
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Ala Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Val Ile Tyr His Asp Gly Ser Tyr Lys Tyr Tyr Glu Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ala Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Tyr Asn Trp Asn His Trp Tyr Phe Asp Val Trp Gly Arg Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
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<400> 38
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            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Val Ile Ser Tyr Asp Glu Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ala Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Asn Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Asp Arg Pro Phe Gly Leu Val Thr Gly Trp Phe Asp Pro Trp
            100   105   110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

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ccaggcaagg ggctggagtg ggtgacaatt atatggtatg atggaagtat taaatactat 180
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            20   25   30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Thr Ile Ile Trp Tyr Asp Gly Ser Ile Lys Tyr Tyr Ala Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65   70   75   80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Gly Gly Tyr Ser Gly Tyr Leu Tyr Phe Asp Tyr Trp Gly Gln
            100   105   110
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 35 40 45
Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Ala Tyr Tyr Asn Pro Ser

50 55 60

Leu Lys Ser Arg Gly Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe
85 90 95
Cys Val Lys Leu Arg Phe Leu Glu Trp Phe Leu Gly Gly Trp Phe Gly
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Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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ccagggaagg gcctggaatg ggtctcagct attactggtg gtggtggtag cacatactac 180
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Gly Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
Ser Ala Ile Thr Gly Gly Gly Gly Ser Thr Tyr Tyr Ser Asn Ser Val
 50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
65 70 75 80
Leu Arg Met Asn Ser Val Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
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Ala Lys Tyr Lys Trp Asn Phe Val Asp Asp Trp Gly Gln Gly Thr Thr
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Gly Phe Thr Phe Ser Asn Tyr Gly
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<400> 73
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60
tcctgtgttg cctctggatt caccttcaat aaatacgaca tgcactgggt ccgccaaact 120
actggaaaag gtctagagtg ggtctcaggt attgatactg atggtgacac atactatcca 180
ggctccgtga agggccgatt caccatctcc agagaaaatg ccgagaactc cctgtatctt 240
caaatgaacg gcctgagagt cggggacacg gctgtgtatt actgtgcaag atggccttgg 300
agtggtttct atggtgcttt tgatatctgg ggccaaggga caatggtcac cgtctcttca 360

<210> 74
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 74
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Asn Lys Tyr
            20   25   30
Asp Met His Trp Val Arg Gln Thr Thr Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ser Gly Ile Asp Thr Asp Gly Asp Thr Tyr Tyr Pro Gly Ser Val Lys
    50   55   60
Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Glu Asn Ser Leu Tyr Leu
65   70   75   80
Gln Met Asn Gly Leu Arg Val Gly Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Trp Pro Trp Ser Gly Phe Tyr Gly Ala Phe Asp Ile Trp Gly Gln
            100   105   110
Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 75
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 75
ggattcacct tcaataaata cgac 24

<210> 76
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 76
Gly Phe Thr Phe Asn Lys Tyr Asp
1 5

<210> 77
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 77
attgatactg atggtgacac a 21

<210> 78
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 78
Ile Asp Thr Asp Gly Asp Thr
1 5

<210> 79
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 79
gcaagatggc cttggagtgg tttctatggt gcttttgata tc 42

<210> 80
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 80
Ala Arg Trp Pro Trp Ser Gly Phe Tyr Gly Ala Phe Asp Ile
1 5 10

<210> 81
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 81
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagc agtggtaatt actactggaa ctggatccgc 120
caacagccag gagagggcct ggagtggatt gcttacatct atcacaatgg ggtcaccaac 180
ttcaatccgt ccctcaagag tcgacttact atatcagtag acacgtctaa gactcagttc 240
tccctgaagt tgaggtctgt gactgccgcg gacacggccg tttattactg tgcgagatca 300
ggcagctggt tcgagaactg gtacttcgat ctctggggcc gtggcaccct ggtcactgtc 360
tcctca 366

<210> 82
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 82
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20   25   30
Asn Tyr Tyr Trp Asn Trp Ile Arg Gln Gln Pro Gly Glu Gly Leu Glu
        35   40   45
Trp Ile Ala Tyr Ile Tyr His Asn Gly Val Thr Asn Phe Asn Pro Ser
    50   55   60
Leu Lys Ser Arg Leu Thr Ile Ser Val Asp Thr Ser Lys Thr Gln Phe
65   70   75   80
Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85   90   95
Cys Ala Arg Ser Gly Ser Trp Phe Glu Asn Trp Tyr Phe Asp Leu Trp
            100   105   110
Gly Arg Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 83
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 83
ggtggctcca tcagcagtgg taattactac   30

<210> 84
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 84
Gly Gly Ser Ile Ser Ser Gly Asn Tyr Tyr
 1   5   10

<210> 85
<211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 85
atctatcaca atggggtcac c 21

<210> 86
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 86
Ile Tyr His Asn Gly Val Thr
1 5

<210> 87
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 87
gcgagatcag gcagctggtt cgagaactgg tacttcgatc tc 42

<210> 88
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 88
Ala Arg Ser Gly Ser Trp Phe Glu Asn Trp Tyr Phe Asp Leu
1 5 10

<210> 89
<211> 324

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 89
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccttg gacgttcggc 300
caagggacca aggtggaaat caaa 324

<210> 90
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

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

<210> 91
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 91

cagagtgtta gcagcagcta c 21

<210> 92
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 92
Gln Ser Val Ser Ser Ser Tyr
1 5

<210> 93
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 93
ggtgcatcc 9

<210> 94
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 94
Gly Ala Ser
1

<210> 95
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 95

cagcagtatg gtagctcacc ttggacg 27

<210> 96
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 96
Gln Gln Tyr Gly Ser Ser Pro Trp Thr
 1 5

<210> 97
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 97
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagt aattcctact ggagctggat ccggcagccc 120
ccagggaagg gactggagtg gattggatat gtctattccc gtgggaacac caagtacaac 180
ccctccctca cgagtcgagt caccatgtca tttgacacgt ccaagaacca gttctccctg 240
aaactgaggt ctgtgaccgc cgcagacacg gccgtgtatt actgtgcgag aagcagcagc 300
tggtacgagg actggtactt cgatctctgg ggccgtggca ccctggtcac tgtctcctca 360

<210> 98
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 98
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Asn Ser
 20 25 30
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
Gly Tyr Val Tyr Ser Arg Gly Asn Thr Lys Tyr Asn Pro Ser Leu Thr

50 55 60

Ser Arg Val Thr Met Ser Phe Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80
Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Ser Ser Ser Trp Tyr Glu Asp Trp Tyr Phe Asp Leu Trp Gly Arg
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 99
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 99
ggtggctcca tcagtaattc ctac 24

<210> 100
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 100
Gly Gly Ser Ile Ser Asn Ser Tyr
1 5

<210> 101
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 101
gtctattccc gtgggaacac c 21

<210> 102
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 102
Val Tyr Ser Arg Gly Asn Thr
 1   5

<210> 103
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 103
gcgagaagca gcagctggta cgaggactgg tacttcgatc tc   42

<210> 104
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 104
Ala Arg Ser Ser Ser Trp Tyr Glu Asp Trp Tyr Phe Asp Leu
 1   5   10

<210> 105
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 105
caggtgcagc tacagcagtg gggcgcaggg ctgtttaagc cttcggagac cctgtccctc 60
acctgcgatg tctatggtgg gtccttcaga ggttattatt ggagttggat ccgccagccc 120
ccagggaagg ggctggagtg gattggggaa atcagttata gtggtttcac caattacaac 180
ccgtccctca agagtcgagt catcatatca atagatacgt ccaagaacca gttctccctg 240

aagatgagct ctgtgaccgc cgcggacacg gctgtttatt actgtgcgag agttacctat 300
ggttatggga cctttgatta ttggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 106
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 106
Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Phe Lys Pro Ser Glu
 1   5   10   15
Thr Leu Ser Leu Thr Cys Asp Val Tyr Gly Gly Ser Phe Arg Gly Tyr
            20   25   30
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45
Gly Glu Ile Ser Tyr Ser Gly Phe Thr Asn Tyr Asn Pro Ser Leu Lys
    50   55   60
Ser Arg Val Ile Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu
65   70   75   80
Lys Met Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85   90   95
Arg Val Thr Tyr Gly Tyr Gly Thr Phe Asp Tyr Trp Gly Gln Gly Thr
            100   105   110
Leu Val Thr Val Ser Ser
        115

<210> 107
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 107
ggtgggtcct tcagaggtta ttat 24

<210> 108
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 108
Gly Gly Ser Phe Arg Gly Tyr Tyr
 1   5

<210> 109
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 109
atcagttata gtggtttcac c   21

<210> 110
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 110
Ile Ser Tyr Ser Gly Phe Thr
 1   5

<210> 111
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 111
gcgagagtta cctatggtta tgggaccttt gattat   36

<210> 112
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 112
Ala Arg Val Thr Tyr Gly Tyr Gly Thr Phe Asp Tyr
 1   5   10

<210> 113
<211> 1165
<212> PRT
<213> Artificial Sequence

<220>
<223> hLEPR Accession No P48357

<400> 113
Met Ile Cys Gln Lys Phe Cys Val Val Leu Leu His Trp Glu Phe Ile
 1   5   10   15
Tyr Val Ile Thr Ala Phe Asn Leu Ser Tyr Pro Ile Thr Pro Trp Arg
            20   25   30
Phe Lys Leu Ser Cys Met Pro Pro Asn Ser Thr Tyr Asp Tyr Phe Leu
        35   40   45
Leu Pro Ala Gly Leu Ser Lys Asn Thr Ser Asn Ser Asn Gly His Tyr
    50   55   60
Glu Thr Ala Val Glu Pro Lys Phe Asn Ser Ser Gly Thr His Phe Ser
65   70   75   80
Asn Leu Ser Lys Thr Thr Phe His Cys Cys Phe Arg Ser Glu Gln Asp
                85   90   95
Arg Asn Cys Ser Leu Cys Ala Asp Asn Ile Glu Gly Lys Thr Phe Val
            100   105   110
Ser Thr Val Asn Ser Leu Val Phe Gln Gln Ile Asp Ala Asn Trp Asn
        115   120   125
Ile Gln Cys Trp Leu Lys Gly Asp Leu Lys Leu Phe Ile Cys Tyr Val
    130   135   140
Glu Ser Leu Phe Lys Asn Leu Phe Arg Asn Tyr Asn Tyr Lys Val His
145   150   155   160
Leu Leu Tyr Val Leu Pro Glu Val Leu Glu Asp Ser Pro Leu Val Pro
                165   170   175
Gln Lys Gly Ser Phe Gln Met Val His Cys Asn Cys Ser Val His Glu
            180   185   190
Cys Cys Glu Cys Leu Val Pro Val Pro Thr Ala Lys Leu Asn Asp Thr
        195   200   205
Leu Leu Met Cys Leu Lys Ile Thr Ser Gly Gly Val Ile Phe Gln Ser
    210   215   220
Pro Leu Met Ser Val Gln Pro Ile Asn Met Val Lys Pro Asp Pro Pro
225   230   235   240
Leu Gly Leu His Met Glu Ile Thr Asp Asp Gly Asn Leu Lys Ile Ser
                245   250   255
Trp Ser Ser Pro Pro Leu Val Pro Phe Pro Leu Gln Tyr Gln Val Lys

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            260                 265                 270
Tyr Ser Glu Asn Ser Thr Thr Val Ile Arg Glu Ala Asp Lys Ile Val
        275                 280                 285
Ser Ala Thr Ser Leu Leu Val Asp Ser Ile Leu Pro Gly Ser Ser Tyr
    290                 295                 300
Glu Val Gln Val Arg Gly Lys Arg Leu Asp Gly Pro Gly Ile Trp Ser
305                 310                 315                 320
Asp Trp Ser Thr Pro Arg Val Phe Thr Thr Gln Asp Val Ile Tyr Phe
                325                 330                 335
Pro Pro Lys Ile Leu Thr Ser Val Gly Ser Asn Val Ser Phe His Cys
            340                 345                 350
Ile Tyr Lys Lys Glu Asn Lys Ile Val Pro Ser Lys Glu Ile Val Trp
        355                 360                 365
Trp Met Asn Leu Ala Glu Lys Ile Pro Gln Ser Gln Tyr Asp Val Val
    370                 375                 380
Ser Asp His Val Ser Lys Val Thr Phe Phe Asn Leu Asn Glu Thr Lys
385                 390                 395                 400
Pro Arg Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu His
                405                 410                 415
Glu Cys His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile
            420                 425                 430
Asn Ile Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg
        435                 440                 445
Trp Ser Thr Ser Thr Ile Gln Ser Leu Ala Glu Ser Thr Leu Gln Leu
    450                 455                 460
Arg Tyr His Arg Ser Ser Leu Tyr Cys Ser Asp Ile Pro Ser Ile His
465                 470                 475                 480
Pro Ile Ser Glu Pro Lys Asp Cys Tyr Leu Gln Ser Asp Gly Phe Tyr
                485                 490                 495
Glu Cys Ile Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp
            500                 505                 510
Ile Arg Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys
        515                 520                 525
Val Leu Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Ser Val Lys
    530                 535                 540
Ala Glu Ile Thr Ile Asn Ile Gly Leu Leu Lys Ile Ser Trp Glu Lys
545                 550                 555                 560
Pro Val Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu
                565                 570                 575
Ser Gly Lys Glu Val Gln Trp Lys Met Tyr Glu Val Tyr Asp Ala Lys
            580                 585                 590
Ser Lys Ser Val Ser Leu Pro Val Pro Asp Leu Cys Ala Val Tyr Ala
        595                 600                 605
Val Gln Val Arg Cys Lys Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn
    610                 615                 620
Trp Ser Asn Pro Ala Tyr Thr Val Val Met Asp Ile Lys Val Pro Met
625                 630                 635                 640
Arg Gly Pro Glu Phe Trp Arg Ile Ile Asn Gly Asp Thr Met Lys Lys
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645 650 655

Glu Lys Asn Val Thr Leu Leu Trp Lys Pro Leu Met Lys Asn Asp Ser
660 665 670

Leu Cys Ser Val Gln Arg Tyr Val Ile Asn His His Thr Ser Cys Asn
675 680 685

Gly Thr Trp Ser Glu Asp Val Gly Asn His Thr Lys Phe Thr Phe Leu
690 695 700

Trp Thr Glu Gln Ala His Thr Val Thr Val Leu Ala Ile Asn Ser Ile
705 710 715 720

Gly Ala Ser Val Ala Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser
725 730 735

Lys Val Asn Ile Val Gln Ser Leu Ser Ala Tyr Pro Leu Asn Ser Ser
740 745 750

Cys Val Ile Val Ser Trp Ile Leu Ser Pro Ser Asp Tyr Lys Leu Met
755 760 765

Tyr Phe Ile Ile Glu Trp Lys Asn Leu Asn Glu Asp Gly Glu Ile Lys
770 775 780

Trp Leu Arg Ile Ser Ser Ser Val Lys Lys Tyr Tyr Ile His Asp His
785 790 795 800

Phe Ile Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Ile Phe Met
805 810 815

Glu Gly Val Gly Lys Pro Lys Ile Ile Asn Ser Phe Thr Gln Asp Asp
820 825 830

Ile Glu Lys His Gln Ser Asp Ala Gly Leu Tyr Val Ile Val Pro Val
835 840 845

Ile Ile Ser Ser Ser Ile Leu Leu Leu Gly Thr Leu Leu Ile Ser His
850 855 860

Gln Arg Met Lys Lys Leu Phe Trp Glu Asp Val Pro Asn Pro Lys Asn
865 870 875 880

Cys Ser Trp Ala Gln Gly Leu Asn Phe Gln Lys Pro Glu Thr Phe Glu
885 890 895

His Leu Phe Ile Lys His Thr Ala Ser Val Thr Cys Gly Pro Leu Leu
900 905 910

Leu Glu Pro Glu Thr Ile Ser Glu Asp Ile Ser Val Asp Thr Ser Trp
915 920 925

Lys Asn Lys Asp Glu Met Met Pro Thr Thr Val Val Ser Leu Leu Ser
930 935 940

Thr Thr Asp Leu Glu Lys Gly Ser Val Cys Ile Ser Asp Gln Phe Asn
945 950 955 960

Ser Val Asn Phe Ser Glu Ala Glu Gly Thr Glu Val Thr Tyr Glu Asp
965 970 975

Glu Ser Gln Arg Gln Pro Phe Val Lys Tyr Ala Thr Leu Ile Ser Asn
980 985 990

Ser Lys Pro Ser Glu Thr Gly Glu Glu Gln Gly Leu Ile Asn Ser Ser
995 1000 1005

Val Thr Lys Cys Phe Ser Ser Lys Asn Ser Pro Leu Lys Asp Ser Phe
1010 1015 1020

Ser Asn Ser Ser Trp Glu Ile Glu Ala Gln Ala Phe Phe Ile Leu Ser

1025 1030 1035 1040
Asp Gln His Pro Asn Ile Ile Ser Pro His Leu Thr Phe Ser Glu Gly
1045 1050 1055
Leu Asp Glu Leu Leu Lys Leu Glu Gly Asn Phe Pro Glu Glu Asn Asn
1060 1065 1070
Asp Lys Lys Ser Ile Tyr Tyr Leu Gly Val Thr Ser Ile Lys Lys Arg
1075 1080 1085
Glu Ser Gly Val Leu Leu Thr Asp Lys Ser Arg Val Ser Cys Pro Phe
1090 1095 1100
Pro Ala Pro Cys Leu Phe Thr Asp Ile Arg Val Leu Gln Asp Ser Cys
1105 1110 1115 1120
Ser His Phe Val Glu Asn Asn Ile Asn Leu Gly Thr Ser Ser Lys Lys
1125 1130 1135
Thr Phe Ala Ser Tyr Met Pro Gln Phe Gln Thr Cys Ser Thr Gln Thr
1140 1145 1150
His Lys Ile Met Glu Asn Lys Met Cys Asp Leu Thr Val
1155 1160 1165

<210> 114
<211> 846
<212> PRT
<213> Artificial Sequence

<220>
<223> hLEPR.mmh
aa 1-818: F22-D839 of P48357
aa 819-846: myc-myc-hexahistidine tag

<400> 114
Phe Asn Leu Ser Tyr Pro Ile Thr Pro Trp Arg Phe Lys Leu Ser Cys
1 5 10 15
Met Pro Pro Asn Ser Thr Tyr Asp Tyr Phe Leu Leu Pro Ala Gly Leu
20 25 30
Ser Lys Asn Thr Ser Asn Ser Asn Gly His Tyr Glu Thr Ala Val Glu
35 40 45
Pro Lys Phe Asn Ser Ser Gly Thr His Phe Ser Asn Leu Ser Lys Thr
50 55 60
Thr Phe His Cys Cys Phe Arg Ser Glu Gln Asp Arg Asn Cys Ser Leu
65 70 75 80
Cys Ala Asp Asn Ile Glu Gly Lys Thr Phe Val Ser Thr Val Asn Ser
85 90 95
Leu Val Phe Gln Gln Ile Asp Ala Asn Trp Asn Ile Gln Cys Trp Leu
100 105 110
Lys Gly Asp Leu Lys Leu Phe Ile Cys Tyr Val Glu Ser Leu Phe Lys
115 120 125
Asn Leu Phe Arg Asn Tyr Asn Tyr Lys Val His Leu Leu Tyr Val Leu
130 135 140

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Pro Glu Val Leu Glu Asp Ser Pro Leu Val Pro Gln Lys Gly Ser Phe
145                 150                 155                 160
Gln Met Val His Cys Asn Cys Ser Val His Glu Cys Cys Glu Cys Leu
                165                 170                 175
Val Pro Val Pro Thr Ala Lys Leu Asn Asp Thr Leu Leu Met Cys Leu
            180                 185                 190
Lys Ile Thr Ser Gly Gly Val Ile Phe Gln Ser Pro Leu Met Ser Val
        195                 200                 205
Gln Pro Ile Asn Met Val Lys Pro Asp Pro Pro Leu Gly Leu His Met
    210                 215                 220
Glu Ile Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Ser Ser Pro Pro
225                 230                 235                 240
Leu Val Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Ser Glu Asn Ser
                245                 250                 255
Thr Thr Val Ile Arg Glu Ala Asp Lys Ile Val Ser Ala Thr Ser Leu
            260                 265                 270
Leu Val Asp Ser Ile Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg
        275                 280                 285
Gly Lys Arg Leu Asp Gly Pro Gly Ile Trp Ser Asp Trp Ser Thr Pro
    290                 295                 300
Arg Val Phe Thr Thr Gln Asp Val Ile Tyr Phe Pro Pro Lys Ile Leu
305                 310                 315                 320
Thr Ser Val Gly Ser Asn Val Ser Phe His Cys Ile Tyr Lys Lys Glu
                325                 330                 335
Asn Lys Ile Val Pro Ser Lys Glu Ile Val Trp Trp Met Asn Leu Ala
            340                 345                 350
Glu Lys Ile Pro Gln Ser Gln Tyr Asp Val Val Ser Asp His Val Ser
        355                 360                 365
Lys Val Thr Phe Phe Asn Leu Asn Glu Thr Lys Pro Arg Gly Lys Phe
    370                 375                 380
Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu His Glu Cys His His Arg
385                 390                 395                 400
Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu
                405                 410                 415
Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr
            420                 425                 430
Ile Gln Ser Leu Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser
        435                 440                 445
Ser Leu Tyr Cys Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro
    450                 455                 460
Lys Asp Cys Tyr Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln
465                 470                 475                 480
Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His
                485                 490                 495
Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser
            500                 505                 510
Val Val Lys Pro Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile
        515                 520                 525
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Asn Ile Gly Leu Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu
    530                 535                 540
Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val
545                 550                 555                 560
Gln Trp Lys Met Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser
                565                 570                 575
Leu Pro Val Pro Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys
            580                 585                 590
Lys Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala
        595                 600                 605
Tyr Thr Val Val Met Asp Ile Lys Val Pro Met Arg Gly Pro Glu Phe
    610                 615                 620
Trp Arg Ile Ile Asn Gly Asp Thr Met Lys Lys Glu Lys Asn Val Thr
625                 630                 635                 640
Leu Leu Trp Lys Pro Leu Met Lys Asn Asp Ser Leu Cys Ser Val Gln
                645                 650                 655
Arg Tyr Val Ile Asn His His Thr Ser Cys Asn Gly Thr Trp Ser Glu
            660                 665                 670
Asp Val Gly Asn His Thr Lys Phe Thr Phe Leu Trp Thr Glu Gln Ala
        675                 680                 685
His Thr Val Thr Val Leu Ala Ile Asn Ser Ile Gly Ala Ser Val Ala
    690                 695                 700
Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Asn Ile Val
705                 710                 715                 720
Gln Ser Leu Ser Ala Tyr Pro Leu Asn Ser Ser Cys Val Ile Val Ser
                725                 730                 735
Trp Ile Leu Ser Pro Ser Asp Tyr Lys Leu Met Tyr Phe Ile Ile Glu
            740                 745                 750
Trp Lys Asn Leu Asn Glu Asp Gly Glu Ile Lys Trp Leu Arg Ile Ser
        755                 760                 765
Ser Ser Val Lys Lys Tyr Tyr Ile His Asp His Phe Ile Pro Ile Glu
    770                 775                 780
Lys Tyr Gln Phe Ser Leu Tyr Pro Ile Phe Met Glu Gly Val Gly Lys
785                 790                 795                 800
Pro Lys Ile Ile Asn Ser Phe Thr Gln Asp Asp Ile Glu Lys His Gln
                805                 810                 815
Ser Asp Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Gly Glu Gln
            820                 825                 830
Lys Leu Ile Ser Glu Glu Asp Leu His His His His His His
        835                 840                 845
```

<210> 115
<211> 1051
<212> PRT
<213> Artificial Sequence

<220>

<223> hLEPR.mFc
aa 1-818: F22-D839 of P48357
aa 819-1051: mouse IgG2a (E98-K330 of P01863)

<400> 115

```
Phe Asn Leu Ser Tyr Pro Ile Thr Pro Trp Arg Phe Lys Leu Ser Cys
 1               5                  10                  15
Met Pro Pro Asn Ser Thr Tyr Asp Tyr Phe Leu Leu Pro Ala Gly Leu
            20                  25                  30
Ser Lys Asn Thr Ser Asn Ser Asn Gly His Tyr Glu Thr Ala Val Glu
        35                  40                  45
Pro Lys Phe Asn Ser Ser Gly Thr His Phe Ser Asn Leu Ser Lys Thr
    50                  55                  60
Thr Phe His Cys Cys Phe Arg Ser Glu Gln Asp Arg Asn Cys Ser Leu
65                  70                  75                  80
Cys Ala Asp Asn Ile Glu Gly Lys Thr Phe Val Ser Thr Val Asn Ser
                85                  90                  95
Leu Val Phe Gln Gln Ile Asp Ala Asn Trp Asn Ile Gln Cys Trp Leu
            100                 105                 110
Lys Gly Asp Leu Lys Leu Phe Ile Cys Tyr Val Glu Ser Leu Phe Lys
        115                 120                 125
Asn Leu Phe Arg Asn Tyr Asn Tyr Lys Val His Leu Leu Tyr Val Leu
    130                 135                 140
Pro Glu Val Leu Glu Asp Ser Pro Leu Val Pro Gln Lys Gly Ser Phe
145                 150                 155                 160
Gln Met Val His Cys Asn Cys Ser Val His Glu Cys Cys Glu Cys Leu
                165                 170                 175
Val Pro Val Pro Thr Ala Lys Leu Asn Asp Thr Leu Leu Met Cys Leu
            180                 185                 190
Lys Ile Thr Ser Gly Gly Val Ile Phe Gln Ser Pro Leu Met Ser Val
        195                 200                 205
Gln Pro Ile Asn Met Val Lys Pro Asp Pro Pro Leu Gly Leu His Met
    210                 215                 220
Glu Ile Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Ser Ser Pro Pro
225                 230                 235                 240
Leu Val Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Ser Glu Asn Ser
                245                 250                 255
Thr Thr Val Ile Arg Glu Ala Asp Lys Ile Val Ser Ala Thr Ser Leu
            260                 265                 270
Leu Val Asp Ser Ile Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg
        275                 280                 285
Gly Lys Arg Leu Asp Gly Pro Gly Ile Trp Ser Asp Trp Ser Thr Pro
    290                 295                 300
Arg Val Phe Thr Thr Gln Asp Val Ile Tyr Phe Pro Pro Lys Ile Leu
305                 310                 315                 320
Thr Ser Val Gly Ser Asn Val Ser Phe His Cys Ile Tyr Lys Lys Glu
                325                 330                 335
Asn Lys Ile Val Pro Ser Lys Glu Ile Val Trp Trp Met Asn Leu Ala
```

```
            340                 345                 350
Glu Lys Ile Pro Gln Ser Gln Tyr Asp Val Val Ser Asp His Val Ser
        355                 360                 365
Lys Val Thr Phe Phe Asn Leu Asn Glu Thr Lys Pro Arg Gly Lys Phe
    370                 375                 380
Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu His Glu Cys His His Arg
385                 390                 395                 400
Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu
                405                 410                 415
Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr
            420                 425                 430
Ile Gln Ser Leu Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser
        435                 440                 445
Ser Leu Tyr Cys Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro
    450                 455                 460
Lys Asp Cys Tyr Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln
465                 470                 475                 480
Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His
                485                 490                 495
Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser
            500                 505                 510
Val Val Lys Pro Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile
        515                 520                 525
Asn Ile Gly Leu Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu
    530                 535                 540
Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val
545                 550                 555                 560
Gln Trp Lys Met Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser
                565                 570                 575
Leu Pro Val Pro Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys
            580                 585                 590
Lys Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala
        595                 600                 605
Tyr Thr Val Val Met Asp Ile Lys Val Pro Met Arg Gly Pro Glu Phe
    610                 615                 620
Trp Arg Ile Ile Asn Gly Asp Thr Met Lys Lys Glu Lys Asn Val Thr
625                 630                 635                 640
Leu Leu Trp Lys Pro Leu Met Lys Asn Asp Ser Leu Cys Ser Val Gln
                645                 650                 655
Arg Tyr Val Ile Asn His His Thr Ser Cys Asn Gly Thr Trp Ser Glu
            660                 665                 670
Asp Val Gly Asn His Thr Lys Phe Thr Phe Leu Trp Thr Glu Gln Ala
        675                 680                 685
His Thr Val Thr Val Leu Ala Ile Asn Ser Ile Gly Ala Ser Val Ala
    690                 695                 700
Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Asn Ile Val
705                 710                 715                 720
Gln Ser Leu Ser Ala Tyr Pro Leu Asn Ser Ser Cys Val Ile Val Ser
```

725 730 735
Trp Ile Leu Ser Pro Ser Asp Tyr Lys Leu Met Tyr Phe Ile Ile Glu
740 745 750
Trp Lys Asn Leu Asn Glu Asp Gly Glu Ile Lys Trp Leu Arg Ile Ser
755 760 765
Ser Ser Val Lys Lys Tyr Tyr Ile His Asp His Phe Ile Pro Ile Glu
770 775 780
Lys Tyr Gln Phe Ser Leu Tyr Pro Ile Phe Met Glu Gly Val Gly Lys
785 790 795 800
Pro Lys Ile Ile Asn Ser Phe Thr Gln Asp Asp Ile Glu Lys His Gln
805 810 815
Ser Asp Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys
820 825 830
Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro
835 840 845
Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr
850 855 860
Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser
865 870 875 880
Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His
885 890 895
Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile
900 905 910
Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn
915 920 925
Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys
930 935 940
Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu
945 950 955 960
Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe
965 970 975
Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu
980 985 990
Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr
995 1000 1005
Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg
1010 1015 1020
Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His
1025 1030 1035 1040
Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
1045 1050

<210> 116
<211> 1045
<212> PRT
<213> Artificial Sequence

<220>
<223> hLEPR.hFc
aa 1-818: F22-D839 of P48357
aa 819-1045: human IgG1 tag (D104-K330 of P01857)

<400> 116
```
Phe Asn Leu Ser Tyr Pro Ile Thr Pro Trp Arg Phe Lys Leu Ser Cys
 1               5                  10                  15
Met Pro Pro Asn Ser Thr Tyr Asp Tyr Phe Leu Leu Pro Ala Gly Leu
            20                  25                  30
Ser Lys Asn Thr Ser Asn Ser Asn Gly His Tyr Glu Thr Ala Val Glu
        35                  40                  45
Pro Lys Phe Asn Ser Ser Gly Thr His Phe Ser Asn Leu Ser Lys Thr
    50                  55                  60
Thr Phe His Cys Cys Phe Arg Ser Glu Gln Asp Arg Asn Cys Ser Leu
65                  70                  75                  80
Cys Ala Asp Asn Ile Glu Gly Lys Thr Phe Val Ser Thr Val Asn Ser
                85                  90                  95
Leu Val Phe Gln Gln Ile Asp Ala Asn Trp Asn Ile Gln Cys Trp Leu
            100                 105                 110
Lys Gly Asp Leu Lys Leu Phe Ile Cys Tyr Val Glu Ser Leu Phe Lys
        115                 120                 125
Asn Leu Phe Arg Asn Tyr Asn Tyr Lys Val His Leu Leu Tyr Val Leu
    130                 135                 140
Pro Glu Val Leu Glu Asp Ser Pro Leu Val Pro Gln Lys Gly Ser Phe
145                 150                 155                 160
Gln Met Val His Cys Asn Cys Ser Val His Glu Cys Cys Glu Cys Leu
                165                 170                 175
Val Pro Val Pro Thr Ala Lys Leu Asn Asp Thr Leu Leu Met Cys Leu
            180                 185                 190
Lys Ile Thr Ser Gly Gly Val Ile Phe Gln Ser Pro Leu Met Ser Val
        195                 200                 205
Gln Pro Ile Asn Met Val Lys Pro Asp Pro Pro Leu Gly Leu His Met
    210                 215                 220
Glu Ile Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Ser Ser Pro Pro
225                 230                 235                 240
Leu Val Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Ser Glu Asn Ser
                245                 250                 255
Thr Thr Val Ile Arg Glu Ala Asp Lys Ile Val Ser Ala Thr Ser Leu
            260                 265                 270
Leu Val Asp Ser Ile Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg
        275                 280                 285
Gly Lys Arg Leu Asp Gly Pro Gly Ile Trp Ser Asp Trp Ser Thr Pro
    290                 295                 300
Arg Val Phe Thr Thr Gln Asp Val Ile Tyr Phe Pro Pro Lys Ile Leu
305                 310                 315                 320
Thr Ser Val Gly Ser Asn Val Ser Phe His Cys Ile Tyr Lys Lys Glu
                325                 330                 335
```

```
Asn Lys Ile Val Pro Ser Lys Glu Ile Val Trp Trp Met Asn Leu Ala
            340                 345                 350
Glu Lys Ile Pro Gln Ser Gln Tyr Asp Val Val Ser Asp His Val Ser
        355                 360                 365
Lys Val Thr Phe Phe Asn Leu Asn Glu Thr Lys Pro Arg Gly Lys Phe
    370                 375                 380
Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu His Glu Cys His His Arg
385                 390                 395                 400
Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu
                405                 410                 415
Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr
            420                 425                 430
Ile Gln Ser Leu Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser
        435                 440                 445
Ser Leu Tyr Cys Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro
    450                 455                 460
Lys Asp Cys Tyr Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln
465                 470                 475                 480
Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His
                485                 490                 495
Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser
            500                 505                 510
Val Val Lys Pro Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile
        515                 520                 525
Asn Ile Gly Leu Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu
    530                 535                 540
Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val
545                 550                 555                 560
Gln Trp Lys Met Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser
                565                 570                 575
Leu Pro Val Pro Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys
            580                 585                 590
Lys Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala
        595                 600                 605
Tyr Thr Val Val Met Asp Ile Lys Val Pro Met Arg Gly Pro Glu Phe
    610                 615                 620
Trp Arg Ile Ile Asn Gly Asp Thr Met Lys Lys Glu Lys Asn Val Thr
625                 630                 635                 640
Leu Leu Trp Lys Pro Leu Met Lys Asn Asp Ser Leu Cys Ser Val Gln
                645                 650                 655
Arg Tyr Val Ile Asn His His Thr Ser Cys Asn Gly Thr Trp Ser Glu
            660                 665                 670
Asp Val Gly Asn His Thr Lys Phe Thr Phe Leu Trp Thr Glu Gln Ala
        675                 680                 685
His Thr Val Thr Val Leu Ala Ile Asn Ser Ile Gly Ala Ser Val Ala
    690                 695                 700
Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Asn Ile Val
705                 710                 715                 720
```

```
Gln Ser Leu Ser Ala Tyr Pro Leu Asn Ser Ser Cys Val Ile Val Ser
                725                 730                 735
Trp Ile Leu Ser Pro Ser Asp Tyr Lys Leu Met Tyr Phe Ile Ile Glu
            740                 745                 750
Trp Lys Asn Leu Asn Glu Asp Gly Glu Ile Lys Trp Leu Arg Ile Ser
        755                 760                 765
Ser Ser Val Lys Lys Tyr Tyr Ile His Asp His Phe Ile Pro Ile Glu
    770                 775                 780
Lys Tyr Gln Phe Ser Leu Tyr Pro Ile Phe Met Glu Gly Val Gly Lys
785                 790                 795                 800
Pro Lys Ile Ile Asn Ser Phe Thr Gln Asp Asp Ile Glu Lys His Gln
                805                 810                 815
Ser Asp Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
            820                 825                 830
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
        835                 840                 845
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
    850                 855                 860
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
865                 870                 875                 880
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
                885                 890                 895
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
            900                 905                 910
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
        915                 920                 925
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
    930                 935                 940
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
945                 950                 955                 960
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
                965                 970                 975
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
            980                 985                 990
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
        995                 1000                1005
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
    1010                1015                1020
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
1025                1030                1035                1040
Leu Ser Pro Gly Lys
                1045
```

<210> 117
<211> 844
<212> PRT
<213> Artificial Sequence

<220>
<223> MfLEPR.mmh
aa 1-816: Macaca fascicularis F22-D837 with a
T827A substitution from XP_005543194.1
aa 817-844: myc-myc-hexahistidine tag

<400> 117

```
Phe Asn Leu Ser Tyr Pro Ile Thr Pro Trp Arg Phe Lys Leu Ser Cys
 1               5                  10                  15
Met Pro Pro Asn Ser Thr Tyr Asp Tyr Phe Leu Leu Pro Ala Gly Leu
            20                  25                  30
Ser Lys Asn Thr Ser Asn Leu Asn Gly His Tyr Glu Thr Ala Val Glu
        35                  40                  45
Phe Asn Ser Ser Asp Thr His Phe Ser Asn Leu Ser Lys Thr Thr Phe
    50                  55                  60
His Cys Cys Phe Arg Ser Glu Gln Asp Arg Asn Cys Ser Leu Cys Ala
65                  70                  75                  80
Asp Asn Ile Glu Gly Lys Thr Phe Val Ser Thr Val Asn Ser Ser Val
                85                  90                  95
Phe Gln Gln Met Gly Ala Asn Trp Asn Ile Gln Cys Trp Leu Lys Gly
            100                 105                 110
Asp Leu Lys Leu Phe Ile Cys Tyr Val Glu Ser Leu Phe Lys Asn Pro
        115                 120                 125
Phe Lys Asn Tyr Lys His Lys Val His Leu Leu Tyr Val Leu Pro Glu
    130                 135                 140
Val Leu Glu Asp Ser Pro Leu Val Pro Gln Lys Gly Ser Phe Gln Met
145                 150                 155                 160
Val His Cys Asn Cys Ser Val His Glu Arg Cys Glu Cys Leu Val Pro
                165                 170                 175
Val Pro Thr Ala Lys Leu Asn Asp Thr Leu Leu Met Cys Leu Lys Ile
            180                 185                 190
Thr Ser Gly Gly Val Ile Phe Gln Ser Pro Leu Met Ser Val Gln Pro
        195                 200                 205
Ile Asn Met Val Lys Pro Asp Pro Pro Leu Gly Leu Arg Met Glu Ile
    210                 215                 220
Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Ser Ser Pro Pro Leu Val
225                 230                 235                 240
Pro Phe Pro Leu Gln Tyr Glu Val Lys Tyr Ser Glu Asn Ser Thr Thr
                245                 250                 255
Val Ile Arg Glu Ala Asp Lys Ile Val Ser Ala Thr Ser Leu Leu Val
            260                 265                 270
Asp Gly Ile Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg Gly Lys
        275                 280                 285
Arg Leu Asp Gly Pro Gly Ile Trp Ser Asp Trp Ser Thr Pro His Val
    290                 295                 300
Phe Thr Thr Gln Asp Val Ile Tyr Phe Pro Pro Lys Ile Leu Thr Ser
305                 310                 315                 320
```

```
Val Gly Ser Asn Val Ser Phe His Cys Ile Tyr Lys Asn Glu Asn Lys
                325                 330                 335
Ile Val Ser Ser Lys Lys Ile Val Trp Trp Met Asn Leu Ala Glu Lys
            340                 345                 350
Ile Pro Gln Ser Gln Tyr Asp Val Val Ser Asp His Val Ser Lys Val
        355                 360                 365
Thr Phe Phe Asn Leu Asn Glu Thr Lys Pro Arg Gly Lys Phe Thr Tyr
    370                 375                 380
Asp Ala Val Tyr Cys Cys Asn Glu His Glu Cys His His Arg Tyr Ala
385                 390                 395                 400
Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr Asp
                405                 410                 415
Gly His Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Asn Thr Ile Gln
            420                 425                 430
Ser Leu Ala Gly Ser Thr Leu Gln Leu Arg Tyr Arg Arg Ser Ser Leu
        435                 440                 445
Tyr Cys Phe Asp Ile Pro Ser Ile His Pro Ile Ser Lys Pro Lys Asp
    450                 455                 460
Cys Tyr Leu Gln Ser Asp Gly Phe Tyr Glu Cys Val Phe Gln Pro Ile
465                 470                 475                 480
Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Pro Leu
                485                 490                 495
Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val
            500                 505                 510
Lys Pro Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Ile Lys Asn Ile
        515                 520                 525
Gly Leu Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn
    530                 535                 540
Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Ile Gln Trp
545                 550                 555                 560
Lys Met Tyr Asp Val Tyr Asp Ala Lys Ser Lys Ser Val Ser Leu Pro
                565                 570                 575
Val Pro Asp Phe Cys Ala Val Tyr Ala Val Gln Val Arg Cys Lys Arg
            580                 585                 590
Ser Asp Gly Leu Gly Leu Trp Ser Asn Trp Ser Asn Pro Ala Tyr Thr
        595                 600                 605
Val Val Met Asp Ile Lys Val Pro Met Arg Gly Pro Glu Phe Trp Arg
    610                 615                 620
Ile Ile Asn Gly Asp Thr Met Lys Lys Glu Lys Asn Val Thr Leu Leu
625                 630                 635                 640
Trp Lys Pro Leu Met Lys Asn Asp Ser Leu Cys Ser Val Gln Arg Tyr
                645                 650                 655
Val Ile Asn His His Thr Ser Cys Asn Gly Thr Trp Ser Glu Asp Val
            660                 665                 670
Gly Asn His Thr Lys Phe Thr Phe Leu Trp Thr Glu Gln Ala His Thr
        675                 680                 685
Val Thr Val Leu Ala Ile Asn Ser Ile Gly Ala Ser Val Ala Asn Phe
    690                 695                 700
```

```
Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Asn Ile Val Gln Ser
705                 710                 715                 720
Leu Ser Ala Tyr Pro Leu Asn Ser Ser Cys Val Ile Leu Ser Trp Ile
                725                 730                 735
Leu Ser Pro Ser Asp Tyr Lys Leu Met Tyr Phe Ile Ile Glu Trp Lys
            740                 745                 750
Asn Leu Asn Glu Asp Gly Glu Ile Lys Trp Leu Arg Ile Ser Ser Ser
        755                 760                 765
Val Lys Lys Tyr Tyr Ile His Asp His Phe Ile Pro Ile Glu Lys Tyr
    770                 775                 780
Gln Phe Ser Leu Tyr Pro Ile Phe Met Glu Gly Val Gly Lys Pro Lys
785                 790                 795                 800
Ile Ile Asn Ser Phe Ala Gln Asp Asn Thr Glu Lys His Gln Asn Asp
                805                 810                 815
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Gly Glu Gln Lys Leu
            820                 825                 830
Ile Ser Glu Glu Asp Leu His His His His His His
        835                 840
```

<210> 118
<211> 846
<212> PRT
<213> Artificial Sequence

<220>
<223> mLEPR.mmh
aa 1-818: Mouse LEPR (L22-G839 of NP_666258.2)
aa 817-846: myc-myc-hexahistidine tag

<400> 118

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

```
    130                 135                 140
Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro Leu Lys Asp Ser Phe
145                 150                 155                 160
Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly Cys Glu Cys His Val
                165                 170                 175
Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu Leu Met Tyr Leu Glu
            180                 185                 190
Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro Leu Met Ser Leu Gln
        195                 200                 205
Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu Gly Leu His Met Glu
    210                 215                 220
Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Asp Ser Gln Thr Met
225                 230                 235                 240
Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Leu Glu Asn Ser Thr
                245                 250                 255
Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala Thr Ser Leu Leu Val
            260                 265                 270
Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg Ser Lys
        275                 280                 285
Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp Ser Ser Pro Gln Val
    290                 295                 300
Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro Lys Ile Leu Thr Ser
305                 310                 315                 320
Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr Lys Asn Glu Asn Gln
                325                 330                 335
Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg Asn Leu Ala Glu Lys
            340                 345                 350
Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp Arg Val Ser Lys Val
        355                 360                 365
Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg Gly Lys Phe Thr Tyr
    370                 375                 380
Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys His His Arg Tyr Ala
385                 390                 395                 400
Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr Asp
                405                 410                 415
Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Pro Ser Thr Ile Gln
            420                 425                 430
Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr His Arg Arg Ser Leu
        435                 440                 445
Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr Ser Glu Pro Lys Asn
    450                 455                 460
Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys Val Phe Gln Pro Ile
465                 470                 475                 480
Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu
                485                 490                 495
Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val
            500                 505                 510
Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu Ile Thr Val Asn Thr
```

```
        515                 520                 525
Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn
    530                 535                 540
Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Ile Gln Trp
545                 550                 555                 560
Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys Ser Ala Ser Leu Leu
                565                 570                 575
Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln Val Arg Cys Arg Arg
            580                 585                 590
Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser Ser Pro Ala Tyr Thr
        595                 600                 605
Leu Val Met Asp Val Lys Val Pro Met Arg Gly Pro Glu Phe Trp Arg
    610                 615                 620
Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg Asn Val Thr Leu Leu
625                 630                 635                 640
Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys Ser Val Arg Arg Tyr
                645                 650                 655
Val Val Lys His Arg Thr Ala His Asn Gly Thr Trp Ser Glu Asp Val
            660                 665                 670
Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr Glu Pro Ala His Thr
        675                 680                 685
Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala Ser Leu Val Asn Phe
    690                 695                 700
Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Ser Ala Val Glu Ser
705                 710                 715                 720
Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val Ile Leu Ser Trp Thr
                725                 730                 735
Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu Val Ile Glu Trp Lys
            740                 745                 750
Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu Arg Ile Pro Ser Asn
        755                 760                 765
Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile Pro Ile Glu Lys Tyr
    770                 775                 780
Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly Val Gly Lys Pro Lys
785                 790                 795                 800
Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp Lys Gln Gln Asn Asp
                805                 810                 815
Ala Gly Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Gly Glu Gln
            820                 825                 830
Lys Leu Ile Ser Glu Glu Asp Leu His His His His His His
        835                 840                 845
```

<210> 119
<211> 846
<212> PRT
<213> Artificial Sequence

<220>
<223> rLEPR.mmh
aa 1-818: Rat LEPR (L22-G839 of NP_036728.1)
aa 819-846: myc-myc-hexahistidine tag

<400> 119
Leu Asn Leu Ala Tyr Pro Thr Ser Pro Trp Arg Phe Lys Leu Phe Cys
 1   5   10   15
Ala Pro Pro Ser Thr Thr Asp Asp Ser Phe Leu Ser Pro Ala Gly Val
            20   25   30
Pro Asn Asn Thr Ser Ser Leu Lys Gly Ala Ser Glu Ala Leu Val Glu
        35   40   45
Ala Lys Phe Asn Ser Thr Gly Ile Tyr Val Ser Glu Leu Ser Lys Thr
    50   55   60
Ile Phe His Cys Cys Phe Gly Asn Glu Gln Gly Gln Asn Cys Ser Ala
65   70   75   80
Leu Thr Gly Asn Thr Glu Gly Lys Thr Leu Ala Ser Val Val Lys Pro
                85   90   95
Leu Val Phe Arg Gln Leu Gly Val Asn Trp Asp Ile Glu Cys Trp Met
            100   105   110
Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met Glu Pro Leu Leu Lys
        115   120   125
Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His Leu Leu Tyr Asp Leu
    130   135   140
Pro Glu Val Ile Asp Asp Leu Pro Leu Pro Pro Leu Lys Asp Ser Phe
145   150   155   160
Gln Thr Val Gln Cys Asn Cys Ser Val Arg Glu Cys Glu Cys His Val
                165   170   175
Pro Val Pro Arg Ala Lys Val Asn Tyr Ala Leu Leu Met Tyr Leu Glu
            180   185   190
Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro Leu Met Ser Leu Gln
        195   200   205
Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu Gly Leu Arg Met Glu
    210   215   220
Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Asp Ser Gln Thr Lys
225   230   235   240
Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Leu Glu Asn Ser Thr
                245   250   255
Ile Val Arg Glu Ala Ala Glu Ile Val Ser Asp Thr Ser Leu Leu Val
            260   265   270
Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg Ser Lys
        275   280   285
Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp Ser Leu Pro Gln Leu
    290   295   300
Phe Thr Thr Gln Asp Val Met Tyr Phe Pro Pro Lys Ile Leu Thr Ser
305   310   315   320
Val Gly Ser Asn Ala Ser Phe Cys Cys Ile Tyr Lys Asn Glu Asn Gln
                325   330   335

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Thr Ile Ser Ser Lys Gln Ile Val Trp Trp Met Asn Leu Ala Glu Lys
            340                 345                 350
Ile Pro Glu Thr Gln Tyr Asn Thr Val Ser Asp His Ile Ser Lys Val
        355                 360                 365
Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg Gly Lys Phe Thr Tyr
    370                 375                 380
Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys His His Arg Tyr Ala
385                 390                 395                 400
Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr Asp
                405                 410                 415
Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Pro Ser Thr Ile Gln
            420                 425                 430
Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr His Arg Arg Ser Leu
        435                 440                 445
Tyr Cys Pro Asp Asn Pro Ser Ile Arg Pro Thr Ser Glu Leu Lys Asn
    450                 455                 460
Cys Val Leu Gln Thr Asp Gly Phe Tyr Glu Cys Val Phe Gln Pro Ile
465                 470                 475                 480
Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu
                485                 490                 495
Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val
            500                 505                 510
Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu Ile Thr Ile Asn Thr
        515                 520                 525
Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn
    530                 535                 540
Leu Gln Phe Gln Ile Arg Tyr Gly Leu Asn Gly Lys Glu Ile Gln Trp
545                 550                 555                 560
Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys Ser Ala Ser Leu Pro
                565                 570                 575
Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln Val Arg Cys Arg Arg
            580                 585                 590
Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser Ser Pro Ala Tyr Thr
        595                 600                 605
Leu Val Met Asp Val Lys Val Pro Met Arg Gly Pro Glu Phe Trp Arg
    610                 615                 620
Ile Met Asp Gly Asp Ile Thr Lys Lys Glu Arg Asn Val Thr Leu Leu
625                 630                 635                 640
Trp Lys Pro Leu Met Lys Asn Asp Ser Leu Cys Ser Val Arg Arg Tyr
                645                 650                 655
Val Val Lys His Arg Thr Ala His Asn Gly Thr Trp Ser Gln Asp Val
            660                 665                 670
Gly Asn Gln Thr Asn Leu Thr Phe Leu Trp Ala Glu Ser Ala His Thr
        675                 680                 685
Val Thr Val Leu Ala Ile Asn Ser Ile Gly Ala Ser Leu Val Asn Phe
    690                 695                 700
Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Asn Ala Val Gln Ser
705                 710                 715                 720
```

```
Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val Ile Leu Ser Trp Thr
                725                 730                 735
Leu Ser Pro Asn Asp Tyr Ser Leu Leu Tyr Leu Val Ile Glu Trp Lys
            740                 745                 750
Asn Leu Asn Asp Asp Asp Gly Met Lys Trp Leu Arg Ile Pro Ser Asn
        755                 760                 765
Val Asn Lys Tyr Tyr Ile His Asp Asn Phe Ile Pro Ile Glu Lys Tyr
    770                 775                 780
Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly Val Gly Lys Pro Lys
785                 790                 795                 800
Ile Ile Asn Gly Phe Thr Lys Asp Asp Ile Ala Lys Gln Gln Asn Asp
                805                 810                 815
Ala Gly Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Gly Glu Gln
            820                 825                 830
Lys Leu Ile Ser Glu Glu Asp Leu His His His His His His
        835                 840                 845
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<210> 120
<211> 1045
<212> PRT
<213> Artificial Sequence

<220>
<223> mLEPR.hFc
aa 1-818: Mouse LEPR (L22-G839 of NP_666258.2)
aa 819-1045: human IgG1 tag (D104-K330 of P01857)

<400> 120

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

```
145                 150                 155                 160
Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly Cys Glu Cys His Val
                165                 170                 175
Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu Leu Met Tyr Leu Glu
            180                 185                 190
Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro Leu Met Ser Leu Gln
        195                 200                 205
Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu Gly Leu His Met Glu
    210                 215                 220
Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Asp Ser Gln Thr Met
225                 230                 235                 240
Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Leu Glu Asn Ser Thr
                245                 250                 255
Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala Thr Ser Leu Leu Val
            260                 265                 270
Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg Ser Lys
        275                 280                 285
Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp Ser Ser Pro Gln Val
    290                 295                 300
Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro Lys Ile Leu Thr Ser
305                 310                 315                 320
Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr Lys Asn Glu Asn Gln
                325                 330                 335
Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg Asn Leu Ala Glu Lys
            340                 345                 350
Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp Arg Val Ser Lys Val
        355                 360                 365
Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg Gly Lys Phe Thr Tyr
    370                 375                 380
Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys His His Arg Tyr Ala
385                 390                 395                 400
Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr Asp
                405                 410                 415
Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Pro Ser Thr Ile Gln
            420                 425                 430
Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr His Arg Arg Ser Leu
        435                 440                 445
Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr Ser Glu Pro Lys Asn
    450                 455                 460
Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys Val Phe Gln Pro Ile
465                 470                 475                 480
Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu
                485                 490                 495
Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val
            500                 505                 510
Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu Ile Thr Val Asn Thr
        515                 520                 525
Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn
```

```
    530                 535                 540
Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Ile Gln Trp
545                 550                 555                 560
Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys Ser Ala Ser Leu Leu
                565                 570                 575
Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln Val Arg Cys Arg Arg
            580                 585                 590
Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser Ser Pro Ala Tyr Thr
        595                 600                 605
Leu Val Met Asp Val Lys Val Pro Met Arg Gly Pro Glu Phe Trp Arg
    610                 615                 620
Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg Asn Val Thr Leu Leu
625                 630                 635                 640
Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys Ser Val Arg Arg Tyr
                645                 650                 655
Val Val Lys His Arg Thr Ala His Asn Gly Thr Trp Ser Glu Asp Val
            660                 665                 670
Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr Glu Pro Ala His Thr
        675                 680                 685
Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala Ser Leu Val Asn Phe
    690                 695                 700
Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Ser Ala Val Glu Ser
705                 710                 715                 720
Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val Ile Leu Ser Trp Thr
                725                 730                 735
Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu Val Ile Glu Trp Lys
            740                 745                 750
Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu Arg Ile Pro Ser Asn
        755                 760                 765
Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile Pro Ile Glu Lys Tyr
    770                 775                 780
Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly Val Gly Lys Pro Lys
785                 790                 795                 800
Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp Lys Gln Gln Asn Asp
                805                 810                 815
Ala Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
            820                 825                 830
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
        835                 840                 845
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
    850                 855                 860
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
865                 870                 875                 880
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
                885                 890                 895
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
            900                 905                 910
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
```

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        915                 920                 925
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
    930                 935                 940
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
945                 950                 955                 960
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
                965                 970                 975
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
            980                 985                 990
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
        995                 1000                1005
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
    1010                1015                1020
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
1025                1030                1035                1040
Leu Ser Pro Gly Lys
                1045
```