

SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.
Gromada, Jesper
Stavis, Panayiotis
Altarejos, Judith

<120> Antigen-Binding Proteins That Antagonize Leptin Receptor

<130> 10271W001

<140> TBD

<141> 2017-11-08

<150> 62/419,062

<151> 2016-11-08

<160> 95

<170> PatentIn version 3.5

<210> 1

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1

cagctgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc	60
acctgcactg tctctggtgc ctctatcagc agtagtcgtt tctacggggg ctggatccgc	120
cagccccag ggaaggggtct ggagtggatt ggggatatct attatagtgg gaatacctac	180
tacaaccctg ccctccagag tcgagtcacc atatccgtag acacgtcaa gaatcagttc	240
tccctgaagc tgagctctgt gaccgccgca gacacggctg tgtattactg tgcgagacac	300
cttatgatta cgtttggggg acttatcgtc gagggttttg atatttgggg ccaagggaca	360
atggtcaccg tctcttca	378

<210> 2

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 2

Gln Leu 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 Ala Ser Ile Ser Ser Ser
20 25 30

Arg Phe Tyr Gly Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Asp Ile Tyr Tyr Ser Gly Asn Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Gln Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg His Leu Met Ile Thr Phe Gly Gly Leu Ile Val Glu Gly
100 105 110

Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120 125

<210> 3
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 3
ggtagcctcta tcagcagtag tcgtttctac

30

<210> 4
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 4

Gly Ala Ser Ile Ser Ser Ser Arg Phe Tyr
1 5 10

<210> 5
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 5
atctattata gtggaatac c 21

<210> 6
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 6

Ile Tyr Tyr Ser Gly Asn Thr
1 5

<210> 7
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 7
gcgagacacc ttatgattac gtttggggga cttatcgtcg agggttttga tatt 54

<210> 8
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 8

Ala Arg His Leu Met Ile Thr Phe Gly Gly Leu Ile Val Glu Gly Phe

1

5

10

15

Asp Ile

<210> 9

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 9

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccgtca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> 10

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 10

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr

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
100 105

<210> 11
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 11
cagagcatta gcagctat

18

<210> 12
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 12

Gln Ser Ile Ser Ser Tyr
1 5

<210> 13
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 13
gctgcatcc

9

<210> 14
<211> 3
<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 14

Ala Ala Ser

1

<210> 15

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 15

caacagagtt acagtacccc tccgatcacc

30

<210> 16

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 16

Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr

1

5

10

<210> 17

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 17

caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc

60

tcctgtgcag cctctggatt cactttcagt agctatggca tccactgggt ccgccaggct

120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaaataa taaatactat

180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cagctgtat

240

ctgcaaatga acagcctgag agctgaggac acggctgtat attactgtgc gaaagatcta	300
tttttggagt ggttatttca cggtatgggc gtctggggcc aagggaccac ggtcaccgtc	360
tcctca	366

$\langle 210 \rangle$	18
$\langle 211 \rangle$	122
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial Sequence

<220>
<223> synthetic

<400> 18

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Asn Asn 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 Lys Asp Leu Phe Leu Glu Trp Leu Phe His Gly Met Gly Val Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210>	19
<211>	24
<212>	DNA
<213>	Artificial Sequence

<220>

<223> synthetic

<400> 19

ggattcactt tcagtagcta tggc

24

<210> 20

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 20

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 21

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 21

atatcatatg atggaaataa taaa

24

<210> 22

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 22

Ile Ser Tyr Asp Gly Asn Asn Lys
1 5

<210> 23

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 23
gcgaaagatc tatttttggg gtggttattt cacggtatgg gcgtc 45

<210> 24
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 24

Ala Lys Asp Leu Phe Leu Glu Trp Leu Phe His Gly Met Gly Val
1 5 10 15

<210> 25
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 25
cagctgcagc tgcaggagtc gggcccagga ctagtgaagc cttcggagac cctgtccctc 60
acctgcattg tctctggtgg cgacatcacc agtagtagtt attactggaa ctggatccgc 120
cagccccag ggaaagggtt ggagtggatt gggaatatct attatagtgg aagcaccaac 180
tacaaccgt ccctcaagag tcgagtcacc atatccatag acacgtcaa gagccagttc 240
tccctgaagc tgaggtctgt gaccgccgca gacacggctg tttattactg tgcgagatta 300
ttacgatatt ttgactggtc aaaaggatac cttgactact ggggccaggg aaccctggtc 360
accgtctcct ca 372

<210> 26
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 26

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

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

<210> 27
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 27
 ggtggcgaca tcaccagtag tagttattac

30

<210> 28
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 28

Gly Gly Asp Ile Thr Ser Ser Ser Tyr Tyr

1 5 10

<210> 29
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 29
atctattata gtggaagcac c 21

<210> 30
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 30

Ile Tyr Tyr Ser Gly Ser Thr
1 5

<210> 31
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 31
gcgagattat tacgatattt tgactgggtca aaaggatacc ttgactac 48

<210> 32
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 32

Ala Arg Leu Leu Arg Tyr Phe Asp Trp Ser Lys Gly Tyr Leu Asp Tyr
1 5 10 15

<210> 33
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 33
caggtgcagc tgggtggagtc tggggggaggc atgggtcaagc ctggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt gactactata tgagctggat ccgccaggct 120
ccagggaagg gtctggagtg gatttcacac attagtatta ctggtagcac catatactac 180
gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagaa ttcactgtat 240
ttggaaatga acagactgag agacgaggac acggccgtat attactgtac gagagatgag 300
ccggatattg tactagtaag gtacggtatg gacgtctggg gcccaaggac cacggtcacc 360
gtctcctca 369

<210> 34
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 34

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Ser His Ile Ser Ile Thr Gly Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Glu Met Asn Arg Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Asp Glu Pro Asp Ile Val Leu Val Arg Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 35
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 35
ggattcacct tcagtgacta ctat

24

<210> 36
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 36

Gly Phe Thr Phe Ser Asp Tyr Tyr
1 5

<210> 37
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 37
attagtatta ctggtagcac cata

24

<210> 38
<211> 8
<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 38

Ile Ser Ile Thr Gly Ser Thr Ile
1 5

<210> 39

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 39

acgagagatg agccggatat tgtactagta aggtacggta tggacgtc 48

<210> 40

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 40

Thr Arg Asp Glu Pro Asp Ile Val Leu Val Arg Tyr Gly Met Asp Val
1 5 10 15

<210> 41

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 41

gaggtgcagc tgggtggagtc tgggggaagt gtggtacggc ctggggaatc cctgagactc 60

tcctgtgcag cctctggatt cacatttgat gattatggca tgagctgggt ccgccaagct 120

ccagggaagg ggctggagtg ggtctctggt attagttgga atggtggcat cacagtttat 180

gcagactctg tgaagggccg attcaccgtc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agccgaggac acggccctct atcactgtgc gagagcccgt 300
 tatgggtggcg ccgactactg gggccaggga accctgggtca ccgtctcctc a 351

<210> 42
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 42

Glu Val Gln Leu Val Glu Ser Gly Gly Ser Val Val Arg Pro Gly Glu
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Ser Trp Asn Gly Gly Ile Thr Val Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His Cys
 85 90 95

Ala Arg Ala Arg Tyr Gly Gly Ala Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 43
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 43
ggattcacat ttgatgatta tggc

24

<210> 44
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 44

Gly Phe Thr Phe Asp Asp Tyr Gly
1 5

<210> 45
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 45
attagttgga atggtggcat caca

24

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 46

Ile Ser Trp Asn Gly Gly Ile Thr
1 5

<210> 47
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 47

gcgagagccc gttatggtgg cgccgactac

30

<210> 48
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 48

Ala Arg Ala Arg Tyr Gly Gly Ala Asp Tyr
1 5 10

<210> 49
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 49

gaggtgcagc tgggtggagtc tggggggagac ttggtacagc ctgggcggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttagc agttttgcc a tgagctgggt ccgccaggct 120
ccagggaggg gactggagt ggtctcaagt ctcagtgata gtggtgataa cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaaaaa tacgttgtat 240
ctgcaaatga acaacctgag agccgaggac acggccgttt attactgtgc gaaagatctc 300
ttttcggggg ggttattcca tggttttgat gtctggggcc aagggacaat ggtcaccgtc 360
tcttca 366

<210> 50
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 50

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
35 40 45

Ser Ser Leu Ser Asp Ser Gly Asp Asn Thr 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 Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Leu Phe Ser Gly Trp Leu Phe His Gly Phe Asp Val Trp
100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 51
ggattcacct ttagcagttt tgcc

24

<210> 52
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 52

Gly Phe Thr Phe Ser Ser Phe Ala
1 5

<210> 53
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 53
ctcagtgata gtggtgataa caca

24

<210> 54
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 54

Leu Ser Asp Ser Gly Asp Asn Thr
1 5

<210> 55
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 55
gcgaaagatc tcttttcggg gtggttattc catggttttg atgtc

45

<210> 56
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 56

Ala Lys Asp Leu Phe Ser Gly Trp Leu Phe His Gly Phe Asp Val
1 5 10 15

<210> 57

<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 57
caggttcagc tggatgcagtc tggacctgaa gtgaaaaaac ctggggcctc agtgaaggtc 60
tcttgtaagg gttctggtta caccttttcc tggatatggaa tcagctggat ccgacaggcc 120
cctggacacg gccttgaatg gatgggatgg atcagcgctt ccagtggtaa tacaagattt 180
gcacagaagg tccagggcag actcaccatg accacagaca catcgacgag tacagcctac 240
atggagctga ggagcctgag atctgacgac acggccgttt attactgtgc gagaacgggg 300
actcggccct ttgactattg gggccaggga accctgggtca ccgtctcctc a 351

<210> 58
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 58

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

Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe Ser Trp Tyr
20 25 30

Gly Ile Ser Trp Ile Arg Gln Ala Pro Gly His Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Ala Ser Ser Gly Asn Thr Arg Phe Ala Gln Lys Val
50 55 60

Gln Gly Arg Leu Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Thr Gly Thr Arg Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 59
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 59
ggttacacct tttcctggta tgga

24

<210> 60
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 60

Gly Tyr Thr Phe Ser Trp Tyr Gly
1 5

<210> 61
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 61
atcagcgctt ccagtggtaa taca

24

<210> 62
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 62

Ile Ser Ala Ser Ser Gly Asn Thr
1 5

<210> 63

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 63

gcgagaacgg ggactcggcc ctttgactat

30

<210> 64

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 64

Ala Arg Thr Gly Thr Arg Pro Phe Asp Tyr
1 5 10

<210> 65

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 65

gaggtgcagc tgggtggagtc tggggggaggc ttggtccagc cggggggggtc cctgagactc 60

tcctgtacag cctctggatt caccttcagt agctatggtc tgcactgggt ccgccaggct 120

ccaggggaagg gactggaata tgtttcaagt attaatacata atgggggtag taaatattat 180

gcagactctg tgaagggcag attcaccatc tccagagaca attcgaagaa cacgctgttt 240

cttcaaatgg gcagcctgaa aactgaggac atggctgttt attactgtgc gagagatctc 300

tttttggagt ggttattcca tggttttgat atctggggcc aagggacaat ggtcaccgtc 360

tcttca

366

<210> 66
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 66

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 Thr Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Leu His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val
35 40 45

Ser Ser Ile Asn His Asn Gly Gly Ser 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 Phe
65 70 75 80

Leu Gln Met Gly Ser Leu Lys Thr Glu Asp Met Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Phe Leu Glu Trp Leu Phe His Gly Phe Asp Ile Trp
100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 67
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 67

ggattcacct tcagtagcta tggc

24

<210> 68
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 68

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 69
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 69
attaatcata atgggggtag taaa

24

<210> 70
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 70

Ile Asn His Asn Gly Gly Ser Lys
1 5

<210> 71
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 71
gcgagagatc tctttttgga gtggttattc catggttttg atatc

45

<210> 72
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 72

Ala	Arg	Asp	Leu	Phe	Leu	Glu	Trp	Leu	Phe	His	Gly	Phe	Asp	Ile
1			5					10					15	

<210> 73
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 73

caggtgcagc	tcgaggagtc	gggcccagga	ctggtgaagc	cttcacagac	cctgtccctc	60
acctgttctg	tctctggtgg	ctccataaac	actggttctt	acttctggac	ttggatccgc	120
cagcaccag	gggagggcct	ggagtggatt	gggtacatct	attacaatgg	agacacctac	180
tacaatccgt	ccctcaagag	tcgagttacc	ttatcactag	acacgtctaa	gaaccagttc	240
tccctgaagc	tgaactctct	gactgccggg	gacacggccg	tttattactg	tgcgagaagt	300
gactggaact	ccctttttga	ccactggggc	caggggaccc	tggtcaccgt	ctcctca	357

<210> 74
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 74

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	Ser	Val	Ser	Gly	Gly	Ser	Ile	Asn	Thr	Gly
			20					25					30		

Ser Tyr Phe Trp Thr Trp Ile Arg Gln His Pro Gly Glu Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Asn Gly Asp Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Leu Ser Leu Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Asn Ser Leu Thr Ala Gly Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ser Asp Trp Asn Ser Leu Phe Asp His Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 75
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 75
ggtggctcca taaacactgg ttcttacttc

30

<210> 76
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 76

Gly Gly Ser Ile Asn Thr Gly Ser Tyr Phe
1 5 10

<210> 77
<211> 21
<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 77

atctattaca atggagacac c

21

<210> 78

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 78

Ile Tyr Tyr Asn Gly Asp Thr

1 5

<210> 79

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 79

gcgagaagtg actggaactc cctttttgac cac

33

<210> 80

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 80

Ala Arg Ser Asp Trp Asn Ser Leu Phe Asp His

1 5 10

<210> 81

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 81

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> 82

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 82

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> 83
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 83
cagagtgtta gcagcagcta c

21

<210> 84
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 84

Gln Ser Val Ser Ser Ser Tyr
1 5

<210> 85
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 85
ggtgcatcc

9

<210> 86
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 86

Gly Ala Ser
1

<210> 87

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

<220>
<223> synthetic

<400> 87
cagcagtatg gtagctcacc ttggacg

27

<210> 88
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 88

Gln Gln Tyr Gly Ser Ser Pro Trp Thr
1 5

<210> 89
<211> 1165
<212> PRT
<213> Artificial Sequence

<220>
<223> hLEPR P48357

<400> 89

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
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
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
1010 1015 1020

Phe Ser Asn Ser Ser Trp Glu Ile Glu Ala Gln Ala Phe Phe Ile
1025 1030 1035

Leu Ser Asp Gln His Pro Asn Ile Ile Ser Pro His Leu Thr Phe
1040 1045 1050

Ser Glu Gly Leu Asp Glu Leu Leu Lys Leu Glu Gly Asn Phe Pro
1055 1060 1065

Glu Glu Asn Asn Asp Lys Lys Ser Ile Tyr Tyr Leu Gly Val Thr
1070 1075 1080

Ser Ile Lys Lys Arg Glu Ser Gly Val Leu Leu Thr Asp Lys Ser
1085 1090 1095

Arg Val Ser Cys Pro Phe Pro Ala Pro Cys Leu Phe Thr Asp Ile
1100 1105 1110

Arg Val Leu Gln Asp Ser Cys Ser His Phe Val Glu Asn Asn Ile
1115 1120 1125

Asn Leu Gly Thr Ser Ser Lys Lys Thr Phe Ala Ser Tyr Met Pro
1130 1135 1140

Gln Phe Gln Thr Cys Ser Thr Gln Thr His Lys Ile Met Glu Asn

1145

1150

1155

Lys Met Cys Asp Leu Thr Val
1160 1165

<210> 90

<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> 90

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 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> 91

<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> 91

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
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
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
820 825 830 835

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
 1010 1015 1020

Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn
 1025 1030 1035

His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
 1040 1045 1050

<210> 92

<211> 1045

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 92

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
1010 1015 1020

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
1025 1030 1035

Leu Ser Leu Ser Pro Gly Lys
1040 1045

<210> 93

<211> 844

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 93

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> 94
<211> 846
<212> PRT
<213> Artificial Sequence

<220>
<223> mLEPR-mmh aa 1-818: mouse LEPR (L22-G839 of NP_666258.2) aa
819-846: myc-myc-hexahistidine tag

<400> 94

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> 95

<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> 95

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

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