

SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.

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

<130> 10178W001

<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

<160> 120

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1

```
caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggaagtc cctgagactc 60
tcctgtgtag cgtctggatt caccttcagt tccgatgcca tgtactgggt ccgccaggct 120
ccaggcaagg ggctggaatg ggtggcagtt atttattatg atggaaatta tcaatactat 180
gaagactccg ttaagggtcg attcaccatc tccagagaca attcccagaa cacgctggat 240
ctgcaaatga acagcctgag agtcgacgac acggctgtat atttctgtgc gcgtctcaac 300
tgggattact ggtatctcga tctctggggc cgtggcaccc tggtcactgt ctctca 357
```

<210> 2

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 2

```

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Lys
 1           5           10           15
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ser Asp
 20           25           30
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
100          105          110
Thr Leu Val Thr Val Ser Ser
115

```

<210> 3

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 3

ggattcacct tcagttccga tgcc

24

<210> 4

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 4

```

Gly Phe Thr Phe Ser Ser Asp Ala
 1           5

```

<210> 5

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 5

atttattatg atggaaatta tcaa

24

<210> 6

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 6

Ile Tyr Tyr Asp Gly Asn Tyr Gln

1

5

<210> 7

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 7

gcgcgtctca actgggatta ctggtatctc gatctc

36

<210> 8

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 8

Ala Arg Leu Asn Trp Asp Tyr Trp Tyr Leu Asp Leu

1

5

10

<210> 9

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 9

```

gacatccaga tgacccagtc 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

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<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

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<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> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 17
 caggtgcagc tgggtggagtc cggggggaggc gtggtccagc ctgggagggtc cctgagactc 60
 tcctgtacag cgtctggatt caccttcagt agttatgccca tgtactgggt cccagggt 120
 ccaggcaagg ggctggagtg ggtgtcagtt atatactatg atggaagtta taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatgg acagcctgag agccgaggac acggctgtct attactgtgc gagttataac 300
 tggaactact ggtacttcga tttctggggc cgtggcaccc tggtcactgt ctcctca 357

<210> 18
 <211> 119
 <212> PRT
 <213> 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 Thr Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 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

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

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			
	115		

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

<220>
 <223> synthetic

<400> 19
 ggattcacct tcagtagtta tgcc 24

<210> 20
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 20
 Gly Phe Thr Phe Ser Ser Tyr Ala
 1 5

<210> 21
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 21
 atatactatg atggaagtta taaa 24

<210> 22
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 22

Ile Tyr Tyr Asp Gly Ser Tyr Lys

1

5

<210> 23

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 23

gcgagttata actggaacta ctggtacttc gatttc

36

<210> 24

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 24

Ala Ser Tyr Asn Trp Asn Tyr Trp Tyr Phe Asp Phe

1

5

10

<210> 25

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 25

cagggtgcagc tgggtggagtc tgggggaagc gtggtccagc ctgggaggct cctgagactc 60
 tcctgtgcag cgtctggatt caccttcagt acatatgcca tgtactgggt ccgccagact 120
 ccaggcaagg ggctggagtg ggtggctgtt ttatactctg atggaagtaa taaatactat 180
 atagactccg tgaagggccg attcaccatc tccagagaca cttccacgaa cactctgtat 240
 ctgcaaatga gcagcctgcg agccgacgac tcggctctat attactgtgc gcgtctcaac 300
 tgggattact ggtacttcga tctctggggc cgtggcacc tggtcactgt ctctca 357

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<210> 26
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 26
 Gln Val Gln Leu Val Glu Ser Gly Gly Ser Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
 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
 115

<210> 27
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 27
 ggattcacct tcagtacata tgcc

24

<210> 28
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 28

Gly Phe Thr Phe Ser Thr Tyr Ala
1 5

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 29
ttatactctg atggaagtaa taaa 24

<210> 30
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 30
Leu Tyr Ser Asp Gly Ser Asn Lys
1 5

<210> 31
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 31
gcgcgctctca actgggatta ctggtacttc gatctc 36

<210> 32
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 32

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

Ala Arg Leu Asn Trp Asp Tyr Trp Tyr Phe Asp Leu
1 5 10

<210> 33
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 33
cagggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggagggtc cctgagactc 60
tcctgtgaag cgtctggatt cagcagcagt gacaatgcca tgtactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtgtcagtt atatatcatg atggaagtta taaatactat 180
gaagactccg tgaagggccg attcaccatc gccagagaca attccaagaa cacgctttat 240
ttgcaaatga acagcctgag agccgaggac acggctgtat attactgtgc gaggtataac 300
tggaaccact ggtacttcga tgtctggggc cgtggcaccc tggtcactgt ctcctca 357

<210> 34
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 34
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 Glu Ala Ser Gly Phe Ser Ser Ser Asp Asn
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 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
115

<210> 35

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 35

ggattcagca gcagtgacaa tgcc

24

<210> 36

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 36

Gly Phe Ser Ser Ser Asp Asn Ala
1 5

<210> 37

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 37

atatatcatg atggaagtta taaa

24

<210> 38

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 38

Ile Tyr His Asp Gly Ser Tyr Lys
1 5

<210> 39

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 39

gcgagggtata actggaacca ctggtacttc gatgtc

36

<210> 40

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 40

Ala Arg Tyr Asn Trp Asn His Trp Tyr Phe Asp Val

1

5

10

<210> 41

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 41

cagggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt acctatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtgtcagtt atatcatatg acgaaagtaa taagtactat 180
gcagactccg tgaagggccg attcaccatt tctagagaca attccaagaa cgcgctgtat 240
ttacaaatga acagcctgag aaatgaggac acggctgtgt attactgtgc gagagatcgg 300
ccttttggat tggttaccgg atggttcgac ccctggggcc aggggaaccct ggtcaccgtc 360
tcctca 366

<210> 42

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<400> 42

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	Thr	Tyr
			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									

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 43

ggattcacct tcagtaccta tggc

24

<210> 44

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 44

Gly	Phe	Thr	Phe	Ser	Thr	Tyr	Gly
1				5			

<210> 45

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 45

atatcatatg acgaaagtaa taag

24

<210> 46

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 46

Ile Ser Tyr Asp Glu Ser Asn Lys

1

5

<210> 47

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 47

gcgagagatc ggccttttgg attggttacc ggatggttcg acccc

45

<210> 48

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 48

Ala Arg Asp Arg Pro Phe Gly Leu Val Thr Gly Trp Phe Asp Pro

1

5

10

15

<210> 49

<211> 360

<212> DNA

<213> Artificial Sequence

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<220>

<223> synthetic

<400> 49

```
caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggagggtc cctgagactc 60
tcctgtgcag cgtctggatt cagtttcaat acctatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtgacaatt atatggtatg atggaagtat taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attattgtgc gagagggtgga 300
tatagtggct acctctactt tgactactgg ggccagggaa ccctgggtcac cgtctcctca 360
```

<210> 50

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 50

```
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 Ser Phe Asn Thr Tyr
 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
Gly Thr Leu Val Thr Val Ser Ser
115          120
```

<210> 51

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 51

ggattcagtt tcaataccta tggc 24

<210> 52

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 52

Gly Phe Ser Phe Asn Thr Tyr Gly

1 5

<210> 53

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 53

atatggtatg atggaagtat taaa

24

<210> 54

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 54

Ile Trp Tyr Asp Gly Ser Ile Lys

1 5

<210> 55

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 55

gcgagaggtg gatatagtagg ctacctctac ttgactac 39

<210> 56

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 56

Ala Arg Gly Gly Tyr Ser Gly Tyr Leu Tyr Phe Asp Tyr
1 5 10

<210> 57

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 57

caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagc agcgggtggtg actactggag ctggatccgc 120
cagctcccag ggaagggcct ggagtggatt gggtagatct attacagtgg gagcgctac 180
tataatccgt ccctcaagag tcgaggtacc atatcaatag acacgtctaa gaaccagttc 240
tccctgaagc tgacctctgt gactgccgcg gacacggccg tatatttctg tgtgaaatta 300
cgatttttgg agtggttctt ggggggctgg ttcggcccct ggggccaggg aaccctggtc 360
accgtctcct ca 372

<210> 58

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 58

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

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

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
	100						105						110		
Pro	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser				
	115					120									

<210> 59
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 59
 ggtggctcca tcagcagcgg tgggtgactac 30

<210> 60
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 60
 Gly Gly Ser Ile Ser Ser Gly Gly Asp Tyr
 1 5 10

<210> 61
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 61
 atctattaca gtgggagcgc c 21

<210> 62
 <211> 7

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 62

Ile Tyr Tyr Ser Gly Ser Ala

1

5

<210> 63

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 63

gtgaaattac gatttttggga gtggttcttg gggggctggt tcggcccc

48

<210> 64

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 64

Val Lys Leu Arg Phe Leu Glu Trp Phe Leu Gly Gly Trp Phe Gly Pro

1

5

10

15

<210> 65

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 65

gaggtgcagc tgggtggagtc tgggggaggc ttggtacagc cggggggggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttttagc aactatggca tgacctgggt ccgccaggct 120
 ccagggaagg gcctggaatg ggtctcagct attactgggtg gtggtggtag cacatactac 180
 tcaaactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacggtgtat 240

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

ctgcgaatga acagtgtgag agccgaggac acggccgtat attactgtgc gaaatataag 300
 tggaaacttcg tggacgactg gggccaggga accacgggtca ccgtctcctc a 351

<210> 66
 <211> 117
 <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 Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30
 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
 85 90 95
 Ala Lys Tyr Lys Trp Asn Phe Val Asp Asp Trp Gly Gln Gly Thr Thr
 100 105 110
 Val Thr Val Ser Ser
 115

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

<220>
 <223> synthetic

<400> 67
 ggattcacct ttagcaacta tggc 24

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

<220>
 <223> synthetic

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<400> 68

Gly Phe Thr Phe Ser Asn Tyr Gly
1 5

<210> 69

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 69

attactggtg gtggtgtag caca 24

<210> 70

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 70

Ile Thr Gly Gly Gly Gly Ser Thr
1 5

<210> 71

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 71

gcgaaatata agtgggaactt cgtggacgac 30

<210> 72

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<400> 72

Ala Lys Tyr Lys Trp Asn Phe Val Asp Asp
1 5 10

<210> 73

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 73

gaggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgttg cctctggatt caccttcaat aaatacgaca tgcactgggt ccgccaaact 120
actggaaaaag gtctagagtg ggtctcaggt attgatactg atggtgacac atactatcca 180
ggctccgtga agggccgatt caccatctcc agagaaaatg ccgagaactc cctgtatctt 240
caaataaacg gcctgagagt cggggacacg gctgtgtatt actgtgcaag atggccttgg 300
agtggtttct atggtgcttt tgatatctgg ggccaaggga caatgggtcac 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

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<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 tttctatggg 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 tctctgggtg ctccatcagc agtggtaatt actactggaa ctggatccgc 120
 caacagccag gagagggcct ggagtggatt gcttacatct atcacaatgg ggtcaccaac 180
 ttcaatccgt cctcaagag tcgacttact atatcagtag acacgtctaa gactcagttc 240
 tccctgaagt tgaggtctgt gactgccgcg gacacggccg tttattactg tgcgagatca 300
 ggagctggt 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 gcagctgggt 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

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<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 ttgcagtgtg ttactgtcag cagtatggta gctcaccttg gacgttcggc 300
caagggaacca 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

cagggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
 acctgcactg tctctggtgg ctccatcagt aattcctact ggagctggat ccggcagccc 120
 ccagggaagg gactggagtg gattggatat gtctattccc gtgggaacac caagtacaac 180
 ccctccctca cgagtcgagt caccatgtca ttgacacgt ccaagaacca gttctccctg 240
 aaactgaggt ctgtgaccgc cgcagacacg gccgtgtatt actgtgcgag aagcagcagc 300
 tggtagcagg actggtactt cgatctctgg ggccgtggca ccctgggtcac 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

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

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

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<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 tacttcgata 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 tctatgggtg gtccttcaga gggtattatt ggagttggat ccgccagccc 120
ccagggaagg ggctggagtg gattggggaa atcagttata gtggtttcac caattacaac 180
ccgtccctca agagtcgagt catcatatca atagatacgt ccaagaacca gttctccctg 240

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

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										

<210> 107

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 107

ggtgggtcct tcagaggcta ttat

24

<210> 108

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<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 cctatgggta tgggaccttt gattat 36

<210> 112

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<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

2016 10 11 10178W001 Sequence Listing as Filed ST25

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									

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

```

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

```

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

```

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

```

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

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			

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

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>

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<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								415	
Thr	Asp	Gly	Tyr	Leu	Thr	Lys	Met	Thr	Cys	Arg	Trp	Ser	Thr	Ser	Thr
														430	
Ile	Gln	Ser	Leu	Ala	Glu	Ser	Thr	Leu	Gln	Leu	Arg	Tyr	His	Arg	Ser
Ser	Leu	Tyr	Cys	Ser	Asp	Ile	Pro	Ser	Ile	His	Pro	Ile	Ser	Glu	Pro
Lys	Asp	Cys	Tyr	Leu	Gln	Ser	Asp	Gly	Phe	Tyr	Glu	Cys	Ile	Phe	Gln
465															480
Pro	Ile	Phe	Leu	Leu	Ser	Gly	Tyr	Thr	Met	Trp	Ile	Arg	Ile	Asn	His
Ser	Leu	Gly	Ser	Leu	Asp	Ser	Pro	Pro	Thr	Cys	Val	Leu	Pro	Asp	Ser
Val	Val	Lys	Pro	Leu	Pro	Pro	Ser	Ser	Val	Lys	Ala	Glu	Ile	Thr	Ile
Asn	Ile	Gly	Leu	Leu	Lys	Ile	Ser	Trp	Glu	Lys	Pro	Val	Phe	Pro	Glu
Asn	Asn	Leu	Gln	Phe	Gln	Ile	Arg	Tyr	Gly	Leu	Ser	Gly	Lys	Glu	Val
545															560
Gln	Trp	Lys	Met	Tyr	Glu	Val	Tyr	Asp	Ala	Lys	Ser	Lys	Ser	Val	Ser
Leu	Pro	Val	Pro	Asp	Leu	Cys	Ala	Val	Tyr	Ala	Val	Gln	Val	Arg	Cys
Lys	Arg	Leu	Asp	Gly	Leu	Gly	Tyr	Trp	Ser	Asn	Trp	Ser	Asn	Pro	Ala
Tyr	Thr	Val	Val	Met	Asp	Ile	Lys	Val	Pro	Met	Arg	Gly	Pro	Glu	Phe
Trp	Arg	Ile	Ile	Asn	Gly	Asp	Thr	Met	Lys	Lys	Glu	Lys	Asn	Val	Thr
625															640
Leu	Leu	Trp	Lys	Pro	Leu	Met	Lys	Asn	Asp	Ser	Leu	Cys	Ser	Val	Gln
Arg	Tyr	Val	Ile	Asn	His	His	Thr	Ser	Cys	Asn	Gly	Thr	Trp	Ser	Glu
Asp	Val	Gly	Asn	His	Thr	Lys	Phe	Thr	Phe	Leu	Trp	Thr	Glu	Gln	Ala
His	Thr	Val	Thr	Val	Leu	Ala	Ile	Asn	Ser	Ile	Gly	Ala	Ser	Val	Ala
Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	Asn	Ile	Val
705															720
Gln	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	As							

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

```

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

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<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	

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

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	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
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
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
																		720

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

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
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
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
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
Leu	Ser	Pro	Gly	Lys												1045		

<210> 117

<211> 844

<212> PRT

<213> Artificial Sequence

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<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

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

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
						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				

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

```

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

```

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

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

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

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

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

<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	

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
						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
						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											

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

```

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

```

<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

```

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

```

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

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

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

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		

2016_10_11_10178W001_Sequence_Listing_as_Filed_ST25

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
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
Leu Ser Pro Gly Lys		1040
1045		