SEQUENCE LISTING

<110> Lo, Kin-Ming
Zhang, Jinyang
Gillies, Stephen D.

<120> Expression and Export of Anti-Obesity Proteins as Fc Fusion Proteins

<130> LEX-008PC

<140>
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<150> US 60/115,079
<151> 1999-01-07

<160> 20

<170> PatentIn Ver. 2.0

<210> 1
<211> 441
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(441)
<223> Hu-Leptin

<400> 1

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Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr
  1               5                  10                  15

att gtc acc agg atc aat gac att tca cac acg cag tca gtc tcc tcc   96
Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser
             20                  25                  30

aaa cag aaa gtc acc ggt ttg gac ttc att cct ggg ctc cac ccc atc   144
Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile
         35                  40                  45

ctg acc tta tcc aag atg gac cag aca ctg gca gtc tac caa cag atc   192
Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Ile
     50                  55                  60

ctc acc agt atg cct tcc aga aac gtg atc caa ata tcc aac gac ctg   240
Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu
 65                  70                  75                  80

gag aac ctc cgg gat ctt ctt cac gtg ctg gcc ttc tct aag agc tgc   288
Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys
                 85                  90                  95

cac ttg ccc tgg gcc agt ggc ctg gag acc ttg gac agc ctg ggg ggt   336
His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly
            100                 105                 110

gtc ctg gaa gct tca ggc tac tcc aca gag gtg gtg gcc ctg agc agg   384
Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg
        115                 120                 125
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ctg cag ggg tct ctg cag gac atg ctg tgg cag ctg gac ctc agc cct 432
Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser Pro
130 135 140

ggg tgc tga 441
Gly Cys
145

<210> 2
<211> 146
<212> PRT
<213> Homo sapiens

<400> 2
Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr
1 5 10 15

Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser
20 25 30

Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile
35 40 45

Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Ile
50 55 60

Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu
65 70 75 80

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

His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly
100 105 110

Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg
115 120 125

Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser Pro
130 135 140

Gly Cys
145

<210> 3
<211> 441
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(441)
<223> Mu-Leptin

<400> 3
gtg cct atc cag aaa gtc cag gat gac acc aaa acc ctc atc aag acc 48
Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr
1 5 10 15

att gtc acc agg atc aat gac att tca cac acg cag tcg gta tcc gcc 96
Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ala
20 25 30

aag cag agg gtc act ggc ttg gac ttc att cct ggg ctt cac ccc att 144

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Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile
          35                  40                  45

ctg agt ttg tcc aag atg gac cag act ctg gca gtc tat caa cag gtc   192
Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Val
     50                  55                  60

ctc acc agc ctg cct tcc caa aat gtg ctg cag ata gcc aat gac ctg   240
Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp Leu
 65                  70                  75                  80

gag aat ctc cga gac ctc ctc cat ctg ctg gcc ttc tcc aag agc tgc   288
Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys
                85                  90                  95

tcc ctg cct cag acc agt ggc ctg cag aag cca gag agc ctg gat ggc   336
Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp Gly
            100                 105                 110

gtc ctg gaa gcc tca ctc tac tcc aca gag gtg gtg gct ttg agc agg   384
Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg
        115                 120                 125

ctg cag ggc tct ctg cag gac att ctt caa cag ttg gat gtt agc cct   432
Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser Pro
    130                 135                 140

gaa tgc tga                                                      441
Glu Cys
145
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<210> 4
<211> 146
<212> PRT
<213> Mus musculus

<400> 4

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Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr
 1               5                  10                  15

Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ala
            20                  25                  30

Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile
        35                  40                  45

Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Val
    50                  55                  60

Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp Leu
65                  70                  75                  80

Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys
                85                  90                  95

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

Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg
        115                 120                 125

Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser Pro
    130                 135                 140

Glu Cys
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145

<210> 5
<211> 696
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(696)
<223> HuFc

<400> 5

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gag ccc aaa tct tct gac aaa act cac aca tgc cca ccg tgc cca gca   48
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
  1               5                  10                  15

cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc   96
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
             20                  25                  30

aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg   144
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
         35                  40                  45

gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg   192
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
     50                  55                  60

gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag   240
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65                  70                  75                  80

tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag   288
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                 85                  90                  95

gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc   336
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc   384
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

cga gaa cca cag gtg tac acc ctg ccc cca tca cgg gag gag atg acc   432
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140

aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc   480
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac   528
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tat   576
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc   624
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205
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tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag   672
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

agc ctc tcc ctg tcc ccg ggt aaa                                  696
Ser Leu Ser Leu Ser Pro Gly Lys
225                 230
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<210> 6
<211> 232
<212> PRT
<213> Homo sapiens

<400> 6

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Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1               5                  10                  15

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

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210                 215                 220

Ser Leu Ser Leu Ser Pro Gly Lys
225                 230
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<210> 7
<211> 699
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(699)
<223> MuFc

<400> 7

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gag ccc aga ggg ccc aca atc aag ccc tgt cct cca tgc aaa tgc cca   48
Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro
  1               5                  10                  15

gca cct aac ctc ttg ggt gga cca tcc gtc ttc atc ttc cct cca aag   96
Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
            20                  25                  30

atc aag gat gta ctc atg atc tcc ctg agc ccc ata gtc aca tgt gtg   144
Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
        35                  40                  45

gtg gtg gat gtg agc gag gat gac cca gat gtc cag atc agc tgg ttt   192
Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
    50                  55                  60

gtg aac aac gtg gaa gta cac aca gct cag aca caa acc cat aga gag   240
Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
65                  70                  75                  80

gat tac aac agt act ctc cgg gtg gtc agt gcc ctc ccc atc cag cac   288
Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
                85                  90                  95

cag gac tgg atg agt ggc aag gag ttc aaa tgc aag gtc aac aac aaa   336
Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
            100                 105                 110

gac ctc cca gcg ccc atc gag aga acc atc tca aaa ccc aaa ggg tca   384
Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser
        115                 120                 125

gta aga gct cca cag gta tat gtc ttg cct cca cca gaa gaa gag atg   432
Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met
    130                 135                 140

act aag aaa cag gtc act ctg acc tgc atg gtc aca gac ttc atg cct   480
Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro
145                 150                 155                 160

gaa gac att tac gtg gag tgg acc aac aac ggg aaa aca gag cta aac   528
Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn
                165                 170                 175

tac aag aac act gaa cca gtc ctg gac tct gat ggt tct tac ttc atg   576
Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met
            180                 185                 190

tac agc aag ctg aga gtg gaa aag aag aac tgg gtg gaa aga aat agc   624
Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser
        195                 200                 205

tac tcc tgt tca gtg gtc cac gag ggt ctg cac aat cac cac acg act   672
Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr
    210                 215                 220

aag agc ttc tcc cgg acc ccg ggt aaa                              699
Lys Ser Phe Ser Arg Thr Pro Gly Lys
225                 230
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<210> 8
<211> 233
<212> PRT
<213> Mus musculus

<400> 8

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

Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
            20                  25                  30

Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
        35                  40                  45

Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
    50                  55                  60

Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
65                  70                  75                  80

Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
                85                  90                  95

Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
            100                 105                 110

Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser
        115                 120                 125

Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met
    130                 135                 140

Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro
145                 150                 155                 160

Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn
                165                 170                 175

Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met
            180                 185                 190

Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser
        195                 200                 205

Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr
    210                 215                 220

Lys Ser Phe Ser Arg Thr Pro Gly Lys
225                 230
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<210> 9
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:forward primer to clone and adapt the murine leptin cDNA

<400> 9
cccgggtaaa gtgcctatcc agaaagtcc 29

<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:reverse primer to clone and adapt the murine leptin cDNA

<400> 10
ctcgagtcag cattcagggc taacatc 27

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:forward primer to clone and adapt human leptin cDNA

<400> 11
cccgggtaaa gtgcccatcc aaaaagtcca 30

<210> 12
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:carboxy terminus of the immunoglobulin heavy chain

<400> 12
cccgggtaaa 10

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:reverse primer to clone and adapt human leptin cDNA

<400> 13
ctcgagtcag cacccagggc tgaggtc 27

<210> 14
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:forward primer to adapt murine leptin cDNA

<400> 14
cttaagcgtg cctatccaga aagtcca 27

<210> 15

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

<220>
<223> Description of Artificial Sequence:reverse primer to adapt murine leptin cDNA

<400> 15
gatatcgcat tcagggctaa catc 24

<210> 16
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:EcoRI/AflII linker-adaptor

<400> 16
aattcgatat c 11

<210> 17
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:EcoRI/AflII linker-adaptor

<400> 17
ttaagatatc g 11

<210> 18
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:linker

<400> 18
ggcgcaggag gttctggcgg atcc 24

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

<220>
<223> Description of Artificial Sequence:linker

<400> 19
ggatccgcca gaacctcctg cgcc 24

<210> 20
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus leptin sequence

<220>
<223> wherein Xaa represents any amino acid, and wherein each Xaa is independently selected

<400> 20

Val Pro Xaa Xaa Xaa Xaa Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr
1 5 10 15

Ile Val Xaa Arg Ile Asn Asp Ile Ser His Thr Xaa Ser Val Ser Xaa
20 25 30

Xaa Gln Xaa Val Xaa Gly Leu Asp Phe Ile Pro Gly Leu Xaa Pro Xaa
35 40 45

Leu Xaa Leu Ser Xaa Met Asp Gln Thr Leu Ala Xaa Tyr Gln Gln Xaa
50 55 60

Leu Xaa Xaa Xaa Xaa Ser Xaa Asn Xaa Xaa Gln Ile Xaa Xaa Asp Leu
65 70 75 80

Glu Asn Leu Arg Asp Leu Leu His Xaa Leu Ala Xaa Ser Lys Ser Cys
85 90 95

Xaa Leu Pro Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Ser Leu Xaa Xaa
100 105 110

Val Leu Glu Ala Ser Xaa Tyr Ser Thr Glu Val Val Ala Leu Ser Arg
115 120 125

Leu Gln Xaa Xaa Leu Gln Asp Xaa Leu Xaa Xaa Leu Asp Xaa Ser Pro
130 135 140

Xaa Cys
145