

seq list_5104975_1 (2)
SEQUENCE LISTING

<110> NATIONAL UNIVERSITY CORPORATION HOKKAIDO UNIVERSITY

<120> Anti-PD-L1 antibodies

<130> FP-221PCT

<150> JP P2016-159088

<151> 2016-08-15

<150> JP P2016-159089

<151> 2016-08-15

<150> JP P2017-110723

<151> 2017-06-05

<150> JP P2017-61454

<151> 2017-03-27

<160> 138

<170> PatentIn version 3.5

<210> 1

<211> 133

<212> PRT

<213> Rattus norvegicus

<400> 1

Met Glu Ser Gln Thr His Val Leu Ile Ser Leu Leu Leu Ser Val Ser
1 5 10 15

Gly Thr Tyr Gly Asp Ile Ala Ile Thr Gln Ser Pro Ser Ser Val Ala
20 25 30

Val Ser Val Gly Glu Thr Val Thr Leu Ser Cys Lys Ser Ser Gln Ser
35 40 45

Leu Leu Tyr Ser Glu Asn Gln Lys Asp Tyr Leu Gly Trp Tyr Gln Gln
50 55 60

Lys Pro Gly Gln Thr Pro Lys Pro Leu Ile Tyr Trp Ala Thr Asn Arg
65 70 75 80

His Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Ile Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr
100 105 110

Tyr Cys Gly Gln Tyr Leu Val Tyr Pro Phe Thr Phe Gly Pro Gly Thr
115 120 125

Lys Leu Glu Leu Lys
130

<210> 2

seq list_5104975_1 (2)

<211> 137
<212> PRT
<213> Rattus norvegicus

<400> 2

Met Gly Trp Ser Gln Ile Ile Leu Phe Leu Val Ala Ala Ala Thr Cys
1 5 10 15

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys
20 25 30

Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Ser Asn Phe Met His Trp Val Lys Gln Gln Pro Gly Asn Gly Leu
50 55 60

Glu Trp Ile Gly Trp Ile Tyr Pro Glu Tyr Gly Asn Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Asp Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Phe Cys Ala Ser Glu Glu Ala Val Ile Ser Leu Val Tyr Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser
130 135

<210> 3
<211> 105
<212> PRT
<213> Canis lupus

<400> 3

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

Glu Leu Gly Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
20 25 30

Tyr Pro Ser Gly Val Thr Val Ala Trp Lys Ala Ser Gly Ser Pro Val
35 40 45

Thr Gln Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys
50 55 60

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

seq list_5104975_1 (2)

His Ser Ser Phe Ser Cys Leu Val Thr His Glu Gly Ser Thr Val Glu
85 90 95

Lys Lys Val Ala Pro Ala Glu Cys Ser
100 105

<210> 4
<211> 331
<212> PRT
<213> Canis lupus
<400> 4

Ala Ser Thr Thr Ala Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly
1 5 10 15

Ser Thr Ser Gly Ser Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr
20 25 30

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

Gly Val His Thr Phe Pro Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Thr Val Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr
65 70 75 80

Phe Thr Cys Asn Val Val His Pro Ala Ser Asn Thr Lys Val Asp Lys
85 90 95

Pro Val Pro Lys Glu Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val
100 105 110

Pro Glu Ser Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro
115 120 125

Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro Glu Ile Thr Cys Val Val
130 135 140

Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val
145 150 155 160

Asp Gly Lys Glu Val His Thr Ala Lys Thr Gln Pro Arg Glu Gln Gln
165 170 175

Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Glu His Gln
180 185 190

Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Arg Val Asn His Ile Gly
195 200 205

seq list_5104975_1 (2)

Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala
210 215 220

His Gln Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu Ser
225 230 235 240

Ser Ser Asp Thr Val Thr Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro
245 250 255

Pro Glu Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Pro Glu Pro Glu
260 265 270

Ser Lys Tyr His Thr Thr Ala Pro Gln Leu Asp Glu Asp Gly Ser Tyr
275 280 285

Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Gln Gly
290 295 300

Asp Thr Phe Thr Cys Ala Val Met His Glu Ala Leu Gln Asn His Tyr
305 310 315 320

Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys
325 330

<210> 5
<211> 399
<212> DNA
<213> Rattus norvegicus

<400> 5
atggaatcac agacgcatgt cctcatttcc cttctgctct cggtatctgg tacctatggg 60
gacattgcga taaccagtc tccatcctct gtggctgtgt cagtaggaga gacggtcact 120
ctgagctgca agtccagtc gagtctttta tacagtga aaacaaaagga ctatttgggc 180
tggtaccagc agaaaccagg gcagactcct aaaccctta tctactgggc aaccaaccgg 240
cacactgggg tccctgatcg cttcacaggt agtggatccg ggacagactt cactctgatc 300
atcagcagtg tgcaggctga agacctggct gattattact gtgggcagta ccttgtctat 360
ccgttcacgt ttggacctgg gaccaagctg gaactgaaa 399

<210> 6
<211> 411
<212> DNA
<213> Rattus norvegicus

<400> 6
atgggatgga gccagatcat cctctttctg gtggcagcag ctacatgtgt tactcccag 60
gtacagctgc agcaatctgg ggctgaatta gtgaagcctg ggtcctcagt gaaaatttcc 120
tgcaaggctt ctggctacac cttcaccagt aactttatgc actgggtaaa gcagcagcct 180
ggaaatggcc ttgagtggat tgggtggatt tatcctgaat atggtaatac taagtacaat 240
caaaagttcg atgggaaggc aacactcact gcagacaaat cctccagcac agcctatatg 300

seq list_5104975_1 (2)

cagctcagca gcctgacatc tgaggactct gcagtctatt tctgtgcaag tgaggaggca 360
gttatatccc ttgtttactg gggccaaggc actctggtca ctgtctcttc a 411

<210> 7
<211> 318
<212> DNA
<213> Canis lupus

<400> 7
cagcccaagg cctccccctc ggtcacactc ttcccgcctt cctctgagga gctcggcgcc 60
aacaaggcca ccctggtgtg cctcatcagc gacttctacc ccagcggcgt gacggtggcc 120
tggaaggcaa gcggcagccc cgtcaccagc ggcgtggaga ccaccaagcc ctccaagcag 180
agcaacaaca agtacgcggc cagcagctac ctgagcctga cgcctgacaa gtggaaatct 240
cacagcagct tcagctgcct ggtcacgcac gaggggagca ccgtggagaa gaaggtggcc 300
cccgcagagt gctcttag 318

<210> 8
<211> 996
<212> DNA
<213> Canis lupus

<400> 8
gcctccacca cggccccctc ggttttccca ctggccccca gctgcgggtc cacttccggc 60
tccacggtgg ccctggcctg cctggtgtca ggctacttcc ccgagcctgt aactgtgtcc 120
tggaattccg gtccttgac cagcgggtgtg cacaccttcc cgtccgtcct gcagtcctca 180
gggctctact ccctcagcag cacggtgaca gtgccctcca gcaggtggcc cagcgagacc 240
ttcacctgca acgtggtcca cccggccagc aacactaaag tagacaagcc agtgcccaaa 300
gagtccacct gcaagtgtat atcccatgac ccagtccttg aatcactggg agggccttcg 360
gtcttcatct ttccccgaa acccaaggac atcctcagga ttaccggaac acccgagatc 420
acctgtgtgg tgtagatct gggccgtgag gaccctgagg tgcagatcag ctggttcgtg 480
gatggtaagg aggtgcacac agccaagacg cagcctcgtg agcagcagtt caacagcacc 540
taccgtgtgg tcagcgtcct cccattgag caccaggact ggctcaccgg aaaggagttc 600
aagtgcagag tcaaccacat aggcctcccc tccccatcg agaggactat ctccaaagcc 660
agagggcaag cccatcagcc cagtgtgtat gtcctgccac catccccaaa ggagttgtca 720
tccagtgaca cggtcaccct gacctgcctg atcaaagact tcttcccacc tgagattgat 780
gtggagtggc agagcaatgg acagccggag cccgagagca agtaccacac gactgcgccc 840
cagctggacg aggacgggtc ctacttcctg tacagcaagc tctctgtgga caagagccgc 900
tggcagcagg gagacacctt cacatgtgag gtgatgcatg aagctctaca gaaccactac 960
acagatctat ccctctccca ttctccgggt aaatga 996

<210> 9
<211> 238

seq list_5104975_1 (2)

<212> PRT
<213> Artificial Sequence

<220>
<223> chimeric L chain

<400> 9

Met Glu Ser Gln Thr His Val Leu Ile Ser Leu Leu Leu Ser Val Ser
1 5 10 15

Gly Thr Tyr Gly Asp Ile Ala Ile Thr Gln Ser Pro Ser Ser Val Ala
20 25 30

Val Ser Val Gly Glu Thr Val Thr Leu Ser Cys Lys Ser Ser Gln Ser
35 40 45

Leu Leu Tyr Ser Glu Asn Gln Lys Asp Tyr Leu Gly Trp Tyr Gln Gln
50 55 60

Lys Pro Gly Gln Thr Pro Lys Pro Leu Ile Tyr Trp Ala Thr Asn Arg
65 70 75 80

His Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Ile Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr
100 105 110

Tyr Cys Gly Gln Tyr Leu Val Tyr Pro Phe Thr Phe Gly Pro Gly Thr
115 120 125

Lys Leu Glu Leu Lys Gln Pro Lys Ala Ser Pro Ser Val Thr Leu Phe
130 135 140

Pro Pro Ser Ser Glu Glu Leu Gly Ala Asn Lys Ala Thr Leu Val Cys
145 150 155 160

Leu Ile Ser Asp Phe Tyr Pro Ser Gly Val Thr Val Ala Trp Lys Ala
165 170 175

Ser Gly Ser Pro Val Thr Gln Gly Val Glu Thr Thr Lys Pro Ser Lys
180 185 190

Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro
195 200 205

Asp Lys Trp Lys Ser His Ser Ser Phe Ser Cys Leu Val Thr His Glu
210 215 220

Gly Ser Thr Val Glu Lys Lys Val Ala Pro Ala Glu Cys Ser
225 230 235

seq list_5104975_1 (2)

<210> 10
 <211> 468
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> chimeric H chain

<400> 10

Met Gly Trp Ser Gln Ile Ile Leu Phe Leu Val Ala Ala Ala Thr Cys
 1 5 10 15

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys
 20 25 30

Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Ser Asn Phe Met His Trp Val Lys Gln Gln Pro Gly Asn Gly Leu
 50 55 60

Glu Trp Ile Gly Trp Ile Tyr Pro Glu Tyr Gly Asn Thr Lys Tyr Asn
 65 70 75 80

Gln Lys Phe Asp Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Phe Cys Ala Ser Glu Glu Ala Val Ile Ser Leu Val Tyr Trp Gly
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser
 130 135 140

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

Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val
 165 170 175

Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val
 195 200 205

Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His
 210 215 220

Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr
 225 230 235 240

seq list_5104975_1 (2)

Cys Lys Cys Ile Ser₂₄₅ Pro Cys Pro Val₂₅₀ Pro Glu Ser Leu Gly₂₅₅ Gly Pro
 Ser Val Phe Ile₂₆₀ Phe Pro Pro Lys₂₆₅ Lys Asp Ile Leu Arg₂₇₀ Ile Thr
 Arg Thr Pro₂₇₅ Glu Ile Thr Cys Val₂₈₀ Val Leu Asp Leu Gly₂₈₅ Arg Glu Asp
 Pro Glu Val Gln Ile Ser Trp₂₉₅ Phe Val Asp Gly Lys₃₀₀ Glu Val His Thr
 Ala Lys Thr Gln Pro Arg₃₁₀ Glu Gln Gln Phe Asn₃₁₅ Ser Thr Tyr Arg Val₃₂₀
 Val Ser Val Leu Pro₃₂₅ Ile Glu His Gln Asp₃₃₀ Trp Leu Thr Gly Lys₃₃₅ Glu
 Phe Lys Cys Arg₃₄₀ Val Asn His Ile Gly₃₄₅ Leu Pro Ser Pro Ile₃₅₀ Glu Arg
 Thr Ile Ser₃₅₅ Lys Ala Arg Gly Gln₃₆₀ Ala His Gln Pro Ser₃₆₅ Val Tyr Val
 Leu Pro₃₇₀ Pro Ser Pro Lys Glu₃₇₅ Leu Ser Ser Ser Asp₃₈₀ Thr Val Thr Leu
 Thr Cys Leu Ile Lys Asp₃₉₀ Phe Phe Pro Pro Glu₃₉₅ Ile Asp Val Glu Trp₄₀₀
 Gln Ser Asn Gly Gln₄₀₅ Pro Glu Pro Glu Ser₄₁₀ Lys Tyr His Thr Thr₄₁₅ Ala
 Pro Gln Leu Asp₄₂₀ Glu Asp Gly Ser Tyr₄₂₅ Phe Leu Tyr Ser Lys₄₃₀ Leu Ser
 Val Asp Lys₄₃₅ Ser Arg Trp Gln Gln₄₄₀ Gly Asp Thr Phe Thr₄₄₅ Cys Ala Val
 Met His Glu Ala Leu Gln Asn₄₅₅ His Tyr Thr Asp Leu₄₆₀ Ser Leu Ser His
 Ser Pro Gly Lys
 465

<210> 11
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 11

seq list_5104975_1 (2)

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 12
<211> 326
<212> PRT
<213> Homo sapiens

<400> 12

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser
1 5 10 15

Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
20 25 30

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

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
50 55 60

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr
65 70 75 80

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg
85 90 95

Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu
100 105 110

Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
115 120 125

seq list_5104975_1 (2)

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
130 135 140

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145 150 155 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
165 170 175

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
180 185 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
195 200 205

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
210 215 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
225 230 235 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
245 250 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
260 265 270

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
275 280 285

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
290 295 300

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Leu Gly Lys
325

<210> 13
<211> 321
<212> DNA
<213> Homo sapiens

<400> 13
actgtggctg caccatctgt cttcatcttc ccgccatctg atgagcagtt gaaatctgga 60
actgcctctg ttgtgtgcct gctgaataac ttctatccca gagaggccaa agtacagtgg 120
aaggtggata acgccctcca atcgggtaac tcccaggaga gtgtcacaga gcaggacagc 180
aaggacagca cctacagcct cagcagcacc ctgacgctga gcaaagcaga ctacgagaaa 240
caciaagtct acgcctgcga agtcacccat cagggcctga gctcgcccgt caciaagagc 300

seq list_5104975_1 (2) 321

<210> 14
<211> 981
<212> DNA
<213> Homo sapiens

<400> 14
tccaccaagg gcccatccgt cttccccctg gcgccctgct ccaggagcac ctccgagagc 60
acagccgccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 120
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga 180
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac gaagacctac 240
acctgcaacg tagatcacia gccagcaac accaagggtg acaagagagt tgagtccaaa 300
tatggtcccc catgcccata atgccagca cctgagttcc tggggggacc atcagtcttc 360
ctgttcccc caaaaccaa ggacactctc atgatctccc ggaccctga ggtcacgtgc 420
gtggtggtgg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc 480
gtggagggtg ataatgcaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt 540
gtggtcagcg tcctcaccgt cctgcaccag gactggctga acggcaagga gtacaagtgc 600
aaggtctcca acaaaggcct cccgtcctcc atcgagaaaa ccatctcaa agccaaaggg 660
cagccccgag agccacaggt gtacaccctg ccccatccc aggaggagat gaccaagaac 720
caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 780
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 840
ggctccttct tcctctacag caggctaacc gtggacaaga gcaggtggca ggaggggaat 900
gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacaca gaagagcctc 960
tccctgtctc tgggtaaata a 981

<210> 15
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> codon-optimized sequence

<400> 15
atggaatctc aaactcatgt ttgatttca ttacttctga gtgtttccgg aacctacggt 60
gatatcgcta tcaactaatc tccctcctct gttgctgtgt ctgtgggcga aaccgttacc 120
ctgtcctgca agtccagtca gtctcttctc tactccgaga atcaaaagga ctacctgggc 180
tggtaccaac agaagcccgg ccagaccca aagccactga tatactgggc aaccaacagg 240
cacaccggag tgcccagacg gttcacaggc agtggatctg gcaccgactt taccttgatc 300
atttcaagcg tgcaggctga agatctggcc gactactact gtggtcagta tctggtgtat 360
cctttcactt tcgggccagg gacaaaattg gaattgaag 399

seq list_5104975_1 (2)

<210> 16
 <211> 411
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon-optimized sequence

<400> 16
 atgggttggt ctcaaattat cttgtttttg gttgctgcag ccacttgtgt tcattctcag 60
 gtgcagctgc aacaaagcgg cgcagaactg gtgaaacctg gcagcagcgt gaaaatatct 120
 tgtaaggcca gcggatatac tttcacctcc aatttcatgc attgggtcaa acagcagccc 180
 ggcaacggac tcgagtggat cggctggatc taccctgagt atggcaacac aaaatataac 240
 caaaaatttg atggaaaggc taccctgact gccgataagt cctccagcac cgcatacatg 300
 caactctcct ccctgacctc cgaggatagc gctgtctact tctgtgcttc cgaagaggct 360
 gtcatatcct tgggtctattg gggccaagga actctggtga ccgtctcatc t 411

<210> 17
 <211> 318
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon-optimized sequence

<400> 17
 cagcccaaag cctctcccag cgtcacctc ttcccacctt ccagtgagga gctgggggca 60
 aacaaagcca ctttgggtgtg tctcatctcc gatttttacc cctccgggggt cacagtcgca 120
 tggaaggcct ccggatcccc tgtgacacag ggagtggaga caacaaaacc tagcaagcag 180
 agtaacaata agtatgccgc ctcaagctat ctcagcctta ctcctgataa gtggaagtca 240
 catagcagtt ttagttgcct cgtaacacat gaggggttcaa ctgtggagaa aaaagtagct 300
 ccagctgagt gtcatga 318

<210> 18
 <211> 996
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon-optimized sequence

<400> 18
 gctagcacia ccgctccctc cgttttttccc ctgcgcccat cctgcgggtc aaccagcgga 60
 tccaccgtcg ctctggcttg tctggtgtca ggatacttcc ccgagcctgt caccgtttct 120
 tggaatagcg gcagccttac ttccggcgtg cataccttcc ctagcgtgct tcagtcctcc 180
 ggtctgtatt ccctcagctc caccgtaact gtcccaagct caagggtggcc ctctgagaca 240
 ttacctgca atgtggtcca tcctgcttca aataccaaag tggacaagcc cgtcccaaaa 300
 gagtctacct gcaaatgtat cagtccttgt cccgtgcccg agtctctggg cggaccctca 360
 gtctttatct tcccaccaa gccaaaggac atattgcgca ttacacggac acccgaaatc 420

seq list_5104975_1 (2)

acctgtgttg	tgttgatct	cggccgggaa	gatcctgagg	tgagattag	ttggtttgtt	480
gatggcaagg	aggtgcacac	agcaaaaaca	cagcccagag	aacagcagtt	caacagtact	540
tatagagtag	tgagtgtgtt	gcctatagag	catcaggact	ggctgacagg	caaagaattc	600
aaatgtaggg	ttaaccacat	tggcctccct	agtccaatcg	agaggacaat	ctctaaagcc	660
cgaggccagg	ctcatcagcc	ttctgtgtac	gttctgcctc	ctagtcctaa	ggaactgtct	720
tcttcagaca	cagtaacact	cacttgcctg	attaaggact	tttttcctcc	agagattgat	780
gtggaatggc	agtctaacgg	gcagccagag	ccagaatcta	agtaccacac	tactgcacca	840
cagctggatg	aggatgggtc	ttacttcctg	tacagtaagc	tgagtgtgga	caagtctcga	900
tggcagcagg	gggatacttt	tacttgcgca	gtaatgcacg	aagcattgca	gaaccactac	960
actgacctgt	cacttagtca	ctcaccaggg	aagtaa			996

<210> 19
 <211> 717
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon-optimized sequence

<400> 19	
atggaatctc	aaactcatgt
tttgatttca	ttactttctga
gtgtttccgg	aacctacggt
	60
gatatcgcta	tcactcaatc
tccctcctct	gttgctgtgt
ctgtgggcga	aaccgttacc
	120
ctgtcctgca	agtccagtca
gtctcttctc	tactccgaga
atcaaaagga	ctacctgggc
	180
tggtagcaac	agaagcccgg
ccagacccca	aagccactga
tatactgggc	aaccaacagg
	240
cacaccggag	tgcccagacg
gttcacaggc	agtggatctg
gcaccgactt	taccttgatc
	300
atttcaagcg	tgagggtga
agatctggcc	gactactact
gtggtcagta	tctggtgtat
	360
cctttcactt	tcggggccagg
gacaaaattg	gaattgaagc
agcccaaagc	ctctcccagc
	420
gtcacctctt	ttccaccttc
cagtgaggag	ctggggggcaa
acaaagccac	tttggtgtgt
	480
ctcatctccg	atcttttacc
ctccgggggc	acagtcgcat
ggaaggcctc	cggatcccct
	540
gtgacacagg	gagtggagac
aacaaaacct	agcaagcaga
gtaacaataa	gtatgccgcc
	600
tcaagctatc	tcagccttac
tcctgataag	tggaagtcac
atagcagttt	tagttgcctc
	660
gtaacacatg	agggttcaac
tgtggagaaa	aaagtagctc
cagctgagtg	ctcatga
	717

<210> 20
 <211> 1407
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon-optimized sequence

<400> 20	
atgggttggt	ctcaaattat
cttggtttttg	gttgctgcag
ccacttgtgt	tcattctcag
	60
gtgcagctgc	aacaaagcgg
cgcagaactg	gtgaaacctg
gcagcagcgt	gaaaatatct
	120

seq list_5104975_1 (2)

tgtaaggcca gcggatatac tttcacctcc aatttcatgc attgggtcaa acagcagccc	180
ggcaacggac tcgagtggat cggctggatc taccgagat atggcaacac aaaatataac	240
caaaaatttg atggaaaggc taccctgact gccgataagt cctccagcac cgcatacatg	300
caactctcct ccctgacctc cgaggatagc gctgtctact tctgtgcttc cgaagaggct	360
gtcatatcct tgggtctattg gggccaagga actctggtga ccgtctcatc tgctagcaca	420
accgctccct ccgtttttcc cctcgcccca tcctgcgggt caaccagcgg atccaccgtc	480
gctctggctt gtctggtgtc aggatacttc cccgagcctg tcaccgtttc ttggaatagc	540
ggcagcctta cttccggcgt gcataccttc cctagcgtgc ttcagtcctc cggctctgtat	600
tccctcagct ccaccgtaac tgtcccaagc tcaagggtggc cctctgagac atttacctgc	660
aatgtggtcc atcctgcttc aaataccaaa gtggacaagc ccgtcccaa agagtctacc	720
tgcaaagtga tcagtccttg tcccgtgccc gagtctctgg gcggaccctc agtctttatc	780
ttcccacca agccaaagga catattgctc attacacgga caccgaaat cacctgtgtt	840
gtgttggtatc tcggccggga agatcctgag gtgcagatta gttggtttgt tgatggcaag	900
gaggtgcaca cagcaaaaac acagcccaga gaacagcagt tcaacagtac ttatagagta	960
gtgagtgtgt tgcctataga gcatcaggac tggctgacag gcaaagaatt caaatgtagg	1020
gttaaccaca ttggcctccc tagtccaatc gagaggacaa tctctaaagc ccgaggccag	1080
gctcatcagc cttctgtgta cgttctgcct cctagtccta aggaactgtc ttcttcagac	1140
acagtaacac tcacttgcct gattaaggac ttttttcctc cagagattga tgtggaatgg	1200
cagtctaacg ggcagccaga gccagaatct aagtaccaca ctactgcacc acagctggat	1260
gaggatgggt cttacttcct gtacagtaag ctgagtgtgg acaagtctcg atggcagcag	1320
ggggatactt ttacttgcgc agtaatgcac gaagcattgc agaaccacta cactgacctg	1380
tcacttagtc actcaccagg gaagtaa	1407

<210> 21
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 21
 aggatggctc ctagactccc 20

<210> 22
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 22
 agacgatggg ggcatactcg 20

seq list_5104975_1 (2)

<210> 23
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 23
 atgagaatgt ttagtgtctt 20

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

<220>
 <223> primer

<400> 24
 ttatgtctct tcaaattgta tatc 24

<210> 25
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 25
 gttgatctgt gtgttg 16

<210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 26
 cgggacttcc acatgagcat 20

<210> 27
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 27
 ttttagacag aaagtga 17

<210> 28
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

seq list_5104975_1 (2)

<223>	primer	
<400>	28	
	gaccagctct tcttggggaa	20
<210>	29	
<211>	29	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	29	
	ccgctcgaga tggggagccg gcgggggcc	29
<210>	30	
<211>	30	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	30	
	cgcggtatcct gaggggccac aggccgggtc	30
<210>	31	
<211>	26	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	31	
	gaagatctat gagaatgttt agtgtc	26
<210>	32	
<211>	28	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	32	
	ggaattctgt ctcttcaaatt tgtatatc	28
<210>	33	
<211>	30	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	33	
	cgcggttagc atggggagcc ggcgggggcc	30
<210>	34	
<211>	30	

seq list_5104975_1 (2)

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 34
 cgcgatatc cagcccctgc aactggccgc 30

<210> 35
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 35
 cgcggctagc atgagaatgt ttagtgtctt 30

<210> 36
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 36
 cgcgatatc agtcctctca cttgctggaa 30

<210> 37
 <211> 12
 <212> PRT
 <213> Rattus norvegicus
 <400> 37
 Gln Ser Leu Leu Tyr Ser Glu Asn Gln Lys Asp Tyr
 1 5 10

<210> 38
 <211> 9
 <212> PRT
 <213> Rattus norvegicus
 <400> 38

Gly Gln Tyr Leu Val Tyr Pro Phe Thr
 1 5

<210> 39
 <211> 8
 <212> PRT
 <213> Rattus norvegicus
 <400> 39

Gly Tyr Thr Phe Thr Ser Asn Phe
 1 5

<210> 40

seq list_5104975_1 (2)

<211> 8
<212> PRT
<213> Rattus norvegicus

<400> 40

Ile Tyr Pro Glu Tyr Gly Asn Thr
1 5

<210> 41
<211> 11
<212> PRT
<213> Rattus norvegicus

<400> 41

Ala Ser Glu Glu Ala Val Ile Ser Leu Val Tyr
1 5 10

<210> 42
<211> 331
<212> PRT
<213> Ovis aries

<400> 42

Ala Ser Thr Thr Pro Pro Lys Val Tyr Pro Leu Thr Ser Cys Cys Gly
1 5 10 15

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

Met Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Ile Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ala Ser Thr Ser Gly Ala Gln Thr
65 70 75 80

Phe Ile Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Gly Cys Pro Asp Pro Cys Lys His Cys Arg Cys Pro
100 105 110

Pro Pro Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
115 120 125

Pro Lys Asp Thr Leu Thr Ile Ser Gly Thr Pro Glu Val Thr Cys Val
130 135 140

Val Val Asp Val Gly Gln Asp Asp Pro Glu Val Gln Phe Ser Trp Phe
145 150 155 160

seq list_5104975_1 (2)

Val Asp Asn Val Glu Val Arg Thr Ala Arg Thr Lys Pro Arg Glu Glu
165 170 175

Gln Phe Asn Ser Thr Phe Arg Val Val Ser Ala Leu Pro Ile Gln His
180 185 190

Gln Asp Trp Thr Gly Gly Lys Glu Phe Lys Cys Lys Val His Asn Glu
195 200 205

Ala Leu Pro Ala Pro Ile Val Arg Thr Ile Ser Arg Thr Lys Gly Gln
210 215 220

Ala Arg Glu Pro Gln Val Tyr Val Leu Ala Pro Pro Gln Glu Glu Leu
225 230 235 240

Ser Lys Ser Thr Leu Ser Val Thr Cys Leu Val Thr Gly Phe Tyr Pro
245 250 255

Asp Tyr Ile Ala Val Glu Trp Gln Lys Asn Gly Gln Pro Glu Ser Glu
260 265 270

Asp Lys Tyr Gly Thr Thr Thr Ser Gln Leu Asp Ala Asp Gly Ser Tyr
275 280 285

Phe Leu Tyr Ser Arg Leu Arg Val Asp Lys Asn Ser Trp Gln Glu Gly
290 295 300

Asp Thr Tyr Ala Cys Val Val Met His Glu Ala Leu His Asn His Tyr
305 310 315 320

Thr Gln Lys Ser Ile Ser Lys Pro Pro Gly Lys
325 330

<210> 43
<211> 996
<212> DNA
<213> Ovis aries

<400> 43
gcctcaacaa ccccccgaa agtctaccct ctgacttctt gctgcgggga cacgtccagc 60
tccatcgtga ccctgggctg cctggtctcc agctatatgc ccgagccggt gaccgtgacc 120
tggaactctg gtgccctgac cagcggcgtg cacaccttcc cggccatcct gcagtcctcc 180
gggctctact ctctcagcag cgtggtgacc gtgccggcca gcacctcagg agcccagacc 240
ttcatctgca acgtagccca cccggccagc agcaccaagg tggacaagcg tgttgagccc 300
ggatgcccgg acccatgcaa acattgccga tgcccacccc ctgagctccc cggaggaccg 360
tctgtcttca tcttcccacc gaaacccaag gacaccctta caatctctgg aacgcccag 420
gtcacgtgtg tgggtggtgga cgtgggcccag gatgaccccg aggtgcagtt ctcttggttc 480
gtggacaacg tggaggtgcg cacggccagg acaaagccga gagaggagca gttcaacagc 540

seq list_5104975_1 (2)

accttccgcg tggtcagcgc cctgcccatac cagcaccaag actggactgg aggaaaggag	600
ttcaagtgca aggtccacaa cgaagccctc ccggcccca tcgtgaggac catctccagg	660
accaaagggc agggccggga gccgcaggtg tacgtcctgg cccacccca ggaagagctc	720
agcaaaagca cgctcagcgt cacctgcctg gtcaccggct tctaccaga ctacatcgcc	780
gtggagtggc agaaaaatgg gcagcctgag tcggaggaca agtacggcac gaccacatcc	840
cagctggacg ccgacggctc ctacttcctg tacagcaggc tcagggtgga caagaacagc	900
tggcaagaag gagacaccta cgcgtgtgtg gtgatgcacg aggctctgca caaccactac	960
acacagaagt cgatctctaa gcctccgggt aaatga	996

<210> 44
 <211> 329
 <212> PRT
 <213> Ovis aries

<400> 44

Ala	Ser	Thr	Thr	Ala	Pro	Lys	Val	Tyr	Pro	Leu	Thr	Ser	Cys	Cys	Gly
1				5					10					15	

Asp	Thr	Ser	Ser	Ser	Ser	Ile	Val	Thr	Leu	Gly	Cys	Leu	Val	Ser	
		20					25					30			

Ser	Tyr	Met	Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Ala	Leu
		35					40					45			

Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Ile	Leu	Gln	Ser	Ser	Gly	Leu
		50				55					60				

Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ala	Ser	Thr	Ser	Gly	Ala
65					70					75					80

Gln	Thr	Phe	Ile	Cys	Asn	Val	Ala	His	Pro	Ala	Ser	Ser	Ala	Lys	Val
				85					90					95	

Asp	Lys	Arg	Val	Gly	Ile	Ser	Ser	Asp	Tyr	Ser	Lys	Cys	Ser	Lys	Pro
			100					105					110		

Pro	Cys	Val	Ser	Arg	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys
		115					120					125			

Asp	Ser	Leu	Met	Ile	Thr	Gly	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val
	130					135					140				

Asp	Val	Gly	Gln	Gly	Asp	Pro	Glu	Val	Gln	Phe	Ser	Trp	Phe	Val	Asp
145					150					155					160

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

seq list_5104975_1 (2)

Asn Ser Thr Phe Arg Val Val Ser Ala Leu Pro Ile Gln His Asp His
180 185 190

Trp Thr Gly Gly Lys Glu Phe Lys Cys Lys Val His Ser Lys Gly Leu
195 200 205

Pro Ala Pro Ile Val Arg Thr Ile Ser Arg Ala Lys Gly Gln Ala Arg
210 215 220

Glu Pro Gln Val Tyr Val Leu Ala Pro Pro Gln Glu Glu Leu Ser Lys
225 230 235 240

Ser Thr Leu Ser Val Thr Cys Leu Val Thr Gly Phe Tyr Pro Asp Tyr
245 250 255

Ile Ala Val Glu Trp Gln Arg Ala Arg Gln Pro Glu Ser Glu Asp Lys
260 265 270

Tyr Gly Thr Thr Thr Ser Gln Leu Asp Ala Asp Gly Ser Tyr Phe Leu
275 280 285

Tyr Ser Arg Leu Arg Val Asp Lys Ser Ser Trp Gln Arg Gly Asp Thr
290 295 300

Tyr Ala Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
305 310 315 320

Lys Ser Ile Ser Lys Pro Pro Gly Lys
325

<210> 45
<211> 990
<212> DNA
<213> Ovis aries

<400> 45
gcctccacca cagccccgaa agtctaccct ctgacttctt gctgcgggga cacgtccagc 60
tccagctcca tcgtgaccct gggctgcctg gtctccagct atatgccga gccggtgacc 120
gtgacctgga actctggtgc cctgaccagc ggcgtgcaca cttcccggc catcctgcag 180
tcctccgggc tctactctct cagcagcgtg gtgaccgtgc cggccagcac ctcaggagcc 240
cagacattca tctgcaacgt agcccacccg gccagcagcg ccaaggtgga caagcgtgtt 300
gggatctcca gtgactactc caagtgttct aaaccgcctt gcgtgagccg accgtctgtc 360
ttcatcttcc ccccgaaacc caaggacagc ctcatgatca caggaacgcc cgaggtcacg 420
tgtgtggtgg tggacgtggg ccagggtgac cccgaggtgc agttctcctg gttcgtggac 480
aacgtggagg tgcgcacggc caggacaaag ccgagagagg agcagttcaa cagcaccttc 540
cgcgtggtca gcgccctgcc catccagcac gaccactgga ctggaggaaa ggagttcaag 600
tgcaagggtc acagcaaagg cctcccggcc cccatcgtga ggaccatctc cagggccaaa 660

seq list_5104975_1 (2)

gggcaggccc gggagccgca ggtgtacgtc ctggccccac cccaggaaga gctcagcaaa	720
agcacgtca gcgtcacctg cctggtcacc ggcttctacc cagactacat cgccgtggag	780
tggcagagag cgcggcagcc tgagtcggag gacaagtacg gcacgaccac atcccagctg	840
gacgccgacg gctcctactt cctgtacagc aggctcaggg tggacaagag cagctggcaa	900
agaggagaca cctacgcgtg tgtggtgatg cacgaggctc tgcacaacca ctacacacag	960
aagtcgatct ctaagcctcc gggtaaatga	990

<210> 46
 <211> 102
 <212> PRT
 <213> Ovis aries

<400> 46

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

Thr Val Ser Val Val Cys Leu Val Asn Asp Phe Tyr Pro Lys Asp Ile
 20 25 30

Asn Val Lys Val Lys Val Asp Gly Val Thr Gln Asn Ser Asn Phe Gln
 35 40 45

Asn Ser Phe Thr Asp Gln Asp Ser Lys Lys Ser Thr Tyr Ser Leu Ser
 50 55 60

Ser Thr Leu Thr Leu Ser Ser Ser Glu Tyr Gln Ser His Asn Ala Tyr
 65 70 75 80

Ala Cys Glu Val Ser His Lys Ser Leu Pro Thr Ala Leu Val Lys Ser
 85 90 95

Phe Asn Lys Asn Glu Cys
 100

<210> 47
 <211> 309
 <212> DNA
 <213> Ovis aries

<400> 47

ccatccgtct tcctcttcaa accatctgag gaacagctga ggaccggaac tgtctctgtc	60
gtgtgcttgg tgaatgattt ctaccccaaa gatatcaatg tcaaggtgaa agtggatggg	120
gttaccaga acagcaactt ccagaacagc ttcacagacc aggacagcaa gaaaagcacc	180
tacagcctca gcagcaccct gacactgtcc agctcagagt accagagcca taacgcctat	240
gcgtgtgagg tcagccacaa gagcctgccc accgccctcg tcaagagctt caataagaat	300
gaatgtag	309

<210> 48

seq list_5104975_1 (2)

<211> 106
<212> PRT
<213> Ovis aries

<400> 48

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

Glu Glu Leu Ser Thr Asn Lys Ala Thr Val Val Cys Leu Ile Asn Asp
20 25 30

Phe Tyr Pro Gly Ser Val Asn Val Val Trp Lys Ala Asp Gly Ser Thr
35 40 45

Ile Asn Gln Asn Val Lys Thr Thr Gln Ala Ser Lys Gln Ser Asn Ser
50 55 60

Lys Tyr Ala Ala Ser Ser Tyr Leu Thr Leu Thr Gly Ser Glu Trp Lys
65 70 75 80

Ser Lys Ser Ser Tyr Thr Cys Glu Val Thr His Glu Gly Ser Thr Val
85 90 95

Thr Lys Thr Val Lys Pro Ser Glu Cys Ser
100 105

<210> 49
<211> 321
<212> DNA
<213> Ovis aries

<400> 49

ggtcagccca agtccgcacc ctcggtcacc ctgttcccgcc cttccacgga ggagctcagt	60
accaacaagg ccaccgtggt gtgtctcatc aacgacttct acccggttag cgtgaacgtg	120
gtctggaagg cagatggcag caccatcaat cagaacgtga agaccacca ggcctccaaa	180
cagagcaaca gcaagtacgc ggccagcagc tacctgacct tgacgggcag cgagtggaag	240
tctaagagca gttacacctg cgaggtcacg caccgagggga gcaccgtgac gaagacagtg	300
aagccctcag agtgttctta g	321

<210> 50
<211> 328
<212> PRT
<213> Sus scrofa

<400> 50

Ala Pro Lys Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Cys Gly Arg
1 5 10 15

Asp Thr Ser Gly Pro Asn Val Ala Leu Gly Cys Leu Ala Ser Ser Tyr
20 25 30

seq list_5104975_1 (2)

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

Gly Val His Thr Phe Pro Ser Val Leu Gln Pro Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Met Val Thr Val Pro Ala Ser Ser Leu Ser Ser Lys Ser
65 70 75 80

Tyr Thr Cys Asn Val Asn His Pro Ala Thr Thr Thr Lys Val Asp Lys
85 90 95

Arg Val Gly Thr Lys Thr Lys Pro Pro Cys Pro Ile Cys Pro Gly Cys
100 105 110

Glu Val Ala Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp
115 120 125

Thr Leu Met Ile Ser Gln Thr Pro Glu Val Thr Cys Val Val Val Asp
130 135 140

Val Ser Lys Glu His Ala Glu Val Gln Phe Ser Trp Tyr Val Asp Gly
145 150 155 160

Val Glu Val His Thr Ala Glu Thr Arg Pro Lys Glu Glu Gln Phe Asn
165 170 175

Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp
180 185 190

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

Ala Pro Ile Thr Arg Thr Ile Ser Lys Ala Ile Gly Gln Ser Arg Glu
210 215 220

Pro Gln Val Tyr Thr Leu Pro Pro Pro Ala Glu Glu Leu Ser Arg Ser
225 230 235 240

Lys Val Thr Val Thr Cys Leu Val Ile Gly Phe Tyr Pro Pro Asp Ile
245 250 255

His Val Glu Trp Lys Ser Asn Gly Gln Pro Glu Pro Glu Gly Asn Tyr
260 265 270

Arg Thr Thr Pro Pro Gln Gln Asp Val Asp Gly Thr Phe Phe Leu Tyr
275 280 285

Ser Lys Leu Ala Val Asp Lys Ala Arg Trp Asp His Gly Glu Thr Phe
290 295 300

seq list_5104975_1 (2)

Glu Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 305 310 315 320

Ser Ile Ser Lys Thr Gln Gly Lys
 325

<210> 51
 <211> 987
 <212> DNA
 <213> Sus scrofa

<400> 51
 gcccccaaga cggccccatc ggtctaccct ctggccccct gcggcagggg cacgtctggc 60
 cctaacgtgg ccttgggctg cctggcctca agctacttcc ccgagccagt gaccatgacc 120
 tggaactcgg gcgccctgac cagtggcgtg cataccttcc catccgtcct gcagccgtca 180
 gggctctact ccctcagcag catgggtgacc gtgccggcca gcagcctgtc cagcaagagc 240
 tacacctgca atgtcaacca cccggccacc accaccaagg tggacaagcg tggttgaaca 300
 aagaccaaac caccatgtcc catatgccca ggctgtgaag tggccggggc ctcggtcttc 360
 atcttccctc caaaaccaa ggacaccctc atgatctccc agacccccga ggtcacgtgc 420
 gtggtggtgg acgtcagcaa ggagcacgcc gaggtccagt tctcctggta cgtggacggc 480
 gtagagggtg acacggccga gacgagacca aaggaggagc agttcaacag cacctaccgt 540
 gtggtcagcg tcctgcccac ccagcaccag gactggctga aggggaagga gttcaagtgc 600
 aaggtcaaca acgtagacct cccagccccc atcacgagga ccatctccaa ggctataggg 660
 cagagccggg agccgcaggt gtacaccctg cccccaccg ccgaggagct gtccaggagc 720
 aaagtcaccg taacctgcct ggtcattggc ttctaccac ctgacatcca tgttgagtgg 780
 aagagcaacg gacagccgga gccagagggc aattaccgca ccaccccgcc ccagcaggac 840
 gtggacggga ctttcttct gtacagcaag ctcgcggtgg acaaggcaag atgggaccat 900
 ggagaaacat ttgagtgtgc ggtgatgcac gaggtctctgc acaaccacta caccagaag 960
 tccatctcca agactcaggg taaatga 987

<210> 52
 <211> 328
 <212> PRT
 <213> Sus scrofa

<400> 52

Ala Pro Lys Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Cys Gly Arg
 1 5 10 15

Asp Val Ser Gly Pro Asn Val Ala Leu Gly Cys Leu Ala Ser Ser Tyr
 20 25 30

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

seq list_5104975_1 (2)

Gly Val His Thr Phe Pro Ser Val Leu Gln Pro Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Met Val Thr Val Pro Ala Ser Ser Leu Ser Ser Lys Ser
65 70 75 80

Tyr Thr Cys Asn Val Asn His Pro Ala Thr Thr Thr Lys Val Asp Lys
85 90 95

Arg Val Gly Ile His Gln Pro Gln Thr Cys Pro Ile Cys Pro Gly Cys
100 105 110

Glu Val Ala Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp
115 120 125

Thr Leu Met Ile Ser Gln Thr Pro Glu Val Thr Cys Val Val Val Asp
130 135 140

Val Ser Lys Glu His Ala Glu Val Gln Phe Ser Trp Tyr Val Asp Gly
145 150 155 160

Val Glu Val His Thr Ala Glu Thr Arg Pro Lys Glu Glu Gln Phe Asn
165 170 175

Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp
180 185 190

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

Ala Pro Ile Thr Arg Thr Ile Ser Lys Ala Ile Gly Gln Ser Arg Glu
210 215 220

Pro Gln Val Tyr Thr Leu Pro Pro Pro Ala Glu Glu Leu Ser Arg Ser
225 230 235 240

Lys Val Thr Leu Thr Cys Leu Val Ile Gly Phe Tyr Pro Pro Asp Ile
245 250 255

His Val Glu Trp Lys Ser Asn Gly Gln Pro Glu Pro Glu Asn Thr Tyr
260 265 270

Arg Thr Thr Pro Pro Gln Gln Asp Val Asp Gly Thr Phe Phe Leu Tyr
275 280 285

Ser Lys Leu Ala Val Asp Lys Ala Arg Trp Asp His Gly Asp Lys Phe
290 295 300

Glu Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
305 310 315 320

seq list_5104975_1 (2)

Ser Ile Ser Lys Thr Gln Gly Lys
325

<210> 53
 <211> 987
 <212> DNA
 <213> Sus scrofa

```

<400> 53
gccccaaga cggcccatc ggtctaccct ctggccccct gcggcagggg cgtgtctggc      60
cctaactgtg ccttgggctg cctggcctca agctacttcc ccgagccagt gaccgtgacc      120
tggaactcgg gcgccctgac cagtggcgtg cacaccttcc catccgtcct gcagccgtca      180
gggctctact ccctcagcag catggtgacc gtgccggcca gcagcctgtc cagcaagagc      240
tacacctgca atgtcaacca cccggccacc accaccaagg tggacaagcg tgttggaata      300
caccagccgc aaacatgtcc catatgccca ggctgtgaag tggccggggc ctcggtcttc      360
atcttccttc caaaaccaa ggacaccctc atgatctccc agacccccga ggtcacgtgc      420
gtggtggtgg acgtcagcaa ggagcacgcc gaggtccagt tctcctggta cgtggacggc      480
gtagaggtgc acacggccga gacgagacca aaggaggagc agttcaacag cacctaccgt      540
gtggtcagcg tcctgcccac ccagcaccag gactggctga aggggaagga gttcaagtgc      600
aaggtcaaca acgtagacct cccagcccc atcacgagga ccatctccaa ggctataggg      660
cagagccggg agccgcaggt gtacaccctg cccccaccg ccgaggagct gtccaggagc      720
aaagtcacgc taacctgcct ggtcattggc ttctaccac ctgacatcca tgttgagtgg      780
aagagcaacg gacagccgga gccagagaac acataccgca ccaccccgcc ccagcaggac      840
gtggacggga ctttcttcct gtacagcaaa ctgcggtggg acaaggcaag atgggaccat      900
ggagacaaat ttgagtgtgc ggtgatgcac gaggctctgc acaaccacta caccagaag      960
tccatctcca agactcaggg taaatga                                           987
  
```

<210> 54
 <211> 328
 <212> PRT
 <213> Sus scrofa

<400> 54

Ala Pro Lys Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15

Asp Thr Ser Gly Pro Asn Val Ala Leu Gly Cys Leu Ala Ser Ser Tyr
 20 25 30

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

Gly Val His Thr Phe Pro Ser Val Leu Gln Pro Ser Gly Leu Tyr Ser
 50 55 60

seq list_5104975_1 (2)

Leu 65 Ser Ser Met Val 70 Thr Val Pro Ala Ser 75 Ser Leu Ser Ser Lys 80 Ser
 Tyr Thr Cys Asn 85 Val Asn His Pro Ala Thr 90 Thr Thr Lys Val Asp 95 Lys
 Arg Val Gly Thr 100 Lys Thr Lys Pro Pro 105 Cys Pro Ile Cys Pro 110 Ala Cys
 Glu Ser Pro 115 Gly Pro Ser Val Phe 120 Ile Phe Pro Pro Lys 125 Pro Lys Asp
 Thr Leu 130 Met Ile Ser Arg Thr 135 Pro Gln Val Thr Cys 140 Val Val Val Asp
 Val 145 Ser Gln Glu Asn Pro 150 Glu Val Gln Phe Ser 155 Trp Tyr Val Asp Gly 160
 Val Glu Val His Thr 165 Ala Gln Thr Arg Pro 170 Lys Glu Glu Gln Phe 175 Asn
 Ser Thr Tyr Arg 180 Val Val Ser Val Leu 185 Pro Ile Gln His Gln 190 Asp Trp
 Leu Asn Gly 195 Lys Glu Phe Lys Cys 200 Lys Val Asn Asn Lys 205 Asp Leu Pro
 Ala Pro 210 Ile Thr Arg Ile Ile 215 Ser Lys Ala Lys Gly 220 Gln Thr Arg Glu
 Pro Gln Val Tyr Thr 225 Leu Pro Pro His Ala Glu 235 Glu Leu Ser Arg Ser 240
 Lys Val Ser Ile Thr 245 Cys Leu Val Ile Gly 250 Phe Tyr Pro Pro Asp 255 Ile
 Asp Val Glu Trp 260 Gln Arg Asn Gly Gln 265 Pro Glu Pro Glu Gly 270 Asn Tyr
 Arg Thr Thr 275 Pro Pro Gln Gln Asp 280 Val Asp Gly Thr Tyr 285 Phe Leu Tyr
 Ser Lys 290 Phe Ser Val Asp Lys 295 Ala Ser Trp Gln Gly 300 Gly Gly Ile Phe
 Gln Cys Ala Val Met 305 His Glu Ala Leu His Asn 315 His Tyr Thr Gln Lys 320
 Ser Ile Ser Lys Thr 325 Pro Gly Lys

seq list_5104975_1 (2)

<210> 55
 <211> 987
 <212> DNA
 <213> Sus scrofa

<400> 55
 gcccccaaga cggccccatc ggtctaccct ctggccccct gcagcagggg cacgtctggc 60
 cctaacgtgg ccttgggctg cctggcctca agctacttcc ccgagccagt gaccgtgacc 120
 tggaactcgg gcgccctgtc cagtggcgtg cataccttcc catccgtcct gcagccgtca 180
 gggctctact ccctcagcag catggtgacc gtgccggcca gcagcctgtc cagcaagagc 240
 tacacctgca atgtcaacca cccggccacc accaccaagg tggacaagcg tggttgaaca 300
 aagaccaaac caccatgtcc catatgccca gcctgtgaat caccagggcc ctcggtcttc 360
 atcttccctc caaaaccaa ggacaccctc atgatctccc ggacaccca ggtcacgtgc 420
 gtggtggttg atgtgagcca ggagaaccg gaggtccagt tctcctggta cgtggacggc 480
 gtagaggtgc acacggccca gacgaggcca aaggaggagc agttcaacag cacctaccgc 540
 gtggtcagcg tcctacccat ccagcaccag gactggctga acgggaagga gttcaagtgc 600
 aaggtcaaca acaaagacct ccagccccc atcacaagga tcatctcaa ggccaaaggg 660
 cagacccggg agccgcaggt gtacaccctg cccccacacg ccgaggagct gtccaggagc 720
 aaagtcaagc taacctgcct ggtcattggc ttctaccac ctgacatcga tgtcgagtgg 780
 caaagaaacg gacagccgga gccagagggc aattaccgca ccacccgcc ccagcaggac 840
 gtggacggga cctacttctt gtacagcaag ttctcggtgg acaaggccag ctggcagggg 900
 ggaggcatat tccagtgtgc ggtgatgcac gaggtctctg acaaccacta caccagaag 960
 tctatctcca agactccggg taaatga 987

<210> 56
 <211> 328
 <212> PRT
 <213> Sus scrofa

<400> 56
 Ala Pro Lys Thr Ala Pro Leu Val Tyr Pro Leu Ala Pro Cys Gly Arg
 1 5 10 15
 Asp Thr Ser Gly Pro Asn Val Ala Leu Gly Cys Leu Ala Ser Ser Tyr
 20 25 30
 Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 Gly Val His Thr Phe Pro Ser Val Leu Gln Pro Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Met Val Thr Val Pro Ala Ser Ser Leu Ser Ser Lys Ser
 65 70 75 80

seq list_5104975_1 (2)

Tyr Thr Cys Asn Val₈₅ Asn His Pro Ala Thr₉₀ Thr Thr Lys Val₉₅ Asp Lys

Arg Val Gly Thr₁₀₀ Lys Thr Lys Pro Pro₁₀₅ Cys Pro Ile Cys Pro₁₁₀ Ala Cys

Glu Ser Pro₁₁₅ Gly Pro Ser Val₁₂₀ Phe Ile Phe Pro Pro Lys₁₂₅ Pro Lys Asp

Thr Leu₁₃₀ Met Ile Ser Arg Thr₁₃₅ Pro Gln Val Thr Cys₁₄₀ Val Val Val Asp

Val₁₄₅ Ser Gln Glu Asn Pro₁₅₀ Glu Val Gln Phe Ser₁₅₅ Trp Tyr Val Asp Gly₁₆₀

Val Glu Val His Thr₁₆₅ Ala Gln Thr Arg Pro₁₇₀ Lys Glu Glu Gln Phe₁₇₅ Asn

Ser Thr Tyr Arg₁₈₀ Val Val Ser Val₁₈₅ Leu Pro Ile Gln His Gln₁₉₀ Asp Trp

Leu Asn Gly₁₉₅ Lys Glu Phe Lys Cys₂₀₀ Lys Val Asn Asn Lys₂₀₅ Asp Leu Pro

Ala Pro₂₁₀ Ile Thr Arg Ile Ile₂₁₅ Ser Lys Ala Lys Gly₂₂₀ Gln Thr Arg Glu

Pro Gln Val Tyr Thr Leu₂₃₀ Pro Pro His Ala Glu₂₃₅ Glu Leu Ser Arg Ser₂₄₀

Lys Val Ser Ile Thr₂₄₅ Cys Leu Val Ile Gly₂₅₀ Phe Tyr Pro Pro Asp₂₅₅ Ile

Asp Val Glu Trp₂₆₀ Gln Arg Asn Gly Gln₂₆₅ Pro Glu Pro Glu Gly₂₇₀ Asn Tyr

Arg Thr Thr₂₇₅ Pro Pro Gln Gln Asp₂₈₀ Val Asp Gly Thr Tyr₂₈₅ Phe Leu Tyr

Ser Lys₂₉₀ Phe Ser Val Asp Lys₂₉₅ Ala Ser Trp Gln Gly₃₀₀ Gly Gly Ile Phe

Gln Cys Ala Val Met His₃₁₀ Glu Ala Leu His Asn₃₁₅ His Tyr Thr Gln Lys₃₂₀

Ser Ile Ser Lys Thr₃₂₅ Pro Gly Lys

<210> 57
<211> 987
<212> DNA
<213> Sus scrofa

seq list_5104975_1 (2)

```

<400> 57
gcccccaaga cggccccatt ggtctaccct ctggccccct gcggcagggg cacgtctggc      60
cctaactgtg ccttgggctg cctggcctca agctacttcc ccgagccagt gaccgtgacc      120
tggaactcgg gcgccctgac cagtggcgtg cataccttcc catccgtcct gcagccgtca      180
gggctctact ccctcagcag catggtgacc gtgccggcca gcagcctgtc cagcaagagc      240
tacacctgca atgtcaacca cccggccacc accaccaagg tggacaagcg tggttgaaca      300
aagaccaaac caccatgtcc catatgcccga gcctgtgaat cgccagggcc ctcggtcttc      360
atcttccctc caaaacccaa ggacaccctc atgatctccc ggacacccca ggtcacgtgc      420
gtggtagttg atgtgagcca ggagaacccg gaggtccagt tctcctggta cgtggacggc      480
gtagaggtgc acacggccca gacgaggcca aaggaggagc agttcaacag cacctaccgc      540
gtggtcagcg tcctgcccac ccagcaccag gactggctga acgggaagga gttcaagtgc      600
aaggtcaaca acaaagacct cccagccccc atcacaagga tcattctcaa ggccaaaggg      660
cagacccggg agccgcaggt gtacaccctg ccccccacac ccgaggagct gtccaggagc      720
aaagtcagca taacctgcct ggtcattggc ttctaccacac ctgacatcga tgtcgagtgg      780
caaagaaacg gacagccgga gccagagggc aattaccgca ccaccccgcc ccagcaggac      840
gtggacggga cctacttcct gtacagcaag ttctcggtag acaaggccag ctggcagggg      900
ggaggcatat tccagtgtgc ggtgatgcac gaggtctctgc acaaccacta caccagaag      960
tctatctcca agactccggg taaatga      987

```

```

<210> 58
<211> 333
<212> PRT
<213> Sus scrofa

```

```

<400> 58
Ala Tyr Asn Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Cys Gly Arg
1           5           10           15

Asp Val Ser Asp His Asn Val Ala Leu Gly Cys Leu Val Ser Ser Tyr
20           25           30

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

Val Val His Thr Phe Pro Ser Val Leu Gln Pro Ser Gly Leu Tyr Ser
50           55           60

Leu Ser Ser Met Val Ile Val Ala Ala Ser Ser Leu Ser Thr Leu Ser
65           70           75           80

Tyr Thr Cys Asn Val Tyr His Pro Ala Thr Asn Thr Lys Val Asp Lys
85           90           95

```

seq list_5104975_1 (2)

Arg Val Asp Ile Glu Pro Pro Thr Pro Ile Cys Pro Glu Ile Cys Ser
100 105 110

Cys Pro Ala Ala Glu Val Leu Gly Ala Pro Ser Val Phe Leu Phe Pro
115 120 125

Pro Lys Pro Lys Asp Ile Leu Met Ile Ser Arg Thr Pro Lys Val Thr
130 135 140

Cys Val Val Val Asp Val Ser Gln Glu Glu Ala Glu Val Gln Phe Ser
145 150 155 160

Trp Tyr Val Asp Gly Val Gln Leu Tyr Thr Ala Gln Thr Arg Pro Met
165 170 175

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile
180 185 190

Gln His Gln Asp Trp Leu Lys Gly Lys Glu Phe Lys Cys Lys Val Asn
195 200 205

Asn Lys Asp Leu Leu Ser Pro Ile Thr Arg Thr Ile Ser Lys Ala Thr
210 215 220

Gly Pro Ser Arg Val Pro Gln Val Tyr Thr Leu Pro Pro Ala Trp Glu
225 230 235 240

Glu Leu Ser Lys Ser Lys Val Ser Ile Thr Cys Leu Val Thr Gly Phe
245 250 255

Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu
260 265 270

Pro Glu Gly Asn Tyr Arg Thr Thr Pro Pro Gln Gln Asp Val Asp Gly
275 280 285

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

Arg Gly Asp Leu Phe Gln Cys Ala Val Met His Glu Ala Leu His Asn
305 310 315 320

His Tyr Thr Gln Lys Ser Ile Ser Lys Thr Gln Gly Lys
325 330

<210> 59
<211> 1002
<212> DNA
<213> Sus scrofa

<400> 59
gcctacaaca cagctccatc ggtctaccct ctggccccct gtggcagggg cgtgtctgat

60

seq list_5104975_1 (2)

cataacgtgg ccttgggctg ccttgtctca agctacttcc ccgagccagt gaccgtgacc	120
tggaactcgg gtgccctgtc cagagtcgtg cataccttcc catccgtcct gcagccgtca	180
gggctctact ccctcagcag catgggtgatc gtggcggcca gcagcctgtc caccctgagc	240
tacacgtgca acgtctacca cccggccacc aacaccaagg tggacaagcg tgttgacatc	300
gaacccccca caccatctg tcccgaatt tgctcatgcc cagctgcaga ggtcctggga	360
gcaccgtcgg tcttcctctt ccctccaaaa cccaaggaca tcctcatgat ctcccggaca	420
ccaaggtca cgtgcgtggg ggtggacgtg agccaggagg aggtgaagt ccagttctcc	480
tgggtacgtg acggcgtaca gttgtacacg gccagacga ggccaatgga ggagcagttc	540
aacagcacct accgctgggt cagcgtcctg cccatccagc accaggactg gctgaagggg	600
aaggagtcca agtgcaaggt caacaacaaa gacctccttt ccccatcac gaggaccatc	660
tccaaggcta cagggccgag ccgggtgccg caggtgtaca ccctgcccc agcctgggaa	720
gagctgtcca agagcaaagt cagcataacc tgcctgggtc ctggcttcta cccacctgac	780
atcgatgtcg agtggcagag caacggacaa caagagccag agggcaatta ccgcaccacc	840
ccgccccagc aggacgtgga tgggacctac ttctgtaca gcaagctcgc ggtggacaag	900
gtcaggtggc agcgtggaga cctattccag tgtgcggtga tgcacgaggc tctgcacaac	960
cactacaccc agaagtccat ctccaagact cagggtaaat ga	1002

<210> 60
 <211> 277
 <212> PRT
 <213> Sus scrofa

<400> 60

Thr Phe Pro Ser Val Leu Gln Pro Ser Gly Leu Tyr Ser Leu Ser Ser
 1 5 10 15

Met Val Thr Val Pro Ala Ser Ser Leu Ser Ser Lys Ser Tyr Thr Cys
 20 25 30

Asn Val Asn His Pro Ala Thr Thr Thr Lys Val Asp Lys Arg Val Gly
 35 40 45

Thr Lys Thr Lys Pro Pro Cys Pro Ile Cys Pro Ala Cys Glu Gly Pro
 50 55 60

Gly Pro Ser Ala Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 65 70 75 80

Ile Ser Arg Thr Pro Lys Val Thr Cys Val Val Val Asp Val Ser Gln
 85 90 95

Glu Asn Pro Glu Val Gln Phe Ser Trp Tyr Val Asp Gly Val Glu Val
 100 105 110

seq list_5104975_1 (2)

His Thr Ala Gln Thr Arg Pro Lys Glu Glu Gln Phe Asn Ser Thr Tyr
115 120 125

Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu Asn Gly
130 135 140

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

Thr Arg Ile Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro Gln Val
165 170 175

Tyr Thr Leu Pro Pro Pro Thr Glu Glu Leu Ser Arg Ser Lys Val Thr
180 185 190

Leu Thr Cys Leu Val Thr Gly Phe Tyr Pro Pro Asp Ile Asp Val Glu
195 200 205

Trp Gln Arg Asn Gly Gln Pro Glu Pro Glu Gly Asn Tyr Arg Thr Thr
210 215 220

Pro Pro Gln Gln Asp Val Asp Gly Thr Tyr Phe Leu Tyr Ser Lys Leu
225 230 235 240

Ala Val Asp Lys Ala Ser Trp Gln Arg Gly Asp Thr Phe Gln Cys Ala
245 250 255

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Phe
260 265 270

Lys Thr Pro Gly Lys
275

<210> 61
<211> 834
<212> DNA
<213> Sus scrofa

<400> 61
accttcccat ccgtcctgca gccgtcaggg ctctactccc tcagcagcat ggtgaccgtg 60
ccggccagca gcctgtccag caagagctac acctgcaatg tcaaccaccc ggccaccacc 120
accaaggtgg acaagcgtgt tggaacaaag accaaaccac catgtcccat atgcccagcc 180
tgtgaagggc ccggggccctc ggccttcata ttccctccaa aaccaagga caccctcatg 240
atctcccga ccccaaggt cacgtgcgtg gtggtagatg tgagccagga gaaccggag 300
gtccagttct cctggtacgt ggacggcgta gaggtgcaca cggcccagac gaggccaaag 360
gaggagcagt tcaacagcac ctaccgcgtg gtcagcgccc tgcccatcca gcaccaggac 420
tggctgaacg ggaaggagtt caagtgaag gtcaacaaca aagacctccc agccccatc 480
acaaggatca tctccaaggc caaagggcag acccgggagc cgcaggtgta caccctgccc 540

seq list_5104975_1 (2)

ccaccaccg aggagctgtc caggagcaaa gtcacgctaa cctgcctggt cactggcttc 600
taccacactg acatcgatgt cgagtggcaa agaaacggac agccggagcc agagggcaat 660
taccgcacca ccccgcccca gcaggacgtg gacgggacct acttcctgta cagcaagctc 720
gcggtggaca aggccagctg gcagcgtgga gacacattcc agtgtgcggt gatgcacgag 780
gctctgcaca accactacac ccagaagtcc atcttcaaga ctccgggtaa atga 834

<210> 62
<211> 318
<212> PRT
<213> Sus scrofa

<400> 62

Ala Pro Lys Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Cys Gly Arg
1 5 10 15

Asp Val Ser Gly Pro Asn Val Ala Leu Gly Cys Leu Ala Ser Ser Tyr
20 25 30

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

Gly Val His Thr Phe Pro Ser Val Leu Gln Pro Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Met Val Thr Val Pro Ala Ser Ser Leu Ser Ser Lys Ser
65 70 75 80

Tyr Thr Cys Asn Val Asn His Pro Ala Thr Thr Thr Lys Val Asp Lys
85 90 95

Arg Val Gly Ile His Gln Pro Gln Thr Cys Pro Ile Cys Pro Ala Cys
100 105 110

Glu Gly Pro Gly Pro Ser Ala Phe Ile Phe Pro Pro Lys Pro Lys Asp
115 120 125

Thr Leu Met Ile Ser Arg Thr Pro Lys Val Thr Cys Val Val Val Asp
130 135 140

Val Ser Gln Glu Asn Pro Glu Val Gln Phe Ser Trp Tyr Val Asp Gly
145 150 155 160

Val Glu Val His Thr Ala Gln Thr Arg Pro Lys Glu Glu Gln Phe Asn
165 170 175

Ser Thr Tyr Arg Val Val Ser Val Leu Leu Ile Gln His Gln Asp Trp
180 185 190

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

seq list_5104975_1 (2)

Ala Pro Ile Thr Arg Ile Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu
210 215 220

Pro Gln Val Tyr Thr Leu Pro Pro Pro Thr Glu Glu Leu Ser Arg Ser
225 230 235 240

Lys Val Thr Leu Thr Cys Leu Val Thr Gly Phe Tyr Pro Pro Asp Ile
245 250 255

Asp Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Pro Glu Gly Asn Tyr
260 265 270

Arg Thr Thr Pro Pro Gln Gln Asp Val Asp Gly Thr Tyr Phe Leu Tyr
275 280 285

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

Gln Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315

<210> 63
<211> 955
<212> DNA
<213> Sus scrofa

<400> 63
gcccccaaga cggccccatc ggtctaccct ctggccccct gcggcagggg cgtgtctggc 60
cctaacgtgg ccttgggctg cctggcctca agctacttcc ccgagccagt gaccgtgacc 120
tggaactcgg gcgccctgac cagtggcgtg cacaccttcc catccgtcct gcagccgtca 180
gggctctact ccctcagcag catggtgacc gtgccggcca gcagcctgtc cagcaagagc 240
tacacctgca atgtcaacca cccggccacc accaccaagg tggacaagcg tgttggaata 300
caccagccgc aaacatgtcc catatgcca gcctgtgaag ggcccgggcc ctcggccttc 360
atcttcctc caaaaccaa ggacaccctc atgatctccc ggaccccaa ggtcacgtgc 420
gtggtggttg atgtgagcca ggagaacccg gaggtccagt tctcctggta cgtggacggc 480
gtagaggtgc acacggccca gacgaggcca aaggaggagc agttcaacag cacctaccgc 540
gtggtcagcg tcctgctcat ccagcaccag gactggctga acgggaagga gttcaagtgc 600
aaggtaaca acaaagacct ccagccccc atcacaagga tcctctcaa ggccaaaggg 660
cagacccggg agccgcaggt gtacaccctg cccccacca ccgaggagct gtccaggagc 720
aaagtcacgc taacctgcct ggtcactggc ttctaccac ctgacatcga tgtcgagtgg 780
caaagaaacg gacagccgga gccagagggc aattaccgca ccacccgcc ccagcaggac 840
gtggacggga cctacttcct gtacagcaag ctcgcggtgg acaaggccag ctggcagcgt 900
ggagacacat tccagtgtgc ggtgatgcac gaggtctctgc acaaccacta cacc 955

seq list_5104975_1 (2)

<210> 64
 <211> 323
 <212> PRT
 <213> Sus scrofa

<400> 64

Ala Pro Lys Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15

Asp Thr Ser Gly Pro Asn Val Ala Leu Gly Cys Leu Val Ser Ser Tyr
 20 25 30

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

Gly Val His Thr Phe Pro Ser Val Leu Gln Pro Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Met Val Thr Val Pro Ala His Ser Leu Ser Ser Lys Arg
 65 70 75 80

Tyr Thr Cys Asn Val Asn His Pro Ala Thr Lys Thr Lys Val Asp Leu
 85 90 95

Cys Val Gly Arg Pro Cys Pro Ile Cys Pro Gly Cys Glu Val Ala Gly
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Met Ile
 115 120 125

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Lys Glu
 130 135 140

His Ala Glu Val Gln Phe Ser Trp Tyr Val Asp Gly Glu Glu Val His
 145 150 155 160

Thr Ala Glu Thr Arg Pro Lys Glu Glu Gln Phe Asn Ser Thr Tyr Arg
 165 170 175

Val Val Ser Val Leu Pro Ile Gln His Glu Asp Trp Leu Lys Gly Lys
 180 185 190

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

Arg Thr Ile Ser Lys Ala Lys Gly Val Val Arg Ser Pro Glu Val Tyr
 210 215 220

Thr Leu Pro Pro Pro Ala Glu Glu Leu Ser Lys Ser Ile Val Thr Leu
 225 230 235 240

seq list_5104975_1 (2)

Thr Cys Leu Val Lys Ser Ile Phe Pro Phe Ile His Val Glu Trp Lys
 245 250 255

Ile Asn Gly Lys Pro Glu Pro Glu Asn Ala Tyr Arg Thr Thr Pro Pro
 260 265 270

Gln Glu Asp Glu Asp Arg Thr Tyr Phe Leu Tyr Ser Lys Leu Ala Val
 275 280 285

Asp Lys Ala Arg Trp Asp His Gly Glu Thr Phe Glu Cys Ala Val Met
 290 295 300

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Ser Lys Thr
 305 310 315 320

Gln Gly Lys

<210> 65
 <211> 975
 <212> DNA
 <213> Sus scrofa

<220>
 <221> misc_feature
 <222> (748)..(748)
 <223> n is a, c, g, or t

<400> 65
 gccccaaga cgccccatc ggtctaccct ctggccccct gcagcagggg cactgtctggc 60
 cctaactgtg ccttgggctg cctggtctca agctacttcc ccgagccagt gaccgtgacc 120
 tggaactcgg gcgccctgac cagtggcgtg cacaccttcc catccgtcct gcagccgtca 180
 gggctctact ccctcagcag catggtgacc gtgccggccc acagcttgtc cagcaagcgc 240
 tatacgtgca atgtcaacca ccagccacc aaaaccaagg tggacctgtg tgttggacga 300
 ccatgtccca tatgcccagg ctgtgaagtg gccggggcct cggctcttcat cttccctcca 360
 aaaccaagg acatcctcat gatctcccgg acccccgagg tcacgtgcgt ggtggtggac 420
 gtcagcaagg agcacgccga ggtccagttc tcctggtacg tggacggcga agaggtgcac 480
 acggccgaga cgaggccaaa ggaggagcag ttcaacagca cctaccgcgt ggtcagcgtc 540
 ctgcccattc agcacgagga ctggctgaag gggaaggagt tcgagtgcaa ggtcaacaac 600
 gaagacctcc caggcccat cagaggacc atctccaagg ccaaaggggt ggtacggagc 660
 ccggaggtgt acaccctgcc cccaccgcc gaggagctgt ccaagagcat agtcacgcta 720
 acctgcctgg tcaaaagcat cttcccgnc ttcattcatg ttgagtggaa aatcaacgga 780
 aaaccagagc cagagaacgc atatcgacc accccgcctc aggaggacga ggacaggacc 840
 tacttcctgt acagcaagct cgcggtggac aaggcaagat gggaccatgg agaaacattt 900
 gagtgtgcgg tgatgcacga ggctctgcac aaccactaca ccagaagtc catctccaag 960

actcagggtgta aatga

<210> 66
 <211> 317
 <212> PRT
 <213> Sus scrofa

<400> 66

Ala Tyr Asn Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Cys Gly Arg
 1 5 10 15

Asp Val Ser Asp His Asn Val Ala Leu Gly Cys Leu Val Ser Ser Tyr
 20 25 30

Phe Pro Glu Pro Val Thr Val Thr Trp Asn Trp Gly Ala Gln Thr Ser
 35 40 45

Gly Val His Thr Phe Pro Ser Val Leu Gln Pro Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Thr Val Thr Val Pro Ala His Ser Leu Ser Ser Lys Cys
 65 70 75 80

Phe Thr Cys Asn Val Asn His Pro Ala Thr Thr Thr Lys Val Asp Leu
 85 90 95

Cys Val Gly Lys Lys Thr Lys Pro Arg Cys Pro Ile Cys Pro Gly Cys
 100 105 110

Glu Val Ala Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp
 115 120 125

Ile Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 130 135 140

Val Ser Lys Glu His Ala Glu Val Gln Phe Ser Trp Tyr Val Asp Gly
 145 150 155 160

Glu Glu Val His Thr Ala Glu Thr Arg Pro Lys Glu Glu Gln Phe Asn
 165 170 175

Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Glu Asp Trp
 180 185 190

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

Gly Pro Ile Thr Arg Thr Ile Ser Lys Ala Lys Gly Val Val Arg Ser
 210 215 220

Pro Glu Val Tyr Thr Leu Pro Pro Pro Ala Glu Glu Leu Ser Lys Ser
 225 230 235 240

seq list_5104975_1 (2)

Ile Val Thr Leu Thr Cys Leu Val Lys Ser Phe Phe Pro Pro Phe Ile
245 250 255

His Val Glu Trp Lys Ile Asn Gly Lys Pro Glu Pro Glu Asn Ala Tyr
260 265 270

Arg Thr Thr Pro Pro Gln Glu Asp Glu Asp Gly Thr Tyr Phe Leu Tyr
275 280 285

Ser Lys Phe Ser Val Glu Lys Phe Arg Trp His Ser Gly Gly Ile His
290 295 300

Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315

<210> 67
<211> 952
<212> DNA
<213> Sus scrofa

<400> 67
gcctacaaca cagctccatc ggtctaccct ctggccccct gtggcagggg cgtgtctgat 60
cataacgtgg ccttgggctg cctggtctca agctacttcc ccgagccagt gaccgtgacc 120
tggaactggg gcgccagac cagtggcgtg cacaccttcc catccgtcct gcagccgtca 180
gggctctact ccctcagcag cacggtgacc gtgccggccc acagcttgtc cagcaagtgc 240
ttcacgtgca atgtcaacca cccggccacc accaccaagg tggacctgtg tgttgaaaaa 300
aagaccaagc ctcatgttcc catatgccca ggctgtgaag tggccggggc ctcggtcttc 360
atcttccctc caaaaccaa ggacatcctc atgatctccc ggacccccga ggtcacgtgc 420
gtggtggtgg acgtcagcaa ggagcacgcc gaggtccagt tctcctggta cgtggacggc 480
gaagaggtgc acacggccga gacgagacca aaggaggagc agttcaacag cacttaccgc 540
gtggtcagcg tcctgcccac ccagcacgag gactggctga aggggaagga gttcgagtgc 600
aaggtaaca acgaagacct cccaggcccc atcacgagga ccatctcaa ggccaaaggg 660
gtggtacgga gcccggaggt gtacaccctg cccccaccg ccgaggagct gtccaagagc 720
atagtcacgc taacctgcct ggtcaaaagc ttcttcccg ctttcatcca tgttgagtgg 780
aaaatcaacg gaaaaccaga gccagagaac gcataccgca ccaccccgcc ccaggaggac 840
gaggacggga cctacttctt gtacagcaag ttctcggtgg aaaagttcag gtggcacagt 900
ggaggcatcc actgtgcggt gatgcacgag gctctgcaca accactacac cc 952

<210> 68
<211> 314
<212> PRT
<213> Sus scrofa

<400> 68

seq list_5104975_1 (2)

Ala Pro Lys Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Cys Gly Arg
1 5 10 15

Asp Thr Ser Gly Pro Asn Val Ala Leu Gly Cys Leu Ala Ser Ser Tyr
20 25 30

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

Gly Val His Thr Phe Pro Ser Val Leu Gln Pro Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Met Val Thr Val Pro Ala Ser Ser Leu Ser Ser Lys Ser
65 70 75 80

Tyr Thr Cys Asn Val Asn His Pro Ala Thr Thr Thr Lys Val Asp Leu
85 90 95

Cys Val Gly Arg Pro Cys Pro Ile Cys Pro Ala Cys Glu Gly Pro Gly
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
115 120 125

Ser Arg Thr Pro Gln Val Thr Cys Val Val Val Asp Val Ser Gln Glu
130 135 140

Asn Pro Glu Val Gln Phe Ser Trp Tyr Val Asp Gly Val Glu Val His
145 150 155 160

Thr Ala Gln Thr Arg Pro Lys Glu Ala Gln Phe Asn Ser Thr Tyr Arg
165 170 175

Val Val Ser Val Leu Pro Ile Gln His Glu Asp Trp Leu Lys Gly Lys
180 185 190

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

Arg Ile Ile Ser Lys Ala Lys Gly Pro Ser Arg Glu Pro Gln Val Tyr
210 215 220

Thr Leu Ser Pro Ser Ala Glu Glu Leu Ser Arg Ser Lys Val Ser Ile
225 230 235 240

Thr Cys Leu Val Thr Gly Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp
245 250 255

Lys Ser Asn Gly Gln Pro Glu Pro Glu Gly Asn Tyr Arg Thr Thr Pro
260 265 270

seq list_5104975_1 (2)

Pro Gln Gln Asp Val Asp Gly Thr Tyr Phe Leu Tyr Ser Lys Leu Ala
 275 280 285

Val Asp Lys Ala Ser Trp Gln Arg Gly Asp Pro Phe Gln Cys Ala Val
 290 295 300

Met His Glu Ala Leu His Asn His Tyr Thr
 305 310

<210> 69
 <211> 943
 <212> DNA
 <213> Sus scrofa

<400> 69
 gcccccaaga cggccccatc ggtctaccct ctggccccct gcggcagggg cacgtctggc 60
 cctaacgtgg ccttgggctg cctggcctca agctacttcc ccgagccagt gaccctgacc 120
 tggaactcgg gcgccctgac cagtggcgtg cataccttcc catccgtcct gcagccgtca 180
 gggctctact ccctcagcag catggtgacc gtgccggcca gcagcctgtc cagcaagagc 240
 tacacctgca atgtcaacca cccggccacc accaccaagg tggacctgtg tgttggacga 300
 ccatgtccca tatgcccagc ctgtgaaggg cccggggcct cggctcttcat cttccctcca 360
 aaaccaaggg acaccctcat gatctcccgg acaccccagg tcacgtgcgt ggtggtagat 420
 gtgagccagg aaaacccgga ggtccagttc tcctggtatg tggacggtgt agaggtgcac 480
 acggcccaga cgaggccaaa ggaggcgag ttcaacagca cctaccgtgt ggtcagcgtc 540
 ctgcccattc agcacgagga ctggctgaag gggaaggagt tcgagtgcaa ggtcaacaac 600
 aaagacctcc cagcccccat cacaaggatc atctccaagg ccaaagggcc gagccgggag 660
 ccgcaggtgt acaccctgtc cccatccgcc gaggagctgt ccaggagcaa agtcagcata 720
 acctgcctgg tctactggctt ctaccacact gacatcgatg tcgagtggaa gagcaacgga 780
 cagccgggagc cagagggcaa ttaccgcacc accccgcccc agcaggacgt ggacggggacc 840
 tacttcctgt acagcaagct cgcggtggac aaggccagct ggcagcgtgg agaccattc 900
 cagtgtgcgg tgatgcacga ggctctgcac aaccactaca ccc 943

<210> 70
 <211> 320
 <212> PRT
 <213> Sus scrofa

<400> 70

Ala Pro Lys Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Cys Gly Arg
 1 5 10 15

Asp Thr Ser Gly Pro Asn Val Ala Leu Gly Cys Leu Ala Ser Ser Tyr
 20 25 30

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

seq list_5104975_1 (2)

Gly Val His Thr Phe Pro Ser Val Leu Gln Pro Ser Gly Leu Tyr Ser
50 55 60

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

Phe Thr Cys Asn Val Asn His Pro Ala Thr Thr Thr Lys Val Asp Leu
85 90 95

Cys Val Gly Arg Pro Cys Pro Ile Cys Pro Ala Cys Glu Gly Asn Gly
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
115 120 125

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
130 135 140

Asn Pro Glu Val Gln Phe Ser Trp Tyr Val Asp Gly Glu Glu Val His
145 150 155 160

Thr Ala Glu Thr Arg Pro Lys Glu Glu Gln Phe Asn Ser Thr Tyr Arg
165 170 175

Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu Lys Gly Lys
180 185 190

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

Arg Ile Ile Ser Lys Ala Lys Gly Pro Ser Arg Glu Pro Gln Val Tyr
210 215 220

Thr Leu Ser Pro Ser Ala Glu Glu Leu Ser Arg Ser Lys Val Ser Ile
225 230 235 240

Thr Cys Leu Val Thr Gly Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp
245 250 255

Lys Ser Asn Gly Gln Pro Glu Pro Glu Gly Asn Tyr Arg Ser Thr Pro
260 265 270

Pro Gln Glu Asp Glu Asp Gly Thr Tyr Phe Leu Tyr Ser Lys Leu Ala
275 280 285

Val Asp Lys Ala Arg Leu Gln Ser Gly Gly Ile His Cys Ala Val Met
290 295 300

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Ser Lys Thr
305 310 315 320

seq list_5104975_1 (2)

<210> 71
 <211> 960
 <212> DNA
 <213> Sus scrofa

<400> 71
 gcccccaaga cggccccatc ggtctaccct ctggccccct gcggcagga cacgtctggc 60
 cctaacgtgg ccttgggctg cctggcctca agctacttcc ccgagccagt gaccgtgacc 120
 tggaactcgg gcgccctgac cagtggcgtg cacaccttcc catccgtcct gcagccgtca 180
 gggctctact ccctcagcag cacggtgacc gtgccggcca ggagctcgtc cagaaagtgc 240
 ttcacgtgca atgtcaacca cccggccacc accaccaagg tggacctgtg tgttggacga 300
 ccatgtccca tatgccagc ctgtgaaggg aacgggccct cggctcttcat cttccctcca 360
 aaacccaagg acaccctcat gatctcccgg acccccgagg tcacgtgctg ggtggtagat 420
 gtgagccagg aaaacccgga ggtccagttc tcctggtacg tggacggcga agaggtgcac 480
 acggccgaga cgaggccaaa ggaggagcag ttcaacagca cctaccgtgt ggtcagcgtc 540
 ctgccccatcc agcaccagga ctggctgaag ggaaaggagt tcgagtgcaa ggtcaacaac 600
 aaagacctcc cagcccccat cacaaggatc atctccaagg ccaaagggcc gagccgggag 660
 ccgaggtgt acaccctgtc cccatccgcc gaggagctgt ccaggagcaa agtcagcata 720
 acctgcctgg tctactggctt ctaccacct gacatcgatg tcgagtggaa gagcaacgga 780
 cagccggagc cagagggcaa ttaccgctcc accccgcccc aggaggacga ggacgggacc 840
 tacttcctgt acagcaaact cgcggtggac aaggcgaggt tgcagagtgg aggcattccac 900
 tgtgcggtga tgcacgaggc tctgcacaac cactacaccc agaagtccat ctccaagact 960

<210> 72
 <211> 266
 <212> PRT
 <213> Bubalus bubalis

<400> 72
 Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 1 5 10 15
 Ser Leu Ser Ser Thr Val Thr Ala Pro Ala Ser Ala Thr Lys Ser Gln
 20 25 30
 Thr Phe Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp
 35 40 45
 Lys Ala Val Val Pro Pro Cys Arg Pro Lys Pro Cys Asp Cys Cys Pro
 50 55 60
 Pro Pro Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
 65 70 75 80

seq list_5104975_1 (2)

Pro Lys Asp Thr Leu₈₅ Thr Ile Ser Gly Thr₉₀ Pro Glu Val Thr Cys₉₅ Val

Val Val Asp Val₁₀₀ Gly His Asp Asp Pro Glu Val Lys Phe Ser₁₁₀ Trp Phe

Val Asp Asp₁₁₅ Val Glu Val Asn Thr₁₂₀ Ala Arg Thr Lys Pro Arg Glu Glu

Gln Phe₁₃₀ Asn Ser Thr Tyr Arg₁₃₅ Val Val Ser Ala Leu₁₄₀ Pro Ile Gln His

Asn Asp Trp Thr Gly₁₅₀ Gly Lys Glu Phe Lys Cys₁₅₅ Lys Val Tyr Asn Glu₁₆₀

Gly Leu Pro Ala Pro₁₆₅ Ile Val Arg Thr Ile₁₇₀ Ser Arg Thr Lys Gly₁₇₅ Gln

Ala Arg Glu Pro₁₈₀ Gln Val Tyr Val Leu₁₈₅ Ala Pro Pro Gln Asp₁₉₀ Glu Leu

Ser Lys Ser₁₉₅ Thr Val Ser Ile Thr₂₀₀ Cys Met Val Thr Gly₂₀₅ Phe Tyr Pro

Asp Tyr₂₁₀ Ile Ala Val Glu Trp₂₁₅ Gln Lys Asp Gly Gln₂₂₀ Pro Glu Ser Glu

Asp₂₂₅ Lys Tyr Gly Thr Thr₂₃₀ Pro Pro Gln Leu Asp₂₃₅ Ser Asp Gly Ser Tyr₂₄₀

Phe Leu Tyr Ser Arg₂₄₅ Leu Arg Val Asn Lys₂₅₀ Asn Ser Trp Gln Glu₂₅₅ Gly

Gly Ala Tyr Thr₂₆₀ Cys Val Val Met His₂₆₅ Glu

<210> 73
<211> 801
<212> DNA
<213> Bubalus bubalis

<400> 73
gagcggcgtg cacaccttcc cggccgtcct tcagtcctcc gggctctact ctctcagcag 60
cacggtgacc gcgcccacca gcgccacaaa aagccagacc ttcacctgca acgtagccca 120
cccggccagc agcaccaagg tggacaaggc tgttgttccc ccatgcagac cgaaaccctg 180
tgattgctgc ccaccccctg agtcccccg aggaccctct gtcttcatct tcccaccaaa 240
accaaggac accctcacia tctctggaac tcctgaggtc acgtgtgtgg tgggtggacgt 300
gggccacgat gaccccgagg tgaagttctc ctggttcgtg gacgatgtgg aggtaaacac 360
agccaggacg aagccaagag aggagcagtt caacagcacc taccgcgtgg tcagcgcctt 420

seq list_5104975_1 (2)

gccccatccag cacaacgact ggactggagg aaaggagttc aagtgcagg tctacaatga	480
aggcctccca gcccccatcg tgaggaccat ctccaggacc aaagggcagg cccgggagcc	540
gcaggtgtac gtcttgcccc caccacagga cgagctcagc aaaagcacgg tcagcatcac	600
ttgcatggtc actggcttct acccagacta catcgccgta gagtggcaga aagatgggca	660
gcctgagtca gaggacaaat atggcacgac cccgccccag ctggacagcg atggctccta	720
cttcctgtac agcaggctca gggatgaaca gaacagctgg caagaaggag gcgcctacac	780
gtgtgtagtg atgcatgagg c	801

<210> 74
 <211> 309
 <212> PRT
 <213> Bulalububalis
 <400> 74

Ala	Ser	Ile	Thr	Ala	Pro	Lys	Val	Tyr	Pro	Leu	Thr	Ser	Cys	Arg	Gly
1				5					10					15	

Glu	Thr	Ser	Ser	Ser	Thr	Val	Thr	Leu	Gly	Cys	Leu	Val	Ser	Ser	Tyr
			20					25					30		

Met	Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Ala	Leu	Lys	Ser
		35					40					45			

Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
	50					55					60				

Leu	Ser	Ser	Thr	Val	Thr	Ala	Pro	Ala	Ser	Ala	Thr	Lys	Ser	Gln	Thr
65					70					75					80

Phe	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Ser	Ser	Thr	Lys	Val	Asp	Thr
				85					90					95	

Ala	Val	Gly	Phe	Ser	Ser	Asp	Cys	Cys	Lys	Phe	Pro	Lys	Pro	Cys	Val
			100					105					110		

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

Met	Ile	Thr	Gly	Asn	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Gly
	130					135					140				

Arg	Asp	Asn	Pro	Glu	Val	Gln	Phe	Ser	Trp	Phe	Val	Gly	Asp	Val	Glu
145					150					155					160

Val	His	Thr	Gly	Arg	Ser	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr
				165					170					175	

Tyr	Arg	Val	Val	Ser	Thr	Leu	Pro	Ile	Gln	His	Asn	Asp	Trp	Thr	Gly
			180					185					190		

seq list_5104975_1 (2)

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

Ile Val Arg Thr Ile Ser Arg Thr Lys Gly Gln Ala Arg Glu Pro Gln
210 215 220

Val Tyr Val Leu Ala Pro Pro Gln Glu Glu Leu Ser Lys Ser Thr Val
225 230 235 240

Ser Val Thr Cys Met Val Thr Gly Phe Tyr Pro Asp Tyr Ile Ala Val
245 250 255

Glu Trp His Arg Asp Arg Gln Ala Glu Ser Glu Asp Lys Tyr Arg Thr
260 265 270

Thr Pro Pro Gln Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Ser Arg
275 280 285

Leu Lys Val Asn Lys Asn Ser Trp Gln Glu Gly Gly Ala Tyr Thr Cys
290 295 300

Val Val Met His Glu
305

<210> 75
<211> 929
<212> DNA
<213> Bubalus bubalis

<400> 75
gcctccatca cagccccgaa agtctaccct ctgacttctt gccgcgggga aacgtccagc 60
tccaccgtga ccctgggctg cctggtctcc agctacatgc ccgagccggt gaccgtgacc 120
tggaactcgg gtgccctgaa gagcggcgtg cacaccttcc cggccgtcct tcagtcctct 180
gggctctact ctctcagcag cacggtgacc gcgcccgcca gcgccacaaa aagccagacc 240
ttcacctgca acgtagccca cccggccagc agcaccaagg tggacacggc tggtgggttc 300
tccagtgact gctgcaagtt tcctaagcct tgtgtgaggg gaccatctgt cttcatcttc 360
ccgccgaaac ccaaagacac cctgatgatc acaggaaatc ccgaggtcac atgtgtggtg 420
gtggacgtgg gccgggataa ccccaggtg cagttctcct ggttcgtggg tgatgtggag 480
gtgcacacgg gcaggtcgaa gccgagagag gagcagttca acagcaccta ccgcgtggtc 540
agcacctgc ccatccagca caatgactgg actggaggaa aggagttcaa gtgcaaggtc 600
aacaacaaag gcctcccagc ccccatcgtg aggaccatct ccaggaccaa agggcaggcc 660
cgggagccgc aggtgtacgt cctggcccca cccaggaag agctcagcaa aagcacggtc 720
agcgtcactt gcatggtcac tggcttctac ccagactaca tcgccgtaga gtggcataga 780
gaccggcagg ctgagtcgga ggacaagtac cgcacgaccc cgccccagct ggacagcgat 840

seq list_5104975_1 (2)
 ggctcctact tcctgtacag caggctcaag gtgaacaaga acagctggca agaaggaggc 900
 gcctacacgt gtgtagtgat gcatgaggc 929

<210> 76
 <211> 352
 <212> PRT
 <213> Bubalus bubalis

<400> 76

Ala Ser Thr Thr Ala Pro Lys Val Tyr Pro Leu Ala Ser Ser Cys Gly
 1 5 10 15

Asp Thr Ser Ser Ser Thr Val Thr Leu Gly Cys Leu Val Ser Ser Tyr
 20 25 30

Met Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ala Leu Lys Asn
 35 40 45

Gly Val His Thr Phe Pro Ala Val Arg Gln Ser Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Met Val Thr Met Pro Thr Ser Thr Ala Gly Thr Gln Thr
 65 70 75 80

Phe Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Thr
 85 90 95

Ala Val Thr Ala Arg His Pro Val Pro Lys Thr Pro Glu Thr Pro Ile
 100 105 110

His Pro Val Lys Pro Pro Thr Gln Glu Pro Arg Asp Glu Lys Thr Pro
 115 120 125

Cys Gln Cys Pro Lys Cys Pro Glu Pro Leu Gly Gly Leu Ser Val Phe
 130 135 140

Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Thr Ile Ser Gly Thr Pro
 145 150 155 160

Glu Val Thr Cys Val Val Val Asp Val Gly Gln Asp Asp Pro Glu Val
 165 170 175

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Arg Met
 180 185 190

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Ala
 195 200 205

Leu Pro Ile Gln His Gln Asp Trp Leu Arg Glu Lys Glu Phe Lys Cys
 210 215 220

seq list_5104975_1 (2)

Lys Val Asn Asn Lys Gly Leu Pro Ala Pro Ile Val Arg Thr Ile Ser
225 230 235 240

Arg Thr Lys Gly Gln Ala Arg Glu Pro Gln Val Tyr Val Leu Ala Pro
245 250 255

Pro Arg Glu Glu Leu Ser Lys Ser Thr Leu Ser Leu Thr Cys Leu Ile
260 265 270

Thr Gly Phe Tyr Pro Glu Glu Val Asp Val Glu Trp Gln Arg Asn Gly
275 280 285

Gln Pro Glu Ser Glu Asp Lys Tyr His Thr Thr Pro Pro Gln Leu Asp
290 295 300

Ala Asp Gly Ser Tyr Phe Leu Tyr Ser Arg Leu Arg Val Asn Arg Ser
305 310 315 320

Ser Trp Gln Glu Gly Asp His Tyr Thr Cys Ala Val Met His Glu Ala
325 330 335

Leu Arg Asn His Tyr Lys Glu Lys Pro Ile Ser Arg Ser Pro Gly Lys
340 345 350

<210> 77
<211> 1059
<212> DNA
<213> Bubalus bubalis

<400> 77
gcctccacca cagccccgaa agtctaccct ctggcatcca gctgcgggga cacgtccagc 60
tccaccgtga ccctgggctg cctggtctcc agctacatgc ccgagccggt gaccgtgacc 120
tggaactcgg gtgccctgaa gaacggcgtg cacaccttcc cggccgtccg gcagtcctcc 180
gggctctact ctctcagcag catggtgacc atgccacca gcaccgcagg aaccagacc 240
ttcacctgca acgtagccca cccggccagc agcaccaagg tggacacggc tgtcactgca 300
aggcatccgg tcccgaagac accagagaca cctatccatc ctgtaaaacc cccaaccag 360
gagcccagag atgaaaagac accctgccag tgtcccaaat gccagaacc tctgggagga 420
ctgtctgtct tcattcttccc accgaaaccc aaggacaccc tcacaatctc tggaacgccc 480
gaggtcacgt gtgtggtggt ggacgtgggc caggatgacc ccgaagtgca gttctcctgg 540
ttcgtggatg acgtggaggt gcacacagcc aggatgaagc caagagagga gcagttcaac 600
agcacctacc gcgtggtcag cgccctgccc atccagcacc aggactggct gcgggaaaag 660
gagttcaagt gcaaggtcaa caacaaaggc ctcccggccc ccatcgtgag gaccatctcc 720
aggaccaaag ggcaggcccc ggagccacag gtgtatgtcc tggccccacc ccgggaagag 780
ctcagcaaaa gcacgctcag cctcacctgc ctaatcaccg gcttctaccc agaagaggta 840
gacgtggagt ggagagaaa tgggcagcct gagtcagagg acaagtacca cacgacccca 900

seq list_5104975_1 (2)

ccccagctgg acgctgacgg ctcctacttc ctgtacagca ggctcagggg gaacaggagc	960
agctggcagg aaggagacca ctacacgtgt gcagtgatgc atgaagcttt acggaatcac	1020
tacaaagaga agcccatctc gaggtctccg ggtaaata	1059

<210> 78
 <211> 105
 <212> PRT
 <213> Bubalus bubalis

<400> 78

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

Glu Leu Ser Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
 20 25 30

Tyr Pro Gly Ser Met Thr Val Ala Arg Lys Ala Asp Gly Ser Thr Ile
 35 40 45

Thr Arg Asn Val Glu Thr Thr Arg Ala Ser Lys Gln Ser Asn Ser Lys
 50 55 60

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Gly Ser Glu Trp Lys Ser
 65 70 75 80

Lys Gly Ser Tyr Ser Cys Glu Val Thr His Glu Gly Ser Thr Val Thr
 85 90 95

Lys Thr Val Lys Pro Ser Glu Cys Ser
 100 105

<210> 79
 <211> 318
 <212> DNA
 <213> Bubalus buballis

<400> 79

cagcccaagt ccgcaccctc agtcaccctg ttcccaccct ccacggagga gctcagcgcc	60
aacaaggcca ccctgggtgtg tctcatcagc gacttctacc cgggtagcat gaccgtggcc	120
aggaaggcag acggcagcac catcaccgg aacgtggaga ccaccgggc ctccaaacag	180
agcaacagca agtacgcggc cagcagctac ctgagcctga cgggcagcga gtggaaatcg	240
aaaggcagtt acagctgcga ggtcacgcac gaggggagca ccgtgacaaa gacagtgaag	300
ccctcagagt gttcttag	318

<210> 80
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 80

seq list_5104975_1 (2)

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

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

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

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

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

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

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

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

Leu Ser Leu Gly Lys
225

<210> 81
<211> 690
<212> DNA
<213> Homo sapiens

<400> 81
gagtccaaat atggtccccc gtgcccata tgcccagcac ctgagttcct ggggggacca

60

seq list_5104975_1 (2)

tcagtcttcc tgttcccccc aaaacccaag gacactctca tgatctcccg gacccctgag	120
gtcacgtgcg tgggtggtgga cgtgagccag gaagaccccg aggtccagtt caactggtac	180
gtggatggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gttcaacagc	240
acgtaccgtg tggtcagcgt cctcaccgtc gtgcaccagg actggctgaa cggcaaggag	300
tacaagtgca aggtctccaa caaaggcctc ccgtcctcca tcgagaaaac catctccaaa	360
gccaaagggc agccccgaga gccacaggtg tacaccctgc ccccatccca ggaggagatg	420
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc	480
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg	540
gactccgacg gctccttctt cctctacagc aggctaaccg tggacaagag caggtggcag	600
gaggggaatg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag	660
aagagcctct ccctgtctct gggtaaata	690

<210> 82
 <211> 217
 <212> PRT
 <213> Homo sapiens

<400> 82

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 20 25 30

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
 35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 50 55 60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 85 90 95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
 115 120 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 130 135 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 145 150 155 160

seq list_5104975_1 (2)

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

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Leu Gly Lys
210 215

<210> 83
<211> 654
<212> DNA
<213> Homo sapiens

<400> 83
gcacctgagt tcctgggggg accatcagtc ttctgttcc ccccaaaacc caaggacact 60
ctcatgatct cccggacccc tgaggtcacg tgcgtggtgg tggacgtgag ccaggaagac 120
cccgaggtcc agttcaactg gtacgtggat ggcgtggagg tgcataatgc caagacaaag 180
ccgcggggagg agcagttcaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 240
caggactggc tgaacggcaa ggagtacaag tgcaaggtct ccaacaaagg cctcccgtcc 300
tccatcgaga aaaccatctc caaagccaaa gggcagcccc gagagccaca ggtgtacacc 360
ctgcccccat cccaggagga gatgaccaag aaccagggtca gcctgacctg cctgggtcaaa 420
ggcttctacc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 480
tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaagctc 540
accgtggaca agagcaggtg gcaggagggg aacgtcttct catgctccgt gatgcatgag 600
gctctgcaca accactacac gcagaagagc ctctccctgt ctctgggtaa atga 654

<210> 84
<211> 329
<212> PRT
<213> Bos taurus

<400> 84

Ala Ser Thr Thr Ala Pro Lys Val Tyr Pro Leu Ser Ser Cys Cys Gly
1 5 10 15

Asp Lys Ser Ser Ser Thr Val Thr Leu Gly Cys Leu Val Ser Ser Tyr
20 25 30

Met Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ala Leu Lys Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

seq list_5104975_1 (2)

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

seq list_5104975_1 (2)

<210> 85
 <211> 329
 <212> PRT
 <213> Bos taurus

<400> 85

Ala Ser Thr Thr Ala Pro Lys Val Tyr Pro Leu Ser Ser Cys Cys Gly
 1 5 10 15

Asp Lys Ser Ser Ser Thr Val Thr Leu Gly Cys Leu Val Ser Ser Tyr
 20 25 30

Met Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ala Leu Lys Ser
 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Met Val Thr Val Pro Gly Ser Thr Ser Gly Gln Thr Phe
 65 70 75 80

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Ala
 85 90 95

Val Asp Pro Thr Cys Lys Pro Ser Pro Cys Asp Cys Cys Pro Pro Pro
 100 105 110

Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
 115 120 125

Asp Thr Leu Thr Ile Ser Gly Thr Pro Glu Val Thr Cys Val Val Val
 130 135 140

Asp Val Gly His Asp Asp Pro Glu Val Lys Phe Ser Trp Phe Val Asp
 145 150 155 160

Asp Val Glu Val Asn Thr Ala Thr Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Ala Leu Arg Ile Gln His Gln Asp
 180 185 190

Trp Thr Gly Gly Lys Glu Phe Lys Cys Lys Val His Asn Glu Gly Leu
 195 200 205

Pro Ala Pro Ile Val Arg Thr Ile Ser Arg Thr Lys Gly Pro Ala Arg
 210 215 220

Glu Pro Gln Val Tyr Val Leu Ala Pro Pro Gln Glu Glu Leu Ser Lys
 225 230 235 240

seq list_5104975_1 (2)

Ser Thr Val Ser Leu Thr Cys Met Val Thr Ser Phe Tyr Pro Asp Tyr
245 250 255

Ile Ala Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Asp Lys
260 265 270

Tyr Gly Thr Thr Pro Pro Gln Leu Asp Ala Asp Ser Ser Tyr Phe Leu
275 280 285

Tyr Ser Lys Leu Arg Val Asp Arg Asn Ser Trp Gln Glu Gly Asp Thr
290 295 300

Tyr Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
305 310 315 320

Lys Ser Thr Ser Lys Ser Ala Gly Lys
325

<210> 86
<211> 329
<212> PRT
<213> Bos taurus

<400> 86

Ala Ser Thr Thr Ala Pro Lys Val Tyr Pro Leu Ser Ser Cys Cys Gly
1 5 10 15

Asp Lys Ser Ser Ser Thr Val Thr Leu Gly Cys Leu Val Ser Ser Tyr
20 25 30

Met Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ala Leu Lys Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Met Val Thr Val Pro Gly Ser Thr Ser Gly Thr Gln Thr
65 70 75 80

Phe Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
85 90 95

Ala Val Asp Pro Arg Cys Lys Thr Thr Cys Asp Cys Cys Pro Pro Pro
100 105 110

Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Thr Ile Ser Gly Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

seq list_5104975_1 (2)

Asp Val Gly His Asp Asp Pro Glu Val Lys Phe Ser Trp Phe Val Asp
145 150 155 160

Asp Val Glu Val Asn Thr Ala Thr Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Ala Leu Arg Ile Gln His Gln Asp
180 185 190

Trp Thr Gly Gly Lys Glu Phe Lys Cys Lys Val His Asn Glu Gly Leu
195 200 205

Pro Ala Pro Ile Val Arg Thr Ile Ser Arg Thr Lys Gly Pro Ala Arg
210 215 220

Glu Pro Gln Val Tyr Val Leu Ala Pro Pro Gln Glu Glu Leu Ser Lys
225 230 235 240

Ser Thr Val Ser Leu Thr Cys Met Val Thr Ser Phe Tyr Pro Asp Tyr
245 250 255

Ile Ala Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Asp Lys
260 265 270

Tyr Gly Thr Thr Pro Pro Gln Leu Asp Ala Asp Gly Ser Tyr Phe Leu
275 280 285

Tyr Ser Arg Leu Arg Val Asp Arg Asn Ser Trp Gln Glu Gly Asp Thr
290 295 300

Tyr Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
305 310 315 320

Lys Ser Thr Ser Lys Ser Ala Gly Lys
325

<210> 87

<211> 326

<212> PRT

<213> Bos taurus

<400> 87

Ala Ser Thr Thr Ala Pro Lys Val Tyr Pro Leu Ala Ser Ser Cys Gly
1 5 10 15

Asp Thr Ser Ser Ser Thr Val Thr Leu Gly Cys Leu Val Ser Ser Tyr
20 25 30

Met Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ala Leu Lys Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser

seq list_5104975_1 (2)

50

55

60

Leu Ser Ser Met Val Thr Val Pro Ala Ser Ser Ser Gly Gln Thr Phe
65 70 75 80

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Ala
85 90 95

Val Gly Val Ser Ile Asp Cys Ser Lys Cys His Asn Gln Pro Cys Val
100 105 110

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

Met Ile Thr Gly Thr Pro Glu Val Thr Cys Val Val Val Asn Val Gly
130 135 140

His Asp Asn Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu
145 150 155 160

Val His Thr Ala Arg Ser Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
165 170 175

Tyr Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Thr Gly
180 185 190

Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Gly Leu Ser Ala Pro
195 200 205

Ile Val Arg Ile Ile Ser Arg Ser Lys Gly Pro Ala Arg Glu Pro Gln
210 215 220

Val Tyr Val Leu Asp Pro Pro Lys Glu Glu Leu Ser Lys Ser Thr Leu
225 230 235 240

Ser Val Thr Cys Met Val Thr Gly Phe Tyr Pro Glu Asp Val Ala Val
245 250 255

Glu Trp Gln Arg Asn Arg Gln Thr Glu Ser Glu Asp Lys Tyr Arg Thr
260 265 270

Thr Pro Pro Gln Leu Asp Thr Asp Arg Ser Tyr Phe Leu Tyr Ser Lys
275 280 285

Leu Arg Val Asp Arg Asn Ser Trp Gln Glu Gly Asp Ala Tyr Thr Cys
290 295 300

Val Val Met His Glu Ala Leu His Asn His Tyr Met Gln Lys Ser Thr
305 310 315 320

Ser Lys Ser Ala Gly Lys

seq list_5104975_1 (2)

325

<210> 88
 <211> 326
 <212> PRT
 <213> Bos taurus

<400> 88

Ala Ser Thr Thr Ala Pro Lys Val Tyr Pro Leu Ser Ser Cys Cys Gly
 1 5 10 15

Asp Lys Ser Ser Thr Val Thr Leu Gly Cys Leu Val Ser Ser Tyr
 20 25 30

Met Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ala Leu Lys Ser
 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Met Val Thr Val Pro Gly Ser Thr Ser Gly Gln Thr Phe
 65 70 75 80

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Ala
 85 90 95

Val Gly Val Ser Ser Asp Cys Ser Lys Pro Asn Asn Gln His Cys Val
 100 105 110

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

Met Ile Thr Gly Thr Pro Glu Val Thr Cys Val Val Val Asn Val Gly
 130 135 140

His Asp Asn Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu
 145 150 155 160

Val His Thr Ala Arg Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
 165 170 175

Tyr Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Thr Gly
 180 185 190

Gly Lys Glu Phe Lys Cys Lys Val Asn Ile Lys Gly Leu Ser Ala Ser
 195 200 205

Ile Val Arg Ile Ile Ser Arg Ser Lys Gly Pro Ala Arg Glu Pro Gln
 210 215 220

Val Tyr Val Leu Asp Pro Pro Lys Glu Glu Leu Ser Lys Ser Thr Val
 225 230 235 240

seq list_5104975_1 (2)

Ser Val Thr Cys Met Val Ile Gly Phe Tyr Pro Glu Asp Val Asp Val
245 250 255

Glu Trp Gln Arg Asp Arg Gln Thr Glu Ser Glu Asp Lys Tyr Arg Thr
260 265 270

Thr Pro Pro Gln Leu Asp Ala Asp Arg Ser Tyr Phe Leu Tyr Ser Lys
275 280 285

Leu Arg Val Asp Arg Asn Ser Trp Gln Arg Gly Asp Thr Tyr Thr Cys
290 295 300

Val Val Met His Glu Ala Leu His Asn His Tyr Met Gln Lys Ser Thr
305 310 315 320

Ser Lys Ser Ala Gly Lys
325

<210> 89

<211> 327

<212> PRT

<213> Bos taurus

<400> 89

Ala Ser Thr Thr Ala Pro Lys Val Tyr Pro Leu Ser Ser Cys Cys Gly
1 5 10 15

Asp Lys Ser Ser Ser Gly Val Thr Leu Gly Cys Leu Val Ser Ser Tyr
20 25 30

Met Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ala Leu Lys Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Met Val Thr Val Pro Ala Ser Ser Ser Gly Thr Gln Thr
65 70 75 80

Phe Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
85 90 95

Ala Val Gly Val Ser Ser Asp Cys Ser Lys Pro Asn Asn Gln His Cys
100 105 110

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

Leu Met Ile Thr Gly Thr Pro Glu Val Thr Cys Val Val Val Asn Val
130 135 140

seq list_5104975_1 (2)

Gly His Asp Asn Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val
145 150 155 160

Glu Val His Thr Ala Arg Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
165 170 175

Thr Tyr Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Thr
180 185 190

Gly Gly Lys Glu Phe Lys Cys Lys Val Asn Ile Lys Gly Leu Ser Ala
195 200 205

Ser Ile Val Arg Ile Ile Ser Arg Ser Lys Gly Pro Ala Arg Glu Pro
210 215 220

Gln Val Tyr Val Leu Asp Pro Pro Lys Glu Glu Leu Ser Lys Ser Thr
225 230 235 240

Val Ser Leu Thr Cys Met Val Ile Gly Phe Tyr Pro Glu Asp Val Asp
245 250 255

Val Glu Trp Gln Arg Asp Arg Gln Thr Glu Ser Glu Asp Lys Tyr Arg
260 265 270

Thr Thr Pro Pro Gln Leu Asp Ala Asp Arg Ser Tyr Phe Leu Tyr Ser
275 280 285

Lys Leu Arg Val Asp Arg Asn Ser Trp Gln Arg Gly Asp Thr Tyr Thr
290 295 300

Cys Val Val Met His Glu Ala Leu His Asn His Tyr Met Gln Lys Ser
305 310 315 320

Thr Ser Lys Ser Ala Gly Lys
325

<210> 90
<211> 352
<212> PRT
<213> Bos taurus

<400> 90

Ala Ser Thr Thr Ala Pro Lys Val Tyr Pro Leu Ala Ser Ser Cys Gly
1 5 10 15

Asp Thr Ser Ser Ser Thr Val Thr Leu Gly Cys Leu Val Ser Ser Tyr
20 25 30

Met Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ala Leu Lys Ser
35 40 45

seq list_5104975_1 (2)

Gly Val His Thr Phe Pro Ala Val Arg Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Met Val Thr Val Pro Ala Ser Ser Ser Glu Thr Gln Thr
65 70 75 80

Phe Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
85 90 95

Ala Val Thr Ala Arg Arg Pro Val Pro Thr Thr Pro Lys Thr Thr Ile
100 105 110

Pro Pro Gly Lys Pro Thr Thr Pro Lys Ser Glu Val Glu Lys Thr Pro
115 120 125

Cys Gln Cys Ser Lys Cys Pro Glu Pro Leu Gly Gly Leu Ser Val Phe
130 135 140

Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Thr Ile Ser Gly Thr Pro
145 150 155 160

Glu Val Thr Cys Val Val Val Asp Val Gly Gln Asp Asp Pro Glu Val
165 170 175

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Arg Thr
180 185 190

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Ala
195 200 205

Leu Arg Ile Gln His Gln Asp Trp Leu Gln Gly Lys Glu Phe Lys Cys
210 215 220

Lys Val Asn Asn Lys Gly Leu Pro Ala Pro Ile Val Arg Thr Ile Ser
225 230 235 240

Arg Thr Lys Gly Gln Ala Arg Glu Pro Gln Val Tyr Val Leu Ala Pro
245 250 255

Pro Arg Glu Glu Leu Ser Lys Ser Thr Leu Ser Leu Thr Cys Leu Ile
260 265 270

Thr Gly Phe Tyr Pro Glu Glu Ile Asp Val Glu Trp Gln Arg Asn Gly
275 280 285

Gln Pro Glu Ser Glu Asp Lys Tyr His Thr Thr Ala Pro Gln Leu Asp
290 295 300

Ala Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Arg Val Asn Lys Ser
305 310 315 320

seq list_5104975_1 (2)

Ser Trp Gln Glu Gly Asp His Tyr Thr Cys Ala Val Met His Glu Ala
325 330 335

Leu Arg Asn His Tyr Lys Glu Lys Ser Ile Ser Arg Ser Pro Gly Lys
340 345 350

<210> 91
<211> 352
<212> PRT
<213> Bos taurus
<400> 91

Ala Ser Thr Thr Ala Pro Lys Val Tyr Pro Leu Ala Ser Arg Cys Gly
1 5 10 15

Asp Thr Ser Ser Ser Thr Val Thr Leu Gly Cys Leu Val Ser Ser Tyr
20 25 30

Met Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ala Leu Lys Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Met Val Thr Val Pro Ala Ser Thr Ser Glu Thr Gln Thr
65 70 75 80

Phe Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
85 90 95

Ala Val Thr Ala Arg Arg Pro Val Pro Thr Thr Pro Lys Thr Thr Ile
100 105 110

Pro Pro Gly Lys Pro Thr Thr Gln Glu Ser Glu Val Glu Lys Thr Pro
115 120 125

Cys Gln Cys Ser Lys Cys Pro Glu Pro Leu Gly Gly Leu Ser Val Phe
130 135 140

Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Thr Ile Ser Gly Thr Pro
145 150 155 160

Glu Val Thr Cys Val Val Val Asp Val Gly Gln Asp Asp Pro Glu Val
165 170 175

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Arg Thr
180 185 190

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Ala
195 200 205

Leu Arg Ile Gln His Gln Asp Trp Leu Gln Gly Lys Glu Phe Lys Cys
Page 63

seq list_5104975_1 (2)

210

215

220

Lys Val Asn Asn Lys Gly Leu Pro Ala Pro Ile Val Arg Thr Ile Ser
225 230 235 240

Arg Thr Lys Gly Gln Ala Arg Glu Pro Gln Val Tyr Val Leu Ala Pro
245 250 255

Pro Arg Glu Glu Leu Ser Lys Ser Thr Leu Ser Leu Thr Cys Leu Ile
260 265 270

Thr Gly Phe Tyr Pro Glu Glu Ile Asp Val Glu Trp Gln Arg Asn Gly
275 280 285

Gln Pro Glu Ser Glu Asp Lys Tyr His Thr Thr Ala Pro Gln Leu Asp
290 295 300

Ala Asp Gly Ser Tyr Phe Leu Tyr Ser Arg Leu Arg Val Asn Lys Ser
305 310 315 320

Ser Trp Gln Glu Gly Asp His Tyr Thr Cys Ala Val Met His Glu Ala
325 330 335

Leu Arg Asn His Tyr Lys Glu Lys Ser Ile Ser Arg Ser Pro Gly Lys
340 345 350

<210> 92
<211> 990
<212> DNA
<213> Bos taurus

<400> 92
gcctccacca cagccccgaa agtctaccct ctgagttctt gctgcgggga caagtccagc 60
tccaccgtga ccctgggctg cctggtctcc agctacatgc ccgagccggt gaccgtgacc 120
tggaactcgg gtgccctgaa gagcggcggt cacaccttcc cggctgtcct tcagtcctcc 180
gggctgtact ctctcagcag catggtgacc gtgcccggca gcacctcagg acagaccttc 240
acctgcaacg tagccccacc ggccagcagc accaagggtg acaaggctgt tgatcccaca 300
tgcaaaccat caccctgtga ctgttgccca cccctgagc tccccggagg accctctgtc 360
ttcatcttcc caccgaaacc caaggacacc ctcaaatct cggaacgcc cgaggtcacg 420
tgtgtggtgg tggacgtggg ccacgatgac cccgaggtga agttctcctg gttcgtggac 480
gacgtggagg taaacacagc cacgacgaag ccgagagagg agcagttcaa cagcacctac 540
cgctggttca gcgccctgcg catccagcac caggactgga ctggaggaaa ggagttcaag 600
tgcaagggtcc acaacgaagg cctcccggcc cccatcgtga ggaccatctc caggacacaa 660
gggccggccc gggagccgca ggtgtatgtc ctggccccac cccaggaaga gctcagcaaa 720
agcacggtca gcctcacctg catggtcacc agcttctacc cagactacat cgccgtggag 780
tggcagagaa acgggcagcc tgagtcggag gacaagtacg gcacgacccc gcccagctg 840

seq list_5104975_1 (2)

gacgccgaca	gctcctactt	cctgtacagc	aagctcaggg	tggacaggaa	cagctggcag	900
gaaggagaca	cctacacgtg	tgtgggtgatg	cacgaggccc	tgcacaatca	ctacacgcag	960
aagtccacct	ctaagtctgc	gggtaaatga				990

<210> 93
 <211> 990
 <212> DNA
 <213> Bos taurus

<400> 93	
gcctccacca	cagccccgaa agtctaccct ctgagttctt gctgcgggga caagtccagc 60
tccaccgtga	ccctgggctg cctgggtctcc agctacatgc ccgagccggt gaccgtgacc 120
tggaaactcg	gtgccctgaa gagcggcgtg cacaccttcc cggccgtcct tcagtcctcc 180
gggctgtact	ctctcagcag catgggtgacc gtgcccggca gcacctcagg acagaccttc 240
acctgcaacg	tagccccacc ggccagcagc accaagggtg acaaggctgt tgatcccaca 300
tgcaaaccat	caccctgtga ctgttgccca cccctgagc tccccggagg accctctgtc 360
ttcatcttcc	caccgaaacc caaggacacc ctcacaatct cgggaacgcc cgaggtcacg 420
tgtgtggtgg	tggacgtggg ccacgatgac cccgaggtga agttctcctg gttcgtggac 480
gacgtggagg	taaacacagc cacgacgaag ccgagagagg agcagttcaa cagcacctac 540
cgcggtgtca	gcgccctgcg catccagcac caggactgga ctggaggaaa ggagttcaag 600
tgcaagggtc	acaacgaagg cctcccggcc cccatcgtga ggaccatctc caggacccaa 660
gggccggccc	gggagccgca ggtgtatgtc ctggccccac cccaggaaga gctcagcaaa 720
agcacggtca	gcctcacctg catgggtcacc agcttctacc cagactacat cgccgtggag 780
tggcagagaa	acgggcagcc tgagtcggag gacaagtacg gcacgacccc gcccagctg 840
gacgccgaca	gctcctactt cctgtacagc aagctcaggg tggacaggaa cagctggcag 900
gaaggagaca	cctacacgtg tgtgggtgatg cacgaggccc tgcacaatca ctacacgcag 960
aagtccacct	ctaagtctgc gggtaaatga 990

<210> 94
 <211> 990
 <212> DNA
 <213> Bos taurus

<400> 94	
gcctccacca	cagccccgaa agtctaccct ctgagttctt gctgcgggga caagtccagc 60
tccaccgtga	ccctgggctg cctgggtctcc agctacatgc ccgagccggt gaccgtgacc 120
tggaaactcg	gtgccctgaa gagcggcgtg cacaccttcc cggccgtcct tcagtcctcc 180
gggctctact	ctctcagcag catgggtgacc gtgcccggca gcacctcagg aaccagacc 240
ttcacctgca	acgtagccca cccggccagc agcaccaagg tggacaaggc tgttgatccc 300
agatgcaaaa	caacctgtga ctgttgccca ccgcctgagc tccctggagg accctctgtc 360
ttcatcttcc	caccgaaacc caaggacacc ctcacaatct cgggaacgcc cgaggtcacg 420

seq list_5104975_1 (2)

tgtgtggtgg	tggacgtggg	ccacgatgac	cccagagtga	agttctcctg	gttcgtggac	480
gacgtggagg	taaacacagc	cacgacgaag	ccgagagagg	agcagttcaa	cagcacctac	540
cgcgtggtca	gcgccctgcg	catccagcac	caggactgga	ctggaggaaa	ggagttcaag	600
tgcaagggtcc	acaacgaagg	cctcccagcc	cccatcgtga	ggaccatctc	caggaccaaa	660
gggccggccc	gggagccgca	ggtgtatgtc	ctggccccac	cccaggaaga	gctcagcaaa	720
agcacggtca	gcctcacctg	catggtcacc	agcttctacc	cagactacat	cgccgtggag	780
tggcagagaa	atgggcagcc	tgagtcagag	gacaagtacg	gcacgacccc	tcccagctg	840
gacgccgacg	gctcctactt	cctgtacagc	aggctcaggg	tggacaggaa	cagctggcag	900
gaaggagaca	cctacacgtg	tgtggtgatg	cacgaggccc	tgcacaatca	ctacacgcag	960
aagtccacct	ctaagtctgc	gggtaaatga				990

<210> 95
 <211> 981
 <212> DNA
 <213> Bos taurus

<400> 95	
gcctccacca	cagccccgaa agtctaccct ctggcatcca gctgcggaga cacatccagc 60
tccaccgtga	ccctgggctg cctggtgtcc agctacatgc ccgagccggt gaccgtgacc 120
tggaactcgg	gtgccctgaa gagcggcgctg cacaccttcc cggtgtcct tcagtcctcc 180
gggtctact	ctctcagcag catggtgacc gtgcccgcga gcagctcagg acagaccttc 240
acctgcaacg	tagccccacc ggccagcagc accaagggtg acaaggctgt tggggctctcc 300
attgactgct	ccaagtgtca taaccagcct tgcgtgaggg aaccatctgt cttcatcttc 360
ccaccgaaac	caaagacac cctgatgatc acaggaacgc ccgaggtcac gtgtgtggtg 420
gtgaacgtgg	gccacgataa ccccaggtg cagttctcct ggttcgtgga tgacgtggag 480
gtgcacacgg	ccaggtcgaa gccaagagag gagcagttca acagcacgta ccgcgtggtc 540
agcgccctgc	ccatccagca ccaggactgg actggaggaa aggagttcaa gtgcaaggtc 600
aacaacaaag	gcctctcggc ccccatcgtg aggatcatct ccaggagcaa agggccggcc 660
cgggagccgc	aggtgtatgt cctggacca cccaaggaag agctcagcaa aagcacgctc 720
agcgtcacct	gcatggtcac cggcttctac ccagaagatg tagccgtgga gtggcagaga 780
aaccggcaga	ctgagtcgga ggacaagtac cgcacgaccc cgcccagct ggacaccgac 840
cgctcctact	tcctgtacag caagctcagg gtggacagga acagctggca ggaaggagac 900
gcctacacgt	gtgtggtgat gcacgaggcc ctgcacaatc actacatgca gaagtccacc 960
tctaagtctg	cgggtaaatg a 981

<210> 96
 <211> 981
 <212> DNA
 <213> Bos taurus

seq list_5104975_1 (2)

```

<400> 96
gcctccacca cagccccgaa agtctaccct ctgagttctt gctgcgggga caagtccagc      60
tccaccgtga ccctgggctg cctggtgtcc agctacatgc ccgagccggt gaccgtgacc      120
tggaactcgg gtgccctgaa gagcggcgtg cacaccttcc cggccgtcct tcagtcctcc      180
gggctctact ctctcagcag catggtgacc gtgcccggca gcacctcagg acagaccttc      240
acctgcaacg tagccccacc ggccagcagc accaagggtg acaaggctgt tggggctctcc      300
agtgactgct ccaagcctaa taaccagcat tgcgtgaggg aaccatctgt cttcatcttc      360
ccaccgaaac ccaaagacac cctgatgatc acaggaacgc ccgaggtcac gtgtgtggtg      420
gtgaacgtgg gccacgataa ccccgaggtg cagttctcct ggttcgtgga cgacgtggag      480
gtgcacacgg ccaggacgaa gccgagagag gagcagttca acagcacgta ccgctggttc      540
agcgccttgc ccatccagca ccaggactgg actggaggaa aggagttcaa gtgcaaggtc      600
aacatcaaag gcctctcggc ctccatcgtg aggatcatct ccaggagcaa agggccggcc      660
cgggagccgc aggtgtatgt cctggacca cccaaggaag agctcagcaa aagcacggtc      720
agcgtcacct gcatggtcat cggcttctac ccagaagatg tagacgtgga gtggcagaga      780
gaccggcaga ctgagtcgga ggacaagtac cgcacgacct cgccccagct ggacgccgac      840
cgctcctact tcctgtacag caagctcagg gtggacagga acagctggca gagaggagac      900
acctacacgt gtgtggtgat gcacgaggcc ctgcacaatc actacatgca gaagtccacc      960
tctaagtctg cgggtaaatg a                                     981

```

```

<210> 97
<211> 984
<212> DNA
<213> Bos taurus

```

```

<400> 97
gcctccacca cagccccgaa agtctaccct ctgagttctt gctgcgggga caagtccagc      60
tcggggggtga ccctgggctg cctggtctcc agctacatgc ccgagccggt gaccgtgacc      120
tggaactcgg gtgccctgaa gagcggcgtg cacaccttcc cggccgtcct tcagtcctcc      180
gggctctact ctctcagcag catggtgacc gtgcccggca gcagctcagg aaccagacc      240
ttcacctgca acgtagccca cccggccagc agcaccaagg tggacaaggc tgttggggtc      300
tccagtgact gtcceaagcc taataaccag cattgcgtga ggggaaccatc tgtcttcac      360
ttcccaccga aacccaaaga caccctgatg atcacaggaa cgcccaggt cacgtgtgtg      420
gtggtgaacg tggggcacga taaccccgag gtgcagttct cctggttcgt ggacgacgtg      480
gaggtgcaca cggccaggac gaagccgaga gaggagcagt tcaacagcac gtaccgctg      540
gtcagcggcc tgcccatcca gcaccaggac tggactggag gaaaggagtt caagtgaag      600
gtcaacatca aaggcctctc ggcctccatc gtgaggatca tctccaggag caaagggccg      660
gcccgggagc cgcaggtgta tgtcctggac ccaccaagg aagagctcag caaaagcacg      720
gtcagcctca cctgcatggt catcggcttc taccagaag atgtagacgt ggagtggcag      780

```

seq list_5104975_1 (2)

agagaccggc agactgagtc ggaggacaag taccgcacga ccccgcccca gctggacgcc	840
gaccgctcct acttcctgta cagcaagctc aggggtggaca ggaacagctg gcagagagga	900
gacacctaca cgtgtgtggt gatgcacgag gccctgcaca atcactacat gcagaagtcc	960
acctctaagt ctgcgggtaa atga	984

<210> 98
 <211> 1059
 <212> DNA
 <213> Bos taurus

<400> 98	
gcctccacca cagccccgaa agtctaccct ctggcatcca gctgcggaga cacatccagc	60
tccaccgtga ccctgggctg cctgggtctcc agctacatgc ccgagccggt gaccgtgacc	120
tggaaactcg gtgccctgaa gagcggcgtg cacaccttcc cggccgtccg gcagtcctct	180
gggctgtact ctctcagcag catggtgact gtgcccgcga gcagctcaga aaccagacc	240
ttcacctgca acgtagccca cccggccagc agcaccaagg tggacaaggc tgtcactgca	300
aggcgtccag tcccagcagc gccaaagaca actatccctc ctggaaaacc cacaacccca	360
aagtctgaag ttgaaaagac accctgccag tgttccaaat gcccagaacc tctgggagga	420
ctgtctgtct tcattcttccc accgaaaccc aaggacaccc tcacaatctc gggaacgccc	480
gaggtcacgt gtgtggtggt ggacgtgggc caggatgacc ccgaggtgca gttctcctgg	540
ttcgtggacg acgtggaggt gcacacggcc aggacgaagc cgagagagga gcagttcaac	600
agcacctacc gcgtggtcag cggcctgcgc atccagcacc aggactggct gcagggaaag	660
gagttcaagt gcaagggtcaa caacaaaggc ctcccggccc ccattgtgag gaccatctcc	720
aggaccaaag ggcaggcccc ggagccgcag gtgtatgtcc tggccccacc ccgggaagag	780
ctcagcaaaa gcacgctcag cctcacctgc ctgatcaccg gtttctaccc agaagagata	840
gacgtggagt ggcagagaaa tgggcagcct gagtcggagg acaagtacca cagcaccgca	900
ccccagctgg atgctgacgg ctccctacttc ctgtacagca agctcagggt gaacaagagc	960
agctggcagg aaggagacca ctacacgtgt gcagtgatgc acgaagcttt acggaatcac	1020
tacaaagaga agtccatctc gaggtctccg ggtaaata	1059

<210> 99
 <211> 1059
 <212> DNA
 <213> Bos taurus

<400> 99	
gcctccacca cagccccgaa agtctaccct ctggcatccc gctgcggaga cacatccagc	60
tccaccgtga ccctgggctg cctgggtctcc agctacatgc ccgagccggt gaccgtgacc	120
tggaaactcg gtgccctgaa gagtggcgtg cacaccttcc cggccgtcct tcagtcctcc	180
gggctgtact ctctcagcag catggtgacc gtgcccgcga gcacctcaga aaccagacc	240
ttcacctgca acgtagccca cccggccagc agcaccaagg tggacaaggc tgtcactgca	300

seq list_5104975_1 (2)

aggcgtccag tcccgacgac gccaaagaca accatccctc ctggaaaacc cacaaccag	360
gagttctgaag ttgaaaagac accctgccag tgttcctaat gccagaacc tctgggagga	420
ctgtctgtct tcatcttccc accgaaaccc aaggacaccc tcacaatctc gggaacgccc	480
gaggtcacgt gtgtggtggt ggacgtgggc caggatgacc ccgaggtgca gttctcctgg	540
ttcgtggacg acgtggaggt gcacacggcc aggacgaagc cgagagagga gcagttcaac	600
agcacctacc gcgtggctag cgccctgcgc atccagcacc aggactggct gcagggaaag	660
gagttcaagt gcaagggtcaa caacaaaggc ctcccggccc ccattgtgag gaccatctcc	720
aggaccaaag ggcaggcccc ggagccgcag gtgtatgtcc tggccccacc ccgggaagag	780
ctcagcaaaa gcacgctcag cctcacctgc ctgatcaccg gtttctaccc agaagagata	840
gacgtggagt ggcagagaaa tgggcagcct gagtcggagg acaagtacca cacgaccgca	900
ccccagctgg atgctgacgg ctcctacttc ctgtacagca ggctcagggt gaacaagagc	960
agctggcagg aaggagacca ctacacgtgt gcagtgatgc atgaagcttt acggaatcac	1020
tacaaagaga agtccatctc gaggtctccg ggtaaata	1059

<210> 100
 <211> 105
 <212> PRT
 <213> Bos taurus

<400> 100

Gln Pro Lys Ser Pro Pro Ser Val Thr Leu Phe Pro Pro Ser Thr Glu
 1 5 10 15

Glu Leu Asn Gly Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
 20 25 30

Tyr Pro Gly Ser Val Thr Val Val Trp Lys Ala Asp Gly Ser Thr Ile
 35 40 45

Thr Arg Asn Val Glu Thr Thr Arg Ala Ser Lys Gln Ser Asn Ser Lys
 50 55 60

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Ser Ser Asp Trp Lys Ser
 65 70 75 80

Lys Gly Ser Tyr Ser Cys Glu Val Thr His Glu Gly Ser Thr Val Thr
 85 90 95

Lys Thr Val Lys Pro Ser Glu Cys Ser
 100 105

<210> 101
 <211> 318
 <212> DNA
 <213> Bos taurus

<400> 101

seq list_5104975_1 (2)

cagcccaagt cccaccctc ggtcaccctg ttcccgccct ccacggagga gctcaacggc	60
aacaaggcca ccctggtgtg tctcatcagc gacttctacc cgggtagcgt gaccgtggtc	120
tggaaggcag acggcagcac catcacccgc aacgtggaga ccacccgggc ctccaaacag	180
agcaacagca agtacgctgc cagcagctac ctgagcctga cgagcagcga ctggaaatcg	240
aaaggcagtt acagctgcga ggtcacgcac gaggggagca ccgtgacgaa gacagtgaag	300
ccctcagagt gttcttag	318

<210> 102
 <211> 328
 <212> PRT
 <213> Bos taurus

<400> 102

Ala Ser Thr Thr Ala Pro Lys Val Tyr Pro Leu Ser Ser Cys Cys Gly
 1 5 10 15

Asp Lys Ser Ser Ser Thr Val Thr Leu Gly Cys Leu Val Ser Ser Tyr
 20 25 30

Met Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ala Leu Lys Ser
 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Met Val Thr Val Pro Gly Ser Thr Ser Gly Gln Thr Phe
 65 70 75 80

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Ala
 85 90 95

Val Asp Pro Thr Cys Lys Pro Ser Pro Cys Asp Cys Cys Pro Pro Pro
 100 105 110

Pro Val Ala Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp
 115 120 125

Thr Leu Thr Ile Ser Gly Thr Pro Glu Val Thr Cys Val Val Val Asp
 130 135 140

Val Gly His Asp Asp Pro Glu Val Lys Phe Ser Trp Phe Val Asp Asp
 145 150 155 160

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

Ser Thr Tyr Arg Val Val Ser Ala Leu Arg Ile Gln His Gln Asp Trp
 180 185 190

seq list_5104975_1 (2)

Thr Gly Gly Lys Glu Phe Lys Cys Lys Val His Asn Glu Gly Leu Pro
195 200 205

Ser Ser Ile Val Arg Thr Ile Ser Arg Thr Lys Gly Pro Ala Arg Glu
210 215 220

Pro Gln Val Tyr Val Leu Ala Pro Pro Gln Glu Glu Leu Ser Lys Ser
225 230 235 240

Thr Val Ser Leu Thr Cys Met Val Thr Ser Phe Tyr Pro Asp Tyr Ile
245 250 255

Ala Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Asp Lys Tyr
260 265 270

Gly Thr Thr Pro Pro Gln Leu Asp Ala Asp Ser Ser Tyr Phe Leu Tyr
275 280 285

Ser Lys Leu Arg Val Asp Arg Asn Ser Trp Gln Glu Gly Asp Thr Tyr
290 295 300

Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
305 310 315 320

Ser Thr Ser Lys Ser Ala Gly Lys
325

<210> 103
<211> 987
<212> DNA
<213> Bos taurus

<400> 103
gctagcaciaa ctgctcctaa ggtgtacccc ctgagctctt gctgcggcga caagtctagc 60
agcaccgtga ccctcggatg cctcgtcagc agctatatgc ctgagccagt tacagtgaca 120
tggaattctg gtgcccttaa gtccggcgtc cataccttcc ctgctgtgct gcagtcctct 180
ggcctgtaca gtttgtcctc tatggtgaca gtacccggtt ccacctccgg acagaccttt 240
acctgtaatg tggctcatcc cgcctcctcc acaaagggtg ataaggctgt tgacctacc 300
tgtaaaccga gtccatgcga ctgctgtccc cccctccag ttgccggacc ctcagtcttt 360
attttccac ccaaaccga agacaccctg acaatctctg gaacaccaga agtcacctgc 420
gtcgtcgtgg atgtgggcca cgacgatcct gaggtaaaat tctcatggtt cgtcgacgat 480
gtggaagtga atacagctac tacaaaacct cgcgaagagc agtttaactc tacctatcga 540
gtggtttctg ctttgcggat tcagcatcag gattggacag gcggcaaaga gtttaaatgt 600
aaagtccata acgagggact tccttctagt atcgtgcgca ctatcagtag aactaaaggg 660
cctgctcggg aacctcaggt gtacgtcctg gcacctccac aggaagagct gagtaagtct 720
acagtttctc tgacttgtat ggtaacatct ttttatccag attacatcgc agttgaatgg 780

seq list_5104975_1 (2)

cagaggaacg ggcagccaga gagtgaggat aagtacggga ctactccacc acagctggac	840
gcagactcaa gttacttcct gtactcaaag ctgaggggtg acagaaactc atggcaggag	900
ggggacactt acacttgcgt agttatgcac gaggcacttc acaaccacta cactcagaag	960
agtacttcaa agagtgcagg gaagtaa	987

<210> 104
 <211> 318
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon-optimized sequence

<400> 104	
cagcctaaga gtcctccttc tgtaacactc tttccccct ctaccgagga actcaacggc	60
aataaagcta ctttggtttg cttatttct gatttctacc ccgggtctgt gaccgtggtg	120
tggaaagctg atgggtccac cattactcg aatgtgga aa ccaccgggc ttctaagcag	180
tccaactcta aatacgcagc atcctcctat ttgagtctta ctagtagtga ctggaagtca	240
aagggtagtt acagttgcga agtcacacat gaaggttcaa cagtgacaaa gacagtcaag	300
ccctcagagt gtcatag	318

<210> 105
 <211> 238
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> chimeric L chain

<400> 105

Met Glu Ser Gln Thr His Val Leu Ile Ser Leu Leu Leu Ser Val Ser
 1 5 10 15

Gly Thr Tyr Gly Asp Ile Ala Ile Thr Gln Ser Pro Ser Ser Val Ala
 20 25 30

Val Ser Val Gly Glu Thr Val Thr Leu Ser Cys Lys Ser Ser Gln Ser
 35 40 45

Leu Leu Tyr Ser Glu Asn Gln Lys Asp Tyr Leu Gly Trp Tyr Gln Gln
 50 55 60

Lys Pro Gly Gln Thr Pro Lys Pro Leu Ile Tyr Trp Ala Thr Asn Arg
 65 70 75 80

His Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
 85 90 95

Phe Thr Leu Ile Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr
 100 105 110

seq list_5104975_1 (2)

Tyr Cys Gly Gln Tyr Leu Val Tyr Pro Phe Thr Phe Gly Pro Gly Thr
115 120 125

Lys Leu Glu Leu Lys Gln Pro Lys Ser Pro Pro Ser Val Thr Leu Phe
130 135 140

Pro Pro Ser Thr Glu Glu Leu Asn Gly Asn Lys Ala Thr Leu Val Cys
145 150 155 160

Leu Ile Ser Asp Phe Tyr Pro Gly Ser Val Thr Val Val Trp Lys Ala
165 170 175

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

Gln Ser Asn Ser Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Ser
195 200 205

Ser Asp Trp Lys Ser Lys Gly Ser Tyr Ser Cys Glu Val Thr His Glu
210 215 220

Gly Ser Thr Val Thr Lys Thr Val Lys Pro Ser Glu Cys Ser
225 230 235

<210> 106
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<223> chimeric H chain

<400> 106

Met Gly Trp Ser Gln Ile Ile Leu Phe Leu Val Ala Ala Ala Thr Cys
1 5 10 15

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys
20 25 30

Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Ser Asn Phe Met His Trp Val Lys Gln Gln Pro Gly Asn Gly Leu
50 55 60

Glu Trp Ile Gly Trp Ile Tyr Pro Glu Tyr Gly Asn Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Asp Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
Page 73

seq_list_5104975_1 (2)

100

105

110

Tyr Phe Cys₁₁₅ Ala Ser Glu Glu₁₂₀ Ala Val Ile Ser Leu Val₁₂₅ Tyr Trp Gly

Gln Gly₁₃₀ Thr Leu Val Thr₁₃₅ Ser Ser Ala Ser Thr₁₄₀ Thr Ala Pro Lys

Val₁₄₅ Tyr Pro Leu Ser Ser₁₅₀ Cys Cys Gly Asp Lys₁₅₅ Ser Ser Ser Thr Val₁₆₀

Thr Leu Gly Cys Leu₁₆₅ Val Ser Ser Tyr Met₁₇₀ Pro Glu Pro Val Thr₁₇₅ Val

Thr Trp Asn Ser₁₈₀ Gly Ala Leu Lys Ser₁₈₅ Gly Val His Thr Phe₁₉₀ Pro Ala

Val Leu Gln₁₉₅ Ser Ser Gly Leu Tyr₂₀₀ Ser Leu Ser Ser Met₂₀₅ Val Thr Val

Pro Gly₂₁₀ Ser Thr Ser Gly Gln₂₁₅ Thr Phe Thr Cys Asn₂₂₀ Val Ala His Pro

Ala Ser Ser Thr Lys Val₂₃₀ Asp Lys Ala Val Asp₂₃₅ Pro Thr Cys Lys Pro₂₄₀

Ser Pro Cys Asp Cys₂₄₅ Cys Pro Pro Pro₂₅₀ Val Ala Gly Pro Ser₂₅₅ Val

Phe Ile Phe Pro₂₆₀ Pro Lys Pro Lys Asp₂₆₅ Thr Leu Thr Ile Ser₂₇₀ Gly Thr

Pro Glu Val₂₇₅ Thr Cys Val Val₂₈₀ Val Asp Val Gly His Asp₂₈₅ Asp Pro Glu

Val Lys₂₉₀ Phe Ser Trp Phe Val₂₉₅ Asp Asp Val Glu Val₃₀₀ Asn Thr Ala Thr

Thr Lys Pro Arg Glu Glu₃₁₀ Gln Phe Asn Ser Thr₃₁₅ Tyr Arg Val Val Ser₃₂₀

Ala Leu Arg Ile Gln₃₂₅ His Gln Asp Trp Thr₃₃₀ Gly Gly Lys Glu Phe₃₃₅ Lys

Cys Lys Val His₃₄₀ Asn Glu Gly Leu Pro₃₄₅ Ser Ser Ile Val Arg₃₅₀ Thr Ile

Ser Arg Thr₃₅₅ Lys Gly Pro Ala Arg₃₆₀ Glu Pro Gln Val Tyr₃₆₅ Val Leu Ala

Pro Pro Gln Glu Glu Leu Ser Lys Ser Thr Val Ser Leu Thr Cys Met

seq list_5104975_1 (2)

370

375

380

Val Thr Ser Phe Tyr Pro Asp Tyr Ile Ala Val Glu Trp Gln Arg Asn
385 390 395 400

Gly Gln Pro Glu Ser Glu Asp Lys Tyr Gly Thr Thr Pro Pro Gln Leu
405 410 415

Asp Ala Asp Ser Ser Tyr Phe Leu Tyr Ser Lys Leu Arg Val Asp Arg
420 425 430

Asn Ser Trp Gln Glu Gly Asp Thr Tyr Thr Cys Val Val Met His Glu
435 440 445

Ala Leu His Asn His Tyr Thr Gln Lys Ser Thr Ser Lys Ser Ala Gly
450 455 460

Lys
465

<210>	107
<211>	717
<212>	DNA
<213>	Artificial Sequence

<220>
<223> codon-optimized sequence

<400>	107								
atggaatctc	aaactcatgt	tttgatttca	ttacttctga	gtgtttccgg	aacctacggt				60
gatatcgcta	tactcaatc	tccctcctct	gttgcttgt	ctgtgggcga	aaccgttacc				120
ctgtcctgca	agtccagtc	gtctcttctc	tactccgaga	atcaaaagg	ctacctgggc				180
tggtaccaac	agaagcccgg	ccagaccca	aagccactga	tatactgggc	aaccaacagg				240
cacaccggag	tgcccgacag	gttcacaggc	agtggatctg	gcaccgactt	taccttgatc				300
atttcaagcg	tgcaggctga	agatctggcc	gactactact	gtggtcagta	tctgggtgat				360
cctttcactt	tcgggccagg	gacaaaactc	gagctcaaac	agcctaagag	tcctccttct				420
gtaaacactct	ttccccctc	taccgaggaa	ctcaacggca	ataaagctac	cttggtttgc				480
cttatttctg	atttctacco	cgggtctgtg	accgtgggtg	ggaaagctga	tgggtccacc				540
attactcgga	atgtggaaac	caccggggt	tctaagcagt	ccaactctaa	atacgagca				600
tcctcctatt	tgagtcttac	tagtagtgac	tggaagtcaa	agggtagtta	cagttgcgaa				660
gtcacacatg	aaggttcaac	agtgcacaa	acagtcaagc	cctcagagtg	ctcatag				717

<210>	108
<211>	1398
<212>	DNA
<213>	Artificial Sequence

<220>
<223> codon-optimized sequence

seq list_5104975_1 (2)

<400> 108
atggggtggg cccagattat attgttcctc gtcgccgccg ccacttgcg acacagccaa 60
gtgcaacttc aacaaagcgg tgcagaactg gtaaagcccc gtagctctgt gaaaatatcc 120
tgtaaagcca gtggctacac atttaccagc aactttatgc actgggtgaa gcaacagccc 180
ggaaatggct tggagtggat tggctggatc tatcccgaat atggtaacac caagtataat 240
cagaagtctg acggttaaggc caccctcacc gccgataagt catcctccac cgcctatatg 300
cagctcagca gcctgaccag cgaggattcc gctgtgtact tctgtgccag cgaagaggct 360
gtgatctcat tgggtgtattg gggacagggc accctcgtca ccgtgtccag cgctagcaca 420
actgctccta aggtgtaccc cctgagctct tgctgcggcg acaagtctag cagcaccgtg 480
accctcggat gcctcgtcag cagctatatg cctgagccag ttacagtgc atggaattct 540
ggtgccctta agtccggcgt ccataccttc cctgctgtgc tgcagtcctc tggcctgtac 600
agtttgtcct ctatgggtgac agtaccgggt tccacctccg gacagacctt tacctgtaat 660
gtggctcatc ccgcctcctc caciaagggt gataaggctg ttgaccctac ctgtaaacc 720
agtccatgag actgctgtcc cccccctcca gttgccggac cctcagtcctt tattttccca 780
cccaaacca aagacaccct gacaatctct ggaacaccag aagtcacctg cgtcgtcgtg 840
gatgtgggccc acgacgatcc tgaggtaaaa ttctcatggt tcgtcgacga tgtggaagtg 900
aatacagcta ctacaaaacc tcgcgaagag cagtttaact ctacctatcg agtggtttct 960
gctttgcgga ttcagcatca ggattggaca ggcggcaaag agtttaaatg taaagtccat 1020
aacgaggggac ttccttctag tatcgtgcgc actatcagta gaactaaagg gcctgctcgg 1080
gaacctcagg tgtacgtcct ggcacctcca caggaagagc tgagtaagtc tacagtttct 1140
ctgacttgta tggtaacatc tttttatcca gattacatcg cagttgaatg gcagaggaac 1200
gggcagccag agagttagga taagtacggg actactccac cacagctgga cgcagactca 1260
agttacttcc tgtactcaaa gctgaggggt gacagaaact catggcagga gggggacact 1320
tacacttgcg tagttatgca cgaggcactt cacaaccact acactcagaa gagtacttca 1380
aagagtgcag ggaagtaa 1398

<210> 109
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 109
atgaggatat atagtgtctt aacat 25

<210> 110
<211> 20
<212> DNA
<213> Artificial Sequence

seq list_5104975_1 (2)

<220>
 <223> primer
 <400> 110
 ttacgtctcc tcaaaatgtg 20

<210> 111
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 111
 atgaggatat gtagtatctt tacat 25

<210> 112
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 112
 ttacgtctcc tcaaattgtg t 21

<210> 113
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 113
 atgaggatat atagtgtctt 20

<210> 114
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 114
 gccactcagg acttggtgat 20

<210> 115
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 115
 gggggtttac tgttgcttga 20

<210> 116

seq list_5104975_1 (2)

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

<220>
<223> primer

<400> 116
ttacgtctcc tcaaattgt 19

<210> 117
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 117
gaagatctat ggggaccccg cgggcgccg 29

<210> 118
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 118
gacccgggga ggggccagga gcagtgtcc 29

<210> 119
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 119
ccgctcgaga tgaggatata tagtgtct 28

<210> 120
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 120
atcccgggcg tctcctcaaa atgtgtag 28

<210> 121
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 121

	seq list_5104975_1 (2)	
actaagctta tggggacccc gcggg		25
<210> 122		
<211> 26		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer		
<400> 122		
actcccgggg aggggccaag agcagt		26
<210> 123		
<211> 29		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer		
<400> 123		
ccgctcgaga tgaggatatg tagtatctt		29
<210> 124		
<211> 29		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer		
<400> 124		
atcccgggcg tctcctcaaa ttgtgtatc		29
<210> 125		
<211> 28		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer		
<400> 125		
gacgctagca tgaggatata tagtgtct		28
<210> 126		
<211> 28		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer		
<400> 126		
gctctgatat ccctcgtttt tgctggat		28
<210> 127		
<211> 29		
<212> DNA		
<213> Artificial Sequence		

seq list_5104975_1 (2)

<220>
 <223> primer
 <400> 127
 gacgctagca tgaggatatg tagtatctt 29
 <210> 128
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 128
 agcttgatat ccctctttct tgctggatc 29
 <210> 129
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 129
 cgcggtatc atggattaca cagcgaagtg 30
 <210> 130
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 130
 cggggtaccc cagagctggt gctgggtat 29
 <210> 131
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 131
 cgcggtatc atgagaatgt ttagtgtctt 30
 <210> 132
 <211> 49
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer
 <400> 132
 cgcggtatc ttaatggtga tggatgatgg gagtcctctc acttgctgg 49
 <210> 133

seq list_5104975_1 (2)

<211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 133
 atatgcggcc gcatggggac cccgcgggcg ct 32

 <210> 134
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 134
 gcgcaagctt tcagaggggc caggagcagt 30

 <210> 135
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 135
 ctagctagca ccatgaggat atatagtgtc ttaac 35

 <210> 136
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 136
 caatctcgag ttacagacag aagatgactg c 31

 <210> 137
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 137
 gctagcatga ggatatatag tgtcttaac 29

 <210> 138
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 138

seq list_5104975_1 (2)
gatatcattc ctcttttttg ctggat

26