

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> CROSS-SPECIES ANTI-LATENT TGF-BETA 1 ANTIBODIES AND METHODS OF USE

<130> C1-A1921P

<150> JP 2019-155278

<151> 2019-08-28

<160> 73

<170> PatentIn version 3.5

<210> 1

<211> 387

<212> PRT

<213> Artificial Sequence

<220>

<223> flag-tagged human latent TGF-beta 1

<400> 1

Met Lys Trp Val Thr Phe Leu Leu Leu Leu Phe Ile Ser Gly Ser Ala
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Phe Ser Asp Tyr Lys Asp Asp Asp Asp Lys Leu Ser Thr Ser Lys Thr
20 25 30

Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala Ile Arg Gly
35 40 45

Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser Gln Gly Glu
50 55 60

Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu Tyr Asn Ser
65 70 75 80

Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Glu Pro Glu Pro Glu Pro
85 90 95

Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu Met Val Glu
 100 105 110

Thr His Asn Glu Ile Tyr Asp Lys Phe Lys Gln Ser Thr His Ser Ile
 115 120 125

Tyr Met Phe Phe Asn Thr Ser Glu Leu Arg Glu Ala Val Pro Glu Pro
 130 135 140

Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu Lys Leu Lys
 145 150 155 160

Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn Asn Ser Trp
 165 170 175

Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser Pro Glu Trp
 180 185 190

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

Gly Glu Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser Cys Asp Ser
 210 215 220

Arg Asp Asn Thr Leu Gln Val Asp Ile Asn Gly Phe Thr Thr Gly Arg
 225 230 235 240

Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro Phe Leu Leu
 245 250 255

Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu Gln Ser Ser Arg
 260 265 270

His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
 275 280 285

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
 290 295 300

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
305 310 315 320

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
325 330 335

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
340 345 350

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
355 360 365

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
370 375 380

Lys Cys Ser
385

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<211> 1167
<212> DNA
<213> Artificial Sequence

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ttcaagcaga gtacacacag catatatatg ttcttcaaca catcagagct ccgagaagcg 420
gtacctgaac ccgtgttgct ctcccgggca gagctgcgtc tgctgaggct caagttaaaa 480

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gtgcggcagt ggttgagccg tggaggggaa attgagggtt ttcgccttag cgcccactgc      660
tcctgtgaca gcagggataa cacactgcaa gtggacatca acgggttcac taccggccgc      720
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ccgctggaga gggcccagca tctgcaaagc tccgggcacc gccgagccct ggacaccaac      840
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gggccctgcc cctacatttg gagcctggac acgcagtaca gcaaggctcct ggccctgtac     1020
aaccagcata acccgggcgc ctcggcggcg ccgtgctgcg tgccgcaggc gctggagccg     1080
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<210> 3
<211> 387
<212> PRT
<213> Artificial Sequence

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<220>
<223> flag-tagged mouse latent TGF-beta 1

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<400> 3

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

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Phe Ser Asp Tyr Lys Asp Asp Asp Lys Leu Ser Thr Ser Lys Thr
          20          25          30

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Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala Ile Arg Gly
          35          40          45

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Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser Gln Gly Glu
          50          55          60

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Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu Tyr Asn Ser
65 70 75 80

Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu Pro Glu Pro
85 90 95

Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu Met Val Asp
100 105 110

Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser His Ser Ile
115 120 125

Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val Pro Glu Pro
130 135 140

Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu Lys Ser Ser
145 150 155 160

Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn Asn Ser Trp
165 170 175

Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr Pro Glu Trp
180 185 190

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

Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser Cys Asp Ser
210 215 220

Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser Pro Lys Arg
225 230 235 240

Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro Phe Leu Leu
245 250 255

Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His Ser Ser Arg
 260 265 270

His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
 275 280 285

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
 290 295 300

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
 305 310 315 320

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
 325 330 335

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ser Pro Cys
 340 345 350

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
 355 360 365

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
 370 375 380

Lys Cys Ser
 385

<210> 4
 <211> 1167
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> flag-tagged mouse latent TGF-beta 1

<400> 4
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 aaggatgacg atgacaagct ctccacctcc aagaccatcg acatggagct ggtgaaacgg 120
 aagcgcatcg aagccatccg tggccagatc ctgtccaaac taaggctcgc cagtccccca 180

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agccaggggg aggtaccgcc cggcccgtg cccgaggcgg tgctcgcttt gtacaacagc 240
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tatgctaaag aggtcacccg cgtgctaata gtggaccgca acaacgccat ctatgagaaa 360
accaaagaca tctcacacag tatatatatg ttcttcaata cgtcagacat tcgggaagca 420
gtgcccgaac ccccatgtgt gtcccgtgca gagctgcgct tgcagagatt aaaatcaagt 480
gtggagcaac atgtggaact ctaccagaaa tatagcaaca attcctggcg ttaccttggt 540
aaccggctgc tgacccccac tgatacgctt gaggggctgt cttttgacgt cactggagtt 600
gtacggcagt ggctgaacca aggagacgga atacagggct ttcgattcag cgctcactgc 660
tcttgtgaca gcaaagataa caaactccac gtggaaatca acgggatcag ccccaaactg 720
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cccctggaag gggcccagca cctgcacagc tcacggcacc ggagagccct ggataccaac 840
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aaccaacaca acccggggcg ttcggcgta cctgtctgctg tgccgcaggc tttggagcca 1080
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<210> 5
<211> 387
<212> PRT
<213> Artificial Sequence

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<220>
<223> flag-tagged cynomolgus monkey latent TGF-beta 1

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<400> 5

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

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Phe Ser Asp Tyr Lys Asp Asp Asp Lys Leu Ser Thr Ser Lys Thr
 20 25 30

Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala Ile Arg Gly
 35 40 45

Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser Gln Gly Glu
 50 55 60

Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu Tyr Asn Ser
 65 70 75 80

Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Glu Pro Glu Pro Glu Pro
 85 90 95

Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu Met Val Glu
 100 105 110

Thr His Asn Glu Ile Tyr Asp Lys Phe Lys Gln Ser Thr His Ser Ile
 115 120 125

Tyr Met Phe Phe Asn Thr Ser Glu Leu Arg Glu Ala Val Pro Glu Pro
 130 135 140

Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu Lys Leu Lys
 145 150 155 160

Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn Asn Ser Trp
 165 170 175

Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser Pro Glu Trp
 180 185 190

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

Gly Glu Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser Cys Asp Ser
 210 215 220

Lys Asp Asn Thr Leu Gln Val Asp Ile Asn Gly Phe Thr Thr Gly Arg
 225 230 235 240

Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro Phe Leu Leu
 245 250 255

Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu Gln Ser Ser Arg
 260 265 270

His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
 275 280 285

Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
 290 295 300

Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
 305 310 315 320

Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
 325 330 335

Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
 340 345 350

Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
 355 360 365

Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
 370 375 380

Lys Cys Ser
 385

<210> 6
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 <212> DNA
 <213> Artificial Sequence

<220>

<223> flag-tagged cynomolgus monkey latent TGF-beta 1

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aagcgcacg aggccatccg cggccagatc ctgtccaagc tgcggctcgc cagccccccg	180
agccaggggg aggtgccgcc cggcccgtg cccgaggccg tgctcgccct gtacaacagc	240
acccgcgacc ggggtggccg ggagagtgc gaaccggagc ccgagcctga ggccgactac	300
tacgccaagg aggtcaccg cgtgctaag gtggaaacc acaacgaaat ctatgacaag	360
ttcaagcaga gtacacacag catatatatg ttcttcaaca catcagagct ccgagaagcg	420
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cgaggtgacc tggccaccat tcatggcatg aaccggcctt tcctgcttct catggccacc	780
ccgttgaga gggcccagca tctgcaaagc tcccggcacc gccgagccct ggacaccaac	840
tattgcttca gctccacgga gaagaactgc tgcgtgcggc agctgtacat tgacttccgc	900
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aaccagcata acccgggcgc ctggcggcg ccgtgctgcg tgccgcaggc gctggagccg	1080
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<210> 7

<211> 1824

<212> DNA

<213> Rattus norvegicus

<400> 7

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cagcatttca aaggcctagt cctgattgcc ttttcccagt atctccagaa atgcccata	180
gaagagcata tcaaattggt gcaggaagta acagactttg caaaaacatg tgtcgtgat	240
gagaatgccg aaaactgtga caagtccatt cacactctct tcggagacaa gttatgcgcc	300
attccaaagc ttcgcgacaa ctacggtgaa ctggctgact gctgtgcaaa acaagagccc	360
gaaagaaacg agtgtttcct gcagcacaag gatgacaacc ccaacctgcc acccttcag	420
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cactatttgc atgaagtgc caggagacat ccttatttct atgccccaga actcctttac	540
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tgctgacac cgaagcttga tgccgtgaaa gagaaagcac tggctgcagc tgtccgtcag	660
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gctcgtatga gccagcgatt ccccaatgct gagttcgag aaatcaccaa attggaaca	780
gacctacca aaatcaacaa ggagtgtgt cacggcgacc tgttggaatg cgcggtgac	840
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tgttgatccc ttctgaagc tcagagactg ccctgtgtgg aagactatct gtctgccatc	1440

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<210> 8
 <211> 275
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> flag-tagged mouse LAP

<400> 8

Met Lys Trp Val Thr Phe Leu Leu Leu Leu Phe Ile Ser Gly Ser Ala
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Phe Ser Asp Tyr Lys Asp Asp Asp Asp Lys Leu Ser Thr Ser Lys Thr
 20 25 30

Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala Ile Arg Gly
 35 40 45

Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser Gln Gly Glu
 50 55 60

Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu Tyr Asn Ser
 65 70 75 80

Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Asp Pro Glu Pro Glu Pro
 85 90 95

Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu Met Val Asp

13

100

105

110

Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser His Ser Ile
115 120 125

Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val Pro Glu Pro
130 135 140

Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu Lys Ser Ser
145 150 155 160

Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn Asn Ser Trp
165 170 175

Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr Pro Glu Trp
180 185 190

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

Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser Cys Asp Ser
210 215 220

Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser Pro Lys Arg
225 230 235 240

Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro Phe Leu Leu
245 250 255

Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His Ser Ser Arg
260 265 270

His Arg Arg
275

<210> 9

<211> 831

<212> DNA

<213> Artificial Sequence

<220>

<223> flag-tagged mouse LAP

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aagcgcatcg aagccatccg tggccagatc ctgtccaaac taaggctcgc cagtccccc	180
agccaggggg aggtaccgcc cgcccgcgtg cccgaggcgg tgctcgcttt gtacaacagc	240
acccgcgacc ggggtggcagg cgagagcgcc gaccagagc cgagagccga agcggactac	300
tatgctaaag aggtcaccgc cgtgctaata gtggaccgca acaacgccat ctatgagaaa	360
accaaagaca tctcacacag tatatatatg ttcttcaata cgtcagacat tcgggaagca	420
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gtggagcaac atgtggaact ctaccagaaa tatagcaaca attcctggcg ttaccttggt	540
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gtacggcagt ggctgaacca aggagacgga atacagggct ttcgattcag cgctcactgc	660
tcttgtgaca gcaaagataa caaactccac gtggaaatca acgggatcag ccccaaactg	720
cggggcgacc tgggcacccat ccatgacatg aaccggccct tctgtctcct catggccacc	780
cccctggaag gggccagca cctgcacagc tcacggcacc ggagatgatg a	831

<210> 10

<211> 328

<212> PRT

<213> Artificial Sequence

<220>

<223> SG181

<400> 10

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys
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Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr

[illegible]

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

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro
325

<210> 11
<211> 107
<212> PRT
<213> Homo sapiens

<400> 11

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

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

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

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

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

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

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

<210> 12
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> hT0947AE04H VH

<400> 12

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

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

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

Gly Tyr Ile Tyr Thr Ser Gly Thr Thr Tyr His Ala Asn Trp Ala Arg
50 55 60

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

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

Arg Gly Thr Phe Ile Trp Asp Tyr Tyr Tyr Trp Val Met Asp Leu Trp
100 105 110

Gly Pro Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 13
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE04L VL

<400> 13

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Thr Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr Ser Asp Ala Asp Ser
 85 90 95

Val Gly Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 14
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>

<223> hT0947AE07H VH

<400> 14

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

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

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

Gly Tyr Ile Tyr Thr Ser Gly Thr Thr Tyr Arg Ala Asn Trp Ala Arg
50 55 60

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

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

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

Gly Pro Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 15

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> hT0947AE07L VL

<400> 15

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

20

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Thr Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr Ser Asp Gly Asp Ser
85 90 95

Val Gly Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 16
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> hT0947AE08H VH

<400> 16

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

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

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

Gly Tyr Ile Tyr Thr Ser Gly Thr Arg Tyr Arg Ala Asn Trp Ala Arg
50 55 60

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

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

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

Gly Pro Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 17
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> hT0947AE08L VL

<400> 17

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Thr Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr Ser Asp Gly Asp Ser
85 90 95

Val Gly Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 18
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE09H VH

<400> 18

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

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

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

Gly Tyr Ile Tyr Thr Ser Gly Thr Arg Tyr Arg Ala Asn Trp Ala Arg
 50 55 60

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

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

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

Gly Pro Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 19
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>

<223> hT0947AE09L VL

<400> 19

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Thr Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr Ser Asp Ala Asp Ser
 85 90 95

Val Gly Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 20

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> hT0947AE04H HVR-H1

<400> 20

Ser Tyr Ala Met Asn
 1 5

<210> 21

<211> 16

<212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE04H HVR-H2

<400> 21

Tyr	Ile	Tyr	Thr	Ser	Gly	Thr	Thr	Tyr	His	Ala	Asn	Trp	Ala	Arg	Gly
1				5					10					15	

<210> 22
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE04H HVR-H3

<400> 22

Gly	Thr	Phe	Ile	Trp	Asp	Tyr	Tyr	Tyr	Trp	Val	Met	Asp	Leu
1				5					10				

<210> 23
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE04L HVR-L1

<400> 23

Gln	Ala	Ser	Gln	Ser	Ile	Ser	Thr	Tyr	Leu	Ala
1				5					10	

<210> 24
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE04L HVR-L2

<400> 24

Lys Ala Ser Thr Leu Glu Ser
1 5

<210> 25
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> hT0947AE04L HVR-L3

<400> 25

Gln Ser Tyr Ser Asp Ala Asp Ser Val Gly
1 5 10

<210> 26
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> hT0947AE07H HVR-H1

<400> 26

Ser Glu Ala Met Asn
1 5

<210> 27
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> hT0947AE07H HVR-H2

<400> 27

Tyr Ile Tyr Thr Ser Gly Thr Thr Tyr Arg Ala Asn Trp Ala Arg Gly
1 5 10 15

<210> 28
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> hT0947AE07H HVR-H3

<400> 28

Gly	Thr	Gly	Ile	Tyr	Asp	Tyr	Tyr	Tyr	Trp	Val	Met	Asp	Leu
1				5					10				

<210> 29

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> hT0947AE07L HVR-L1

<400> 29

Gln	Ala	Ser	Gln	Ser	Ile	Ser	Thr	Tyr	Leu	Ala
1				5					10	

<210> 30

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> hT0947AE07L HVR-L2

<400> 30

Ala	Ala	Ser	Thr	Leu	Glu	Ser
1				5		

<210> 31

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> hT0947AE07L HVR-L3

<400> 31

Gln	Ser	Tyr	Ser	Asp	Gly	Asp	Ser	Val	Gly
1				5					10

<210> 32
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE08H HVR-H1

<400> 32

Ser Tyr Ala Met Asn
 1 5

<210> 33
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE08H HVR-H2

<400> 33

Tyr Ile Tyr Thr Ser Gly Thr Arg Tyr Arg Ala Asn Trp Ala Arg Gly
 1 5 10 15

<210> 34
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE08H HVR-H3

<400> 34

Gly Thr Asp Ile Tyr Asp Tyr Tyr Tyr Trp Val Met Asp Leu
 1 5 10

<210> 35
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>

<223> hT0947AE08L HVR-L1

<400> 35

Gln	Ala	Ser	Gln	Ser	Ile	Ser	Thr	Tyr	Leu	Ala
1				5					10	

<210> 36

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> hT0947AE08L HVR-L2

<400> 36

Ala	Ala	Ser	Thr	Leu	Glu	Ser
1				5		

<210> 37

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> hT0947AE08L HVR-L3

<400> 37

Gln	Ser	Tyr	Ser	Asp	Gly	Asp	Ser	Val	Gly
1				5					10

<210> 38

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> hT0947AE09H HVR-H1

<400> 38

Ser	Tyr	Ala	Met	Asn
1			5	

<210> 39
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE09H HVR-H2

<400> 39

Tyr Ile Tyr Thr Ser Gly Thr Arg Tyr Arg Ala Asn Trp Ala Arg Gly
 1 5 10 15

<210> 40
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE09H HVR-H3

<400> 40

Gly Thr Asp Ile Tyr Asp Tyr Tyr Tyr Trp Val Met Asp Leu
 1 5 10

<210> 41
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE09L HVR-L1

<400> 41

Gln Ala Ser Gln Ser Ile Ser Thr Tyr Leu Ala
 1 5 10

<210> 42
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE09L HVR-L2

<400> 42

Ala Ala Ser Thr Leu Glu Ser
1 5

<210> 43

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> hT0947AE09L HVR-L3

<400> 43

Gln Ser Tyr Ser Asp Ala Asp Ser Val Gly
1 5 10

<210> 44

<211> 328

<212> PRT

<213> Artificial Sequence

<220>

<223> SG1

<400> 44

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

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr 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 Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

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

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

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

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

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

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

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

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

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

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

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro
 325

<210> 45
 <211> 328
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SG191

<400> 45

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

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr 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 Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80

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

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110

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

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

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

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

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

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

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

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

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255

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

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

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

Val Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ala His Tyr Thr
 305 310 315 320

Arg Lys Glu Leu Ser Leu Ser Pro
 325

<210> 46
 <211> 324
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mF18

<400> 46

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

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

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

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

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

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

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

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

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

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

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

Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn
 180 185 190

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

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

Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val
 225 230 235 240

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

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

Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn
 275 280 285

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

Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
 305 310 315 320

Ser Pro Gly Lys

<210> 47
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE04H-SG181

<400> 47

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

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

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

Gly Tyr Ile Tyr Thr Ser Gly Thr Thr Tyr His Ala Asn Trp Ala Arg
 50 55 60

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

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

Arg Gly Thr Phe Ile Trp Asp Tyr Tyr Tyr Trp Val Met Asp Leu Trp
 100 105 110

Gly Pro Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140

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

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Arg
 225 230 235 240

Arg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445

Ser Pro
 450

<210> 48
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE07H-SG181

<400> 48

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

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

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

Gly Tyr Ile Tyr Thr Ser Gly Thr Thr Tyr Arg Ala Asn Trp Ala Arg
 50 55 60

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

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

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

Gly Pro Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140

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

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Arg
 225 230 235 240

Arg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445

Ser Pro
450

<210> 49
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> hT0947AE08H-SG181

<400> 49

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

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

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

Gly Tyr Ile Tyr Thr Ser Gly Thr Arg Tyr Arg Ala Asn Trp Ala Arg
50 55 60

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

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

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

Gly Pro Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130 135 140

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

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Arg
 225 230 235 240

Arg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445

Ser Pro
 450

<210> 50
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE09H-SG181

<400> 50

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

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

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

Gly Tyr Ile Tyr Thr Ser Gly Thr Arg Tyr Arg Ala Asn Trp Ala Arg
 50 55 60

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

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

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

Gly Pro Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140

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

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Arg
 225 230 235 240

Arg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445

Ser Pro
450

<210> 51
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> hT0947AE04H-SG191

<400> 51

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

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

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

Gly Tyr Ile Tyr Thr Ser Gly Thr Thr Tyr His Ala Asn Trp Ala Arg
50 55 60

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

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

Arg Gly Thr Phe Ile Trp Asp Tyr Tyr Tyr Trp Val Met Asp Leu Trp
100 105 110

Gly Pro Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130 135 140

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

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Arg
 225 230 235 240

Arg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430

Leu His Glu Ala Leu His Ala His Tyr Thr Arg Lys Glu Leu Ser Leu
 435 440 445

Ser Pro
 450

<210> 52
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE07H-SG191

<400> 52

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

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

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

Gly Tyr Ile Tyr Thr Ser Gly Thr Thr Tyr Arg Ala Asn Trp Ala Arg
 50 55 60

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

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

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

Gly Pro Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140

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

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Arg
 225 230 235 240

Arg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430

Leu His Glu Ala Leu His Ala His Tyr Thr Arg Lys Glu Leu Ser Leu
 435 440 445

Ser Pro
 450

<210> 53
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE08H-SG191

<400> 53

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

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

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

Gly Tyr Ile Tyr Thr Ser Gly Thr Arg Tyr Arg Ala Asn Trp Ala Arg
 50 55 60

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

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

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

Gly Pro Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140

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

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Arg
 225 230 235 240

Arg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430

Leu His Glu Ala Leu His Ala His Tyr Thr Arg Lys Glu Leu Ser Leu
 435 440 445

Ser Pro
 450

<210> 54
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE09H-SG191

<400> 54

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

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

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

Gly Tyr Ile Tyr Thr Ser Gly Thr Arg Tyr Arg Ala Asn Trp Ala Arg
 50 55 60

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

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

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

Gly Pro Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140

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

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Arg
225 230 235 240

Arg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430

Leu His Glu Ala Leu His Ala His Tyr Thr Arg Lys Glu Leu Ser Leu
 435 440 445

Ser Pro
 450

<210> 55
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE04H-mF18

<400> 55

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

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

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

Gly Tyr Ile Tyr Thr Ser Gly Thr Thr Tyr His Ala Asn Trp Ala Arg
 50 55 60

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

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

Arg Gly Thr Phe Ile Trp Asp Tyr Tyr Tyr Trp Val Met Asp Leu Trp
 100 105 110

Gly Pro Gly Thr Leu Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro
 115 120 125

Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met
 130 135 140

Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160

Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro
 165 170 175

Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val
 180 185 190

Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His
 195 200 205

Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys
 210 215 220

Gly Cys Lys Pro Cys Ile Cys Thr Val Lys Glu Val Ser Lys Val Phe
 225 230 235 240

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

Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val
 260 265 270

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
 275 280 285

Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu
 290 295 300

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
 305 310 315 320

Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
340 345 350

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile
355 360 365

Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
370 375 380

Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp
385 390 395 400

Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
405 410 415

Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
420 425 430

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
435 440 445

<210>	56
<211>	446
<212>	PRT
<213>	Artificial Sequence

<220>
<223> hT0947AE07H-mF18

<400> 56

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

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

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

Gly Tyr Ile Tyr Thr Ser Gly Thr Thr Tyr Arg Ala Asn Trp Ala Arg
 50 55 60

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

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

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

Gly Pro Gly Thr Leu Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro
 115 120 125

Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met
 130 135 140

Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160

Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro
 165 170 175

Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val
 180 185 190

Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His
 195 200 205

Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys
 210 215 220

Gly Cys Lys Pro Cys Ile Cys Thr Val Lys Glu Val Ser Lys Val Phe
 225 230 235 240

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

Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val
 260 265 270

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
 275 280 285

Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu
 290 295 300

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
 305 310 315 320

Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser
 325 330 335

Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
 340 345 350

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile
 355 360 365

Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
 370 375 380

Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp
 385 390 395 400

Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
 405 410 415

Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
 420 425 430

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 435 440 445

<210> 57
 <211> 446
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE08H-mF18

<400> 57

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

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

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

Gly Tyr Ile Tyr Thr Ser Gly Thr Arg Tyr Arg Ala Asn Trp Ala Arg
 50 55 60

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

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

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

Gly Pro Gly Thr Leu Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro
 115 120 125

Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met
 130 135 140

Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val
180 185 190

Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His
195 200 205

Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys
210 215 220

Gly Cys Lys Pro Cys Ile Cys Thr Val Lys Glu Val Ser Lys Val Phe
225 230 235 240

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

Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val
260 265 270

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
275 280 285

Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu
290 295 300

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
305 310 315 320

Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
340 345 350

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile
 355 360 365

Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
 370 375 380

Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp
 385 390 395 400

Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
 405 410 415

Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
 420 425 430

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 435 440 445

<210> 58

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> hT0947AE09H-mF18

<400> 58

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

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

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

Gly Tyr Ile Tyr Thr Ser Gly Thr Arg Tyr Arg Ala Asn Trp Ala Arg
 50 55 60

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

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

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

Gly Pro Gly Thr Leu Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro
115 120 125

Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met
130 135 140

Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val
180 185 190

Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His
195 200 205

Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys
210 215 220

Gly Cys Lys Pro Cys Ile Cys Thr Val Lys Glu Val Ser Lys Val Phe
225 230 235 240

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

Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val
 260 265 270

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
 275 280 285

Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu
 290 295 300

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
 305 310 315 320

Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser
 325 330 335

Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
 340 345 350

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile
 355 360 365

Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
 370 375 380

Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp
 385 390 395 400

Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
 405 410 415

Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
 420 425 430

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 435 440 445

<210> 59

<211> 107

<212> PRT

<213> Mus musculus

<400> 59

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

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

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
 35 40 45

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
 50 55 60

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

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
 85 90 95

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 100 105

<210> 60

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> hT0947AE04L-SK1

<400> 60

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Thr Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr Ser Asp Ala Asp Ser
 85 90 95

Val Gly Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
 100 105 110

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

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 195 200 205

Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 61

<211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE07L-SK1

<400> 61

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Thr Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr Ser Asp Gly Asp Ser
 85 90 95

Val Gly Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
 100 105 110

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

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu

69

165

170

175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 62
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> hT0947AE08L-SK1

<400> 62

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Thr Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr Ser Asp Gly Asp Ser
85 90 95

Val Gly Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala

70

100

105

110

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

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 63
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> hT0947AE09L-SK1

<400> 63

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Thr Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile

71

35

40

45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr Ser Asp Ala Asp Ser
85 90 95

Val Gly Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

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

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 64

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> hT0947AE04L-mk1

<400> 64

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Thr Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr Ser Asp Ala Asp Ser
85 90 95

Val Gly Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala
100 105 110

Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser
115 120 125

Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp
130 135 140

Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val
145 150 155 160

Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met
165 170 175

Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser
 180 185 190

Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys
 195 200 205

Ser Phe Asn Arg Asn Glu Cys
 210 215

<210> 65
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE07L-mk1

<400> 65

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Thr Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr Ser Asp Gly Asp Ser
 85 90 95

Val Gly Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala
 100 105 110

Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser
 115 120 125

Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp
 130 135 140

Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val
 145 150 155 160

Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met
 165 170 175

Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser
 180 185 190

Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys
 195 200 205

Ser Phe Asn Arg Asn Glu Cys
 210 215

<210> 66
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hT0947AE08L-mk1

<400> 66

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Thr Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 35 40 45

75

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr Ser Asp Gly Asp Ser
85 90 95

Val Gly Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala
100 105 110

Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser
115 120 125

Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp
130 135 140

Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val
145 150 155 160

Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met
165 170 175

Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser
180 185 190

Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys
195 200 205

Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 67
<211> 215
<212> PRT
<213> Artificial Sequence

<220>

<223> hT0947AE09L-mk1

<400> 67

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Thr Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr Ser Asp Ala Asp Ser
 85 90 95

Val Gly Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala
 100 105 110

Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser
 115 120 125

Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp
 130 135 140

Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val
 145 150 155 160

Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met
 165 170 175

Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser

77

180

185

190

Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys
195 200 205

Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 68
<211> 390
<212> PRT
<213> Homo sapiens

<400> 68

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

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

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

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

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
100 105 110

Met Val Glu Thr His Asn Glu Ile Tyr Asp Lys Phe Lys Gln Ser Thr
115 120 125

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
 130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
 145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
 165 170 175

Asn Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
 180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
 195 200 205

Ser Arg Gly Gly Glu Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser
 210 215 220

Cys Asp Ser Arg Asp Asn Thr Leu Gln Val Asp Ile Asn Gly Phe Thr
 225 230 235 240

Thr Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
 245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu Gln
 260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser
 275 280 285

Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys
 290 295 300

Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn
 305 310 315 320

Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr
 325 330 335

Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala
 340 345 350

Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr
 355 360 365

Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val
 370 375 380

Arg Ser Cys Lys Cys Ser
 385 390

<210> 69
 <211> 1173
 <212> DNA
 <213> Homo sapiens

<400> 69
 atgccgccct ccgggtgctg gctgctgccg ctgctgtctac cgctgctgtg gctactggtg 60
 ctgacgcctg gccggccggc cgcgggacta tccacctgca agactatcga catggagctg 120
 gtgaagcgga agcgcacgga ggccatccgc ggccagatcc tgtccaagct gcggctcgcc 180
 agcccccca gccaggggga ggtgccgccc ggcccgtgct ccgaggccgt gctcgccctg 240
 tacaacagca cccgcgaccg ggtggccggg gagagtgcag aaccggagcc cgagcctgag 300
 gccgactact acgccaagga ggtcaccgc gtgctaattg tggaaacca caacgaaatc 360
 tatgacaagt tcaagcagag tacacacagc atatatatgt tcttcaacac atcagagctc 420
 cgagaagcgg tacctgaacc cgtgttgctc tccggggcag agctgcgtct gctgaggctc 480
 aagttaaaag tggagcagca cgtggagctg taccagaaat acagcaacaa ttcctggcga 540
 tacctcagca accggctgct ggcaccagc gactcgccag agtggttatc ttttgatgtc 600
 accggagttg tgcggcagtg gttgagccgt ggaggggaaa ttgagggtt tcgccttagc 660
 gccactgct cctgtgacag cagggataac aactgcaag tggacatcaa cgggttcact 720
 accggccgcc gaggtgacct ggccaccatt catggcatga accggccttt cctgcttctc 780

atggccaccc cgctggagag ggcccagcat ctgcaaagct cccggcaccg ccgagccctg 840
 gacaccaact attgcttcag ctccacggag aagaactgct gcgtgcggca gctgtacatt 900
 gacttccgca aggacctcgg ctggaagtgg atccacgagc ccaagggcta ccatgccaac 960
 ttctgcctcg ggccctgccc ctacatttgg agcctggaca cgcagtacag caaggtcctg 1020
 gccctgtaca accagcataa cccgggcgcc tcggcggcgc cgtgctgctg gccgcaggcg 1080
 ctggagccgc tgcccatcgt gtactacgtg ggccgcaagc ccaaggtgga gcagctgtcc 1140
 aacatgatcg tgcgctcctg caagtgcagc tga 1173

<210> 70
 <211> 390
 <212> PRT
 <213> Mus musculus

<400> 70

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Pro
 1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
 20 25 30

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

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
 50 55 60

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
 65 70 75 80

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

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
 100 105 110

Met Val Asp Arg Asn Asn Ala Ile Tyr Glu Lys Thr Lys Asp Ile Ser
 115 120 125

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Asp Ile Arg Glu Ala Val
 130 135 140

Pro Glu Pro Pro Leu Leu Ser Arg Ala Glu Leu Arg Leu Gln Arg Leu
 145 150 155 160

Lys Ser Ser Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
 165 170 175

Asn Ser Trp Arg Tyr Leu Gly Asn Arg Leu Leu Thr Pro Thr Asp Thr
 180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
 195 200 205

Asn Gln Gly Asp Gly Ile Gln Gly Phe Arg Phe Ser Ala His Cys Ser
 210 215 220

Cys Asp Ser Lys Asp Asn Lys Leu His Val Glu Ile Asn Gly Ile Ser
 225 230 235 240

Pro Lys Arg Arg Gly Asp Leu Gly Thr Ile His Asp Met Asn Arg Pro
 245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
 260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser
 275 280 285

Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys
 290 295 300

Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn
 305 310 315 320

Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr
 325 330 335

Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala
 340 345 350

Ser Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr
 355 360 365

Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val
 370 375 380

Arg Ser Cys Lys Cys Ser
 385 390

<210> 71
 <211> 1173
 <212> DNA
 <213> Mus musculus

<400> 71
 atgccgccct cggggctgcg gctactgccg cttctgctcc cactcccggtg gcttctagtg 60
 ctgacgcccc ggaggccagc cgcgggactc tccacctgca agaccatcga catggagctg 120
 gtgaaacgga agcgcacga agccatccgt ggccagatcc tgtccaaact aaggctcgcc 180
 agtcccccaa gccaggggga ggtaccgccc ggcccgtgc ccgaggcggt gctcgctttg 240
 tacaacagca cccgcgaccg ggtggcaggc gagagcgccg acccagagcc ggagcccga 300
 gcggactact atgctaaaga ggtcaccgc gtgctaattg tggaccgcaa caacgccatc 360
 tatgagaaaa ccaaagacat ctacacagt atatatatgt tcttcaatac gtcagacatt 420
 cgggaagcag tgcccgaacc ccattgctg tcccgtgcag agctgcgctt gcagagatta 480
 aaatcaagtg tggagcaaca tgtggaactc taccagaaat atagcaacaa ttcctggcgt 540
 taccttggtg accggctgct gacccccact gatacgctg agtggctgtc ttttgacgtc 600
 actggagttg tacggcagtg gctgaaccaa ggagacggaa tacagggctt tcgattcagc 660

gctcactgct cttgtgacag caaagataac aaactccacg tggaaatcaa cgggatcagc 720
 cccaaacgtc ggggcgacct gggcaccatc catgacatga accggccctt cctgctcctc 780
 atggccaccc ccctggaaag ggcccagcac ctgcacagct cacggcaccg gagagccctg 840
 gataccaact attgcttcag ctccacagag aagaactgct gtgtgcggca gctgtacatt 900
 gactttagga aggacctggg ttggaagtgg atccacgagc ccaagggcta ccatgccaac 960
 ttctgtctgg gaccctgccc ctatatttgg agcctggaca cacagtacag caaggtcctt 1020
 gccctctaca accaacacaa cccgggcgct tcggcgctcac cgtgctgcgt gccgcaggct 1080
 ttggagccac tgcccatcgt ctactacgtg ggtcgcaagc ccaaggtgga gcagttgtcc 1140
 aacatgattg tgcgctcctg caagtgcagc tga 1173

<210> 72
 <211> 390
 <212> PRT
 <213> *Macaca fascicularis*

<400> 72

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
1 5 10 15

Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
20 25 30

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

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
50 55 60

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
65 70 75 80

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

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
 100 105 110

Met Val Glu Thr His Asn Glu Ile Tyr Asp Lys Phe Lys Gln Ser Thr
 115 120 125

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
 130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
 145 150 155 160

Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
 165 170 175

Asn Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
 180 185 190

Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
 195 200 205

Ser Arg Gly Gly Glu Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser
 210 215 220

Cys Asp Ser Lys Asp Asn Thr Leu Gln Val Asp Ile Asn Gly Phe Thr
 225 230 235 240

Thr Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
 245 250 255

Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu Gln
 260 265 270

Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser
 275 280 285

Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys
 290 295 300

Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn
305 310 315 320

Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr
325 330 335

Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala
340 345 350

Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr
355 360 365

Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val
370 375 380

Arg Ser Cys Lys Cys Ser
385 390

<210> 73
<211> 1173
<212> DNA
<213> *Macaca fascicularis*

<400> 73
atgccgccct ccgggctgcg gctgctgccg ctgctgctac cgctgctgtg gctactggtg 60
ctgacgcctg gccggccggc cgccggacta tccacctgca agactatcga catggagctg 120
gtgaagcgga agcgcacga ggccatccgc ggccagatcc tgtccaagct gcggctcgcc 180
agcccccca gccaggggga ggtgccgccc ggcccgtgc ccgaggccgt gctcgccctg 240
tacaacagca cccgcgaccg ggtggccggg gagagtgcgg agccggaacc cgaaccggag 300
gccgactact acgccaagga ggtcaccgc gtgctaattg tggaaccaca caacgaaatc 360
tatgacaagt tcaagcagag cacacacagc atatatatgt tcttcaacac atcagagctc 420
cgagaagcag tacctgaacc tgtgttgctc tcccgggcag agctgctgtc gctgaggctc 480
aagttaaaag tggagcagca tgtggagctg taccagaaat acagcaacaa ttcttgccga 540

tacctcagca accggtgct ggcgcccagc gactcgccgg agtggttgtc ttttgatgtc	600
accggagttg tgcggcagtg gttgagccgc ggaggggaaa ttgagggtt tcgccttagc	660
gcccactgct cctgtgacag caaagataac aactgcaag tggacatcaa cgggttcact	720
accggccgcc gaggtgacct ggccaccatt catggcatga accggccttt cctgcttctc	780
atggccaccc cgctggagag ggcccaacat ctgcaaagct cccggcaccg ccgagccctg	840
gacaccaact actgcttcag ctccacggag aagaactgct gctgctggca gctgtatatt	900
gacttccgca aggacctcgg ctggaagtgg atccacgagc ccaagggtta ccatgccaac	960
ttctgcctgg gacctgccc ctacatttgg agcctggaca cgagtagag caaggtcctg	1020
gccctgtaca accagcataa cccgggcgcc tcggcggcgc cgtgctgctg gccgcaggcg	1080
ctggagccgc tgcccatcgt gtactacgtg ggccgcaagc ccaagggtga gcagctgtcc	1140
aacatgatcg tgcgctcctg caaatgcagc tga	1173