

SEQUENCE LISTING

<110> The Trustees Of The University Of Pennsylvania
Yang, Xiaolu
Guo, Lili

<120> Compositions and Methods for Degradation of Misfolded Proteins

<130> 046483-6149-00-WO.605285

<150> US 62/168,309

<151> 2015-05-29

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<170> PatentIn version 3.5

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

His Ser Leu Thr Leu Ser Cys Pro Val Cys Arg Gln Thr Ser Ile Leu
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Pro Glu Lys Gly Val Ala Ala Leu Gln Asn Asn Phe Phe Ile Thr Asn
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Leu Met Asp Val Leu Gln Arg Thr Pro Gly Ser Asn Ala Glu Glu Ser
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Pro Thr Val Pro Leu Lys Asp Val Val Glu Gln His Lys Ala Ser Leu
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Ala Ser Ile Val Asp Asp Ile His Ser Thr Phe Asp Glu Leu Gln Lys
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Cys Lys Thr Gly Asn Ala Tyr Leu Thr Ala Glu Leu Ser Thr Pro Asp
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Ala Asp Pro Leu Tyr Gly Pro Gln Gly Leu Ala Leu Thr Ser Asp Gly
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Tyr Ile Pro Ala Gln Ser Leu Thr Leu Ser Cys Pro Val Cys Arg Gln
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Phe Ile Ser Ser Leu Met Glu Ala Met Gln Gln Ala Pro Asp Gly Ala
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His Asp Pro Glu Asp Pro His Pro Leu Ser Val Val Ala Gly Arg Pro
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Leu Ser Cys Pro Asn His Glu Gly Lys Thr Met Glu Phe Tyr Cys Glu
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Arg Lys Ala Glu Ala Leu Ala Gln Ile Ser Ala Ala Phe Glu Asp Leu
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 Phe Lys Phe Gly Ser His Gly Glu Gly Asn Gly Gln Phe Asn Ala Pro
 660 665 670
 Thr Gly Val Ala Val Asp Ser Asn Gly Asn Ile Ile Val Ala Asp Trp
 675 680 685
 Gly Asn Ser Arg Ile Gln Val Phe Asp Ser Ser Gly Ser Phe Leu Ser
 690 695 700
 Tyr Ile Asn Thr Ser Ala Glu Pro Leu Tyr Gly Pro Gln Gly Leu Ala
 705 710 715 720
 Leu Thr Ser Asp Gly His Val Val Val Ala Asp Ala Gly Asn His Cys
 725 730 735
 Phe Lys Ala Tyr Arg Tyr Leu Gln
 740

<210> 7

<211> 1503

<212> DNA

<213> Homo sapiens

<400> 7

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gcgccgggcg gcggccgtt cccctgcccc gaatgtcggc acccatcggc gcccgccgcg 180

ctgcgaccca actgggcctt ggccaggctg actgagaaga cgacgcgccg gcgcctgggc 240
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 gaccagcggc cagtgtgcct ggtgtgcagg gaggcccagg agcaccagac tcacgccatg 360
 gcacccatcg acgaggcctt cgagagctac cggacagga actttgacat ccacgtggat 420
 gaatggaaga gaagactaat taggctgctc ttgtaccatt ttaagcagga ggagaaactt 480
 cttaaagtctc agcgtaatct cgtggccaag atgaagaaag tcatgcattt acaggatgta 540
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<210> 8

<211> 500

<212> PRT

<213> Homo sapiens

<400> 8

Met Glu Ala Glu Asp Ile Gln Glu Glu Leu Thr Cys Pro Ile Cys Leu
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Asp Tyr Phe Gln Asp Pro Val Ser Ile Glu Cys Gly His Asn Phe Cys
20 25 30

Arg Gly Cys Leu His Arg Asn Trp Ala Pro Gly Gly Gly Pro Phe Pro
35 40 45

Cys Pro Glu Cys Arg His Pro Ser Ala Pro Ala Ala Leu Arg Pro Asn
50 55 60

Trp Ala Leu Ala Arg Leu Thr Glu Lys Thr Gln Arg Arg Arg Leu Gly
65 70 75 80

Pro Val Pro Pro Gly Leu Cys Gly Arg His Trp Glu Pro Leu Arg Leu
85 90 95

Phe Cys Glu Asp Asp Gln Arg Pro Val Cys Leu Val Cys Arg Glu Ser
100 105 110

Gln Glu His Gln Thr His Ala Met Ala Pro Ile Asp Glu Ala Phe Glu
115 120 125

Ser Tyr Arg Thr Gly Asn Phe Asp Ile His Val Asp Glu Trp Lys Arg
130 135 140

Arg Leu Ile Arg Leu Leu Leu Tyr His Phe Lys Gln Glu Glu Lys Leu
145 150 155 160

Leu Lys Ser Gln Arg Asn Leu Val Ala Lys Met Lys Lys Val Met His
165 170 175

Leu Gln Asp Val Glu Val Lys Asn Ala Thr Gln Trp Lys Asp Lys Ile
180 185 190

Lys Ser Gln Arg Met Arg Ile Ser Thr Glu Phe Ser Lys Leu His Asn
195 200 205

Phe Leu Val Glu Glu Glu Asp Leu Phe Leu Gln Arg Leu Asn Lys Glu
210 215 220

Glu Glu Glu Thr Lys Lys Lys Leu Asn Glu Asn Thr Leu Lys Leu Asn
225 230 235 240

Gln Thr Ile Ala Ser Leu Lys Lys Leu Ile Leu Glu Val Gly Glu Lys
245 250 255

Ser Gln Ala Pro Thr Leu Glu Leu Leu Gln Asn Pro Lys Glu Val Leu
260 265 270

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

Val Lys Thr Val Cys Gln Ile Pro Leu Met Lys Glu Met Leu Lys Arg
290 295 300

Phe Gln Val Ala Val Asn Leu Ala Glu Asp Thr Ala His Pro Lys Leu
305 310 315 320

Val Phe Ser Gln Glu Gly Arg Tyr Val Lys Asn Thr Ala Ser Ala Ser
325 330 335

Ser Trp Pro Val Phe Ser Ser Ala Trp Asn Tyr Phe Ala Gly Trp Arg
340 345 350

Asn Pro Gln Lys Thr Ala Phe Val Glu Arg Phe Gln His Leu Pro Cys
355 360 365

Val Leu Gly Lys Asn Val Phe Thr Ser Gly Lys His Tyr Trp Glu Val
370 375 380

Glu Ser Arg Asp Ser Leu Glu Val Ala Val Gly Val Cys Arg Glu Asp
385 390 395 400

Val Met Gly Ile Thr Asp Arg Ser Lys Met Ser Pro Asp Val Gly Ile
405 410 415

Trp Ala Ile Tyr Trp Ser Ala Ala Gly Tyr Trp Pro Leu Ile Gly Phe
420 425 430

Pro Gly Thr Pro Thr Gln Gln Glu Pro Ala Leu His Arg Val Gly Val
435 440 445

Tyr Leu Asp Arg Gly Thr Gly Asn Val Ser Phe Tyr Ser Ala Val Asp
450 455 460

Gly Val His Leu His Thr Phe Ser Cys Ser Ser Val Ser Arg Leu Arg
465 470 475 480

Pro Phe Phe Trp Leu Ser Pro Leu Ala Ser Leu Val Ile Pro Pro Val
485 490 495

Thr Asp Arg Lys
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<210> 9

<211> 1482

<212> DNA

<213> Homo sapiens

<400> 9

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gcaaaccaca agaagtccat gctagacaaa ggagagagta gctgccctgt gtgccggatc 180

agttaccagc ctgagaacat acggcctaata cgcatgtag ccaacatagt ggagaagctc 240

agggaggtca agttgagccc agaggggcag aaagttgatc attgtgcacg ccatggagag 300

aaacttctac tcttctgtca ggaggacggg aaggtcattt gctggctttg tgagcgtct 360

caggagcacc gtggcacca cacgttctc acagaggagg ttgcccgga gtaccaagtg 420

aagctccagg cagctctgga gatgctgagg cagaagcagc aggaagctga agagttagaa 480

gctgacatca gagaagagaa agcttcctgg aagactcaaa tacagtatga caaaaccaac 540
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caaaacctgg agaaggagga ggaagacatt ctgaaaagcc ttacgaactc tgaaactgag 660
atggtgcagc agaccagtc cctgagagag ctcatctcag atctggagca tcggctgcag 720
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aatgtggag tcccatgac tctgtgtca ccaagctctt ga 1482

<210> 10

<211> 493

<212> PRT

<213> Homo sapiens

<400> 10

Met Ala Ser Gly Ile Leu Val Asn Val Lys Glu Glu Val Thr Cys Pro

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Ile Cys Leu Glu Leu Leu Thr Gln Pro Leu Ser Leu Asp Cys Gly His

20 25 30

Ser Phe Cys Gln Ala Cys Leu Thr Ala Asn His Lys Lys Ser Met Leu

35 40 45
 Asp Lys Gly Glu Ser Ser Cys Pro Val Cys Arg Ile Ser Tyr Gln Pro
 50 55 60
 Glu Asn Ile Arg Pro Asn Arg His Val Ala Asn Ile Val Glu Lys Leu
 65 70 75 80
 Arg Glu Val Lys Leu Ser Pro Glu Gly Gln Lys Val Asp His Cys Ala
 85 90 95
 Arg His Gly Glu Lys Leu Leu Leu Phe Cys Gln Glu Asp Gly Lys Val
 100 105 110
 Ile Cys Trp Leu Cys Glu Arg Ser Gln Glu His Arg Gly His His Thr
 115 120 125
 Phe Leu Thr Glu Glu Val Ala Arg Glu Tyr Gln Val Lys Leu Gln Ala
 130 135 140
 Ala Leu Glu Met Leu Arg Gln Lys Gln Gln Glu Ala Glu Glu Leu Glu
 145 150 155 160
 Ala Asp Ile Arg Glu Glu Lys Ala Ser Trp Lys Thr Gln Ile Gln Tyr
 165 170 175
 Asp Lys Thr Asn Val Leu Ala Asp Phe Glu Gln Leu Arg Asp Ile Leu
 180 185 190
 Asp Trp Glu Glu Ser Asn Glu Leu Gln Asn Leu Glu Lys Glu Glu Glu
 195 200 205
 Asp Ile Leu Lys Ser Leu Thr Asn Ser Glu Thr Glu Met Val Gln Gln
 210 215 220
 Thr Gln Ser Leu Arg Glu Leu Ile Ser Asp Leu Glu His Arg Leu Gln
 225 230 235 240

Gly Ser Val Met Glu Leu Leu Gln Gly Val Asp Gly Val Ile Lys Arg
245 250 255

Thr Glu Asn Val Thr Leu Lys Lys Pro Glu Thr Phe Pro Lys Asn Gln
260 265 270

Arg Arg Val Phe Arg Ala Pro Asp Leu Lys Gly Met Leu Glu Val Phe
275 280 285

Arg Glu Leu Thr Asp Val Arg Arg Tyr Trp Val Asp Val Thr Val Ala
290 295 300

Pro Asn Asn Ile Ser Cys Ala Val Ile Ser Glu Asp Lys Arg Gln Val
305 310 315 320

Ser Ser Pro Lys Pro Gln Ile Ile Tyr Gly Ala Arg Gly Thr Arg Tyr
325 330 335

Gln Thr Phe Val Asn Phe Asn Tyr Cys Thr Gly Ile Leu Gly Ser Gln
340 345 350

Ser Ile Thr Ser Gly Lys His Tyr Trp Glu Val Asp Val Ser Lys Lys
355 360 365

Thr Ala Trp Ile Leu Gly Val Cys Ala Gly Phe Gln Pro Asp Ala Met
370 375 380

Cys Asn Ile Glu Lys Asn Glu Asn Tyr Gln Pro Lys Tyr Gly Tyr Trp
385 390 395 400

Val Ile Gly Leu Glu Glu Gly Val Lys Cys Ser Ala Phe Gln Asp Ser
405 410 415

Ser Phe His Thr Pro Ser Val Pro Phe Ile Val Pro Leu Ser Val Ile
420 425 430

Ile Cys Pro Asp Arg Val Gly Val Phe Leu Asp Tyr Glu Ala Cys Thr
435 440 445

Val Ser Phe Phe Asn Ile Thr Asn His Gly Phe Leu Ile Tyr Lys Phe
 450 455 460

Ser His Cys Ser Phe Ser Gln Pro Val Phe Pro Tyr Leu Asn Pro Arg
 465 470 475 480

Lys Cys Gly Val Pro Met Thr Leu Cys Ser Pro Ser Ser
 485 490

<210> 11

<211> 1551

<212> DNA

<213> Homo sapiens

<400> 11

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 gtgacctgcc ctatctgcct ggagctccta acagaacccc tgagcataga ctgtggccac 180
 agcttctgcc aagcctgcat cacaccaaat ggcagggaaat cagtgttg tcaagaagg 240
 gaaagaagct gccctgtgtg ccagaccagc taccagccag ggaacctgcg gcctaactcg 300
 catctggcca acatagttag gcggctcaga gaggtagtgt tgggccctgg gaagcagctg 360
 aaagcagttc tttgtcaga ccatggagaa aaactgcagc tcttctgtca ggaggatggg 420
 aaggtcattt gctggctttg tgagcggctc caggagcacc gtgtcacca cacgttctc 480
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 aagaatcaga tggagcctga gagatgcagg atccagacag agtttaatca gctgcgaaat 660
 atcctagaca gaggaggca acgggagctg aaaaagctgg aacaggaaga gaagaagggg 720
 ctacgaatta tagaagaggc tgagaatgat ctgtccacc agaccagtc gctgcgagag 780
 ctcatctcgg atctggagcg tcgatgtcag gggtaacaa tggagctgct gcaggatgtg 840
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 aagctgagaa gtatgttccg agccccagat ctgaaaagga tgctgcgagt gtgtagagag 960

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 aatcttgacc tggctaaaaa ccggagacaa gtgaggttg tgggagctaa agtatctgga 1080
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<210> 12

<211> 516

<212> PRT

<213> Homo sapiens

<400> 12

Met Cys Gly Ser Glu Arg Ile Leu Gln Ala Gly Asn Ile Leu Glu Ile
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Arg Val Gly Gln Ala Gly Ala Arg Arg Val Ala Thr Met Thr Ser Pro
 20 25 30

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

Leu Leu Thr Glu Pro Leu Ser Ile Asp Cys Gly His Ser Phe Cys Gln
 50 55 60

Ala Cys Ile Thr Pro Asn Gly Arg Glu Ser Val Ile Gly Gln Glu Gly
 65 70 75 80

Glu Arg Ser Cys Pro Val Cys Gln Thr Ser Tyr Gln Pro Gly Asn Leu
 85 90 95

Arg Pro Asn Arg His Leu Ala Asn Ile Val Arg Arg Leu Arg Glu Val
100 105 110

Val Leu Gly Pro Gly Lys Gln Leu Lys Ala Val Leu Cys Ala Asp His
115 120 125

Gly Glu Lys Leu Gln Leu Phe Cys Gln Glu Asp Gly Lys Val Ile Cys
130 135 140

Trp Leu Cys Glu Arg Ser Gln Glu His Arg Gly His His Thr Phe Leu
145 150 155 160

Val Glu Glu Val Ala Gln Glu Tyr Gln Glu Lys Phe Gln Glu Ser Leu
165 170 175

Lys Lys Leu Lys Asn Glu Glu Gln Glu Ala Glu Lys Leu Thr Ala Phe
180 185 190

Ile Arg Glu Lys Lys Thr Ser Trp Lys Asn Gln Met Glu Pro Glu Arg
195 200 205

Cys Arg Ile Gln Thr Glu Phe Asn Gln Leu Arg Asn Ile Leu Asp Arg
210 215 220

Val Glu Gln Arg Glu Leu Lys Lys Leu Glu Gln Glu Glu Lys Lys Gly
225 230 235 240

Leu Arg Ile Ile Glu Glu Ala Glu Asn Asp Leu Val His Gln Thr Gln
245 250 255

Ser Leu Arg Glu Leu Ile Ser Asp Leu Glu Arg Arg Cys Gln Gly Ser
260 265 270

Thr Met Glu Leu Leu Gln Asp Val Ser Asp Val Thr Glu Arg Ser Glu
275 280 285

Phe Trp Thr Leu Arg Lys Pro Glu Ala Leu Pro Thr Lys Leu Arg Ser
290 295 300

Met Phe Arg Ala Pro Asp Leu Lys Arg Met Leu Arg Val Cys Arg Glu
305 310 315 320

Leu Thr Asp Val Gln Ser Tyr Trp Val Asp Val Thr Leu Asn Pro His
 325 330 335

Thr Ala Asn Leu Asn Leu Val Leu Ala Lys Asn Arg Arg Gln Val Arg
 340 345 350

Phe Val Gly Ala Lys Val Ser Gly Pro Ser Cys Leu Glu Lys His Tyr
 355 360 365

Asp Cys Ser Val Leu Gly Ser Gln His Phe Ser Ser Gly Lys His Tyr
 370 375 380

Trp Glu Val Asp Val Ala Lys Lys Thr Ala Trp Ile Leu Gly Val Cys
385 390 395 400

Ser Asn Ser Leu Gly Pro Thr Phe Ser Phe Asn His Phe Ala Gln Asn
 405 410 415

His Ser Ala Tyr Ser Arg Tyr Gln Pro Gln Ser Gly Tyr Trp Val Ile
 420 425 430

Gly Leu Gln His Asn His Glu Tyr Arg Ala Tyr Glu Asp Ser Ser Pro
 435 440 445

Ser Leu Leu Leu Ser Met Thr Val Pro Pro Arg Arg Val Gly Val Phe
 450 455 460

Leu Asp Tyr Glu Ala Gly Thr Val Ser Phe Tyr Asn Val Thr Asn His
465 470 475 480

Gly Phe Pro Ile Tyr Thr Phe Ser Lys Tyr Tyr Phe Pro Thr Thr Leu
 485 490 495

Cys Pro Tyr Phe Asn Pro Cys Asn Cys Val Ile Pro Met Thr Leu Arg

Arg Pro Ser Ser
515

<210> 13
<211> 666
<212> DNA
<213> Homo sapiens

<400> 13
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tccgtcagat gcggccacag cttctgccgc gcctgcatag ggcgtgtctg ggagcgcccc 180
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gcctga

<210> 14
<211> 221
<212> PRT
<213> Homo sapiens

<400> 14

Met Ala Ala Val Gly Pro Arg Thr Gly Pro Gly Thr Gly Ala Glu Ala
1 5 10 15

Leu Ala Leu Ala Ala Glu Leu Gln Gly Glu Ala Thr Cys Ser Ile Cys
20 25 30

Leu Glu Leu Phe Arg Glu Pro Val Ser Val Glu Cys Gly His Ser Phe
35 40 45

Cys Arg Ala Cys Ile Gly Arg Cys Trp Glu Arg Pro Gly Ala Gly Ser
50 55 60

Val Gly Ala Ala Thr Arg Ala Pro Pro Phe Pro Leu Pro Cys Pro Gln
65 70 75 80

Cys Arg Glu Pro Ala Arg Pro Ser Gln Leu Arg Pro Asn Arg Gln Leu
85 90 95

Ala Ala Val Ala Thr Leu Leu Arg Arg Phe Ser Leu Pro Ala Ala Ala
100 105 110

Pro Gly Glu His Gly Ser Gln Ala Ala Ala Ala Arg Ala Ala Ala Ala
115 120 125

Arg Cys Gly Gln His Gly Glu Pro Phe Lys Leu Tyr Cys Gln Asp Asp
130 135 140

Gly Arg Ala Ile Cys Val Val Cys Asp Arg Ala Arg Glu His Arg Glu
145 150 155 160

His Ala Val Leu Pro Leu Asp Glu Ala Val Gln Glu Ala Lys Glu Leu
165 170 175

Leu Glu Ser Arg Leu Arg Val Leu Lys Lys Glu Leu Glu Asp Cys Glu
180 185 190

Val Phe Arg Ser Thr Glu Lys Lys Glu Ser Lys Glu Leu Leu Val Ser
195 200 205

Gln Ala Pro Ala Gly Pro Pro Trp Asp Ile Thr Glu Ala
210 215 220

<210> 15

<211> 1656
 <212> DNA
 <213> Homo sapiens

<400> 15
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gagtactcac accgctccc gccacaccc tccgtcccc agtccttcc cagcctggcg 1560
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gggcagccgt ccaccaaaca ctacgtgacg agctaa 1656

<210> 16
<211> 551
<212> PRT
<213> Homo sapiens

<400> 16

Met Ala Glu Asn Trp Lys Asn Cys Phe Glu Glu Glu Leu Ile Cys Pro
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Ile Cys Leu His Val Phe Val Glu Pro Val Gln Leu Pro Cys Lys His
20 25 30

Asn Phe Cys Arg Gly Cys Ile Gly Glu Ala Trp Ala Lys Asp Ser Gly
35 40 45

Leu Val Arg Cys Pro Glu Cys Asn Gln Ala Tyr Asn Gln Lys Pro Gly
50 55 60

Leu Glu Lys Asn Leu Lys Leu Thr Asn Ile Val Glu Lys Phe Asn Ala
65 70 75 80

Leu His Val Glu Lys Pro Pro Ala Ala Leu His Cys Val Phe Cys Arg
85 90 95

Arg Gly Pro Pro Leu Pro Ala Gln Lys Val Cys Leu Arg Cys Glu Ala
100 105 110

Pro Cys Cys Gln Ser His Val Gln Thr His Leu Gln Gln Pro Ser Thr
115 120 125

Ala Arg Gly His Leu Leu Val Glu Ala Asp Asp Val Arg Ala Trp Ser

130	135	140			
Cys	Pro	Gln	His	Asn	Ala
145	150	155	160		
Tyr	Arg	Leu	Tyr	His	Cys
					Glu
					Ala
					Glu
					Gln
Val	Ala	Val	Cys	Gln	Tyr
165	170	175			
Cys	Cys	Tyr	Tyr	Ser	Gly
					Ala
					His
					Gln
					Gly
His	Ser	Val	Cys	Asp	Val
180	185	190			
Glu	Ile	Arg	Arg	Asn	Glu
					Ile
					Arg
					Lys
					Met
Leu	Met	Lys	Gln	Gln	Asp
195	200	205			
Arg	Leu	Glu	Glu	Arg	Glu
					Gln
					Asp
					Ile
					Glu
Asp	Gln	Leu	Tyr	Lys	Leu
210	215	220			
Glu	Ser	Asp	Lys	Arg	Leu
					Val
					Glu
					Glu
					Lys
Val	Asn	Gln	Leu	Lys	Glu
225	230	235	240		
Glu	Glu	Val	Arg	Leu	Gln
					Tyr
					Glu
					Lys
					Leu
					His
Gln	Leu	Leu	Asp	Glu	Asp
245	250	255			
Leu	Arg	Gln	Thr	Val	Glu
					Val
					Leu
					Asp
					Lys
Ala	Gln	Ala	Lys	Phe	Cys
260	265	270			
Ser	Glu	Asn	Ala	Ala	Gln
					Ala
					Leu
					His
					Leu
Gly	Glu	Arg	Met	Gln	Glu
275	280	285			
Ala	Lys	Lys	Leu	Leu	Gly
					Ser
					Leu
					Gln
					Leu
Leu	Phe	Asp	Lys	Thr	Glu
290	295	300			
Val	Ser	Phe	Met	Lys	Asn
					Thr
					Lys
					Ser
Val	Lys	Ile	Leu	Met	Asp
305	310	315	320		
Arg	Thr	Gln	Thr	Cys	Thr
					Ser
					Ser
					Ser
					Leu
Ser	Pro	Thr	Lys	Ile	Gly
325	330	335			
His	Leu	Asn	Ser	Lys	Leu
					Phe
					Leu
					Asn
					Glu

Val Ala Lys Lys Glu Lys Gln Leu Arg Lys Met Leu Glu Gly Pro Phe
340 345 350

Ser Thr Pro Val Pro Phe Leu Gln Ser Val Pro Leu Tyr Pro Cys Gly
355 360 365

Val Ser Ser Ser Gly Ala Glu Lys Arg Lys His Ser Thr Ala Phe Pro
370 375 380

Glu Ala Ser Phe Leu Glu Thr Ser Ser Gly Pro Val Gly Gly Gln Tyr
385 390 395 400

Gly Ala Ala Gly Thr Ala Ser Gly Glu Gly Gln Ser Gly Gln Pro Leu
405 410 415

Gly Pro Cys Ser Ser Thr Gln His Leu Val Ala Leu Pro Gly Gly Ala
420 425 430

Gln Pro Val His Ser Ser Pro Val Phe Pro Pro Ser Gln Tyr Pro Asn
435 440 445

Gly Ser Ala Ala Gln Gln Pro Met Leu Pro Gln Tyr Gly Gly Arg Lys
450 455 460

Ile Leu Val Cys Ser Val Asp Asn Cys Tyr Cys Ser Ser Val Ala Asn
465 470 475 480

His Gly Gly His Gln Pro Tyr Pro Arg Ser Gly His Phe Pro Trp Thr
485 490 495

Val Pro Ser Gln Glu Tyr Ser His Pro Leu Pro Pro Thr Pro Ser Val
500 505 510

Pro Gln Ser Leu Pro Ser Leu Ala Val Arg Asp Trp Leu Asp Ala Ser
515 520 525

Gln Gln Pro Gly His Gln Asp Phe Tyr Arg Val Tyr Gly Gln Pro Ser
530 535 540

Thr Lys His Tyr Val Thr Ser
545 550

<210> 17

<211> 2133

<212> DNA

<213> Homo sapiens

<400> 17

atggaggaga tggagagga gttgaaatgc cccgtgtgcg gctccttcta tcgggagccc 60
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acccagagt ctgaatcccc ccagagccat cgggccgcgg gctccggggg ctccgactat 180
gactatctgg acctggacaa gatgagccta tacagcgagg cggacagcgg ctatggctcc 240
tacggggggg tcgccagcgc cccactacc ccgtgccaga agtccccaa cggcgtccgc 300
gtgtttccc cggctatgcc gccaccggcc acccattgt caccggcct ggccccggtg 360
ccccgcaact cctgtatcac ctgccccag tgtcaccgca gcctcatcct ggatgaccgg 420
gggctcgcg gttccccaa gaatcgcgta ctggaagggg taattgaccg ctaccagcag 480
agcaaagccg cggccctcaa gtgccagctc tgcgagaagg cgccaagga agccaccgctc 540
atgtgcgaac agtgcgatgt ctttactgc gatccgtgcc gcctgcgctg ccacccgccc 600
cgggggcccc tagccaagca ccgcctggtg ccccgggccc agggctgtgt gagccggagg 660
ctgagccac gcaaggtctc cacctgcaca gaccacgagc tggagaacca cagcatgtac 720
tgcgtgcaat gcaagatgcc cgtgtgctac cagtgttgaggaggaggcaa aactccagc 780
cacgaagtca aggctctggg ggccatgtgg aaactacata agagccagct ctcccaggcg 840
ctgaacggac tgtcagacag ggccaaagaa gccaaggagt ttctggtaca gctgcgcaac 900
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gatgccctca tcgatgccct caacagaaga aaagcccagc tgctggcccg cgtaacaag 1020
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cgccagacca caggctcat ggagtactgc ttggaggtga ttaagaaaa tgatcctagt 1140
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 ccagcaaccc ctatctaca gctggaggaa tgtgtaccc acaacaacag cgctacgttg 1380
 tcctggaaac agccacctct gtccacggtg cccgccgatg gatacattct ggagctggat 1440
 gatggcaacg gtggtcaatt ccgggaggtg tatgtgggga aggagacaat gtgcactgtg 1500
 gatggtcttc acttcaacag cacatacaac gctcgggtca aggccttcaa caaacagga 1560
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 gacaataacc ggagctgggt catgcacaac aactcgaca ccaacagaac tgagggaggg 1920
 atcacaaaag gggccacaat tggggtcctc ctgacttaa atagaaaaaa ctgacattt 1980
 tttatcaacg atgaacaaca aggtcccata gcatttgata acgtggaggg cctcttctc 2040
 cctgcggtca gcctgaacag gaacgtgcag gtcacgtgc acaccgggct ccaggtcccc 2100
 gacttctact ccagcagagc atcaatagcc taa 2133

<210> 18

<211> 710

<212> PRT

<213> Homo sapiens

<400> 18

Met Glu Glu Met Glu Glu Glu Leu Lys Cys Pro Val Cys Gly Ser Phe

1 5 10 15

Tyr Arg Glu Pro Ile Ile Leu Pro Cys Ser His Asn Leu Cys Gln Ala

20 25 30

Cys Ala Arg Asn Ile Leu Val Gln Thr Pro Glu Ser Glu Ser Pro Gln

35 40 45

Ser His Arg Ala Ala Gly Ser Gly Val Ser Asp Tyr Asp Tyr Leu Asp
50 55 60

Leu Asp Lys Met Ser Leu Tyr Ser Glu Ala Asp Ser Gly Tyr Gly Ser
65 70 75 80

Tyr Gly Gly Phe Ala Ser Ala Pro Thr Thr Pro Cys Gln Lys Ser Pro
85 90 95

Asn Gly Val Arg Val Phe Pro Pro Ala Met Pro Pro Pro Ala Thr His
100 105 110

Leu Ser Pro Ala Leu Ala Pro Val Pro Arg Asn Ser Cys Ile Thr Cys
115 120 125

Pro Gln Cys His Arg Ser Leu Ile Leu Asp Asp Arg Gly Leu Arg Gly
130 135 140

Phe Pro Lys Asn Arg Val Leu Glu Gly Val Ile Asp Arg Tyr Gln Gln
145 150 155 160

Ser Lys Ala Ala Ala Leu Lys Cys Gln Leu Cys Glu Lys Ala Pro Lys
165 170 175

Glu Ala Thr Val Met Cys Glu Gln Cys Asp Val Phe Tyr Cys Asp Pro
180 185 190

Cys Arg Leu Arg Cys His Pro Pro Arg Gly Pro Leu Ala Lys His Arg
195 200 205

Leu Val Pro Pro Ala Gln Gly Arg Val Ser Arg Arg Leu Ser Pro Arg
210 215 220

Lys Val Ser Thr Cys Thr Asp His Glu Leu Glu Asn His Ser Met Tyr
225 230 235 240

Cys Val Gln Cys Lys Met Pro Val Cys Tyr Gln Cys Leu Glu Glu Gly
245 250 255

Lys His Ser Ser His Glu Val Lys Ala Leu Gly Ala Met Trp Lys Leu
260 265 270

His Lys Ser Gln Leu Ser Gln Ala Leu Asn Gly Leu Ser Asp Arg Ala
275 280 285

Lys Glu Ala Lys Glu Phe Leu Val Gln Leu Arg Asn Met Val Gln Gln
290 295 300

Ile Gln Glu Asn Ser Val Glu Phe Glu Ala Cys Leu Val Ala Gln Cys
305 310 315 320

Asp Ala Leu Ile Asp Ala Leu Asn Arg Arg Lys Ala Gln Leu Leu Ala
325 330 335

Arg Val Asn Lys Glu His Glu His Lys Leu Lys Val Val Arg Asp Gln
340 345 350

Ile Ser His Cys Thr Val Lys Leu Arg Gln Thr Thr Gly Leu Met Glu
355 360 365

Tyr Cys Leu Glu Val Ile Lys Glu Asn Asp Pro Ser Gly Phe Leu Gln
370 375 380

Ile Ser Asp Ala Leu Ile Arg Arg Val His Leu Thr Glu Asp Gln Trp
385 390 395 400

Gly Lys Gly Thr Leu Thr Pro Arg Met Thr Thr Asp Phe Asp Leu Ser
405 410 415

Leu Asp Asn Ser Pro Leu Leu Gln Ser Ile His Gln Leu Asp Phe Val
420 425 430

Gln Val Lys Ala Ser Ser Pro Val Pro Ala Thr Pro Ile Leu Gln Leu
435 440 445

Glu Glu Cys Cys Thr His Asn Asn Ser Ala Thr Leu Ser Trp Lys Gln

450	455	460	
Pro Pro Leu Ser Thr Val Pro Ala Asp Gly Tyr Ile Leu Glu Leu Asp			
465	470	475	480
Asp Gly Asn Gly Gly Gln Phe Arg Glu Val Tyr Val Gly Lys Glu Thr			
	485	490	495
Met Cys Thr Val Asp Gly Leu His Phe Asn Ser Thr Tyr Asn Ala Arg			
	500	505	510
Val Lys Ala Phe Asn Lys Thr Gly Val Ser Pro Tyr Ser Lys Thr Leu			
	515	520	525
Val Leu Gln Thr Ser Glu Val Ala Trp Phe Ala Phe Asp Pro Gly Ser			
	530	535	540
Ala His Ser Asp Ile Ile Leu Ser Asn Asp Asn Leu Thr Val Thr Cys			
545	550	555	560
Ser Ser Tyr Asp Asp Arg Val Val Leu Gly Lys Thr Gly Phe Ser Lys			
	565	570	575
Gly Ile His Tyr Trp Glu Leu Thr Val Asp Arg Tyr Asp Asn His Pro			
	580	585	590
Asp Pro Ala Phe Gly Val Ala Arg Met Asp Val Met Lys Asp Val Met			
	595	600	605
Leu Gly Lys Asp Asp Lys Ala Trp Ala Met Tyr Val Asp Asn Asn Arg			
	610	615	620
Ser Trp Phe Met His Asn Asn Ser His Thr Asn Arg Thr Glu Gly Gly			
625	630	635	640
Ile Thr Lys Gly Ala Thr Ile Gly Val Leu Leu Asp Leu Asn Arg Lys			
	645	650	655

Asn Leu Thr Phe Phe Ile Asn Asp Glu Gln Gln Gly Pro Ile Ala Phe
660 665 670

Asp Asn Val Glu Gly Leu Phe Phe Pro Ala Val Ser Leu Asn Arg Asn
675 680 685

Val Gln Val Thr Leu His Thr Gly Leu Pro Val Pro Asp Phe Tyr Ser
690 695 700

Ser Arg Ala Ser Ile Ala
705 710

<210> 19
<211> 1446
<212> DNA
<213> Homo sapiens

<400> 19
atggcctctg ctgcctctgt gaccagcctg gcagatgaag tcaactgccc catctgtcag 60
ggtagcctga gggagccggt cactatcgac tgcggccaca acttctgccg ggcctgcctt 120
acccgctact gtgagatacc aggcccagac ctggaggagt ccctacttg cccactctgc 180
aaagaacctt tccgtctctg gagcttccgg cccaactggc agctggctaa cgtggtggag 240
aacattgagc gcctccagct ggtgtccaca ctgggtttgg gagaggagga tgtctgcaa 300
gagcacggag agaagatcta cttcttctgt gaggatgatg agatgcagtt gtgcgtggtg 360
tgccggggagg ctggggagca cgctaccac accatgcgct tcctggagga tgcagcggct 420
ccctataggg aacaaatcca taagtgtctt aaatgtctaa gaaaagagag agaggagatt 480
caagaaatcc agtcaagaga aaataaaagg atgcaagtcc tcctgactca ggtgtccacc 540
aagagacaac aggtgatttc tgagttcgca cacctgagga agtttctaga ggaacagcag 600
agcatcctct tagcacaatt ggagagccag gatggggaca tcttaggga acgggatgaa 660
tttgatttgc tgggtgctgg ggagatctgc cggtttagtg ctctattga agaactggag 720
gagaagaatg agaggccagc aaggagctc ctgacggaca tcagaagcac tctaataaga 780
tgtgaaacca gaaagtgccg gaaaccggtg gctgtgtcgc cagagctggg ccagaggatt 840
cgggactttc ccagcaggc cctcccgtg cagagggaga tgaagatgtt tctggaaaaa 900

ctatgctttg agttggacta tgagccagct cacatttctc tagaccctca gacttccac 960
 cccaagctcc tctgtccga ggaccaccag cgagctcagt tctctacaa atggcagaac 1020
 tcaccagaca accccaacg ttttgaccgg gccacctgtg ttctggccca cactggcatc 1080
 acagggggga gacacacgtg ggtggtgagt atagacctgg cccatggggg cagctgcacc 1140
 gtgggcgtgg tgagcgagga tgtgcagcgg aagggggagc ttcggctgcg gccagaggag 1200
 ggggtgtggg ctgtgaggct ggcttggggc ttcgtctcgg ctctgggctc cttcccaca 1260
 cggctgacct tgaaggagca gccccggcag gtgagggtgt ctcttgacta tgaggtgggc 1320
 tgggtgacct tcaccaacgc tgtcacccga gagcccatct acaccttcac tgcctccttc 1380
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 tcctga 1446

<210> 20
 <211> 481
 <212> PRT
 <213> Homo sapiens

<400> 20

Met Ala Ser Ala Ala Ser Val Thr Ser Leu Ala Asp Glu Val Asn Cys
 1 5 10 15

Pro Ile Cys Gln Gly Thr Leu Arg Glu Pro Val Thr Ile Asp Cys Gly
 20 25 30

His Asn Phe Cys Arg Ala Cys Leu Thr Arg Tyr Cys Glu Ile Pro Gly
 35 40 45

Pro Asp Leu Glu Glu Ser Pro Thr Cys Pro Leu Cys Lys Glu Pro Phe
 50 55 60

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

Asn Ile Glu Arg Leu Gln Leu Val Ser Thr Leu Gly Leu Gly Glu Glu
 85 90 95

Asp Val Cys Gln Glu His Gly Glu Lys Ile Tyr Phe Phe Cys Glu Asp
100 105 110

Asp Glu Met Gln Leu Cys Val Val Cys Arg Glu Ala Gly Glu His Ala
115 120 125

Thr His Thr Met Arg Phe Leu Glu Asp Ala Ala Ala Pro Tyr Arg Glu
130 135 140

Gln Ile His Lys Cys Leu Lys Cys Leu Arg Lys Glu Arg Glu Glu Ile
145 150 155 160

Gln Glu Ile Gln Ser Arg Glu Asn Lys Arg Met Gln Val Leu Leu Thr
165 170 175

Gln Val Ser Thr Lys Arg Gln Gln Val Ile Ser Glu Phe Ala His Leu
180 185 190

Arg Lys Phe Leu Glu Glu Gln Gln Ser Ile Leu Leu Ala Gln Leu Glu
195 200 205

Ser Gln Asp Gly Asp Ile Leu Arg Gln Arg Asp Glu Phe Asp Leu Leu
210 215 220

Val Ala Gly Glu Ile Cys Arg Phe Ser Ala Leu Ile Glu Glu Leu Glu
225 230 235 240

Glu Lys Asn Glu Arg Pro Ala Arg Glu Leu Leu Thr Asp Ile Arg Ser
245 250 255

Thr Leu Ile Arg Cys Glu Thr Arg Lys Cys Arg Lys Pro Val Ala Val
260 265 270

Ser Pro Glu Leu Gly Gln Arg Ile Arg Asp Phe Pro Gln Gln Ala Leu
275 280 285

Pro Leu Gln Arg Glu Met Lys Met Phe Leu Glu Lys Leu Cys Phe Glu

290	295	300
Leu Asp Tyr Glu Pro Ala His Ile Ser Leu Asp Pro Gln Thr Ser His		
305	310	315 320
Pro Lys Leu Leu Leu Ser Glu Asp His Gln Arg Ala Gln Phe Ser Tyr		
	325 330	335
Lys Trp Gln Asn Ser Pro Asp Asn Pro Gln Arg Phe Asp Arg Ala Thr		
	340 345	350
Cys Val Leu Ala His Thr Gly Ile Thr Gly Gly Arg His Thr Trp Val		
	355 360	365
Val Ser Ile Asp Leu Ala His Gly Gly Ser Cys Thr Val Gly Val Val		
	370 375	380
Ser Glu Asp Val Gln Arg Lys Gly Glu Leu Arg Leu Arg Pro Glu Glu		
385	390 395	400
Gly Val Trp Ala Val Arg Leu Ala Trp Gly Phe Val Ser Ala Leu Gly		
	405 410	415
Ser Phe Pro Thr Arg Leu Thr Leu Lys Glu Gln Pro Arg Gln Val Arg		
	420 425	430
Val Ser Leu Asp Tyr Glu Val Gly Trp Val Thr Phe Thr Asn Ala Val		
	435 440	445
Thr Arg Glu Pro Ile Tyr Thr Phe Thr Ala Ser Phe Thr Arg Lys Val		
	450 455	460
Ile Pro Phe Phe Gly Leu Trp Gly Arg Gly Ser Ser Phe Ser Leu Ser		
465	470 475	480
Ser		

<210> 21
 <211> 1407
 <212> DNA
 <213> Homo sapiens

<400> 21
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 cggcgctgct ggggcccagc cgagggcccg tacgctgcc ccgagtgcc cgagctgtcc 180
 ccgcagagga acctgcggcc caaccgccg ctgtctaaga tggccgagat ggcgcgggcg 240
 ctgcaccgc cgtgcgggt cccgcagggc gtgtgcccc gcgaccgca gccactggcc 300
 gccttctgtg gcgacgagct gcgcctctg tgtcgccct gcgagcgctc tggggagcac 360
 tgggcgacc gcgtgcggc gctgcaggac gcggccgaag acctcaaggc gaagctggag 420
 aagtactgg agcatctccg gaagcagatg caggatgcgt tgctgttcca agcccaggcg 480
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 gaggaggagg agctggagg gctgccccg ctgcgggagg gcgcagccca ctaggccag 660
 cagagcgccc acctagctga gctcatgcc gagctcgagg gccgctgcca gctgcctgct 720
 ctggggctgc tgcaggacat caaggacgcc ctgcgcaggg tccaggatgt gaagctgcag 780
 ccccagaag ttgtgcctat ggagctgagg accgtgtgca gggccccgg actggtagag 840
 aactgcgga ggtttcgagg ggacgtgacc ttggaccgg acaccgcaa ccctgagctg 900
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 agcccagagc gctttgacct cggcccctgc gtgctgggcc aggagcgctt cacctcaggc 1020
 cgccactact gggaggtgga ggttggggc cgcaccagct gggccctggg ggtgtgcagg 1080
 gagaactga acaggaagga gaaggcgag ctgtccgagg gcaacggctt ctggatcctg 1140
 gtcttctgg ggagctatta caattcctc gaacgggcct tggctccact ccgggacca 1200
 cccaggcgcg tggggatctt tctggactac gaggtggac atctctttt ctacagtgcc 1260
 accgatgggt cactgtatt catctttccc gagatcccct tctcggggac gctgcggccc 1320
 ctcttctcac ccctgtccag cagcccgacc ccgatgacta tctgccggcc gaaagtgagg 1380

tccggggaca ccctggctcc ccagtga

1407

<210> 22

<211> 468

<212> PRT

<213> Homo sapiens

<400> 22

Met Ala Ala Pro Asp Leu Ser Thr Asn Leu Gln Glu Glu Ala Thr Cys
1 5 10 15

Ala Ile Cys Leu Asp Tyr Phe Thr Asp Pro Val Met Thr Asp Cys Gly
20 25 30

His Asn Phe Cys Arg Glu Cys Ile Arg Arg Cys Trp Gly Gln Pro Glu
35 40 45

Gly Pro Tyr Ala Cys Pro Glu Cys Arg Glu Leu Ser Pro Gln Arg Asn
50 55 60

Leu Arg Pro Asn Arg Pro Leu Ala Lys Met Ala Glu Met Ala Arg Arg
65 70 75 80

Leu His Pro Pro Ser Pro Val Pro Gln Gly Val Cys Pro Ala His Arg
85 90 95

Glu Pro Leu Ala Ala Phe Cys Gly Asp Glu Leu Arg Leu Leu Cys Ala
100 105 110

Ala Cys Glu Arg Ser Gly Glu His Trp Ala His Arg Val Arg Pro Leu
115 120 125

Gln Asp Ala Ala Glu Asp Leu Lys Ala Lys Leu Glu Lys Ser Leu Glu
130 135 140

His Leu Arg Lys Gln Met Gln Asp Ala Leu Leu Phe Gln Ala Gln Ala
145 150 155 160

Asp Glu Thr Cys Val Leu Trp Gln Lys Met Val Glu Ser Gln Arg Gln
165 170 175

Asn Val Leu Gly Glu Phe Glu Arg Leu Arg Arg Leu Leu Ala Glu Glu
180 185 190

Glu Gln Gln Leu Leu Gln Arg Leu Glu Glu Glu Glu Leu Glu Val Leu
195 200 205

Pro Arg Leu Arg Glu Gly Ala Ala His Leu Gly Gln Gln Ser Ala His
210 215 220

Leu Ala Glu Leu Ile Ala Glu Leu Glu Gly Arg Cys Gln Leu Pro Ala
225 230 235 240

Leu Gly Leu Leu Gln Asp Ile Lys Asp Ala Leu Arg Arg Val Gln Asp
245 250 255

Val Lys Leu Gln Pro Pro Glu Val Val Pro Met Glu Leu Arg Thr Val
260 265 270

Cys Arg Val Pro Gly Leu Val Glu Thr Leu Arg Arg Phe Arg Gly Asp
275 280 285

Val Thr Leu Asp Pro Asp Thr Ala Asn Pro Glu Leu Ile Leu Ser Glu
290 295 300

Asp Arg Arg Ser Val Gln Arg Gly Asp Leu Arg Gln Ala Leu Pro Asp
305 310 315 320

Ser Pro Glu Arg Phe Asp Pro Gly Pro Cys Val Leu Gly Gln Glu Arg
325 330 335

Phe Thr Ser Gly Arg His Tyr Trp Glu Val Glu Val Gly Asp Arg Thr
340 345 350

Ser Trp Ala Leu Gly Val Cys Arg Glu Asn Val Asn Arg Lys Glu Lys
355 360 365

Gly Glu Leu Ser Ala Gly Asn Gly Phe Trp Ile Leu Val Phe Leu Gly
 370 375 380

Ser Tyr Tyr Asn Ser Ser Glu Arg Ala Leu Ala Pro Leu Arg Asp Pro
 385 390 395 400

Pro Arg Arg Val Gly Ile Phe Leu Asp Tyr Glu Ala Gly His Leu Ser
 405 410 415

Phe Tyr Ser Ala Thr Asp Gly Ser Leu Leu Phe Ile Phe Pro Glu Ile
 420 425 430

Pro Phe Ser Gly Thr Leu Arg Pro Leu Phe Ser Pro Leu Ser Ser Ser
 435 440 445

Pro Thr Pro Met Thr Ile Cys Arg Pro Lys Gly Gly Ser Gly Asp Thr
 450 455 460

Leu Ala Pro Gln
 465

<210> 23
 <211> 894
 <212> DNA
 <213> Mus musculus

<400> 23
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 ctgatggatga aacctgtgag tgcagattgt ggtcacacct tctgccaagg ctgcatcacg 120
 ttgtactttg aatccatcaa atgcgataag aaagtgttca ttgccctgt gtgccgaatt 180
 agttaccagt ttagcaatct gaggcctaata cgaaatgtgg ccaacatagt agagaggctc 240
 aaaatgttca agcccagccc agaagaggag cagaaagtgt ttaactgtgc aagacatgga 300
 aagaaactcc agctcttctg taggaaggac atgatggcca tctgctggct ttgtgagcga 360
 tctcaggagc accgttgtca caaacagct ctattgaag aggtggccca ggagtacaag 420
 gagcagctgc aggtagtctt gcaaaggctg atggcagata agaaaaaatt tgaaaactgg 480

aaagatgacc ttcagaagga tagaacttac tgggagaatc aaatacagaa agatgtgcag 540
 aatgttcggt cagagttaa acgaatgagg gatatcatgg actctgagga gaagaaggaa 600
 ttgcagaagc tgaggcaaga gaaggaagac attctcaaca acctggcaga gtctgaaagt 660
 gagcatgctc agcagagcaa gttgctagaa gacttcatct cagatgtgga acatcagtta 720
 cagtgtcag acatagaaat actgcagggt gtggagaaca tcatagaacg gagtcatact 780
 ttttcgatga agaagcccaa agccatcgcc agggaacaaa gaaagttccg agcccctgac 840
 ctgcaaggca tgctgcaagt gctgcaagag gtcacagagg ctcatcgcta ctag 894

<210> 24

<211> 297

<212> PRT

<213> Mus musculus

<400> 24

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

Val Cys Leu Asn Leu Met Val Lys Pro Val Ser Ala Asp Cys Gly His
 20 25 30

Thr Phe Cys Gln Gly Cys Ile Thr Leu Tyr Phe Glu Ser Ile Lys Cys
 35 40 45

Asp Lys Lys Val Phe Ile Cys Pro Val Cys Arg Ile Ser Tyr Gln Phe
 50 55 60

Ser Asn Leu Arg Pro Asn Arg Asn Val Ala Asn Ile Val Glu Arg Leu
 65 70 75 80

Lys Met Phe Lys Pro Ser Pro Glu Glu Glu Gln Lys Val Phe Asn Cys
 85 90 95

Ala Arg His Gly Lys Lys Leu Gln Leu Phe Cys Arg Lys Asp Met Met
 100 105 110

Ala Ile Cys Trp Leu Cys Glu Arg Ser Gln Glu His Arg Gly His Lys

115 120 125
 Thr Ala Leu Ile Glu Glu Val Ala Gln Glu Tyr Lys Glu Gln Leu Gln
 130 135 140
 Val Val Leu Gln Arg Leu Met Ala Asp Lys Lys Lys Phe Glu Asn Trp
 145 150 155 160
 Lys Asp Asp Leu Gln Lys Asp Arg Thr Tyr Trp Glu Asn Gln Ile Gln
 165 170 175
 Lys Asp Val Gln Asn Val Arg Ser Glu Phe Lys Arg Met Arg Asp Ile
 180 185 190
 Met Asp Ser Glu Glu Lys Lys Glu Leu Gln Lys Leu Arg Gln Glu Lys
 195 200 205
 Glu Asp Ile Leu Asn Asn Leu Ala Glu Ser Glu Ser Glu His Ala Gln
 210 215 220
 Gln Ser Lys Leu Leu Glu Asp Phe Ile Ser Asp Val Glu His Gln Leu
 225 230 235 240
 Gln Cys Ser Asp Ile Glu Ile Leu Gln Gly Val Glu Asn Ile Ile Glu
 245 250 255
 Arg Ser His Thr Phe Ser Met Lys Lys Pro Lys Ala Ile Ala Arg Glu
 260 265 270
 Gln Arg Lys Phe Arg Ala Pro Asp Leu Gln Gly Met Leu Gln Val Leu
 275 280 285
 Gln Glu Val Thr Glu Ala His Arg Tyr
 290 295

<210> 25
 <211> 1224
 <212> DNA
 <213> Homo sapiens

<400> 25
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 cgggttttgc cttgctccca caacttctgc aaaaaatgct tagaaggat cttagaaggg 120
 agtgtgcgga attccttggt gagaccagct ccattcaagt gtcctacatg ccgtaaggaa 180
 acttcagcta ctggaattaa tagcctgcag gtttaattact ccctgaaggg tattgtggaa 240
 aagataaca agatcaagat ctctccaaa atgccagat gcaaaggaca cttggggcag 300
 cctctcaaca ttttctgct gactgatatg cagctgattt gtgggatctg tgctactcgt 360
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 ctgtctgact ttgagacat gaaactgtct gttatgcaag catatgacc agagatcaac 660
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<210> 26
 <211> 407
 <212> PRT
 <213> Homo sapiens

<400> 26

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Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys
20 25 30

Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg
35 40 45

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr
50 55 60

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu
65 70 75 80

Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly
85 90 95

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu
100 105 110

Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe
115 120 125

Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser
130 135 140

Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg
145 150 155 160

Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr
165 170 175

Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr
180 185 190

Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys
195 200 205

Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr
210 215 220

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys
225 230 235 240

Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg
245 250 255

Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu
260 265 270

Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp
275 280 285

Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly
290 295 300

Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu
305 310 315 320

Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu
325 330 335

Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
340 345 350

Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser
355 360 365

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

Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe
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Val Cys Lys Tyr Lys Leu Leu

<210> 27

<211> 1329

<212> DNA

<213> Homo sapiens

<400> 27

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aaggctaagc cagagtcaag taaaacctgg ctgaaggga aattcactga actcagatta    360
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tacacggcca ccgagcagga gatgcagcag cagatgagcc tcggggagct gtgccatccc    600
gtgcccctct cctttgagcc cgtcaagagc tctttaagg gcctcgtgga agccgtggag    660
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ctgccctag 1329

<210> 28

<211> 442

<212> PRT

<213> Homo sapiens

<400> 28

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Val Glu Gly Cys Gly Trp Arg Cys Pro Glu His Gly Asp Arg Val Ala

20 25 30

Glu Leu Phe Cys Arg Arg Cys Arg Arg Cys Val Cys Ala Leu Cys Pro

35 40 45

Val Leu Gly Ala His Arg Gly His Pro Val Gly Leu Ala Leu Glu Ala

50 55 60

Ala Val His Val Gln Lys Leu Ser Gln Glu Cys Leu Lys Gln Leu Ala

65 70 75 80

Ile Lys Lys Gln Gln His Ile Asp Asn Ile Thr Gln Ile Glu Asp Ala

85 90 95

Thr Glu Lys Leu Lys Ala Asn Ala Glu Ser Ser Lys Thr Trp Leu Lys

100 105 110

Gly Lys Phe Thr Glu Leu Arg Leu Leu Leu Asp Glu Glu Glu Ala Leu

115 120 125

Ala Lys Lys Phe Ile Asp Lys Asn Thr Gln Leu Thr Leu Gln Val Tyr

130 135 140

Arg Glu Gln Ala Asp Ser Cys Arg Glu Gln Leu Asp Ile Met Asn Asp

145 150 155 160

Leu Ser Asn Arg Val Trp Ser Ile Ser Gln Glu Pro Asp Pro Val Gln
165 170 175

Arg Leu Gln Ala Tyr Thr Ala Thr Glu Gln Glu Met Gln Gln Gln Met
180 185 190

Ser Leu Gly Glu Leu Cys His Pro Val Pro Leu Ser Phe Glu Pro Val
195 200 205

Lys Ser Phe Phe Lys Gly Leu Val Glu Ala Val Glu Ser Thr Leu Gln
210 215 220

Thr Pro Leu Asp Ile Arg Leu Lys Glu Ser Ile Asn Cys Gln Leu Ser
225 230 235 240

Asp Pro Ser Ser Thr Lys Pro Gly Thr Leu Leu Lys Thr Ser Pro Ser
245 250 255

Pro Glu Arg Ser Leu Leu Leu Lys Tyr Ala Arg Thr Pro Thr Leu Asp
260 265 270

Pro Asp Thr Met His Ala Arg Leu Arg Leu Ser Ala Asp Arg Leu Thr
275 280 285

Val Arg Cys Gly Leu Leu Gly Ser Leu Gly Pro Val Pro Val Leu Arg
290 295 300

Phe Asp Ala Leu Trp Gln Val Leu Ala Arg Asp Cys Phe Ala Thr Gly
305 310 315 320

Arg His Tyr Trp Glu Val Asp Val Gln Glu Ala Gly Ala Gly Trp Trp
325 330 335

Val Gly Ala Ala Tyr Ala Ser Leu Arg Arg Arg Gly Ala Ser Ala Ala
340 345 350

Ala Arg Leu Gly Cys Asn Arg Gln Ser Trp Cys Leu Lys Arg Tyr Asp
355 360 365

Leu Glu Tyr Trp Ala Phe His Asp Gly Gln Arg Ser Arg Leu Arg Pro
 370 375 380

Arg Asp Asp Leu Asp Arg Leu Gly Val Phe Leu Asp Tyr Glu Ala Gly
 385 390 395 400

Val Leu Ala Phe Tyr Asp Val Thr Gly Gly Met Ser His Leu His Thr
 405 410 415

Phe Arg Ala Thr Phe Gln Glu Pro Leu Tyr Pro Ala Leu Arg Leu Trp
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Glu Gly Ala Ile Ser Ile Pro Arg Leu Pro
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<210> 29

<211> 1398

<212> DNA

<213> Homo sapiens

<400> 29

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aaggagctgg aggagaagtg tcagcagcca gcaagtgagc ttctacaaga tgtcagagtc    720

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<210> 30

<211> 465

<212> PRT

<213> Homo sapiens

<400> 30

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Thr Leu Cys Ala Gly Pro Leu Glu Asp Ala Val Thr Ile Pro Cys Gly
20 25 30

His Thr Phe Cys Arg Leu Cys Leu Pro Ala Leu Ser Gln Met Gly Ala
35 40 45

Gln Ser Ser Gly Lys Ile Leu Leu Cys Pro Leu Cys Gln Glu Glu Glu
50 55 60

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

Thr Tyr Cys Glu Glu His Gly Glu Lys Ile Tyr Phe Phe Cys Glu Asn
85 90 95

Asp Ala Glu Phe Leu Cys Val Phe Cys Arg Glu Gly Pro Thr His Gln
100 105 110

Ala His Thr Val Gly Phe Leu Asp Glu Ala Ile Gln Pro Tyr Arg Asp
115 120 125

Arg Leu Arg Ser Arg Leu Glu Ala Leu Ser Thr Glu Arg Asp Glu Ile
130 135 140

Glu Asp Val Lys Cys Gln Glu Asp Gln Lys Leu Gln Val Leu Leu Thr
145 150 155 160

Gln Ile Glu Ser Lys Lys His Gln Val Glu Thr Ala Phe Glu Arg Leu
165 170 175

Gln Gln Glu Leu Glu Gln Gln Arg Cys Leu Leu Leu Ala Arg Leu Arg
180 185 190

Glu Leu Glu Gln Gln Ile Trp Lys Glu Arg Asp Glu Tyr Ile Thr Lys
195 200 205

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

Glu Lys Cys Gln Gln Pro Ala Ser Glu Leu Leu Gln Asp Val Arg Val
225 230 235 240

Asn Gln Ser Arg Cys Glu Met Lys Thr Phe Val Ser Pro Glu Ala Ile
245 250 255

Ser Pro Asp Leu Val Lys Lys Ile Arg Asp Phe His Arg Lys Ile Leu
260 265 270

Thr Leu Pro Glu Met Met Arg Met Phe Ser Glu Asn Leu Ala His His

275	280	285
Leu Glu Ile Asp Ser Gly Val Ile Thr Leu Asp Pro Gln Thr Ala Ser		
290	295	300
Arg Ser Leu Val Leu Ser Glu Asp Arg Lys Ser Val Arg Tyr Thr Arg		
305	310	315
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Gln Lys Lys Ser Leu Pro Asp Ser Pro Leu Arg Phe Asp Gly Leu Pro		
325	330	335
Ala Val Leu Gly Phe Pro Gly Phe Ser Ser Gly Arg His Arg Trp Gln		
340	345	350
Val Asp Leu Gln Leu Gly Asp Gly Gly Gly Cys Thr Val Gly Val Ala		
355	360	365
Gly Glu Gly Val Arg Arg Lys Gly Glu Met Gly Leu Ser Ala Glu Asp		
370	375	380
Gly Val Trp Ala Val Ile Ile Ser His Gln Gln Cys Trp Ala Ser Thr		
385	390	395
		400
Ser Pro Gly Thr Asp Leu Pro Leu Ser Glu Ile Pro Arg Gly Val Arg		
405	410	415
Val Ala Leu Asp Tyr Glu Ala Gly Gln Val Thr Leu His Asn Ala Gln		
420	425	430
Thr Gln Glu Pro Ile Phe Thr Phe Thr Ala Ser Phe Ser Gly Lys Val		
435	440	445
Phe Pro Phe Phe Ala Val Trp Lys Lys Gly Ser Cys Leu Thr Leu Lys		
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Gly		
465		

<210> 31
 <211> 1695
 <212> DNA
 <213> Homo sapiens

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<210> 32
 <211> 564
 <212> PRT
 <213> Homo sapiens

<400> 32

Met Ala Glu Leu Asp Leu Met Ala Pro Gly Pro Leu Pro Arg Ala Thr
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Ala Gln Pro Pro Ala Pro Leu Ser Pro Asp Ser Gly Ser Pro Ser Pro
 20 25 30

Asp Ser Gly Ser Ala Ser Pro Val Glu Glu Glu Asp Val Gly Ser Ser
 35 40 45

Glu Lys Leu Gly Arg Glu Thr Glu Glu Gln Asp Ser Asp Ser Ala Glu
 50 55 60

Gln Gly Asp Pro Ala Gly Glu Gly Lys Glu Val Leu Cys Asp Phe Cys
 65 70 75 80

Leu Asp Asp Thr Arg Arg Val Lys Ala Val Lys Ser Cys Leu Thr Cys
 85 90 95

Met Val Asn Tyr Cys Glu Glu His Leu Gln Pro His Gln Val Asn Ile
 100 105 110

Lys Leu Gln Ser His Leu Leu Thr Glu Pro Val Lys Asp His Asn Trp
 115 120 125

Arg Tyr Cys Pro Ala His His Ser Pro Leu Ser Ala Phe Cys Cys Pro
130 135 140

Asp Gln Gln Cys Ile Cys Gln Asp Cys Cys Gln Glu His Ser Gly His
145 150 155 160

Thr Ile Val Ser Leu Asp Ala Ala Arg Arg Asp Lys Glu Ala Glu Leu
165 170 175

Gln Cys Thr Gln Leu Asp Leu Glu Arg Lys Leu Lys Leu Asn Glu Asn
180 185 190

Ala Ile Ser Arg Leu Gln Ala Asn Gln Lys Ser Val Leu Val Ser Val
195 200 205

Ser Glu Val Lys Ala Val Ala Glu Met Gln Phe Gly Glu Leu Leu Ala
210 215 220

Ala Val Arg Lys Ala Gln Ala Asn Val Met Leu Phe Leu Glu Glu Lys
225 230 235 240

Glu Gln Ala Ala Leu Ser Gln Ala Asn Gly Ile Lys Ala His Leu Glu
245 250 255

Tyr Arg Ser Ala Glu Met Glu Lys Ser Lys Gln Glu Leu Glu Arg Met
260 265 270

Ala Ala Ile Ser Asn Thr Val Gln Phe Leu Glu Glu Tyr Cys Lys Phe
275 280 285

Lys Asn Thr Glu Asp Ile Thr Phe Pro Ser Val Tyr Val Gly Leu Lys
290 295 300

Asp Lys Leu Ser Gly Ile Arg Lys Val Ile Thr Glu Ser Thr Val His
305 310 315 320

Leu Ile Gln Leu Leu Glu Asn Tyr Lys Lys Lys Leu Gln Glu Phe Ser

325	330	335
Lys Glu Glu Glu Tyr Asp Ile Arg Thr Gln Val Ser Ala Val Val Gln		
340	345	350
Arg Lys Tyr Trp Thr Ser Lys Pro Glu Pro Ser Thr Arg Glu Gln Phe		
355	360	365
Leu Gln Tyr Ala Tyr Asp Ile Thr Phe Asp Pro Asp Thr Ala His Lys		
370	375	380
Tyr Leu Arg Leu Gln Glu Glu Asn Arg Lys Val Thr Asn Thr Thr Pro		
385	390	395
Trp Glu His Pro Tyr Pro Asp Leu Pro Ser Arg Phe Leu His Trp Arg		
405	410	415
Gln Val Leu Ser Gln Gln Ser Leu Tyr Leu His Arg Tyr Tyr Phe Glu		
420	425	430
Val Glu Ile Phe Gly Ala Gly Thr Tyr Val Gly Leu Thr Cys Lys Gly		
435	440	445
Ile Asp Arg Lys Gly Glu Glu Arg Asn Ser Cys Ile Ser Gly Asn Asn		
450	455	460
Phe Ser Trp Ser Leu Gln Trp Asn Gly Lys Glu Phe Thr Ala Trp Tyr		
465	470	475
Ser Asp Met Glu Thr Pro Leu Lys Ala Gly Pro Phe Arg Arg Leu Gly		
485	490	495
Val Tyr Ile Asp Phe Pro Gly Gly Ile Leu Ser Phe Tyr Gly Val Glu		
500	505	510
Tyr Asp Thr Met Thr Leu Val His Lys Phe Ala Cys Lys Phe Ser Glu		
515	520	525

Pro Val Tyr Ala Ala Phe Trp Leu Ser Lys Lys Glu Asn Ala Ile Arg
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Ile Val Asp Leu Gly Glu Glu Pro Glu Lys Pro Ala Pro Ser Leu Val
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Gly Thr Ala Pro

<210> 33

<211> 1434

<212> DNA

<213> Homo sapiens

<400> 33

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cagctgagct gggaaaaggc gaggggcaag aaggggaggc ggaagcggaa gggctccttc 180

ccctgccccg agtgcagaga gatgtccccg cagaggaacc tgctgcccac ccggctgctg 240

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<210> 34

<211> 477

<212> PRT

<213> Homo sapiens

<400> 34

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

His Asn Phe Cys Arg Ala Cys Ile Gln Leu Ser Trp Glu Lys Ala Arg
 35 40 45

Gly Lys Lys Gly Arg Arg Lys Arg Lys Gly Ser Phe Pro Cys Pro Glu
 50 55 60

Cys Arg Glu Met Ser Pro Gln Arg Asn Leu Leu Pro Asn Arg Leu Leu
 65 70 75 80

Thr Lys Val Ala Glu Met Ala Gln Gln His Pro Gly Leu Gln Lys Gln
 85 90 95

Asp Leu Cys Gln Glu His His Glu Pro Leu Lys Leu Phe Cys Gln Lys
 100 105 110

Asp Gln Ser Pro Ile Cys Val Val Cys Arg Glu Ser Arg Glu His Arg
115 120 125

Leu His Arg Val Leu Pro Ala Glu Glu Ala Val Gln Gly Tyr Lys Leu
130 135 140

Lys Leu Glu Glu Asp Met Glu Tyr Leu Arg Glu Gln Ile Thr Arg Thr
145 150 155 160

Gly Asn Leu Gln Ala Arg Glu Glu Gln Ser Leu Ala Glu Trp Gln Gly
165 170 175

Lys Val Lys Glu Arg Arg Glu Arg Ile Val Leu Glu Phe Glu Lys Met
180 185 190

Asn Leu Tyr Leu Val Glu Glu Glu Gln Arg Leu Leu Gln Ala Leu Glu
195 200 205

Thr Glu Glu Glu Glu Thr Ala Ser Arg Leu Arg Glu Ser Val Ala Cys
210 215 220

Leu Asp Arg Gln Gly His Ser Leu Glu Leu Leu Leu Gln Leu Glu
225 230 235 240

Glu Arg Ser Thr Gln Gly Pro Leu Gln Met Leu Gln Asp Met Lys Glu
245 250 255

Pro Leu Ser Arg Lys Asn Asn Val Ser Val Gln Cys Pro Glu Val Ala
260 265 270

Pro Pro Thr Arg Pro Arg Thr Val Cys Arg Val Pro Gly Gln Ile Glu
275 280 285

Val Leu Arg Gly Phe Leu Glu Asp Val Val Pro Asp Ala Thr Ser Ala
290 295 300

Tyr Pro Tyr Leu Leu Leu Tyr Glu Ser Arg Gln Arg Arg Tyr Leu Gly
305 310 315 320

Ser Ser Pro Glu Gly Ser Gly Phe Cys Ser Lys Asp Arg Phe Val Ala
325 330 335

Tyr Pro Cys Ala Val Gly Gln Thr Ala Phe Ser Ser Gly Arg His Tyr
340 345 350

Trp Glu Val Gly Met Asn Ile Thr Gly Asp Ala Leu Trp Ala Leu Gly
355 360 365

Val Cys Arg Asp Asn Val Ser Arg Lys Asp Arg Val Pro Lys Cys Pro
370 375 380

Glu Asn Gly Phe Trp Val Val Gln Leu Ser Lys Gly Thr Lys Tyr Leu
385 390 395 400

Ser Thr Phe Ser Ala Leu Thr Pro Val Met Leu Met Glu Pro Pro Ser
405 410 415

His Met Gly Ile Phe Leu Asp Phe Glu Ala Gly Glu Val Ser Phe Tyr
420 425 430

Ser Val Ser Asp Gly Ser His Leu His Thr Tyr Ser Gln Ala Thr Phe
435 440 445

Pro Gly Pro Leu Gln Pro Phe Phe Cys Leu Gly Ala Pro Lys Ser Gly
450 455 460

Gln Met Val Ile Ser Thr Val Thr Met Trp Val Lys Gly
465 470 475

<210> 35

<211> 1945

<212> DNA

<213> Homo sapiens

<400> 35

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<210> 36
<211> 667
<212> PRT
<213> Homo sapiens

<400> 36

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Phe Glu Asp Pro Leu Leu Leu Pro Cys Ala His Ser Leu Cys Phe Asn
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Cys Ala His Arg Ile Leu Val Ser His Cys Ala Thr Asn Glu Ser Val
35 40 45

Glu Ser Ile Thr Ala Phe Gln Cys Pro Thr Cys Arg His Val Ile Thr
50 55 60

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

Asn Ile Ile Asp Arg Phe Gln Lys Ala Ser Val Ser Gly Pro Asn Ser
85 90 95

Pro Ser Glu Thr Arg Arg Glu Arg Ala Phe Asp Ala Asn Thr Met Thr
100 105 110

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

Asp Ala Val Lys Thr Cys Val Thr Cys Glu Val Ser Tyr Cys Asp Glu
130 135 140

Cys Leu Lys Ala Thr His Pro Asn Lys Lys Pro Phe Thr Gly His Arg
145 150 155 160

Leu Ile Glu Pro Ile Pro Asp Ser His Ile Arg Gly Leu Met Cys Leu
165 170 175

Glu His Glu Asp Glu Lys Val Asn Met Tyr Cys Val Thr Asp Asp Gln
180 185 190

Leu Ile Cys Ala Leu Cys Lys Leu Val Gly Arg His Arg Asp His Gln
195 200 205

Val Ala Ala Leu Ser Glu Arg Tyr Asp Lys Leu Lys Gln Asn Leu Glu
210 215 220

Ser Asn Leu Thr Asn Leu Ile Lys Arg Asn Thr Glu Leu Glu Thr Leu
225 230 235 240

Leu Ala Lys Leu Ile Gln Thr Cys Gln His Val Glu Val Asn Ala Ser
245 250 255

Arg Gln Glu Ala Lys Leu Thr Glu Glu Cys Asp Leu Leu Ile Glu Ile
260 265 270

Ile Gln Gln Arg Arg Gln Ile Ile Gly Thr Lys Ile Lys Glu Gly Lys
275 280 285

Val Met Arg Leu Arg Lys Leu Ala Gln Gln Ile Ala Asn Cys Lys Gln
290 295 300

Cys Ile Glu Arg Ser Ala Ser Leu Ile Ser Gln Ala Glu His Ser Leu
305 310 315 320

Lys Glu Asn Asp His Ala Arg Phe Leu Gln Thr Ala Lys Asn Ile Thr
325 330 335

Glu Arg Val Ser Met Ala Thr Ala Ser Ser Gln Val Leu Ile Pro Glu
340 345 350

Ile Asn Leu Asn Asp Thr Phe Asp Thr Phe Ala Leu Asp Phe Ser Arg
355 360 365

Glu Lys Lys Leu Leu Glu Cys Leu Asp Tyr Leu Thr Ala Pro Asn Pro
370 375 380

Pro Thr Ile Arg Glu Glu Leu Cys Thr Ala Ser Tyr Asp Thr Ile Thr
385 390 395 400

Val His Trp Thr Ser Asp Asp Glu Phe Ser Val Val Ser Tyr Glu Leu
405 410 415

Gln Tyr Thr Ile Phe Thr Gly Gln Ala Asn Val Val Ser Leu Cys Asn
420 425 430

Ser Ala Asp Ser Trp Met Ile Val Pro Asn Ile Lys Gln Asn His Tyr
435 440 445

Thr Val His Gly Leu Gln Ser Gly Thr Lys Tyr Ile Phe Met Val Lys
450 455 460

Ala Ile Asn Gln Ala Gly Ser Arg Ser Ser Glu Pro Gly Lys Leu Lys
465 470 475 480

Thr Asn Ser Gln Pro Phe Lys Leu Asp Pro Lys Ser Ala His Arg Lys
485 490 495

Leu Lys Val Ser His Asp Asn Leu Thr Val Glu Arg Asp Glu Ser Ser
500 505 510

Ser Lys Lys Ser His Thr Pro Glu Arg Phe Thr Ser Gln Gly Ser Tyr
515 520 525

Gly Val Ala Gly Asn Val Phe Ile Asp Ser Gly Arg His Tyr Trp Glu
530 535 540

Val Val Ile Ser Gly Ser Thr Trp Tyr Ala Ile Gly Leu Ala Tyr Lys
 545 550 555 560

Ser Ala Pro Lys His Glu Trp Ile Gly Lys Asn Ser Ala Ser Trp Ala
 565 570 575

Leu Cys Arg Cys Asn Asn Asn Trp Val Val Arg His Asn Ser Lys Glu
 580 585 590

Ile Pro Ile Glu Pro Ala Pro His Leu Arg Arg Val Gly Ile Leu Leu
 595 600 605

Asp Tyr Asp Asn Gly Ser Ile Ala Phe Tyr Asp Ala Leu Asn Ser Ile
 610 615 620

His Leu Tyr Thr Phe Asp Val Ala Phe Ala Gln Pro Val Cys Pro Thr
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Phe Thr Val Trp Asn Lys Cys Leu Thr Ile Ile Thr Gly Leu Pro Ile
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Pro Asp His Leu Asp Cys Thr Glu Gln Leu Pro
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<210> 37
 <211> 2649
 <212> DNA
 <213> Homo sapiens

<400> 37
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<210> 38

<211> 882

<212> PRT

<213> Homo sapiens

<400> 38

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Arg Pro Gln Glu Pro Thr Met Pro Pro Pro Glu Thr Pro Ser Glu Gly

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Arg Gln Pro Ser Pro Ser Pro Ser Pro Thr Glu Arg Ala Pro Ala Ser

35 40 45

Glu Glu Glu Phe Gln Phe Leu Arg Cys Gln Gln Cys Gln Ala Glu Ala

50 55 60

Lys Cys Pro Lys Leu Leu Pro Cys Leu His Thr Leu Cys Ser Gly Cys
65 70 75 80

Leu Glu Ala Ser Gly Met Gln Cys Pro Ile Cys Gln Ala Pro Trp Pro
 85 90 95

Leu Gly Ala Asp Thr Pro Ala Leu Asp Asn Val Phe Phe Glu Ser Leu
 100 105 110

Gln Arg Arg Leu Ser Val Tyr Arg Gln Ile Val Asp Ala Gln Ala Val
 115 120 125

Cys Thr Arg Cys Lys Glu Ser Ala Asp Phe Trp Cys Phe Glu Cys Glu
 130 135 140

Gln Leu Leu Cys Ala Lys Cys Phe Glu Ala His Gln Trp Phe Leu Lys
145 150 155 160

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

Phe Leu Asp Gly Thr Arg Lys Thr Asn Asn Ile Phe Cys Ser Asn Pro
 180 185 190

Asn His Arg Thr Pro Thr Leu Thr Ser Ile Tyr Cys Arg Gly Cys Ser
 195 200 205

Lys Pro Leu Cys Cys Ser Cys Ala Leu Leu Asp Ser Ser His Ser Glu
 210 215 220

Leu Lys Cys Asp Ile Ser Ala Glu Ile Gln Gln Arg Gln Glu Glu Leu
225 230 235 240

Asp Ala Met Thr Gln Ala Leu Gln Glu Gln Asp Ser Ala Phe Gly Ala
 245 250 255

Val His Ala Gln Met His Ala Ala Val Gly Gln Leu Gly Arg Ala Arg
 260 265 270

Ala Glu Thr Glu Glu Leu Ile Arg Glu Arg Val Arg Gln Val Val Ala
275 280 285

His Val Arg Ala Gln Glu Arg Glu Leu Leu Glu Ala Val Asp Ala Arg
290 295 300

Tyr Gln Arg Asp Tyr Glu Glu Met Ala Ser Arg Leu Gly Arg Leu Asp
305 310 315 320

Ala Val Leu Gln Arg Ile Arg Thr Gly Ser Ala Leu Val Gln Arg Met
325 330 335

Lys Cys Tyr Ala Ser Asp Gln Glu Val Leu Asp Met His Gly Phe Leu
340 345 350

Arg Gln Ala Leu Cys Arg Leu Arg Gln Glu Glu Pro Gln Ser Leu Gln
355 360 365

Ala Ala Val Arg Thr Asp Gly Phe Asp Glu Phe Lys Val Arg Leu Gln
370 375 380

Asp Leu Ser Ser Cys Ile Thr Gln Gly Lys Asp Ala Ala Val Ser Lys
385 390 395 400

Lys Ala Ser Pro Glu Ala Ala Ser Thr Pro Arg Asp Pro Ile Asp Val
405 410 415

Asp Leu Pro Glu Glu Ala Glu Arg Val Lys Ala Gln Val Gln Ala Leu
420 425 430

Gly Leu Ala Glu Ala Gln Pro Met Ala Val Val Gln Ser Val Pro Gly
435 440 445

Ala His Pro Val Pro Val Tyr Ala Phe Ser Ile Lys Gly Pro Ser Tyr
450 455 460

Gly Glu Asp Val Ser Asn Thr Thr Thr Ala Gln Lys Arg Lys Cys Ser

465	470	475	480
Gln Thr Gln Cys Pro Arg Lys Val Ile Lys Met Glu Ser Glu Glu Gly			
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Lys Glu Ala Arg Leu Ala Arg Ser Ser Pro Glu Gln Pro Arg Pro Ser			
	500	505	510
Thr Ser Lys Ala Val Ser Pro Pro His Leu Asp Gly Pro Pro Ser Pro			
	515	520	525
Arg Ser Pro Val Ile Gly Ser Glu Val Phe Leu Pro Asn Ser Asn His			
	530	535	540
Val Ala Ser Gly Ala Gly Glu Ala Glu Glu Arg Val Val Val Ile Ser			
545	550	555	560
Ser Ser Glu Asp Ser Asp Ala Glu Asn Ser Ser Ser Arg Glu Leu Asp			
	565	570	575
Asp Ser Ser Ser Glu Ser Ser Asp Leu Gln Leu Glu Gly Pro Ser Thr			
	580	585	590
Leu Arg Val Leu Asp Glu Asn Leu Ala Asp Pro Gln Ala Glu Asp Arg			
	595	600	605
Pro Leu Val Phe Phe Asp Leu Lys Ile Asp Asn Glu Thr Gln Lys Ile			
	610	615	620
Ser Gln Leu Ala Ala Val Asn Arg Glu Ser Lys Phe Arg Val Val Ile			
625	630	635	640
Gln Pro Glu Ala Phe Phe Ser Ile Tyr Ser Lys Ala Val Ser Leu Glu			
	645	650	655
Val Gly Leu Gln His Phe Leu Ser Phe Leu Ser Ser Met Arg Arg Pro			
	660	665	670

Ile Leu Ala Cys Tyr Lys Leu Trp Gly Pro Gly Leu Pro Asn Phe Phe
675 680 685

Arg Ala Leu Glu Asp Ile Asn Arg Leu Trp Glu Phe Gln Glu Ala Ile
690 695 700

Ser Gly Phe Leu Ala Ala Leu Pro Leu Ile Arg Glu Arg Val Pro Gly
705 710 715 720

Ala Ser Ser Phe Lys Leu Lys Asn Leu Ala Gln Thr Tyr Leu Ala Arg
725 730 735

Asn Met Ser Glu Arg Ser Ala Met Ala Ala Val Leu Ala Met Arg Asp
740 745 750

Leu Cys Arg Leu Leu Glu Val Ser Pro Gly Pro Gln Leu Ala Gln His
755 760 765

Val Tyr Pro Phe Ser Ser Leu Gln Cys Phe Ala Ser Leu Gln Pro Leu
770 775 780

Val Gln Ala Ala Val Leu Pro Arg Ala Glu Ala Arg Leu Leu Ala Leu
785 790 795 800

His Asn Val Ser Phe Met Glu Leu Leu Ser Ala His Arg Arg Asp Arg
805 810 815

Gln Gly Gly Leu Lys Lys Tyr Ser Arg Tyr Leu Ser Leu Gln Thr Thr
820 825 830

Thr Leu Pro Pro Ala Gln Pro Ala Phe Asn Leu Gln Ala Leu Gly Thr
835 840 845

Tyr Phe Glu Gly Leu Leu Glu Gly Pro Ala Leu Ala Arg Ala Glu Gly
850 855 860

Val Ser Thr Pro Leu Ala Gly Arg Gly Leu Ala Glu Arg Ala Ser Gln
865 870 875 880

Gln Ser

<210> 39

<211> 2346

<212> DNA

<213> Homo sapiens

<400> 39

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ccccggagcc agatccagag agccaggccg gtgaagatgg ccactctgct ggtcacctac    180
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 gactga 2346

<210> 40

<211> 781

<212> PRT

<213> Homo sapiens

<400> 40

Met Ala Lys Thr Pro Ser Asp His Leu Leu Ser Thr Leu Glu Glu Leu

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Val Pro Tyr Asp Phe Glu Lys Phe Lys Phe Lys Leu Gln Asn Thr Ser
20 25 30

Val Gln Lys Glu His Ser Arg Ile Pro Arg Ser Gln Ile Gln Arg Ala
35 40 45

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

Tyr Ala Val Gln Leu Thr Leu Gln Val Leu Arg Ala Ile Asn Gln Arg
65 70 75 80

Leu Leu Ala Glu Glu Leu His Arg Ala Ala Ile Gln Glu Tyr Ser Thr
85 90 95

Gln Glu Asn Gly Thr Asp Asp Ser Ala Ala Ser Ser Ser Leu Gly Glu
100 105 110

Asn Lys Pro Arg Ser Leu Lys Thr Pro Asp His Pro Glu Gly Asn Glu
115 120 125

Gly Asn Gly Pro Arg Pro Tyr Gly Gly Gly Ala Ala Ser Leu Arg Cys
130 135 140

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

Arg Arg Glu Lys Ala Ser Glu Gly Leu Asp Ala Gln Gly Lys Pro Arg
165 170 175

Thr Arg Ser Pro Ala Leu Pro Gly Gly Arg Ser Pro Gly Pro Cys Arg
180 185 190

Ala Leu Glu Gly Gly Gln Ala Glu Val Arg Leu Arg Arg Asn Ala Ser
195 200 205

Ser Ala Gly Arg Leu Gln Gly Leu Ala Gly Gly Ala Pro Gly Gln Lys
210 215 220

Glu Cys Arg Pro Phe Glu Val Tyr Leu Pro Ser Gly Lys Met Arg Pro
225 230 235 240

Arg Ser Leu Glu Val Thr Ile Ser Thr Gly Glu Lys Ala Pro Ala Asn
 245 250 255

Pro Glu Ile Leu Leu Thr Leu Glu Glu Lys Thr Ala Ala Asn Leu Asp
 260 265 270

Ser Ala Thr Glu Pro Arg Ala Arg Pro Thr Pro Asp Gly Gly Ala Ser
 275 280 285

Ala Asp Leu Lys Glu Gly Pro Gly Asn Pro Glu His Ser Val Thr Gly
 290 295 300

Arg Pro Pro Asp Thr Ala Ala Ser Pro Arg Cys His Ala Gln Glu Gly
305 310 315 320

Asp Pro Val Asp Gly Thr Cys Val Arg Asp Ser Cys Ser Phe Pro Glu
 325 330 335

Ala Val Ser Gly His Pro Gln Ala Ser Gly Ser Arg Ser Pro Gly Cys
 340 345 350

Pro Arg Cys Gln Asp Ser His Glu Arg Lys Ser Pro Gly Ser Leu Ser
 355 360 365

Pro Gln Pro Leu Pro Gln Cys Lys Arg His Leu Lys Gln Val Gln Leu
 370 375 380

Leu Phe Cys Glu Asp His Asp Glu Pro Ile Cys Leu Ile Cys Ser Leu
385 390 395 400

Ser Gln Glu His Gln Gly His Arg Val Arg Pro Ile Glu Glu Val Ala
 405 410 415

Leu Glu His Lys Lys Lys Ile Gln Lys Gln Leu Glu His Leu Lys Lys

420	425	430
Leu Arg Lys Ser Gly Glu Glu Gln Arg Ser Tyr Gly Glu Glu Lys Ala		
435	440	445
Val Ser Phe Leu Lys Gln Thr Glu Ala Leu Lys Gln Arg Val Gln Arg		
450	455	460
Lys Leu Glu Gln Val Tyr Tyr Phe Leu Glu Gln Gln Glu His Phe Phe		
465	470	475 480
Val Ala Ser Leu Glu Asp Val Gly Gln Met Val Gly Gln Ile Arg Lys		
485	490	495
Ala Tyr Asp Thr Arg Val Ser Gln Asp Ile Ala Leu Leu Asp Ala Leu		
500	505	510
Ile Gly Glu Leu Glu Ala Lys Glu Cys Gln Ser Glu Trp Glu Leu Leu		
515	520	525
Gln Asp Ile Gly Asp Ile Leu His Arg Ala Lys Thr Val Pro Val Pro		
530	535	540
Glu Lys Trp Thr Thr Pro Gln Glu Ile Lys Gln Lys Ile Gln Leu Leu		
545	550	555 560
His Gln Lys Ser Glu Phe Val Glu Lys Ser Thr Lys Tyr Phe Ser Glu		
565	570	575
Thr Leu Arg Ser Glu Met Glu Met Phe Asn Val Pro Glu Leu Ile Gly		
580	585	590
Ala Gln Ala His Ala Val Asn Val Ile Leu Asp Ala Glu Thr Ala Tyr		
595	600	605
Pro Asn Leu Ile Phe Ser Asp Asp Leu Lys Ser Val Arg Leu Gly Asn		
610	615	620

Lys Trp Glu Arg Leu Pro Asp Gly Pro Gln Arg Phe Asp Ser Cys Ile
 625 630 635 640

Ile Val Leu Gly Ser Pro Ser Phe Leu Ser Gly Arg Arg Tyr Trp Glu
 645 650 655

Val Glu Val Gly Asp Lys Thr Ala Trp Ile Leu Gly Ala Cys Lys Thr
 660 665 670

Ser Ile Ser Arg Lys Gly Asn Met Thr Leu Ser Pro Glu Asn Gly Tyr
 675 680 685

Trp Val Val Ile Met Met Lys Glu Asn Glu Tyr Gln Ala Ser Ser Val
 690 695 700

Pro Pro Thr Arg Leu Leu Ile Lys Glu Pro Pro Lys Arg Val Gly Ile
 705 710 715 720

Phe Val Asp Tyr Arg Val Gly Ser Ile Ser Phe Tyr Asn Val Thr Ala
 725 730 735

Arg Ser His Ile Tyr Thr Phe Ala Ser Cys Ser Phe Ser Gly Pro Leu
 740 745 750

Gln Pro Ile Phe Ser Pro Gly Thr Arg Asp Gly Gly Lys Asn Thr Ala
 755 760 765

Pro Leu Thr Ile Cys Pro Val Gly Gly Gln Gly Pro Asp
 770 775 780

<210> 41

<211> 1428

<212> DNA

<213> Homo sapiens

<400> 41

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tctcaggttg ggaaaggtgg gggcagcgtc tgtcctgtgt gccggcagcg ctttctgctc 180

aagaatctcc ggccaatcg acagctagcc aacatggtga acaaccttaa agaatcagc 240
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ctgttctgtg agaaagatgg gaaggccctt tgctgggtat gtgccagtc tcggaaacac 360
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cctctgcggc ctttctcag tcctggttc aatgatggag gaaaaaacac agcccctcta 1380
accctctgtc cactgaatat tggatcacia ggatccactg actattga 1428

<210> 42

<211> 475

<212> PRT

<213> Homo sapiens

<400> 42

Met Ala Ser Ala Ala Arg Leu Thr Met Met Trp Glu Glu Val Thr Cys
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Pro Ile Cys Leu Asp Pro Phe Val Glu Pro Val Ser Ile Glu Cys Gly
20 25 30

His Ser Phe Cys Gln Glu Cys Ile Ser Gln Val Gly Lys Gly Gly Gly
35 40 45

Ser Val Cys Pro Val Cys Arg Gln Arg Phe Leu Leu Lys Asn Leu Arg
50 55 60

Pro Asn Arg Gln Leu Ala Asn Met Val Asn Asn Leu Lys Glu Ile Ser
65 70 75 80

Gln Glu Ala Arg Glu Gly Thr Gln Gly Glu Arg Cys Ala Val His Gly
85 90 95

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

Val Cys Ala Gln Ser Arg Lys His Arg Asp His Ala Met Val Pro Leu
115 120 125

Glu Glu Ala Ala Gln Glu Tyr Gln Glu Lys Leu Gln Val Ala Leu Gly
130 135 140

Glu Leu Arg Arg Lys Gln Glu Leu Ala Glu Lys Leu Glu Val Glu Ile
145 150 155 160

Ala Ile Lys Arg Ala Asp Trp Lys Lys Thr Val Glu Thr Gln Lys Ser
165 170 175

Arg Ile His Ala Glu Phe Val Gln Gln Lys Asn Phe Leu Val Glu Glu
180 185 190

Glu Gln Arg Gln Leu Gln Glu Leu Glu Lys Asp Glu Arg Glu Gln Leu
195 200 205

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

Leu Gln Glu Leu Ile Ser Glu Leu Asp Arg Arg Cys His Ser Ser Ala
225 230 235 240

Leu Glu Leu Leu Gln Glu Val Ile Ile Val Leu Glu Arg Ser Glu Ser
245 250 255

Trp Asn Leu Lys Asp Leu Asp Ile Thr Ser Pro Glu Leu Arg Ser Val
260 265 270

Cys His Val Pro Gly Leu Lys Lys Met Leu Arg Thr Cys Ala Val His
275 280 285

Ile Thr Leu Asp Pro Asp Thr Ala Asn Pro Trp Leu Ile Leu Ser Glu
290 295 300

Asp Arg Arg Gln Val Arg Leu Gly Asp Thr Gln Gln Ser Ile Pro Gly
305 310 315 320

Asn Glu Glu Arg Phe Asp Ser Tyr Pro Met Val Leu Gly Ala Gln His
325 330 335

Phe His Ser Gly Lys His Tyr Trp Glu Val Asp Val Thr Gly Lys Glu
340 345 350

Ala Trp Asp Leu Gly Val Cys Arg Asp Ser Val Arg Arg Lys Gly His
355 360 365

Phe Leu Leu Ser Ser Lys Ser Gly Phe Trp Thr Ile Trp Leu Trp Asn
370 375 380

Lys Gln Lys Tyr Glu Ala Gly Thr Tyr Pro Gln Thr Pro Leu His Leu
385 390 395 400

Gln Val Pro Pro Cys Gln Val Gly Ile Phe Leu Asp Tyr Glu Ala Gly
405 410 415

Met Val Ser Phe Tyr Asn Ile Thr Asp His Gly Ser Leu Ile Tyr Ser
 420 425 430

Phe Ser Glu Cys Ala Phe Thr Gly Pro Leu Arg Pro Phe Phe Ser Pro
 435 440 445

Gly Phe Asn Asp Gly Gly Lys Asn Thr Ala Pro Leu Thr Leu Cys Pro
 450 455 460

Leu Asn Ile Gly Ser Gln Gly Ser Thr Asp Tyr
 465 470 475

<210> 43

<211> 1497

<212> DNA

<213> Homo sapiens

<400> 43

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 gcaaagatca aggagtcagt gatcatctca agaggggaaa gcagctgtcc tgtgtgtcag 180
 accagattcc agcctgggaa cctccgacct aatcggcatc tggccaacat agttgagaga 240
 gtcaaagagg tcaagatgag cccacaggag gggcagaaga gagatgtctg tgagcaccat 300
 ggaaaaaac tccagatctt ctgtaaggag gatggaaaag tcatttgctg ggtttgtgaa 360
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 cagaagattc tgaaggggtt caatgaaatg agagtcattt tggacaatga ggagcagaga 600
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<210> 44

<211> 498

<212> PRT

<213> Homo sapiens

<400> 44

Met Asp Phe Ser Val Lys Val Asp Ile Glu Lys Glu Val Thr Cys Pro

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Ile Cys Leu Glu Leu Leu Thr Glu Pro Leu Ser Leu Asp Cys Gly His

20 25 30

Ser Phe Cys Gln Ala Cys Ile Thr Ala Lys Ile Lys Glu Ser Val Ile

35 40 45

Ile Ser Arg Gly Glu Ser Ser Cys Pro Val Cys Gln Thr Arg Phe Gln

50 55 60

Pro Gly Asn Leu Arg Pro Asn Arg His Leu Ala Asn Ile Val Glu Arg

65 70 75 80

Val Lys Glu Val Lys Met Ser Pro Gln Glu Gly Gln Lys Arg Asp Val
85 90 95

Cys Glu His His Gly Lys Lys Leu Gln Ile Phe Cys Lys Glu Asp Gly
100 105 110

Lys Val Ile Cys Trp Val Cys Glu Leu Ser Gln Glu His Gln Gly His
115 120 125

Gln Thr Phe Arg Ile Asn Glu Val Val Lys Glu Cys Gln Glu Lys Leu
130 135 140

Gln Val Ala Leu Gln Arg Leu Ile Lys Glu Asp Gln Glu Ala Glu Lys
145 150 155 160

Leu Glu Asp Asp Ile Arg Gln Glu Arg Thr Ala Trp Lys Asn Tyr Ile
165 170 175

Gln Ile Glu Arg Gln Lys Ile Leu Lys Gly Phe Asn Glu Met Arg Val
180 185 190

Ile Leu Asp Asn Glu Glu Gln Arg Glu Leu Gln Lys Leu Glu Glu Gly
195 200 205

Glu Val Asn Val Leu Asp Asn Leu Ala Ala Ala Thr Asp Gln Leu Val
210 215 220

Gln Gln Arg Gln Asp Ala Ser Thr Leu Ile Ser Asp Leu Gln Arg Arg
225 230 235 240

Leu Arg Gly Ser Ser Val Glu Met Leu Gln Asp Val Ile Asp Val Met
245 250 255

Lys Arg Ser Glu Ser Trp Thr Leu Lys Lys Pro Lys Ser Val Ser Lys
260 265 270

Lys Leu Lys Ser Val Phe Arg Val Pro Asp Leu Ser Gly Met Leu Gln
275 280 285

Val Leu Lys Glu Leu Thr Asp Val Gln Tyr Tyr Trp Val Asp Val Met
290 295 300

Leu Asn Pro Gly Ser Ala Thr Ser Asn Val Ala Ile Ser Val Asp Gln
305 310 315 320

Arg Gln Val Lys Thr Val Arg Thr Cys Thr Phe Lys Asn Ser Asn Pro
325 330 335

Cys Asp Phe Ser Ala Phe Gly Val Phe Gly Cys Gln Tyr Phe Ser Ser
340 345 350

Gly Lys Tyr Tyr Trp Glu Val Asp Val Ser Gly Lys Ile Ala Trp Ile
355 360 365

Leu Gly Val His Ser Lys Ile Ser Ser Leu Asn Lys Arg Lys Ser Ser
370 375 380

Gly Phe Ala Phe Asp Pro Ser Val Asn Tyr Ser Lys Val Tyr Ser Arg
385 390 395 400

Tyr Arg Pro Gln Tyr Gly Tyr Trp Val Ile Gly Leu Gln Asn Thr Cys
405 410 415

Glu Tyr Asn Ala Phe Glu Asp Ser Ser Ser Ser Asp Pro Lys Val Leu
420 425 430

Thr Leu Phe Met Ala Val Pro Pro Cys Arg Ile Gly Val Phe Leu Asp
435 440 445

Tyr Glu Ala Gly Ile Val Ser Phe Phe Asn Val Thr Asn His Gly Ala
450 455 460

Leu Ile Tyr Lys Phe Ser Gly Cys Arg Phe Ser Arg Pro Ala Tyr Pro
465 470 475 480

Tyr Phe Asn Pro Trp Asn Cys Leu Val Pro Met Thr Val Cys Pro Pro
485 490 495

Ser Ser

<210> 45

<211> 1725

<212> DNA

<213> Homo sapiens

<400> 45

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<210> 46
 <211> 574
 <212> PRT
 <213> Homo sapiens

<400> 46

Met Ala Thr Leu Val Val Asn Lys Leu Gly Ala Gly Val Asp Ser Gly
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Arg Gln Gly Ser Arg Gly Thr Ala Val Val Lys Val Leu Glu Cys Gly
 20 25 30

Val Cys Glu Asp Val Phe Ser Leu Gln Gly Asp Lys Val Pro Arg Leu
 35 40 45

Leu Leu Cys Gly His Thr Val Cys His Asp Cys Leu Thr Arg Leu Pro
 50 55 60

Leu His Gly Arg Ala Ile Arg Cys Pro Phe Asp Arg Gln Val Thr Asp
 65 70 75 80

Leu Gly Asp Ser Gly Val Trp Gly Leu Lys Lys Asn Phe Ala Leu Leu
 85 90 95

Glu Leu Leu Glu Arg Leu Gln Asn Gly Pro Ile Gly Gln Tyr Gly Ala
100 105 110

Ala Glu Glu Ser Ile Gly Ile Ser Gly Glu Ser Ile Ile Arg Cys Asp
115 120 125

Glu Asp Glu Ala His Leu Ala Ser Val Tyr Cys Thr Val Cys Ala Thr
130 135 140

His Leu Cys Ser Glu Cys Ser Gln Val Thr His Ser Thr Lys Thr Leu
145 150 155 160

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

Met Cys Ser Gln His Gln Val His Ala Ile Glu Phe Val Cys Leu Glu
180 185 190

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

Gly Lys His Gln Gly His Lys His Ser Val Leu Glu Pro Glu Ala Asn
210 215 220

Gln Ile Arg Ala Ser Ile Leu Asp Met Ala His Cys Ile Arg Thr Phe
225 230 235 240

Thr Glu Glu Ile Ser Asp Tyr Ser Arg Lys Leu Val Gly Ile Val Gln
245 250 255

His Ile Glu Gly Gly Glu Gln Ile Val Glu Asp Gly Ile Gly Met Ala
260 265 270

His Thr Glu His Val Pro Gly Thr Ala Glu Asn Ala Arg Ser Cys Ile
275 280 285

Arg Ala Tyr Phe Tyr Asp Leu His Glu Thr Leu Cys Arg Gln Glu Glu
290 295 300

Met Ala Leu Ser Val Val Asp Ala His Val Arg Glu Lys Leu Ile Trp
305 310 315 320

Leu Arg Gln Gln Gln Glu Asp Met Thr Ile Leu Leu Ser Glu Val Ser
 325 330 335

Ala Ala Cys Leu His Cys Glu Lys Thr Leu Gln Gln Asp Asp Cys Arg
 340 345 350

Val Val Leu Ala Lys Gln Glu Ile Thr Arg Leu Leu Glu Thr Leu Gln
 355 360 365

Lys Gln Gln Gln Gln Phe Thr Glu Val Ala Asp His Ile Gln Leu Asp
 370 375 380

Ala Ser Ile Pro Val Thr Phe Thr Lys Asp Asn Arg Val His Ile Gly
385 390 395 400

Pro Lys Met Glu Ile Arg Val Val Thr Leu Gly Leu Asp Gly Ala Gly
 405 410 415

Lys Thr Thr Ile Leu Phe Lys Leu Lys Gln Asp Glu Phe Met Gln Pro
 420 425 430

Ile Pro Thr Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Leu
 435 440 445

Lys Phe Thr Ile Trp Asp Val Gly Gly Lys His Lys Leu Arg Pro Leu
 450 455 460

Trp Lys His Tyr Tyr Leu Asn Thr Gln Ala Val Val Phe Val Val Asp
465 470 475 480

Ser Ser His Arg Asp Arg Ile Ser Glu Ala His Ser Glu Leu Ala Lys
 485 490 495

Leu Leu Thr Glu Lys Glu Leu Arg Asp Ala Leu Leu Leu Ile Phe Ala
 500 505 510

Asn Lys Gln Asp Val Ala Gly Ala Leu Ser Val Glu Glu Ile Thr Glu
 515 520 525

Leu Leu Ser Leu His Lys Leu Cys Cys Gly Arg Ser Trp Tyr Ile Gln
 530 535 540

Gly Cys Asp Ala Arg Ser Gly Met Gly Leu Tyr Glu Gly Leu Asp Trp
 545 550 555 560

Leu Ser Arg Gln Leu Val Ala Ala Gly Val Leu Asp Val Ala
 565 570

<210> 47
 <211> 3153
 <212> DNA
 <213> Homo sapiens

<400> 47
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acaaaataca taaaattcac aggaaatcag atccaaaaca gaattattga agtaaatcaa 900
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ctaaagaacc tctatccaga aaaaagggtt ccaaaccag aattcaggaa tgaatcagaa 3060
gataataaat ttagtgatga ttcagatgat gactttgtac agccccggaa gaaacgcctc 3120
aaaagcattg aagaacgcca gttgcttaaa taa 3153

<210> 48

<211> 1050

<212> PRT

<213> Homo sapiens

<400> 48

Met Glu Val Ala Val Glu Lys Ala Val Ala Ala Ala Ala Ala Ser

1 5 10 15

Ala Ala Ala Ser Gly Gly Pro Ser Ala Ala Pro Ser Gly Glu Asn Glu

20 25 30

Ala Glu Ser Arg Gln Gly Pro Asp Ser Glu Arg Gly Gly Glu Ala Ala

35 40 45

Arg Leu Asn Leu Leu Asp Thr Cys Ala Val Cys His Gln Asn Ile Gln

50 55 60

Ser Arg Ala Pro Lys Leu Leu Pro Cys Leu His Ser Phe Cys Gln Arg
65 70 75 80

Cys Leu Pro Ala Pro Gln Arg Tyr Leu Met Leu Pro Ala Pro Met Leu
 85 90 95

Gly Ser Ala Glu Thr Pro Pro Pro Val Pro Ala Pro Gly Ser Pro Val
 100 105 110

Ser Gly Ser Ser Pro Phe Ala Thr Gln Val Gly Val Ile Arg Cys Pro
 115 120 125

Val Cys Ser Gln Glu Cys Ala Glu Arg His Ile Ile Asp Asn Phe Phe
 130 135 140

Val Lys Asp Thr Thr Glu Val Pro Ser Ser Thr Val Glu Lys Ser Asn
145 150 155 160

Gln Val Cys Thr Ser Cys Glu Asp Asn Ala Glu Ala Asn Gly Phe Cys
 165 170 175

Val Glu Cys Val Glu Trp Leu Cys Lys Thr Cys Ile Arg Ala His Gln
 180 185 190

Arg Val Lys Phe Thr Lys Asp His Thr Val Arg Gln Lys Glu Glu Val
 195 200 205

Ser Pro Glu Ala Val Gly Val Thr Ser Gln Arg Pro Val Phe Cys Pro
 210 215 220

Phe His Lys Lys Glu Gln Leu Lys Leu Tyr Cys Glu Thr Cys Asp Lys
225 230 235 240

Leu Thr Cys Arg Asp Cys Gln Leu Leu Glu His Lys Glu His Arg Tyr
 245 250 255

Gln Phe Ile Glu Glu Ala Phe Gln Asn Gln Lys Val Ile Ile Asp Thr
 260 265 270

Leu Ile Thr Lys Leu Met Glu Lys Thr Lys Tyr Ile Lys Phe Thr Gly
275 280 285

Asn Gln Ile Gln Asn Arg Ile Ile Glu Val Asn Gln Asn Gln Lys Gln
290 295 300

Val Glu Gln Asp Ile Lys Val Ala Ile Phe Thr Leu Met Val Glu Ile
305 310 315 320

Asn Lys Lys Gly Lys Ala Leu Leu His Gln Leu Glu Ser Leu Ala Lys
325 330 335

Asp His Arg Met Lys Leu Met Gln Gln Gln Gln Glu Val Ala Gly Leu
340 345 350

Ser Lys Gln Leu Glu His Val Met His Phe Ser Lys Trp Ala Val Ser
355 360 365

Ser Gly Ser Ser Thr Ala Leu Leu Tyr Ser Lys Arg Leu Ile Thr Tyr
370 375 380

Arg Leu Arg His Leu Leu Arg Ala Arg Cys Asp Ala Ser Pro Val Thr
385 390 395 400

Asn Asn Thr Ile Gln Phe His Cys Asp Pro Ser Phe Trp Ala Gln Asn
405 410 415

Ile Ile Asn Leu Gly Ser Leu Val Ile Glu Asp Lys Glu Ser Gln Pro
420 425 430

Gln Met Pro Lys Gln Asn Pro Val Val Glu Gln Asn Ser Gln Pro Pro
435 440 445

Ser Gly Leu Ser Ser Asn Gln Leu Ser Lys Phe Pro Thr Gln Ile Ser
450 455 460

Leu Ala Gln Leu Arg Leu Gln His Met Gln Gln Gln Val Met Ala Gln

465	470	475	480
Arg Gln Gln Val Gln Arg Arg Pro Ala Pro Val Gly Leu Pro Asn Pro			
	485	490	495
Arg Met Gln Gly Pro Ile Gln Gln Pro Ser Ile Ser His Gln Gln Pro			
	500	505	510
Pro Pro Arg Leu Ile Asn Phe Gln Asn His Ser Pro Lys Pro Asn Gly			
	515	520	525
Pro Val Leu Pro Pro His Pro Gln Gln Leu Arg Tyr Pro Pro Asn Gln			
	530	535	540
Asn Ile Pro Arg Gln Ala Ile Lys Pro Asn Pro Leu Gln Met Ala Phe			
545	550	555	560
Leu Ala Gln Gln Ala Ile Lys Gln Trp Gln Ile Ser Ser Gly Gln Gly			
	565	570	575
Thr Pro Ser Thr Thr Asn Ser Thr Ser Ser Thr Pro Ser Ser Pro Thr			
	580	585	590
Ile Thr Ser Ala Ala Gly Tyr Asp Gly Lys Ala Phe Gly Ser Pro Met			
	595	600	605
Ile Asp Leu Ser Ser Pro Val Gly Gly Ser Tyr Asn Leu Pro Ser Leu			
	610	615	620
Pro Asp Ile Asp Cys Ser Ser Thr Ile Met Leu Asp Asn Ile Val Arg			
625	630	635	640
Lys Asp Thr Asn Ile Asp His Gly Gln Pro Arg Pro Pro Ser Asn Arg			
	645	650	655
Thr Val Gln Ser Pro Asn Ser Ser Val Pro Ser Pro Gly Leu Ala Gly			
	660	665	670

Pro Val Thr Met Thr Ser Val His Pro Pro Ile Arg Ser Pro Ser Ala
675 680 685

Ser Ser Val Gly Ser Arg Gly Ser Ser Gly Ser Ser Ser Lys Pro Ala
690 695 700

Gly Ala Asp Ser Thr His Lys Val Pro Val Val Met Leu Glu Pro Ile
705 710 715 720

Arg Ile Lys Gln Glu Asn Ser Gly Pro Pro Glu Asn Tyr Asp Phe Pro
725 730 735

Val Val Ile Val Lys Gln Glu Ser Asp Glu Glu Ser Arg Pro Gln Asn
740 745 750

Ala Asn Tyr Pro Arg Ser Ile Leu Thr Ser Leu Leu Leu Asn Ser Ser
755 760 765

Gln Ser Ser Thr Ser Glu Glu Thr Val Leu Arg Ser Asp Ala Pro Asp
770 775 780

Ser Thr Gly Asp Gln Pro Gly Leu His Gln Asp Asn Ser Ser Asn Gly
785 790 795 800

Lys Ser Glu Trp Leu Asp Pro Ser Gln Lys Ser Pro Leu His Val Gly
805 810 815

Glu Thr Arg Lys Glu Asp Asp Pro Asn Glu Asp Trp Cys Ala Val Cys
820 825 830

Gln Asn Gly Gly Glu Leu Leu Cys Cys Glu Lys Cys Pro Lys Val Phe
835 840 845

His Leu Ser Cys His Val Pro Thr Leu Thr Asn Phe Pro Ser Gly Glu
850 855 860

Trp Ile Cys Thr Phe Cys Arg Asp Leu Ser Lys Pro Glu Val Glu Tyr
865 870 875 880

Asp Cys Asp Ala Pro Ser His Asn Ser Glu Lys Lys Lys Thr Glu Gly
885 890 895

Leu Val Lys Leu Thr Pro Ile Asp Lys Arg Lys Cys Glu Arg Leu Leu
900 905 910

Leu Phe Leu Tyr Cys His Glu Met Ser Leu Ala Phe Gln Asp Pro Val
915 920 925

Pro Leu Thr Val Pro Asp Tyr Tyr Lys Ile Ile Lys Asn Pro Met Asp
930 935 940

Leu Ser Thr Ile Lys Lys Arg Leu Gln Glu Asp Tyr Ser Met Tyr Ser
945 950 955 960

Lys Pro Glu Asp Phe Val Ala Asp Phe Arg Leu Ile Phe Gln Asn Cys
965 970 975

Ala Glu Phe Asn Glu Pro Asp Ser Glu Val Ala Asn Ala Gly Ile Lys
980 985 990

Leu Glu Asn Tyr Phe Glu Glu Leu Leu Lys Asn Leu Tyr Pro Glu Lys
995 1000 1005

Arg Phe Pro Lys Pro Glu Phe Arg Asn Glu Ser Glu Asp Asn Lys
1010 1015 1020

Phe Ser Asp Asp Ser Asp Asp Asp Phe Val Gln Pro Arg Lys Lys
1025 1030 1035

Arg Leu Lys Ser Ile Glu Glu Arg Gln Leu Leu Lys
1040 1045 1050

<210> 49

<211> 1893

<212> DNA

<213> Homo sapiens

<400> 49

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 tgggcagtcc agggctcgcc atacctgtgc ccgcagtgcc gcgccgtcta ccaggcgcga 180
 ccgcagtgc acaagaacac ggtgctgtgc aacgtggtgg agcagttcct gcaggccgac 240
 ctggcccggg agccacccgc cgacgtctgg acgccgccc cccgcgcctc tgcaccacg 300
 ccgaatgccc aggtggcctg cgaccactgc ctgaaggagg ccgccgtgaa gacgtgcttg 360
 gtgtgcatgg cctccttctg tcaggagcac ctgcagccgc acttcgacag cccgccttc 420
 caggaccacc cgctgcagcc gcccgttcgc gacctgtgc gccgcaaatg ttcccagcac 480
 aatcggctgc gggaatttt ctgccccgag cacagcgagt gcatctgcca catctgcctg 540
 gtggagcata agacctgtc tcccgcgtcc ctgagccagg ccagcgcga cctggaggcc 600
 accctgaggc acaactaac tgtcatgtac agtcagatca acggggcgtc gagagcactg 660
 gatgatgtga gaaacaggca gcaggatgtg cggatgactg caaacagaaa ggtggagcag 720
 ctacaacaag aatacacgga aatgaaggct ctcttgacg cctcagagac cacctcgaca 780
 aggaagataa aggaagagga gaagagggtc aacagcaagt ttgacacat ttatcagatt 840
 ctctcaaga agaagagtga gatccagacc ttgaaggagg agattgaaca gacgctgacc 900
 aagagggatg agttcgagtt tctggagaaa gcatcaaac tgcgaggaat ctcaacaaag 960
 ccagtctaca tccccgaggt ggaactgaac cacaagctga taaaaggcat ccaccagagc 1020
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 agttcaggtg accctggaga gcatgacca gcgtccacac acaaatccac acgccctgtg 1140
 aagaaggtct ccaaagagga aaagaaatcc aagaaacctc cccctgtccc tgccttacc 1200
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 gaggctgcag ccaaagccac cagctcacat ccgaactcaa catctctcaa ggccaagggtg 1320
 ctggagacct tcttgccaa gtccagacct gagctcctgg agtattacat taaagtcac 1380
 ctggactaca acaccgcca caacaaagt gctctgtcag agtgctatac agtagcttct 1440
 gtggctgaga tgcctcagaa ctaccggccg catccccaga ggttcacata ctgctctcag 1500
 gtgctgggcc tgactgcta caagaagggg atccactact gggaggtgga gctgcagaag 1560

aacaacttct gtgggtagg catctgctac ggaagcatga accggcaggg cccagaaagc 1620
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tggcacaata acgtggagaa aacctgccc tccaccaagg ccacgcgggt gggcgtgctt 1740
ctcaactgtg accacggctt tgtcatcttc ttcgctgtg ccgacaaggt ccacctgatg 1800
tataagttca ggggtggactt tactgaggct ttgtaccgg ctttctgggt atttctgct 1860
ggtgccacac tctcatctg ctccccaag tag 1893

<210> 50
<211> 630
<212> PRT
<213> Homo sapiens

<400> 50

Met Ala Glu Leu Cys Pro Leu Ala Glu Glu Leu Ser Cys Ser Ile Cys
1 5 10 15

Leu Glu Pro Phe Lys Glu Pro Val Thr Thr Pro Cys Gly His Asn Phe
20 25 30

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

Leu Cys Pro Gln Cys Arg Ala Val Tyr Gln Ala Arg Pro Gln Leu His
50 55 60

Lys Asn Thr Val Leu Cys Asn Val Val Glu Gln Phe Leu Gln Ala Asp
65 70 75 80

Leu Ala Arg Glu Pro Pro Ala Asp Val Trp Thr Pro Pro Ala Arg Ala
85 90 95

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

Glu Ala Ala Val Lys Thr Cys Leu Val Cys Met Ala Ser Phe Cys Gln
115 120 125

Glu His Leu Gln Pro His Phe Asp Ser Pro Ala Phe Gln Asp His Pro
130 135 140

Leu Gln Pro Pro Val Arg Asp Leu Leu Arg Arg Lys Cys Ser Gln His
145 150 155 160

Asn Arg Leu Arg Glu Phe Phe Cys Pro Glu His Ser Glu Cys Ile Cys
165 170 175

His Ile Cys Leu Val Glu His Lys Thr Cys Ser Pro Ala Ser Leu Ser
180 185 190

Gln Ala Ser Ala Asp Leu Glu Ala Thr Leu Arg His Lys Leu Thr Val
195 200 205

Met Tyr Ser Gln Ile Asn Gly Ala Ser Arg Ala Leu Asp Asp Val Arg
210 215 220

Asn Arg Gln Gln Asp Val Arg Met Thr Ala Asn Arg Lys Val Glu Gln
225 230 235 240

Leu Gln Gln Glu Tyr Thr Glu Met Lys Ala Leu Leu Asp Ala Ser Glu
245 250 255

Thr Thr Ser Thr Arg Lys Ile Lys Glu Glu Glu Lys Arg Val Asn Ser
260 265 270

Lys Phe Asp Thr Ile Tyr Gln Ile Leu Leu Lys Lys Lys Ser Glu Ile
275 280 285

Gln Thr Leu Lys Glu Glu Ile Glu Gln Ser Leu Thr Lys Arg Asp Glu
290 295 300

Phe Glu Phe Leu Glu Lys Ala Ser Lys Leu Arg Gly Ile Ser Thr Lys
305 310 315 320

Pro Val Tyr Ile Pro Glu Val Glu Leu Asn His Lys Leu Ile Lys Gly

325	330	335
Ile His Gln Ser Thr Ile Asp Leu Lys Asn Glu Leu Lys Gln Cys Ile		
340	345	350
Gly Arg Leu Gln Glu Pro Thr Pro Ser Ser Gly Asp Pro Gly Glu His		
355	360	365
Asp Pro Ala Ser Thr His Lys Ser Thr Arg Pro Val Lys Lys Val Ser		
370	375	380
Lys Glu Glu Lys Lys Ser Lys Lys Pro Pro Pro Val Pro Ala Leu Pro		
385	390	395
		400
Ser Lys Leu Pro Thr Phe Gly Ala Pro Glu Gln Leu Val Asp Leu Lys		
405	410	415
Gln Ala Gly Leu Glu Ala Ala Ala Lys Ala Thr Ser Ser His Pro Asn		
420	425	430
Ser Thr Ser Leu Lys Ala Lys Val Leu Glu Thr Phe Leu Ala Lys Ser		
435	440	445
Arg Pro Glu Leu Leu Glu Tyr Tyr Ile Lys Val Ile Leu Asp Tyr Asn		
450	455	460
Thr Ala His Asn Lys Val Ala Leu Ser Glu Cys Tyr Thr Val Ala Ser		
465	470	475
		480
Val Ala Glu Met Pro Gln Asn Tyr Arg Pro His Pro Gln Arg Phe Thr		
485	490	495
Tyr Cys Ser Gln Val Leu Gly Leu His Cys Tyr Lys Lys Gly Ile His		
500	505	510
Tyr Trp Glu Val Glu Leu Gln Lys Asn Asn Phe Cys Gly Val Gly Ile		
515	520	525

Cys Tyr Gly Ser Met Asn Arg Gln Gly Pro Glu Ser Arg Leu Gly Arg
 530 535 540

Asn Ser Ala Ser Trp Cys Val Glu Trp Phe Asn Thr Lys Ile Ser Ala
 545 550 555 560

Trp His Asn Asn Val Glu Lys Thr Leu Pro Ser Thr Lys Ala Thr Arg
 565 570 575

Val Gly Val Leu Leu Asn Cys Asp His Gly Phe Val Ile Phe Phe Ala
 580 585 590

Val Ala Asp Lys Val His Leu Met Tyr Lys Phe Arg Val Asp Phe Thr
 595 600 605

Glu Ala Leu Tyr Pro Ala Phe Trp Val Phe Ser Ala Gly Ala Thr Leu
 610 615 620

Ser Ile Cys Ser Pro Lys
 625 630

<210> 51

<211> 1620

<212> DNA

<213> Homo sapiens

<400> 51

atggccacgt cagccccact acggagcctg gaagaggagg tgacctgctc catctgtctt 60

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acagacgtcc gcccacatctc agggagccgc cccgtctgcc cactctgcaa gaagcctttt 180

aagaaggaga acatccgacc cgtgtggcaa ctggccagcc tggaggagaa cattgagcgg 240

ctgaaggtgg acaagggcag gcagccggga gaggtgacct gggagcagca ggatgcaaag 300

ttgtgcgagc gacaccgaga gaagctgcac tactactgtg aggacgacgg gaagctgctg 360

tgcgtgatgt gccgggagtc ccgggagcac agggcccaca cgccgtcct catggagaag 420

gccgcccagc cccacaggga aaaaatcctg aaccacctga gtaccctaag gagggacaga 480

gacaaaattc agggcttcca ggcaaaggga gaagctgata tcctggccgc gctgaagaag 540

ctccaggacc agaggcagta cattgtggct gaggttgagc agggatcatca gttcctgagg 600
 gagcgggagg aacacctgct ggaacagctg gcgaagctgg agcaggagct cacggagggc 660
 agggagaagt tcaagagccg gggcgtcggg gagcttgccc ggctggccct ggtcatctcc 720
 gaactggagg gcaaggcgca gcagccagct gcagagctca tgcaggacac gagagacttc 780
 ctaaacaggt atccacggaa gaagttctgg gttgggaaac ccattgctcg agtgggtaaa 840
 aaaaagaccg gagaattctc agataaactc ctctctctgc aacgaggcct gaggggaattc 900
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 aagggttca cctggggcaa ggtctactgg gaagtggaag tggagaggga gggctggtct 1140
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 tgggcgtgc gcctctctc ctccggcatc tgggccaaca ccagccccga ggctgagctt 1440
 ttccagcac tgcggccccg gagagtgggc atcgccctgg attatgaagg gggcaccgtg 1500
 actttacca acgcagagtc acaggaactc atctacact tcaactccac cttcaccgg 1560
 cgcctgtgcc cttctctgtg gctcaagtgg ccaggaacac gcctctgtct aagaccctga 1620

<210> 52

<211> 539

<212> PRT

<213> Homo sapiens

<400> 52

Met Ala Thr Ser Ala Pro Leu Arg Ser Leu Glu Glu Glu Val Thr Cys

1 5 10 15

Ser Ile Cys Leu Asp Tyr Leu Arg Asp Pro Val Thr Ile Asp Cys Gly

20 25 30

His Val Phe Cys Arg Ser Cys Thr Thr Asp Val Arg Pro Ile Ser Gly
35 40 45

Ser Arg Pro Val Cys Pro Leu Cys Lys Lys Pro Phe Lys Lys Glu Asn
50 55 60

Ile Arg Pro Val Trp Gln Leu Ala Ser Leu Val Glu Asn Ile Glu Arg
65 70 75 80

Leu Lys Val Asp Lys Gly Arg Gln Pro Gly Glu Val Thr Arg Glu Gln
85 90 95

Gln Asp Ala Lys Leu Cys Glu Arg His Arg Glu Lys Leu His Tyr Tyr
100 105 110

Cys Glu Asp Asp Gly Lys Leu Leu Cys Val Met Cys Arg Glu Ser Arg
115 120 125

Glu His Arg Pro His Thr Ala Val Leu Met Glu Lys Ala Ala Gln Pro
130 135 140

His Arg Glu Lys Ile Leu Asn His Leu Ser Thr Leu Arg Arg Asp Arg
145 150 155 160

Asp Lys Ile Gln Gly Phe Gln Ala Lys Gly Glu Ala Asp Ile Leu Ala
165 170 175

Ala Leu Lys Lys Leu Gln Asp Gln Arg Gln Tyr Ile Val Ala Glu Phe
180 185 190

Glu Gln Gly His Gln Phe Leu Arg Glu Arg Glu Glu His Leu Leu Glu
195 200 205

Gln Leu Ala Lys Leu Glu Gln Glu Leu Thr Glu Gly Arg Glu Lys Phe
210 215 220

Lys Ser Arg Gly Val Gly Glu Leu Ala Arg Leu Ala Leu Val Ile Ser

225	230	235	240
Glu Leu Glu Gly Lys Ala Gln Gln Pro Ala Ala Glu Leu Met Gln Asp			
	245	250	255
Thr Arg Asp Phe Leu Asn Arg Tyr Pro Arg Lys Lys Phe Trp Val Gly			
	260	265	270
Lys Pro Ile Ala Arg Val Val Lys Lys Lys Thr Gly Glu Phe Ser Asp			
	275	280	285
Lys Leu Leu Ser Leu Gln Arg Gly Leu Arg Glu Phe Gln Gly Lys Leu			
	290	295	300
Leu Arg Asp Leu Glu Tyr Lys Thr Val Ser Val Thr Leu Asp Pro Gln			
305	310	315	320
Ser Ala Ser Gly Tyr Leu Gln Leu Ser Glu Asp Trp Lys Cys Val Thr			
	325	330	335
Tyr Thr Ser Leu Tyr Lys Ser Ala Tyr Leu His Pro Gln Gln Phe Asp			
	340	345	350
Cys Glu Pro Gly Val Leu Gly Ser Lys Gly Phe Thr Trp Gly Lys Val			
	355	360	365
Tyr Trp Glu Val Glu Val Glu Arg Glu Gly Trp Ser Glu Asp Glu Glu			
	370	375	380
Glu Gly Asp Glu Glu Glu Glu Gly Glu Glu Glu Glu Glu Glu			
385	390	395	400
Ala Gly Tyr Gly Asp Gly Tyr Asp Asp Trp Glu Thr Asp Glu Asp Glu			
	405	410	415
Glu Ser Leu Gly Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu			
	420	425	430

Val Leu Glu Ser Cys Met Val Gly Val Ala Arg Asp Ser Val Lys Arg
 435 440 445

Lys Gly Asp Leu Ser Leu Arg Pro Glu Asp Gly Val Trp Ala Leu Arg
 450 455 460

Leu Ser Ser Ser Gly Ile Trp Ala Asn Thr Ser Pro Glu Ala Glu Leu
 465 470 475 480

Phe Pro Ala Leu Arg Pro Arg Arg Val Gly Ile Ala Leu Asp Tyr Glu
 485 490 495

Gly Gly Thr Val Thr Phe Thr Asn Ala Glu Ser Gln Glu Leu Ile Tyr
 500 505 510

Thr Phe Thr Ala Thr Phe Thr Arg Arg Leu Val Pro Phe Leu Trp Leu
 515 520 525

Lys Trp Pro Gly Thr Arg Leu Leu Leu Arg Pro
 530 535

<210> 53

<211> 1542

<212> DNA

<213> Homo sapiens

<400> 53

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 cagtacttcg cagagcccat gatgctcgac tgcggccata acatctgttg cgcgtgcctc 120
 gcccgtgct ggggcacggc agagactaac gtgtcgtgcc cgcagtgccg ggagaccttc 180
 ccgcagaggc acatgcggcc caaccggcac ctggccaacg tgaccaact ggtaaagcag 240
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 tccgcgagc accgcggcca cagcgtgctg ccgctcgagg aggcggtgga gggcttcaag 420
 gagcaaatcc agaaccagct cgaccattta aaaagagtga aagatttaa gaagagacgt 480
 cgggcccagg gggaacaggc acgagctgaa ctcttgagcc taaccagat ggagagggag 540

aagattgttt gggagtttga gcagctgtat cactccttaa aggagcatga gtatcgctc 600
ctggcccgcc ttgaggagct agacttgcc atctacaata gcatcaatgg tgccatcacc 660
cagttctctt gcaacatctc ccacctcagc agcctgatcg ctgagctaga agagaagcag 720
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atcaggattc ctgaaccttg gatcacacct ccagatttgc aagagaaaat ccacattttt 840
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catgttggga atcatgtgca ttcatggag acctcccctt ga 1542

<210> 54

<211> 513

<212> PRT

<213> Homo sapiens

<400> 54

Met Ala Ser Gly Ser Val Ala Glu Cys Leu Gln Gln Glu Thr Thr Cys

1 5 10 15

Pro Val Cys Leu Gln Tyr Phe Ala Glu Pro Met Met Leu Asp Cys Gly

20 25 30

His Asn Ile Cys Cys Ala Cys Leu Ala Arg Cys Trp Gly Thr Ala Glu
35 40 45

Thr Asn Val Ser Cys Pro Gln Cys Arg Glu Thr Phe Pro Gln Arg His
50 55 60

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

Leu Arg Thr Glu Arg Pro Ser Gly Pro Gly Gly Glu Met Gly Val Cys
85 90 95

Glu Lys His Arg Glu Pro Leu Lys Leu Tyr Cys Glu Glu Asp Gln Met
100 105 110

Pro Ile Cys Val Val Cys Asp Arg Ser Arg Glu His Arg Gly His Ser
115 120 125

Val Leu Pro Leu Glu Glu Ala Val Glu Gly Phe Lys Glu Gln Ile Gln
130 135 140

Asn Gln Leu Asp His Leu Lys Arg Val Lys Asp Leu Lys Lys Arg Arg
145 150 155 160

Arg Ala Gln Gly Glu Gln Ala Arg Ala Glu Leu Leu Ser Leu Thr Gln
165 170 175

Met Glu Arg Glu Lys Ile Val Trp Glu Phe Glu Gln Leu Tyr His Ser
180 185 190

Leu Lys Glu His Glu Tyr Arg Leu Leu Ala Arg Leu Glu Glu Leu Asp
195 200 205

Leu Ala Ile Tyr Asn Ser Ile Asn Gly Ala Ile Thr Gln Phe Ser Cys
210 215 220

Asn Ile Ser His Leu Ser Ser Leu Ile Ala Gln Leu Glu Glu Lys Gln
225 230 235 240

Gln Gln Pro Thr Arg Glu Leu Leu Gln Asp Ile Gly Asp Thr Leu Ser
245 250 255

Arg Ala Glu Arg Ile Arg Ile Pro Glu Pro Trp Ile Thr Pro Pro Asp
260 265 270

Leu Gln Glu Lys Ile His Ile Phe Ala Gln Lys Cys Leu Phe Leu Thr
275 280 285

Glu Ser Leu Lys Gln Phe Thr Glu Lys Met Gln Ser Asp Met Glu Lys
290 295 300

Ile Gln Glu Leu Arg Glu Ala Gln Leu Tyr Ser Val Asp Val Thr Leu
305 310 315 320

Asp Pro Asp Thr Ala Tyr Pro Ser Leu Ile Leu Ser Asp Asn Leu Arg
325 330 335

Gln Val Arg Tyr Ser Tyr Leu Gln Gln Asp Leu Pro Asp Asn Pro Glu
340 345 350

Arg Phe Asn Leu Phe Pro Cys Val Leu Gly Ser Pro Cys Phe Ile Ala
355 360 365

Gly Arg His Tyr Trp Glu Val Glu Val Gly Asp Lys Ala Lys Trp Thr
370 375 380

Ile Gly Val Cys Glu Asp Ser Val Cys Arg Lys Gly Gly Val Thr Ser
385 390 395 400

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

Tyr Trp Ala Leu Thr Ser Pro Met Thr Ala Leu Pro Leu Arg Thr Pro
420 425 430

Leu Gln Arg Val Gly Ile Phe Leu Asp Tyr Asp Ala Gly Glu Val Ser
435 440 445

Phe Tyr Asn Val Thr Glu Arg Cys His Thr Phe Thr Phe Ser His Ala
 450 455 460

Thr Phe Cys Gly Pro Val Arg Pro Tyr Phe Ser Leu Ser Tyr Ser Gly
 465 470 475 480

Gly Lys Ser Ala Ala Pro Leu Ile Ile Cys Pro Met Ser Gly Ile Asp
 485 490 495

Gly Phe Ser Gly His Val Gly Asn His Gly His Ser Met Glu Thr Ser
 500 505 510

Pro

<210> 55
 <211> 2508
 <212> DNA
 <213> Homo sapiens

<400> 55
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 ctgccctgtt tgactcggc ctgtagtgcc tgcttagggc ccgcgggccc cgccgccgcc 300
 aacagctcgg gggacggcgg ggcggcgggc gacggcaccg tggcggactg tcccgtgtgc 360
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 aaggctgcca ccgacgcca ggatgcgaac cagtgtgca ctagctgtga ggataatgcc 480
 ccagccacca gctacttgtt ggagtgtctg ggcctctgt gtgagacctg ttagaggcg 540
 caccagcggg tgaagtacac caaggacat actgtgcgct ctactgggcc agccaagtct 600
 cgggatggtg aacgtactgt ctattgcaac gtacacaagc atgaaccct tgtgtgttt 660
 tgtgagagct gtgatactct cacctgccga gactgccagc tcaatgccca caaggaccac 720

cagtaccagt tcttagagga tgcaagtagg aaccagcgca agtcctggc ctactggtg 780
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<210> 56
 <211> 835
 <212> PRT
 <213> Homo sapiens

<400> 56

Met Ala Ala Ser Ala Ala Ala Ser Ala Ala Ala Ser Ala Ala
 1 5 10 15

Ser Gly Ser Pro Gly Pro Gly Glu Gly Ser Ala Gly Gly Glu Lys Arg
 20 25 30

Ser Thr Ala Pro Ser Ala Ala Ala Ser Ala Ser Ala Ser Ala Ala Ala
 35 40 45

Ser Ser Pro Ala Gly Gly Gly Ala Glu Ala Leu Glu Leu Leu Glu His
 50 55 60

Cys Gly Val Cys Arg Glu Arg Leu Arg Pro Glu Arg Glu Pro Arg Leu
 65 70 75 80

Leu Pro Cys Leu His Ser Ala Cys Ser Ala Cys Leu Gly Pro Ala Ala
 85 90 95

Pro Ala Ala Ala Asn Ser Ser Gly Asp Gly Gly Ala Ala Gly Asp Gly
 100 105 110

Thr Val Val Asp Cys Pro Val Cys Lys Gln Gln Cys Phe Ser Lys Asp
 115 120 125

Ile Val Glu Asn Tyr Phe Met Arg Asp Ser Gly Ser Lys Ala Ala Thr

130	135	140	
Asp Ala Gln Asp Ala Asn Gln Cys Cys Thr Ser Cys Glu Asp Asn Ala			
145	150	155	160
Pro Ala Thr Ser Tyr Cys Val Glu Cys Ser Glu Pro Leu Cys Glu Thr			
	165	170	175
Cys Val Glu Ala His Gln Arg Val Lys Tyr Thr Lys Asp His Thr Val			
	180	185	190
Arg Ser Thr Gly Pro Ala Lys Ser Arg Asp Gly Glu Arg Thr Val Tyr			
	195	200	205
Cys Asn Val His Lys His Glu Pro Leu Val Leu Phe Cys Glu Ser Cys			
	210	215	220
Asp Thr Leu Thr Cys Arg Asp Cys Gln Leu Asn Ala His Lys Asp His			
	225	230	235
			240
Gln Tyr Gln Phe Leu Glu Asp Ala Val Arg Asn Gln Arg Lys Leu Leu			
	245	250	255
Ala Ser Leu Val Lys Arg Leu Gly Asp Lys His Ala Thr Leu Gln Lys			
	260	265	270
Ser Thr Lys Glu Val Arg Ser Ser Ile Arg Gln Val Ser Asp Val Gln			
	275	280	285
Lys Arg Val Gln Val Asp Val Lys Met Ala Ile Leu Gln Ile Met Lys			
	290	295	300
Glu Leu Asn Lys Arg Gly Arg Val Leu Val Asn Asp Ala Gln Lys Val			
	305	310	315
			320
Thr Glu Gly Gln Gln Glu Arg Leu Glu Arg Gln His Trp Thr Met Thr			
	325	330	335

Lys Ile Gln Lys His Gln Glu His Ile Leu Arg Phe Ala Ser Trp Ala
340 345 350

Leu Glu Ser Asp Asn Asn Thr Ala Leu Leu Leu Ser Lys Lys Leu Ile
355 360 365

Tyr Phe Gln Leu His Arg Ala Leu Lys Met Ile Val Asp Pro Val Glu
370 375 380

Pro His Gly Glu Met Lys Phe Gln Trp Asp Leu Asn Ala Trp Thr Lys
385 390 395 400

Ser Ala Glu Ala Phe Gly Lys Ile Val Ala Glu Arg Pro Gly Thr Asn
405 410 415

Ser Thr Gly Pro Ala Pro Met Ala Pro Pro Arg Ala Pro Gly Pro Leu
420 425 430

Ser Lys Gln Gly Ser Gly Ser Ser Gln Pro Met Glu Val Gln Glu Gly
435 440 445

Tyr Gly Phe Gly Ser Gly Asp Asp Pro Tyr Ser Ser Ala Glu Pro His
450 455 460

Val Ser Gly Val Lys Arg Ser Arg Ser Gly Glu Gly Glu Val Ser Gly
465 470 475 480

Leu Met Arg Lys Val Pro Arg Val Ser Leu Glu Arg Leu Asp Leu Asp
485 490 495

Leu Thr Ala Asp Ser Gln Pro Pro Val Phe Lys Val Phe Pro Gly Ser
500 505 510

Thr Thr Glu Asp Tyr Asn Leu Ile Val Ile Glu Arg Gly Ala Ala Ala
515 520 525

Ala Ala Thr Gly Gln Pro Gly Thr Ala Pro Ala Gly Thr Pro Gly Ala
530 535 540

Pro Pro Leu Ala Gly Met Ala Ile Val Lys Glu Glu Glu Thr Glu Ala
545 550 555 560

Ala Ile Gly Ala Pro Pro Thr Ala Thr Glu Gly Pro Glu Thr Lys Pro
 565 570 575

Val Leu Met Ala Leu Ala Glu Gly Pro Gly Ala Glu Gly Pro Arg Leu
 580 585 590

Ala Ser Pro Ser Gly Ser Thr Ser Ser Gly Leu Glu Val Val Ala Pro
 595 600 605

Glu Gly Thr Ser Ala Pro Gly Gly Gly Pro Gly Thr Leu Asp Asp Ser
 610 615 620

Ala Thr Ile Cys Arg Val Cys Gln Lys Pro Gly Asp Leu Val Met Cys
625 630 635 640

Asn Gln Cys Glu Phe Cys Phe His Leu Asp Cys His Leu Pro Ala Leu
 645 650 655

Gln Asp Val Pro Gly Glu Glu Trp Ser Cys Ser Leu Cys His Val Leu
 660 665 670

Pro Asp Leu Lys Glu Glu Asp Gly Ser Leu Ser Leu Asp Gly Ala Asp
 675 680 685

Ser Thr Gly Val Val Ala Lys Leu Ser Pro Ala Asn Gln Arg Lys Cys
 690 695 700

Glu Arg Val Leu Leu Ala Leu Phe Cys His Glu Pro Cys Arg Pro Leu
705 710 715 720

His Gln Leu Ala Thr Asp Ser Thr Phe Ser Leu Asp Gln Pro Gly Gly
 725 730 735

Thr Leu Asp Leu Thr Leu Ile Arg Ala Arg Leu Gln Glu Lys Leu Ser
 740 745 750

Pro Pro Tyr Ser Ser Pro Gln Glu Phe Ala Gln Asp Val Gly Arg Met
 755 760 765

Phe Lys Gln Phe Asn Lys Leu Thr Glu Asp Lys Ala Asp Val Gln Ser
 770 775 780

Ile Ile Gly Leu Gln Arg Phe Phe Glu Thr Arg Met Asn Glu Ala Phe
 785 790 795 800

Gly Asp Thr Lys Phe Ser Ala Val Leu Val Glu Pro Pro Pro Met Ser
 805 810 815

Leu Pro Gly Ala Gly Leu Ser Ser Gln Glu Leu Ser Gly Gly Pro Gly
 820 825 830

Asp Gly Pro
 835

<210> 57

<211> 1767

<212> DNA

<213> Homo sapiens

<400> 57

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agcccgctcg gcccagtgg cagcctggag aatggcacca aggctgacgg caaggatgcc 120

aagaccacca acgggcacgg cggggaggca gctgagggca agagcctggg cagcgcctg 180

aagccagggg aaggtaggag cgccctgttc gcgggcaatg agtggcggcg acccatcatc 240

cagtttgtcg agtccgggga cgacaagaac tccaactact tcagcatgga ctctatggaa 300

ggcaagaggt cgccgtacgc agggctccag ctgggggctg ccaagaagcc acccgttacc 360

tttgccgaaa agggcgagct gcgcaagtcc attttctcg agtcccggaa gccacggtg 420

tccatcatgg agcccgggga gaccggcgga aacagctacc cccgggccga cacgggcctt 480

ttttcacggt ccaagtccgg ctccgaggag gtgctgtgcg actcctgcat cggcaacaag 540

cagaaggcgg tcaagtctg cctggtgtgc caggcctct tctgcgagct gcatttcaag 600

cccacctgg agggcgccgc cttccgagac caccagctgc tcgagcccat ccgggacttt 660
 gaggcccgca agtgtcccg tcatggcaag acgatggagc tcttctgcca gaccgaccag 720
 acctgcatct gctacctttg catgttccag gagcacaaga atcatagcac cgtgacagtg 780
 gaggaggcca aggccgagaa ggagacggag ctgtcattgc aaaaggagca gctgcagctc 840
 aagatcattg agattgagga tgaagctgag aagtggcaga aggagaagga ccgcatcaag 900
 agcttcacca ccaatgagaa ggccatcctg gagcagaact tccgggacct ggtgcgggac 960
 ctggagaagc aaaaggagga agtgagggt gcgctggagc agcgggagca ggatgctgtg 1020
 gaccaagtga aggtgatcat ggatgctctg gatgagagag ccaaggtgct gcatgaggac 1080
 aagcagaccg gggagcagct gcatagcatc agcgactctg tgtgtttct gcaggaattt 1140
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 cacatggaga acggtggtga ccacgctat gtgaacaact acacgaacag ctcgggggt 1380
 gagtggagtg caccggacac catgaagaga tactccatgt acctgacacc caaagtgagg 1440
 gtccggacat cataccagcc ctctctctt ggccgcttca ccaaggagac caccagaag 1500
 aatttaaca atctctatgg cacaaagg taaactacct cccgggtctg ggagtactcc 1560
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 ctgaaaggct atccctcct catgaggagc caaagcccca aggccagcc ccagacttg 1680
 aaatctggca agcagactat gctgtctcac taccggccat tctacgtcaa caaaggcaac 1740
 gggattgggt ccaacgaagc cccatga 1767

<210> 58

<211> 588

<212> PRT

<213> Homo sapiens

<400> 58

Met Glu Ala Ala Asp Ala Ser Arg Ser Asn Gly Ser Ser Pro Glu Ala

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Arg Asp Ala Arg Ser Pro Ser Gly Pro Ser Gly Ser Leu Glu Asn Gly
20 25 30

Thr Lys Ala Asp Gly Lys Asp Ala Lys Thr Thr Asn Gly His Gly Gly
35 40 45

Glu Ala Ala Glu Gly Lys Ser Leu Gly Ser Ala Leu Lys Pro Gly Glu
50 55 60

Gly Arg Ser Ala Leu Phe Ala Gly Asn Glu Trp Arg Arg Pro Ile Ile
65 70 75 80

Gln Phe Val Glu Ser Gly Asp Asp Lys Asn Ser Asn Tyr Phe Ser Met
85 90 95

Asp Ser Met Glu Gly Lys Arg Ser Pro Tyr Ala Gly Leu Gln Leu Gly
100 105 110

Ala Ala Lys Lys Pro Pro Val Thr Phe Ala Glu Lys Gly Glu Leu Arg
115 120 125

Lys Ser Ile Phe Ser Glu Ser Arg Lys Pro Thr Val Ser Ile Met Glu
130 135 140

Pro Gly Glu Thr Arg Arg Asn Ser Tyr Pro Arg Ala Asp Thr Gly Leu
145 150 155 160

Phe Ser Arg Ser Lys Ser Gly Ser Glu Glu Val Leu Cys Asp Ser Cys
165 170 175

Ile Gly Asn Lys Gln Lys Ala Val Lys Ser Cys Leu Val Cys Gln Ala
180 185 190

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

Arg Asp His Gln Leu Leu Glu Pro Ile Arg Asp Phe Glu Ala Arg Lys

210	215	220	
Cys Pro Val His Gly Lys Thr Met Glu Leu Phe Cys Gln Thr Asp Gln			
225	230	235	240
Thr Cys Ile Cys Tyr Leu Cys Met Phe Gln Glu His Lys Asn His Ser			
245	250	255	
Thr Val Thr Val Glu Glu Ala Lys Ala Glu Lys Glu Thr Glu Leu Ser			
260	265	270	
Leu Gln Lys Glu Gln Leu Gln Leu Lys Ile Ile Glu Ile Glu Asp Glu			
275	280	285	
Ala Glu Lys Trp Gln Lys Glu Lys Asp Arg Ile Lys Ser Phe Thr Thr			
290	295	300	
Asn Glu Lys Ala Ile Leu Glu Gln Asn Phe Arg Asp Leu Val Arg Asp			
305	310	315	320
Leu Glu Lys Gln Lys Glu Glu Val Arg Ala Ala Leu Glu Gln Arg Glu			
325	330	335	
Gln Asp Ala Val Asp Gln Val Lys Val Ile Met Asp Ala Leu Asp Glu			
340	345	350	
Arg Ala Lys Val Leu His Glu Asp Lys Gln Thr Arg Glu Gln Leu His			
355	360	365	
Ser Ile Ser Asp Ser Val Leu Phe Leu Gln Glu Phe Gly Ala Leu Met			
370	375	380	
Ser Asn Tyr Ser Leu Pro Pro Pro Leu Pro Thr Tyr His Val Leu Leu			
385	390	395	400
Glu Gly Glu Gly Leu Gly Gln Ser Leu Gly Asn Phe Lys Asp Asp Leu			
405	410	415	

Leu Asn Val Cys Met Arg His Val Glu Lys Met Cys Lys Ala Asp Leu
420 425 430

Ser Arg Asn Phe Ile Glu Arg Asn His Met Glu Asn Gly Gly Asp His
435 440 445

Arg Tyr Val Asn Asn Tyr Thr Asn Ser Phe Gly Gly Glu Trp Ser Ala
450 455 460

Pro Asp Thr Met Lys Arg Tyr Ser Met Tyr Leu Thr Pro Lys Gly Gly
465 470 475 480

Val Arg Thr Ser Tyr Gln Pro Ser Ser Pro Gly Arg Phe Thr Lys Glu
485 490 495

Thr Thr Gln Lys Asn Phe Asn Asn Leu Tyr Gly Thr Lys Gly Asn Tyr
500 505 510

Thr Ser Arg Val Trp Glu Tyr Ser Ser Ser Ile Gln Asn Ser Asp Asn
515 520 525

Asp Leu Pro Val Val Gln Gly Ser Ser Ser Phe Ser Leu Lys Gly Tyr
530 535 540

Pro Ser Leu Met Arg Ser Gln Ser Pro Lys Ala Gln Pro Gln Thr Trp
545 550 555 560

Lys Ser Gly Lys Gln Thr Met Leu Ser His Tyr Arg Pro Phe Tyr Val
565 570 575

Asn Lys Gly Asn Gly Ile Gly Ser Asn Glu Ala Pro
580 585

<210> 59

<211> 1491

<212> DNA

<213> Mus musculus

<400> 59

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 ctgaattatg agtccaacag aaacacagac gggaaggga actgccctgt atgccgagtt 180
 ccttaccat ttgggaatct gaggcctaata ctacatgtgg ccaacatagt agagaggctc 240
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 gagaaactcc ggctcttctg taggaaggac atgatggta tctgctggct ttgtgagcga 360
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 gagaagctgc agggagctct gtggaagctg atgaaaaagg caaaaatatg tgatgaatgg 480
 caggatgacc ttcaactgca gagagttgac tgggagaacc aaatacagat caatgtagaa 540
 aatgttcaga gacagtttaa aggactaaga gacctctgg actccaagga gaatgaggag 600
 ctgcagaagc tgaagaaaga gaagaaagag gttatggaaa agctggaaga gtctgaaaat 660
 gagctggagg atcagacaga gttgtgaga gacctcatct cagatgtgga acatcattg 720
 gagctctcaa ccttagaaat gctgcagggt gcaaattgtg tctgagaag gagtcagtc 780
 ttaagcctgc aacagcccca aactgtccc caaaagagaa aaagaacatt ccaagctcca 840
 gatctgaaag gcatgtgca agtgtatcaa ggactcatgg atatccagca atactgggtt 900
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 aatcctatga aatgttcaga gccaatgact atatgcgggc caccctcta a 1491

<210> 60

<211> 496

<212> PRT

<213> Mus musculus

<400> 60

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

Ser Phe Cys Arg Ala Cys Ile Thr Leu Asn Tyr Glu Ser Asn Arg Asn
35 40 45

Thr Asp Gly Lys Gly Asn Cys Pro Val Cys Arg Val Pro Tyr Pro Phe
50 55 60

Gly Asn Leu Arg Pro Asn Leu His Val Ala Asn Ile Val Glu Arg Leu
65 70 75 80

Lys Gly Phe Lys Ser Ile Pro Glu Glu Glu Gln Lys Val Asn Ile Cys
85 90 95

Ala Gln His Gly Glu Lys Leu Arg Leu Phe Cys Arg Lys Asp Met Met
100 105 110

Val Ile Cys Trp Leu Cys Glu Arg Ser Gln Glu His Arg Gly His Gln
115 120 125

Thr Ala Leu Ile Glu Glu Val Asp Gln Glu Tyr Lys Glu Lys Leu Gln
130 135 140

Gly Ala Leu Trp Lys Leu Met Lys Lys Ala Lys Ile Cys Asp Glu Trp
145 150 155 160

Gln Asp Asp Leu Gln Leu Gln Arg Val Asp Trp Glu Asn Gln Ile Gln
165 170 175

Ile Asn Val Glu Asn Val Gln Arg Gln Phe Lys Gly Leu Arg Asp Leu

180	185	190
Leu Asp Ser Lys Glu Asn Glu Glu Leu Gln Lys Leu Lys Lys Glu Lys		
195	200	205
Lys Glu Val Met Glu Lys Leu Glu Glu Ser Glu Asn Glu Leu Glu Asp		
210	215	220
Gln Thr Glu Leu Val Arg Asp Leu Ile Ser Asp Val Glu His His Leu		
225	230	235 240
Glu Leu Ser Thr Leu Glu Met Leu Gln Gly Ala Asn Cys Val Leu Arg		
245	250	255
Arg Ser Gln Ser Leu Ser Leu Gln Gln Pro Gln Thr Val Pro Gln Lys		
260	265	270
Arg Lys Arg Thr Phe Gln Ala Pro Asp Leu Lys Gly Met Leu Gln Val		
275	280	285
Tyr Gln Gly Leu Met Asp Ile Gln Gln Tyr Trp Val His Met Thr Leu		
290	295	300
His Ala Arg Asn Asn Ala Val Ile Ala Ile Asn Lys Glu Lys Arg Gln		
305	310	315 320
Ile Gln Tyr Arg Ser Tyr Asn Thr Val Pro Val Ser Glu Ile Tyr His		
325	330	335
Leu Gly Val Leu Gly Tyr Pro Ala Leu Ser Ser Gly Lys His Tyr Trp		
340	345	350
Glu Val Asp Ile Ser Arg Ser Asp Ala Trp Leu Leu Gly Leu Asn Asp		
355	360	365
Gly Lys Cys Ala Gln Pro Gln Leu His Ser Lys Glu Glu Met Gly Ile		
370	375	380

Lys Lys Asn Leu His Ser Gln Ile Lys Gln Asn Val Leu Phe Gln Pro
 385 390 395 400

Lys Cys Gly Tyr Trp Val Ile Gly Met Lys Asn Pro Ser Val Tyr Lys
 405 410 415

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

Ser Leu Pro Asp Arg Pro Ser Arg Val Gly Val Phe Leu Asp Arg Lys
 435 440 445

Ala Gly Thr Leu Ser Phe Tyr Asp Val Ser Asn Cys Gly Ala Leu Ile
 450 455 460

Tyr Arg Phe Tyr Asp Pro Ala Phe Pro Val Glu Val Tyr Pro Tyr Phe
 465 470 475 480

Asn Pro Met Lys Cys Ser Glu Pro Met Thr Ile Cys Gly Pro Pro Ser
 485 490 495

<210> 61

<211> 1278

<212> DNA

<213> Homo sapiens

<400> 61

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gacattctgc agaaacctgt caccatcgac tgtgggcaca atttctgcct caaatgcatc 120

actcagattg gggaaacatc atgtggattt ttcaaatgtc ccctctgcaa aactccgta 180

aggaagaacg caatcaggtt caactcgctg ttgcggaatc tggaggagaa aatccaagct 240

ctacaagcct ctgaggtgca gtccaaaagg aaagaggcta catgcccag gaccaggag 300

atgttcact atttctgca g gatgatggg aagttcctct gttttgtgt tcgtgaatcc 360

aaggaccaca aatcccataa tgtcagcttg atcgaagaag ctgccagaa ttatcagggg 420

cagattcaag agcagatcca agtcttgca caaaaggaga aggagacagt acaagtgaag 480

gcacaaggtg tacacaggtt cgatgtcttc acggaccagg tagaacatga gaagcaaagg 540

atcctcacag aatttgaact cctgcatcaa gtcctagagg aggagaagaa tttcctgcta 600
 tcacggattt actggctggg tcatgaggga acggaagcgg ggaaacacta tgtgcctcc 660
 actgagccac agttgaacga tctcaagaag ctggttgatt ccctgaagac caagcagaac 720
 atgccacca ggcagctgct ggaggatata aaagtcgtct tgtgcagaag tgaagagttt 780
 cagtttctca acccaacccc tgttcctctg gaactggaga aaaaactcag tgaagcaaaa 840
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 gatgagattt ctggtcaagg agcgagctct caggatacga agacattga cgttgcgctg 1200
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 gaggttcctt caagctaa 1278

<210> 62

<211> 425

<212> PRT

<213> Homo sapiens

<400> 62

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

His Asn Phe Cys Leu Lys Cys Ile Thr Gln Ile Gly Glu Thr Ser Cys
 35 40 45

Gly Phe Phe Lys Cys Pro Leu Cys Lys Thr Ser Val Arg Lys Asn Ala
 50 55 60

Ile Arg Phe Asn Ser Leu Leu Arg Asn Leu Val Glu Lys Ile Gln Ala
65 70 75 80

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

Arg His Gln Glu Met Phe His Tyr Phe Cys Glu Asp Asp Gly Lys Phe
 100 105 110

Leu Cys Phe Val Cys Arg Glu Ser Lys Asp His Lys Ser His Asn Val
 115 120 125

Ser Leu Ile Glu Glu Ala Ala Gln Asn Tyr Gln Gly Gln Ile Gln Glu
 130 135 140

Gln Ile Gln Val Leu Gln Gln Lys Glu Lys Glu Thr Val Gln Val Lys
145 150 155 160

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

Glu Lys Gln Arg Ile Leu Thr Glu Phe Glu Leu Leu His Gln Val Leu
 180 185 190

Glu Glu Glu Lys Asn Phe Leu Leu Ser Arg Ile Tyr Trp Leu Gly His
 195 200 205

Glu Gly Thr Glu Ala Gly Lys His Tyr Val Ala Ser Thr Glu Pro Gln
 210 215 220

Leu Asn Asp Leu Lys Lys Leu Val Asp Ser Leu Lys Thr Lys Gln Asn
225 230 235 240

Met Pro Pro Arg Gln Leu Leu Glu Asp Ile Lys Val Val Leu Cys Arg
 245 250 255

Ser Glu Glu Phe Gln Phe Leu Asn Pro Thr Pro Val Pro Leu Glu Leu
 260 265 270

Glu Lys Lys Leu Ser Glu Ala Lys Ser Arg His Asp Ser Ile Thr Gly
275 280 285

Ser Leu Lys Lys Phe Lys Asp Gln Leu Gln Ala Asp Arg Lys Lys Asp
290 295 300

Glu Asn Arg Phe Phe Lys Ser Met Asn Lys Asn Asp Met Lys Ser Trp
305 310 315 320

Gly Leu Leu Gln Lys Asn Asn His Lys Met Asn Lys Thr Ser Glu Pro
325 330 335

Gly Ser Ser Ser Ala Gly Gly Arg Thr Thr Ser Gly Pro Pro Asn His
340 345 350

His Ser Ser Ala Pro Ser His Ser Leu Phe Arg Ala Ser Ser Ala Gly
355 360 365

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

Gly Gln Gly Ala Ser Ser Gln Asp Thr Lys Thr Phe Asp Val Ala Leu
385 390 395 400

Ser Glu Glu Leu His Ala Ala Leu Ser Glu Trp Leu Thr Ala Ile Arg
405 410 415

Ala Trp Phe Cys Glu Val Pro Ser Ser
420 425

<210> 63

<211> 1962

<212> DNA

<213> Homo sapiens

<400> 63

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cataccatct gccgccagt cctggagaag ctattggcca gtagcatcaa tgggtgccgc 180
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aagatctaca gctaccatct gagaagatat tccaccccat ag 1962

<210> 64

<211> 653

<212> PRT

<213> Homo sapiens

<400> 64

Met Ala Ala Ala Ala Ala Ser His Leu Asn Leu Asp Ala Leu Arg Glu
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Val Leu Glu Cys Pro Ile Cys Met Glu Ser Phe Thr Glu Glu Gln Leu
20 25 30

Arg Pro Lys Leu Leu His Cys Gly His Thr Ile Cys Arg Gln Cys Leu
35 40 45

Glu Lys Leu Leu Ala Ser Ser Ile Asn Gly Val Arg Cys Pro Phe Cys
50 55 60

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

Thr Val Leu Lys Ile Ile Asp Thr Ala Gly Leu Ser Glu Ala Val Gly
85 90 95

Leu Leu Met Cys Arg Ser Cys Gly Arg Arg Leu Pro Arg Gln Phe Cys
100 105 110

Arg Ser Cys Gly Leu Val Leu Cys Glu Pro Cys Arg Glu Ala Asp His
115 120 125

Gln Pro Pro Gly His Cys Thr Leu Pro Val Lys Glu Ala Ala Glu Glu
130 135 140

Arg Arg Arg Asp Phe Gly Glu Lys Leu Thr Arg Leu Arg Glu Leu Met
145 150 155 160

Gly Glu Leu Gln Arg Arg Lys Ala Ala Leu Glu Gly Val Ser Lys Asp
165 170 175

Leu Gln Ala Arg Tyr Lys Ala Val Leu Gln Glu Tyr Gly His Glu Glu
180 185 190

Arg Arg Val Gln Asp Glu Leu Ala Arg Ser Arg Lys Phe Phe Thr Gly
195 200 205

Ser Leu Ala Glu Val Glu Lys Ser Asn Ser Gln Val Val Glu Glu Gln
210 215 220

Ser Tyr Leu Leu Asn Ile Ala Glu Val Gln Ala Val Ser Arg Cys Asp
225 230 235 240

Tyr Phe Leu Ala Lys Ile Lys Gln Ala Asp Val Ala Leu Leu Glu Glu
245 250 255

Thr Ala Asp Glu Glu Glu Pro Glu Leu Thr Ala Ser Leu Pro Arg Glu
260 265 270

Leu Thr Leu Gln Asp Val Glu Leu Leu Lys Val Gly His Val Gly Pro
275 280 285

Leu Gln Ile Gly Gln Ala Val Lys Lys Pro Arg Thr Val Asn Val Glu
290 295 300

Asp Ser Trp Ala Met Glu Ala Thr Ala Ser Ala Ala Ser Thr Ser Val
305 310 315 320

Thr Phe Arg Glu Met Asp Met Ser Pro Glu Glu Val Val Ala Ser Pro
325 330 335

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

Gln Gln Cys Leu Phe Leu Lys Lys Met Gly Ala Lys Gly Ser Thr Pro
355 360 365

Gly Met Phe Asn Leu Pro Val Ser Leu Tyr Val Thr Ser Gln Gly Glu
370 375 380

Val Leu Val Ala Asp Arg Gly Asn Tyr Arg Ile Gln Val Phe Thr Arg
385 390 395 400

Lys Gly Phe Leu Lys Glu Ile Arg Arg Ser Pro Ser Gly Ile Asp Ser
405 410 415

Phe Val Leu Ser Phe Leu Gly Ala Asp Leu Pro Asn Leu Thr Pro Leu
420 425 430

Ser Val Ala Met Asn Cys Gln Gly Leu Ile Gly Val Thr Asp Ser Tyr
435 440 445

Asp Asn Ser Leu Lys Val Tyr Thr Leu Asp Gly His Cys Val Ala Cys
450 455 460

His Arg Ser Gln Leu Ser Lys Pro Trp Gly Ile Thr Ala Leu Pro Ser
465 470 475 480

Gly Gln Phe Val Val Thr Asp Val Glu Gly Gly Lys Leu Trp Cys Phe
485 490 495

Thr Val Asp Arg Gly Ser Gly Val Val Lys Tyr Ser Cys Leu Cys Ser
500 505 510

Ala Val Arg Pro Lys Phe Val Thr Cys Asp Ala Glu Gly Thr Val Tyr
515 520 525

Phe Thr Gln Gly Leu Gly Leu Asn Leu Glu Asn Arg Gln Asn Glu His
530 535 540

His Leu Glu Gly Gly Phe Ser Ile Gly Ser Val Gly Pro Asp Gly Gln
 545 550 555 560

Leu Gly Arg Gln Ile Ser His Phe Phe Ser Glu Asn Glu Asp Phe Arg
 565 570 575

Cys Ile Ala Gly Met Cys Val Asp Ala Arg Gly Asp Leu Ile Val Ala
 580 585 590

Asp Ser Ser Arg Lys Glu Ile Leu His Phe Pro Lys Gly Gly Gly Tyr
 595 600 605

Ser Val Leu Ile Arg Glu Gly Leu Thr Cys Pro Val Gly Ile Ala Leu
 610 615 620

Thr Pro Lys Gly Gln Leu Leu Val Leu Asp Cys Trp Asp His Cys Ile
 625 630 635 640

Lys Ile Tyr Ser Tyr His Leu Arg Arg Tyr Ser Thr Pro
 645 650

<210> 65

<211> 3384

<212> DNA

<213> Homo sapiens

<400> 65

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gtgctggtgg aggaggagga ggaggaaggc ggcagggccg gcgctgaggg cggcgcggcc 180

ggggccgacg acgggggggt ggccgcggcc tcctcgggct cggcccaggc tgcttcatct 240

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gagagaccag tacatataaa gtaa 3384

<210> 66

<211> 1127

<212> PRT

<213> Homo sapiens

<400> 66

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

Glu Gly Gly Arg Ala Gly Ala Glu Gly Gly Ala Ala Gly Pro Asp Asp
50 55 60

Gly Gly Val Ala Ala Ala Ser Ser Gly Ser Ala Gln Ala Ala Ser Ser
65 70 75 80

Pro Ala Ala Ser Val Gly Thr Gly Val Ala Gly Gly Ala Val Ser Thr
85 90 95

Pro Ala Pro Ala Pro Ala Ser Ala Pro Ala Pro Gly Pro Ser Ala Gly
100 105 110

Pro Pro Pro Gly Pro Pro Ala Ser Leu Leu Asp Thr Cys Ala Val Cys
115 120 125

Gln Gln Ser Leu Gln Ser Arg Arg Glu Ala Glu Pro Lys Leu Leu Pro
130 135 140

Cys Leu His Ser Phe Cys Leu Arg Cys Leu Pro Glu Pro Glu Arg Gln
145 150 155 160

Leu Ser Val Pro Ile Pro Gly Gly Ser Asn Gly Asp Ile Gln Gln Val
165 170 175

Gly Val Ile Arg Cys Pro Val Cys Arg Gln Glu Cys Arg Gln Ile Asp
180 185 190

Leu Val Asp Asn Tyr Phe Val Lys Asp Thr Ser Glu Ala Pro Ser Ser
195 200 205

Ser Asp Glu Lys Ser Glu Gln Val Cys Thr Ser Cys Glu Asp Asn Ala
210 215 220

Ser Ala Val Gly Phe Cys Val Glu Cys Gly Glu Trp Leu Cys Lys Thr
225 230 235 240

Cys Ile Glu Ala His Gln Arg Val Lys Phe Thr Lys Asp His Leu Ile
245 250 255

Arg Lys Lys Glu Asp Val Ser Glu Ser Val Gly Ala Ser Gly Gln Arg
260 265 270

Pro Val Phe Cys Pro Val His Lys Gln Glu Gln Leu Lys Leu Phe Cys
275 280 285

Glu Thr Cys Asp Arg Leu Thr Cys Arg Asp Cys Gln Leu Leu Glu His
290 295 300

Lys Glu His Arg Tyr Gln Phe Leu Glu Glu Ala Phe Gln Asn Gln Lys
305 310 315 320

Gly Ala Ile Glu Asn Leu Leu Ala Lys Leu Leu Glu Lys Lys Asn Tyr
325 330 335

Val His Phe Ala Ala Thr Gln Val Gln Asn Arg Ile Lys Glu Val Asn
340 345 350

Glu Thr Asn Lys Arg Val Glu Gln Glu Ile Lys Val Ala Ile Phe Thr
355 360 365

Leu Ile Asn Glu Ile Asn Lys Lys Gly Lys Ser Leu Leu Gln Gln Leu
370 375 380

Glu Asn Val Thr Lys Glu Arg Gln Met Lys Leu Leu Gln Gln Gln Asn

385 390 395 400

 Asp Ile Thr Gly Leu Ser Arg Gln Val Lys His Val Met Asn Phe Thr
 405 410 415

 Asn Trp Ala Ile Ala Ser Gly Ser Ser Thr Ala Leu Leu Tyr Ser Lys
 420 425 430

 Arg Leu Ile Thr Phe Gln Leu Arg His Ile Leu Lys Ala Arg Cys Asp
 435 440 445

 Pro Val Pro Ala Ala Asn Gly Ala Ile Arg Phe His Cys Asp Pro Thr
 450 455 460

 Phe Trp Ala Lys Asn Val Val Asn Leu Gly Asn Leu Val Ile Glu Ser
 465 470 475 480

 Lys Pro Ala Pro Gly Tyr Thr Pro Asn Val Val Val Gly Gln Val Pro
 485 490 495

 Pro Gly Thr Asn His Ile Ser Lys Thr Pro Gly Gln Ile Asn Leu Ala
 500 505 510

 Gln Leu Arg Leu Gln His Met Gln Gln Gln Val Tyr Ala Gln Lys His
 515 520 525

 Gln Gln Leu Gln Gln Met Arg Met Gln Gln Pro Pro Ala Pro Val Pro
 530 535 540

 Thr Thr Thr Thr Thr Thr Gln Gln His Pro Arg Gln Ala Ala Pro Gln
 545 550 555 560

 Met Leu Gln Gln Gln Pro Pro Arg Leu Ile Ser Val Gln Thr Met Gln
 565 570 575

 Arg Gly Asn Met Asn Cys Gly Ala Phe Gln Ala His Gln Met Arg Leu
 580 585 590

Ala Gln Asn Ala Ala Arg Ile Pro Gly Ile Pro Arg His Ser Gly Pro
595 600 605

Gln Tyr Ser Met Met Gln Pro His Leu Gln Arg Gln His Ser Asn Pro
610 615 620

Gly His Ala Gly Pro Phe Pro Val Val Ser Val His Asn Thr Thr Ile
625 630 635 640

Asn Pro Thr Ser Pro Thr Thr Ala Thr Met Ala Asn Ala Asn Arg Gly
645 650 655

Pro Thr Ser Pro Ser Val Thr Ala Ile Glu Leu Ile Pro Ser Val Thr
660 665 670

Asn Pro Glu Asn Leu Pro Ser Leu Pro Asp Ile Pro Pro Ile Gln Leu
675 680 685

Glu Asp Ala Gly Ser Ser Ser Leu Asp Asn Leu Leu Ser Arg Tyr Ile
690 695 700

Ser Gly Ser His Leu Pro Pro Gln Pro Thr Ser Thr Met Asn Pro Ser
705 710 715 720

Pro Gly Pro Ser Ala Leu Ser Pro Gly Ser Ser Gly Leu Ser Asn Ser
725 730 735

His Thr Pro Val Arg Pro Pro Ser Thr Ser Ser Thr Gly Ser Arg Gly
740 745 750

Ser Cys Gly Ser Ser Gly Arg Thr Ala Glu Lys Thr Ser Leu Ser Phe
755 760 765

Lys Ser Asp Gln Val Lys Val Lys Gln Glu Pro Gly Thr Glu Asp Glu
770 775 780

Ile Cys Ser Phe Ser Gly Gly Val Lys Gln Glu Lys Thr Glu Asp Gly
785 790 795 800

Arg Arg Ser Ala Cys Met Leu Ser Ser Pro Glu Ser Ser Leu Thr Pro
805 810 815

Pro Leu Ser Thr Asn Leu His Leu Glu Ser Glu Leu Asp Ala Leu Ala
820 825 830

Ser Leu Glu Asn His Val Lys Ile Glu Pro Ala Asp Met Asn Glu Ser
835 840 845

Cys Lys Gln Ser Gly Leu Ser Ser Leu Val Asn Gly Lys Ser Pro Ile
850 855 860

Arg Ser Leu Met His Arg Ser Ala Arg Ile Gly Gly Asp Gly Asn Asn
865 870 875 880

Lys Asp Asp Asp Pro Asn Glu Asp Trp Cys Ala Val Cys Gln Asn Gly
885 890 895

Gly Asp Leu Leu Cys Cys Glu Lys Cys Pro Lys Val Phe His Leu Thr
900 905 910

Cys His Val Pro Thr Leu Leu Ser Phe Pro Ser Gly Asp Trp Ile Cys
915 920 925

Thr Phe Cys Arg Asp Ile Gly Lys Pro Glu Val Glu Tyr Asp Cys Asp
930 935 940

Asn Leu Gln His Ser Lys Lys Gly Lys Thr Ala Gln Gly Leu Ser Pro
945 950 955 960

Val Asp Gln Arg Lys Cys Glu Arg Leu Leu Leu Tyr Leu Tyr Cys His
965 970 975

Glu Leu Ser Ile Glu Phe Gln Glu Pro Val Pro Ala Ser Ile Pro Asn
980 985 990

Tyr Tyr Lys Ile Ile Lys Lys Pro Met Asp Leu Ser Thr Val Lys Lys
995 1000 1005

Lys Leu Gln Lys Lys His Ser Gln His Tyr Gln Ile Pro Asp Asp
 1010 1015 1020

Phe Val Ala Asp Val Arg Leu Ile Phe Lys Asn Cys Glu Arg Phe
 1025 1030 1035

Asn Glu Met Met Lys Val Val Gln Val Tyr Ala Asp Thr Gln Glu
 1040 1045 1050

Ile Asn Leu Lys Ala Asp Ser Glu Val Ala Gln Ala Gly Lys Ala
 1055 1060 1065

Val Ala Leu Tyr Phe Glu Asp Lys Leu Thr Glu Ile Tyr Ser Asp
 1070 1075 1080

Arg Thr Phe Ala Pro Leu Pro Glu Phe Glu Gln Glu Glu Asp Asp
 1085 1090 1095

Gly Glu Val Thr Glu Asp Ser Asp Glu Asp Phe Ile Gln Pro Arg
 1100 1105 1110

Arg Lys Arg Leu Lys Ser Asp Glu Arg Pro Val His Ile Lys
 1115 1120 1125

<210> 67

<211> 1467

<212> DNA

<213> Homo sapiens

<400> 67

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gtgagcaaca aggaggcagt gaccagcatg ggaggaaaaa gcagctgtcc tgtgtgtggt 180

atcagttact catttgaaca tctacaggct aatcagcatc tggccaacat agtggagaga 240

ctcaaggagg tcaagttgag cccagacaat gggaagaaga gagatctctg tgatcatcat 300

ggagagaaac tcctactctt ctgtaaggag gataggaaag tcatttgctg gctttgtgag 360

cggtctcagg agcaccgtgg tcaccacaca gtctcacgg aggaagtatt caaggaatgt 420
 caggagaaac tccaggcagt cctcaagagg ctgaagaagg aagaggagga agctgagaag 480
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<210> 68

<211> 488

<212> PRT

<213> Homo sapiens

<400> 68

Met Ala Ser Lys Ile Leu Leu Asn Val Gln Glu Glu Val Thr Cys Pro

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Ile Cys Leu Glu Leu Leu Thr Glu Pro Leu Ser Leu Asp Cys Gly His
20 25 30

Ser Leu Cys Arg Ala Cys Ile Thr Val Ser Asn Lys Glu Ala Val Thr
35 40 45

Ser Met Gly Gly Lys Ser Ser Cys Pro Val Cys Gly Ile Ser Tyr Ser
50 55 60

Phe Glu His Leu Gln Ala Asn Gln His Leu Ala Asn Ile Val Glu Arg
65 70 75 80

Leu Lys Glu Val Lys Leu Ser Pro Asp Asn Gly Lys Lys Arg Asp Leu
85 90 95

Cys Asp His His Gly Glu Lys Leu Leu Leu Phe Cys Lys Glu Asp Arg
100 105 110

Lys Val Ile Cys Trp Leu Cys Glu Arg Ser Gln Glu His Arg Gly His
115 120 125

His Thr Val Leu Thr Glu Glu Val Phe Lys Glu Cys Gln Glu Lys Leu
130 135 140

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

Leu Glu Ala Asp Ile Arg Glu Glu Lys Thr Ser Trp Lys Tyr Gln Val
165 170 175

Gln Thr Glu Arg Gln Arg Ile Gln Thr Glu Phe Asp Gln Leu Arg Ser
180 185 190

Ile Leu Asn Asn Glu Glu Gln Arg Glu Leu Gln Arg Leu Glu Glu Glu
195 200 205

Glu Lys Lys Thr Leu Asp Lys Phe Ala Glu Ala Glu Asp Glu Leu Val
210 215 220

Gln Gln Lys Gln Leu Val Arg Glu Leu Ile Ser Asp Val Glu Cys Arg
225 230 235 240

Ser Gln Trp Ser Thr Met Glu Leu Leu Gln Asp Met Ser Gly Ile Met
 245 250 255

Lys Trp Ser Glu Ile Trp Arg Leu Lys Lys Pro Lys Met Val Ser Lys
 260 265 270

Lys Leu Lys Thr Val Phe His Ala Pro Asp Leu Ser Arg Met Leu Gln
 275 280 285

Met Phe Arg Glu Leu Thr Ala Val Arg Cys Tyr Trp Val Asp Val Thr
 290 295 300

Leu Asn Ser Val Asn Leu Asn Leu Asn Leu Val Leu Ser Glu Asp Gln
305 310 315 320

Arg Gln Val Ile Ser Val Pro Ile Trp Pro Phe Gln Cys Tyr Asn Tyr
 325 330 335

Gly Val Leu Gly Ser Gln Tyr Phe Ser Ser Gly Lys His Tyr Trp Glu
 340 345 350

Val Asp Val Ser Lys Lys Thr Ala Trp Ile Leu Gly Val Tyr Cys Arg
 355 360 365

Thr Tyr Ser Arg His Met Lys Tyr Val Val Arg Arg Cys Ala Asn Arg
 370 375 380

Gln Asn Leu Tyr Thr Lys Tyr Arg Pro Leu Phe Gly Tyr Trp Val Ile
385 390 395 400

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

Ser Asp Pro Glu Val Leu Thr Leu Ser Met Ala Val Pro Pro Cys Arg
 420 425 430

Val Gly Val Phe Leu Asp Tyr Glu Ala Gly Ile Val Ser Phe Phe Asn
 435 440 445

Val Thr Ser His Gly Ser Leu Ile Tyr Lys Phe Ser Lys Cys Cys Phe
 450 455 460

Ser Gln Pro Val Tyr Pro Tyr Phe Asn Pro Trp Asn Cys Pro Ala Pro
 465 470 475 480

Met Thr Leu Cys Pro Pro Ser Ser
 485

<210> 69
 <211> 1482
 <212> DNA
 <213> Homo sapiens

<400> 69
 atggagcggga gtcccgcacgt gtccccggg ccttcccgt cttcaagga ggagttgctc 60
 tgcgccgtct gctacgaccc cttccgcgac gcagtcactc tgcgtgcgg ccacaacttc 120
 tgccgcgggt gcgtgagccg ctgctgggag gtgcaggtgt cggccacctg cccagtgtgc 180
 aaagaccgcg cgtcaccgcg cgacctgctg accaaccaca ccctcaaca cctggtggag 240
 aagctgctgc gcgaggaggc cgagggcgcg cgctggacca gctaccgctt ctgcgtgtc 300
 tgccgcctgc accgcggaca gctcagcctc ttctgcctcg aggacaagga gctgctgtgc 360
 tgctcctgcc aggccgaccc ccgacaccag gggcaccgcg tgagccggt gaaggacact 420
 gcccacgact ttcgggcca gtgcaggaac atggagcatg cactgcggga gaaggccaag 480
 gccttctggg ccatgcggcg ctccatgag gccatcgcca agcacaatca ggtggaggct 540
 gcatggctgg aaggccgat ccggcaggag ttgataagc ttcgcgagtt cttgagagt 600
 gaggagcagg ccattctgga tgccatggcc gaggagacaa ggcagaagca acttctggcc 660
 gacgagaaga tgaagcagct cacagaggag acggaggtgc tggcacatga gatcgagcgg 720
 ctgcagatgg agatgaagga ggacgacgtt tcttttctca tgaacacaa gagccgaaaa 780
 cgccgactct tctgcacat ggagccagag ccagtccagc ccggcatgct tatcgatgct 840

tgcaagtacc tgggctccct gcagtaccgc gtctggaaga agatgcttgc atctgtggaa 900
 tctgtaccct tcagctttga cccaacacc gcagctggct ggctctccgt gtctgacgac 960
 ctcaccagcg tcaccaacca tggctaccgc gtgcaggtgg agaaccgga acgcttctcc 1020
 tcggcgccct gcctgtggg ctccgtgtc ttctcacagg gctcgacgc ctgggaggtg 1080
 gcccttgggg ggctgcagag ctggagggtg ggctgtgtac gtgtgcgcca ggactcgggc 1140
 gctgagggcc actcacacag ctgctaccac gacacacgt cggttcttg gtatgtctgc 1200
 cgcacgcagg gcgtggagg ggaccactgc gtgacctgg acccagccac gtcgccctg 1260
 gtcctggcca tcccacgccc cctgcgtgtg gagctggagt gtgaggagg cgagctgtct 1320
 ttctatgacg cggagcgcca ctgccactg tacacctcc acgccgctt tgggaggtt 1380
 cgccctact tctacctgg gggtgcacgg ggccgggc ctccagagcc ttgcgcatc 1440
 tgcccctgc acatcagtgt caaggaaga ctggatggct ga 1482

<210> 70

<211> 493

<212> PRT

<213> Homo sapiens

<400> 70

Met Glu Arg Ser Pro Asp Val Ser Pro Gly Pro Ser Arg Ser Phe Lys

1 5 10 15

Glu Glu Leu Leu Cys Ala Val Cys Tyr Asp Pro Phe Arg Asp Ala Val

20 25 30

Thr Leu Arg Cys Gly His Asn Phe Cys Arg Gly Cys Val Ser Arg Cys

35 40 45

Trp Glu Val Gln Val Ser Pro Thr Cys Pro Val Cys Lys Asp Arg Ala

50 55 60

Ser Pro Ala Asp Leu Arg Thr Asn His Thr Leu Asn Asn Leu Val Glu

65 70 75 80

Lys Leu Leu Arg Glu Glu Ala Glu Gly Ala Arg Trp Thr Ser Tyr Arg
85 90 95

Phe Ser Arg Val Cys Arg Leu His Arg Gly Gln Leu Ser Leu Phe Cys
100 105 110

Leu Glu Asp Lys Glu Leu Leu Cys Cys Ser Cys Gln Ala Asp Pro Arg
115 120 125

His Gln Gly His Arg Val Gln Pro Val Lys Asp Thr Ala His Asp Phe
130 135 140

Arg Ala Lys Cys Arg Asn Met Glu His Ala Leu Arg Glu Lys Ala Lys
145 150 155 160

Ala Phe Trp Ala Met Arg Arg Ser Tyr Glu Ala Ile Ala Lys His Asn
165 170 175

Gln Val Glu Ala Ala Trp Leu Glu Gly Arg Ile Arg Gln Glu Phe Asp
180 185 190

Lys Leu Arg Glu Phe Leu Arg Val Glu Glu Gln Ala Ile Leu Asp Ala
195 200 205

Met Ala Glu Glu Thr Arg Gln Lys Gln Leu Leu Ala Asp Glu Lys Met
210 215 220

Lys Gln Leu Thr Glu Glu Thr Glu Val Leu Ala His Glu Ile Glu Arg
225 230 235 240

Leu Gln Met Glu Met Lys Glu Asp Asp Val Ser Phe Leu Met Lys His
245 250 255

Lys Ser Arg Lys Arg Arg Leu Phe Cys Thr Met Glu Pro Glu Pro Val
260 265 270

Gln Pro Gly Met Leu Ile Asp Val Cys Lys Tyr Leu Gly Ser Leu Gln
275 280 285

Tyr Arg Val Trp Lys Lys Met Leu Ala Ser Val Glu Ser Val Pro Phe
290 295 300

Ser Phe Asp Pro Asn Thr Ala Ala Gly Trp Leu Ser Val Ser Asp Asp
305 310 315 320

Leu Thr Ser Val Thr Asn His Gly Tyr Arg Val Gln Val Glu Asn Pro
325 330 335

Glu Arg Phe Ser Ser Ala Pro Cys Leu Leu Gly Ser Arg Val Phe Ser
340 345 350

Gln Gly Ser His Ala Trp Glu Val Ala Leu Gly Gly Leu Gln Ser Trp
355 360 365

Arg Val Gly Val Val Arg Val Arg Gln Asp Ser Gly Ala Glu Gly His
370 375 380

Ser His Ser Cys Tyr His Asp Thr Arg Ser Gly Phe Trp Tyr Val Cys
385 390 395 400

Arg Thr Gln Gly Val Glu Gly Asp His Cys Val Thr Ser Asp Pro Ala
405 410 415

Thr Ser Pro Leu Val Leu Ala Ile Pro Arg Arg Leu Arg Val Glu Leu
420 425 430

Glu Cys Glu Glu Gly Glu Leu Ser Phe Tyr Asp Ala Glu Arg His Cys
435 440 445

His Leu Tyr Thr Phe His Ala Arg Phe Gly Glu Val Arg Pro Tyr Phe
450 455 460

Tyr Leu Gly Gly Ala Arg Gly Ala Gly Pro Pro Glu Pro Leu Arg Ile
465 470 475 480

Cys Pro Leu His Ile Ser Val Lys Glu Glu Leu Asp Gly
485 490

<210> 71
 <211> 2187
 <212> DNA
 <213> Homo sapiens

<400> 71
 atgtcggagt ctggggagat gagtgaattt ggctacatca tggaattgat agctaaaggc 60
 aaggttacca ttaagaatat cgaaaggag ctcatgtgcc cagcatgcaa ggagctgttt 120
 acccaccat tgattctccc ttgccaacat agtatctgtc ataatgtgt aaaagaactc 180
 ctgctgactc tcgatgattc attcaacgat gtgggatcag acaactcaa tcaaagcagt 240
 cctcgacttc ggctccctc ccctagtatg gataaaattg accgaattaa cagaccaggc 300
 tggaagcgca attcattgac cccgaggaca actgttttcc cttgccctgg ctgtgagcat 360
 gatgtggatc ttggagaacg aggaatcaat ggtctgttc gaaactcac ttggaaact 420
 attgtgaaa gatatctca agcagctagg gcagccacag ccattatgtg tgaccttgt 480
 aaaccaccac ctcaagaatc caaaaaagc tgcattggact gtagtgcaag ttactgcaat 540
 gaatgctca aaattcatca ccctgggggt actataaaag ctcaaatga gtatgttgg 600
 ccaactacta acttcagacc caagatttta atgtgccag aacatgaaac agagagaata 660
 aacatgtact gtgaattatg taggaggcca gtttgccatc tgtgtaagt gggtggtaat 720
 catgccaaac accgtgtaac cactatgagc agtcctaca aaacctaaa ggaaaagctt 780
 tcaaaggata ttgattacct tattggaag gaaagccagg tgaagagtca aatatctgaa 840
 ctaaactgt taatgaaaga aacagagtgt aatggagaga gggctaaaga agaagcaatt 900
 acacatttg aaaagctctt tgaagtctg gaagagagga aatcatctgt ttgaaagca 960
 attgactcct ctaagaaact aagattagac aaattcaga ctcaaatgga agagtaccag 1020
 ggacttctag agaacaatgg acttgaggga tatgctcaag aagtgctaaa ggagacagat 1080
 cagtcttgct ttgtcgagac agcaaagcag ctccacctca gaatacagaa agccacagaa 1140
 tctttgaaga gctttagacc tgcagctcag acttctttg aagactatgt tgtaataacc 1200
 tctaaacaaa cagaacttct tggagaatta tccttttct ctatggcat agacgtgcc 1260
 gagatcaatg aggaacagag caaagttat acaatgcct tgataaattg gcaccatcca 1320

gaaaaggata aagctgatag ctatgttctt gaatatcgga aaatcaatag agatgatgaa 1380
 atgtcatgga atgagataga agtgtgtgga acaagtaaaa taattcaaga cttggaaaac 1440
 agtagtacct atgctttcag agtaagagct tacaagggtt caatctgtag tccttcgagc 1500
 agagaattga ttcttcatac tcctccagct ccagttttca gcttcctctt tgatgaaaaa 1560
 tgtggctata ataatgaaca cctcctgctg aacttgaaga gagaccgtgt agagagtaga 1620
 gctggattta atcttctgct tgctgcagaa cgcatccaag tgggttatta cacaagctta 1680
 gactacatca ttggagatac tggcattaca aaaggaaaac acttctgggc cttccgtgtg 1740
 gaaccatatt catacctggt aaaagtggga gttgcttcta gcgataaact acaagaatgg 1800
 ctccgttctc cccgggatgc agttagtcca agatatgagc aagacagtgg gcatgacagt 1860
 ggaagtgagg atgcctgttt tgattcttca caaccattta ccttagttac tataggcatg 1920
 cagaaatfff ttatacccaa gtcacctact tcttctaag aacctgaaa tagagttctc 1980
 cctatgccaa caagtattgg gattttcctt gactgtgata aaggcaaagt agatttctat 2040
 gatatggatc agatgaaatg cctttatgaa cgccaagtgg actgttcaca tacactgtat 2100
 ccagcatttg cattaatggg cagtgaggga attcagcttg aagaacccat cacagcaaaa 2160
 tatctggaat accaagagga catgtag 2187

<210> 72

<211> 728

<212> PRT

<213> Homo sapiens

<400> 72

Met Ser Glu Ser Gly Glu Met Ser Glu Phe Gly Tyr Ile Met Glu Leu

1 5 10 15

Ile Ala Lys Gly Lys Val Thr Ile Lys Asn Ile Glu Arg Glu Leu Ile

20 25 30

Cys Pro Ala Cys Lys Glu Leu Phe Thr His Pro Leu Ile Leu Pro Cys

35 40 45

Gln His Ser Ile Cys His Lys Cys Val Lys Glu Leu Leu Thr Leu
50 55 60

Asp Asp Ser Phe Asn Asp Val Gly Ser Asp Asn Ser Asn Gln Ser Ser
65 70 75 80

Pro Arg Leu Arg Leu Pro Ser Pro Ser Met Asp Lys Ile Asp Arg Ile
85 90 95

Asn Arg Pro Gly Trp Lys Arg Asn Ser Leu Thr Pro Arg Thr Thr Val
100 105 110

Phe Pro Cys Pro Gly Cys Glu His Asp Val Asp Leu Gly Glu Arg Gly
115 120 125

Ile Asn Gly Leu Phe Arg Asn Phe Thr Leu Glu Thr Ile Val Glu Arg
130 135 140

Tyr Arg Gln Ala Ala Arg Ala Ala Thr Ala Ile Met Cys Asp Leu Cys
145 150 155 160

Lys Pro Pro Pro Gln Glu Ser Thr Lys Ser Cys Met Asp Cys Ser Ala
165 170 175

Ser Tyr Cys Asn Glu Cys Phe Lys Ile His His Pro Trp Gly Thr Ile
180 185 190

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

Ile Leu Met Cys Pro Glu His Glu Thr Glu Arg Ile Asn Met Tyr Cys
210 215 220

Glu Leu Cys Arg Arg Pro Val Cys His Leu Cys Lys Leu Gly Gly Asn
225 230 235 240

His Ala Asn His Arg Val Thr Thr Met Ser Ser Ala Tyr Lys Thr Leu
245 250 255

Lys Glu Lys Leu Ser Lys Asp Ile Asp Tyr Leu Ile Gly Lys Glu Ser
260 265 270

Gln Val Lys Ser Gln Ile Ser Glu Leu Asn Leu Leu Met Lys Glu Thr
275 280 285

Glu Cys Asn Gly Glu Arg Ala Lys Glu Glu Ala Ile Thr His Phe Glu
290 295 300

Lys Leu Phe Glu Val Leu Glu Glu Arg Lys Ser Ser Val Leu Lys Ala
305 310 315 320

Ile Asp Ser Ser Lys Lys Leu Arg Leu Asp Lys Phe Gln Thr Gln Met
325 330 335

Glu Glu Tyr Gln Gly Leu Leu Glu Asn Asn Gly Leu Val Gly Tyr Ala
340 345 350

Gln Glu Val Leu Lys Glu Thr Asp Gln Ser Cys Phe Val Gln Thr Ala
355 360 365

Lys Gln Leu His Leu Arg Ile Gln Lys Ala Thr Glu Ser Leu Lys Ser
370 375 380

Phe Arg Pro Ala Ala Gln Thr Ser Phe Glu Asp Tyr Val Val Asn Thr
385 390 395 400

Ser Lys Gln Thr Glu Leu Leu Gly Glu Leu Ser Phe Phe Ser Ser Gly
405 410 415

Ile Asp Val Pro Glu Ile Asn Glu Glu Gln Ser Lys Val Tyr Asn Asn
420 425 430

Ala Leu Ile Asn Trp His His Pro Glu Lys Asp Lys Ala Asp Ser Tyr
435 440 445

Val Leu Glu Tyr Arg Lys Ile Asn Arg Asp Asp Glu Met Ser Trp Asn
450 455 460

Glu Ile Glu Val Cys Gly Thr Ser Lys Ile Ile Gln Asp Leu Glu Asn
465 470 475 480

Ser Ser Thr Tyr Ala Phe Arg Val Arg Ala Tyr Lys Gly Ser Ile Cys
 485 490 495

Ser Pro Cys Ser Arg Glu Leu Ile Leu His Thr Pro Pro Ala Pro Val
 500 505 510

Phe Ser Phe Leu Phe Asp Glu Lys Cys Gly Tyr Asn Asn Glu His Leu
 515 520 525

Leu Leu Asn Leu Lys Arg Asp Arg Val Glu Ser Arg Ala Gly Phe Asn
 530 535 540

Leu Leu Leu Ala Ala Glu Arg Ile Gln Val Gly Tyr Tyr Thr Ser Leu
545 550 555 560

Asp Tyr Ile Ile Gly Asp Thr Gly Ile Thr Lys Gly Lys His Phe Trp
 565 570 575

Ala Phe Arg Val Glu Pro Tyr Ser Tyr Leu Val Lys Val Gly Val Ala
 580 585 590

Ser Ser Asp Lys Leu Gln Glu Trp Leu Arg Ser Pro Arg Asp Ala Val
 595 600 605

Ser Pro Arg Tyr Glu Gln Asp Ser Gly His Asp Ser Gly Ser Glu Asp
 610 615 620

Ala Cys Phe Asp Ser Ser Gln Pro Phe Thr Leu Val Thr Ile Gly Met
625 630 635 640

Gln Lys Phe Phe Ile Pro Lys Ser Pro Thr Ser Ser Asn Glu Pro Glu
 645 650 655

Asn Arg Val Leu Pro Met Pro Thr Ser Ile Gly Ile Phe Leu Asp Cys

660 665 670
 Asp Lys Gly Lys Val Asp Phe Tyr Asp Met Asp Gln Met Lys Cys Leu
 675 680 685

Tyr Glu Arg Gln Val Asp Cys Ser His Thr Leu Tyr Pro Ala Phe Ala
 690 695 700

Leu Met Gly Ser Gly Gly Ile Gln Leu Glu Glu Pro Ile Thr Ala Lys
 705 710 715 720

Tyr Leu Glu Tyr Gln Glu Asp Met
 725

<210> 73
 <211> 2895
 <212> DNA
 <213> Homo sapiens

<400> 73
 atggatgaac agagcgtgga gagcattgct gaggttttcc gatgtttcat ttgtatggag 60
 aaattgcggg atgcacgcct gtgtcctcat tgcctcaaac tgtgttggtt cagctgtatt 120
 aggcgctggc tgacagagca gagagctcaa tgtcctcatt gccgtgctcc actccagcta 180
 cgagaactag taaattgtcg ttgggcagaa gaagtaacac aacagcttga tactcttcaa 240
 ctctgcagtc tcaccaaaaca tgaagaaaat gaaaaggaca aatgtgaaaa tcacatgaa 300
 aaacttagtg tattttgctg gacttgaag aagtgtatct gccatcagtg tgcactttgg 360
 ggaggaatgc atggcggaca tacctttaa cctttggcag aaatttatga gcaacacgct 420
 actaaagtga atgaagaggt agccaaactt cgtcggcgtc tcatggaact gatcagctta 480
 gttcaagaag tggaaggaa ttagaagct gtaagaaatg caaagatga gcgtgttcgg 540
 gaaattagga atgcagtgga gatgatgatt gcacggttag acacacagct gaagaataag 600
 cttataacac tgatgggtca gaagacatct ctaaccaag aaacagagct tttggaatcc 660
 ttacttcagg aggtggagca ccagttcggg tctttagta agagtgagtt gatatctaag 720
 agctcagaga tccttatgat gtttcagcaa gttcatcgga agcccatggc atcttttgtt 780

accactcctg ttccaccaga ctttaccagt gaattagtgc catcttacga ttcagctact 840
 tttgttttag agaatttcag cactttgcgt cagagagcag atcctgttta cagtccacct 900
 cttcaagttt caggactttg ctggagggtta aaagtttacc cagatggaaa tggagtgtg 960
 cgaggttact acttatctgt gtttctggag ctctcagctg gcttcctga aacttctaaa 1020
 tatgaatcgc gtgtagagat gggtcaccag tcctgtaatg atcctacaaa aaatatcatt 1080
 cgagaatttg catctgactt tgaagttgga gaatgctggg gctataatag attttccgt 1140
 ttggacttac tcgcaaatga aggatacttg aatccacaaa atgatacagt gattttaagg 1200
 tttcaggtag gttcaccaac tttcttcaa aaatcccggg accagcattg gtacattact 1260
 cagttggaag ctgcacagac tagttatc caacaaataa acaacctta agagagactt 1320
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 cttctgaag gtggtctac tacagcttct gtaagagagg ccaaagagga tgaagaagat 1500
 gaggagaaga ttcagaatga agattatcat cagagcttt cagatggaga tctggatctg 1560
 gatctgttt atgaggatga agtaaatcag ctcatggca gcagttcctc tgtagttcc 1620
 acagcaaca gtaatacaga agaaaatgat attgatgaag aaactatgtc tggagaaaat 1680
 gatgtggaat ataacaacat ggaattagaa gagggagaac tcatggaaga tgcagctgct 1740
 gcaggaccg caggtagtag ccatggttat gtgggttcca gtagtagaat atcaagaaga 1800
 acacattat gctccgctgc taccagtagt ttactagaca ttgatccatt aattttaata 1860
 cattgttgg accttaagga cggagcagt atagaaaatt tgtggggctt acagcctcgc 1920
 ccactgctt cacttctgca gcccacagca tcatattctc gaaaagataa agaccaaagg 1980
 aagcaacagg caatgtggcg agtgcctct gatttaaaga tgctaaaag actcaaaact 2040
 caaatggccg aagttcgatg tatgaaaact gatgtaaaga atacacttc agaaataaaa 2100
 agcagcagt ctgcttctgg agacatgcag acaagccttt tttctgctga ccaggcagct 2160
 ctggctgcat gtggaactga aaactctggc agattgcagg atttggaat ggaactcctg 2220
 gcaaagtcag cagttgcaa ttgttacata cgaaactcca caaataagaa gagtaattcg 2280
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ggagaaaata gtcgttcaaa gggagactgt cagactctgt ctgaaggctc cccaggaagc 2400
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 attctgccaa aaactgaaga ccggcagtgt aaagcttgg attcagatgc tgttgtggtt 2520
 gcagttttca gtggcttgcc tgcggttgag aaaaggagga aaatggtcac cttgggggct 2580
 aatgctaaag gaggtcatct ggaaggactg cagatgactg atttggaata taattctgaa 2640
 actggagagt tacacctgt actacctgaa ggagcttcag ctgccctga agaaggaatg 2700
 agtagcgaca gtgacattga atgtgacact gagaatgagg agcaggaaga gcataccagt 2760
 gtgggcgggt ttacgactc cttcatggtc atgacacagc ccccgatga agatacacat 2820
 tccagtttct ctgatggtga acaaataggc cctgaagatc tcagcttcaa tacagatgaa 2880
 aatagtggaa ggtaa 2895

<210> 74
 <211> 964
 <212> PRT
 <213> Homo sapiens

<400> 74

Met Asp Glu Gln Ser Val Glu Ser Ile Ala Glu Val Phe Arg Cys Phe
 1 5 10 15

Ile Cys Met Glu Lys Leu Arg Asp Ala Arg Leu Cys Pro His Cys Ser
 20 25 30

Lys Leu Cys Cys Phe Ser Cys Ile Arg Arg Trp Leu Thr Glu Gln Arg
 35 40 45

Ala Gln Cys Pro His Cys Arg Ala Pro Leu Gln Leu Arg Glu Leu Val
 50 55 60

Asn Cys Arg Trp Ala Glu Glu Val Thr Gln Gln Leu Asp Thr Leu Gln
 65 70 75 80

Leu Cys Ser Leu Thr Lys His Glu Glu Asn Glu Lys Asp Lys Cys Glu
 85 90 95

Asn His His Glu Lys Leu Ser Val Phe Cys Trp Thr Cys Lys Lys Cys
100 105 110

Ile Cys His Gln Cys Ala Leu Trp Gly Gly Met His Gly Gly His Thr
115 120 125

Phe Lys Pro Leu Ala Glu Ile Tyr Glu Gln His Val Thr Lys Val Asn
130 135 140

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

Val Gln Glu Val Glu Arg Asn Val Glu Ala Val Arg Asn Ala Lys Asp
165 170 175

Glu Arg Val Arg Glu Ile Arg Asn Ala Val Glu Met Met Ile Ala Arg
180 185 190

Leu Asp Thr Gln Leu Lys Asn Lys Leu Ile Thr Leu Met Gly Gln Lys
195 200 205

Thr Ser Leu Thr Gln Glu Thr Glu Leu Leu Glu Ser Leu Leu Gln Glu
210 215 220

Val Glu His Gln Leu Arg Ser Cys Ser Lys Ser Glu Leu Ile Ser Lys
225 230 235 240

Ser Ser Glu Ile Leu Met Met Phe Gln Gln Val His Arg Lys Pro Met
245 250 255

Ala Ser Phe Val Thr Thr Pro Val Pro Pro Asp Phe Thr Ser Glu Leu
260 265 270

Val Pro Ser Tyr Asp Ser Ala Thr Phe Val Leu Glu Asn Phe Ser Thr
275 280 285

Leu Arg Gln Arg Ala Asp Pro Val Tyr Ser Pro Pro Leu Gln Val Ser

290	295	300	
Gly Leu Cys Trp Arg Leu Lys Val Tyr Pro Asp Gly Asn Gly Val Val			
305	310	315	320
Arg Gly Tyr Tyr Leu Ser Val Phe Leu Glu Leu Ser Ala Gly Leu Pro			
	325	330	335
Glu Thr Ser Lys Tyr Glu Tyr Arg Val Glu Met Val His Gln Ser Cys			
	340	345	350
Asn Asp Pro Thr Lys Asn Ile Ile Arg Glu Phe Ala Ser Asp Phe Glu			
	355	360	365
Val Gly Glu Cys Trp Gly Tyr Asn Arg Phe Phe Arg Leu Asp Leu Leu			
	370	375	380
Ala Asn Glu Gly Tyr Leu Asn Pro Gln Asn Asp Thr Val Ile Leu Arg			
385	390	395	400
Phe Gln Val Arg Ser Pro Thr Phe Phe Gln Lys Ser Arg Asp Gln His			
	405	410	415
Trp Tyr Ile Thr Gln Leu Glu Ala Ala Gln Thr Ser Tyr Ile Gln Gln			
	420	425	430
Ile Asn Asn Leu Lys Glu Arg Leu Thr Ile Glu Leu Ser Arg Thr Gln			
	435	440	445
Lys Ser Arg Asp Leu Ser Pro Pro Asp Asn His Leu Ser Pro Gln Asn			
	450	455	460
Asp Asp Ala Leu Glu Thr Arg Ala Lys Lys Ser Ala Cys Ser Asp Met			
465	470	475	480
Leu Leu Glu Gly Gly Pro Thr Thr Ala Ser Val Arg Glu Ala Lys Glu			
	485	490	495

Asp Glu Glu Asp Glu Glu Lys Ile Gln Asn Glu Asp Tyr His His Glu
500 505 510

Leu Ser Asp Gly Asp Leu Asp Leu Asp Leu Val Tyr Glu Asp Glu Val
515 520 525

Asn Gln Leu Asp Gly Ser Ser Ser Ser Ala Ser Ser Thr Ala Thr Ser
530 535 540

Asn Thr Glu Glu Asn Asp Ile Asp Glu Glu Thr Met Ser Gly Glu Asn
545 550 555 560

Asp Val Glu Tyr Asn Asn Met Glu Leu Glu Glu Gly Glu Leu Met Glu
565 570 575

Asp Ala Ala Ala Ala Gly Pro Ala Gly Ser Ser His Gly Tyr Val Gly
580 585 590

Ser Ser Ser Arg Ile Ser Arg Arg Thr His Leu Cys Ser Ala Ala Thr
595 600 605

Ser Ser Leu Leu Asp Ile Asp Pro Leu Ile Leu Ile His Leu Leu Asp
610 615 620

Leu Lys Asp Arg Ser Ser Ile Glu Asn Leu Trp Gly Leu Gln Pro Arg
625 630 635 640

Pro Pro Ala Ser Leu Leu Gln Pro Thr Ala Ser Tyr Ser Arg Lys Asp
645 650 655

Lys Asp Gln Arg Lys Gln Gln Ala Met Trp Arg Val Pro Ser Asp Leu
660 665 670

Lys Met Leu Lys Arg Leu Lys Thr Gln Met Ala Glu Val Arg Cys Met
675 680 685

Lys Thr Asp Val Lys Asn Thr Leu Ser Glu Ile Lys Ser Ser Ser Ala
690 695 700

Ala Ser Gly Asp Met Gln Thr Ser Leu Phe Ser Ala Asp Gln Ala Ala
705 710 715 720

Leu Ala Ala Cys Gly Thr Glu Asn Ser Gly Arg Leu Gln Asp Leu Gly
725 730 735

Met Glu Leu Leu Ala Lys Ser Ser Val Ala Asn Cys Tyr Ile Arg Asn
740 745 750

Ser Thr Asn Lys Lys Ser Asn Ser Pro Lys Pro Ala Arg Ser Ser Val
755 760 765

Ala Gly Ser Leu Ser Leu Arg Arg Ala Val Asp Pro Gly Glu Asn Ser
770 775 780

Arg Ser Lys Gly Asp Cys Gln Thr Leu Ser Glu Gly Ser Pro Gly Ser
785 790 795 800

Ser Gln Ser Gly Ser Arg His Ser Ser Pro Arg Ala Leu Ile His Gly
805 810 815

Ser Ile Gly Asp Ile Leu Pro Lys Thr Glu Asp Arg Gln Cys Lys Ala
820 825 830

Leu Asp Ser Asp Ala Val Val Val Ala Val Phe Ser Gly Leu Pro Ala
835 840 845

Val Glu Lys Arg Arg Lys Met Val Thr Leu Gly Ala Asn Ala Lys Gly
850 855 860

Gly His Leu Glu Gly Leu Gln Met Thr Asp Leu Glu Asn Asn Ser Glu
865 870 875 880

Thr Gly Glu Leu Gln Pro Val Leu Pro Glu Gly Ala Ser Ala Ala Pro
885 890 895

Glu Glu Gly Met Ser Ser Asp Ser Asp Ile Glu Cys Asp Thr Glu Asn
900 905 910

Glu Glu Gln Glu Glu His Thr Ser Val Gly Gly Phe His Asp Ser Phe
 915 920 925

Met Val Met Thr Gln Pro Pro Asp Glu Asp Thr His Ser Ser Phe Pro
 930 935 940

Asp Gly Glu Gln Ile Gly Pro Glu Asp Leu Ser Phe Asn Thr Asp Glu
 945 950 955 960

Asn Ser Gly Arg

<210> 75
 <211> 1398
 <212> DNA
 <213> Homo sapiens

<400> 75
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 acagacttct ttaaaaaccc aagccaaaag caactgaggc aggagacatt ctgctgtccc 180
 cagtgtcggg ctccatttca tatggatagc ctccgacca acaagcagct gggaagcctc 240
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<210> 76

<211> 465

<212> PRT

<213> Homo sapiens

<400> 76

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys
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Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly
 20 25 30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser
 35 40 45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala
 50 55 60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu
 65 70 75 80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His
 85 90 95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys
100 105 110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu
115 120 125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val
130 135 140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser
145 150 155 160

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg
165 170 175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu
180 185 190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr
195 200 205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn
210 215 220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser
225 230 235 240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp
245 250 255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr
260 265 270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
275 280 285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu

290 295 300
 Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
 305 310 315 320
 Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
 325 330 335
 Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
 340 345 350
 Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
 355 360 365
 Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
 370 375 380
 Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
 385 390 395 400
 Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
 405 410 415
 Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
 420 425 430
 His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
 435 440 445
 Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly
 450 455 460

Asp
 465

<210> 77
 <211> 1557
 <212> DNA
 <213> Homo sapiens

<400> 77

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<210> 78

<211> 518

<212> PRT

<213> Homo sapiens

<400> 78

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Ala Ala Ala Leu Glu Asn Leu Gln Val Glu Ala Ser Cys Ser Val Cys

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Leu Glu Tyr Leu Lys Glu Pro Val Ile Ile Glu Cys Gly His Asn Phe

35 40 45

Cys Lys Ala Cys Ile Thr Arg Trp Trp Glu Asp Leu Glu Arg Asp Phe

50 55 60

Pro Cys Pro Val Cys Arg Lys Thr Ser Arg Tyr Arg Ser Leu Arg Pro

65 70 75 80

Asn Arg Gln Leu Gly Ser Met Val Glu Ile Ala Lys Gln Leu Gln Ala

85 90 95

Val Lys Arg Lys Ile Arg Asp Glu Ser Leu Cys Pro Gln His His Glu

100 105 110

Ala Leu Ser Leu Phe Cys Tyr Glu Asp Gln Glu Ala Val Cys Leu Ile

115 120 125

Cys Ala Ile Ser His Thr His Arg Ala His Thr Val Val Pro Leu Asp

130 135 140

Asp Ala Thr Gln Glu Tyr Lys Glu Lys Leu Gln Lys Cys Leu Glu Pro

145 150 155 160

Leu Glu Gln Lys Leu Gln Glu Ile Thr Arg Cys Lys Ser Ser Glu Glu
165 170 175

Lys Lys Pro Gly Glu Leu Lys Arg Leu Val Glu Ser Arg Arg Gln Gln
180 185 190

Ile Leu Arg Glu Phe Glu Glu Leu His Arg Arg Leu Asp Glu Glu Gln
195 200 205

Gln Val Leu Leu Ser Arg Leu Glu Glu Glu Glu Gln Asp Ile Leu Gln
210 215 220

Arg Leu Arg Glu Asn Ala Ala His Leu Gly Asp Lys Arg Arg Asp Leu
225 230 235 240

Ala His Leu Ala Ala Glu Val Glu Gly Lys Cys Leu Gln Ser Gly Phe
245 250 255

Glu Met Leu Lys Asp Val Lys Ser Thr Leu Glu Lys Asn Ile Pro Arg
260 265 270

Lys Phe Gly Gly Ser Leu Ser Thr Ile Cys Pro Arg Asp His Lys Ala
275 280 285

Leu Leu Gly Leu Val Lys Glu Ile Asn Arg Cys Glu Lys Val Lys Thr
290 295 300

Met Glu Val Thr Ser Val Ser Ile Glu Leu Glu Lys Asn Phe Ser Asn
305 310 315 320

Phe Pro Arg Gln Tyr Phe Ala Leu Arg Lys Ile Leu Lys Gln Leu Ile
325 330 335

Ala Asp Val Thr Leu Asp Pro Glu Thr Ala His Pro Asn Leu Val Leu
340 345 350

Ser Glu Asp Arg Lys Ser Val Lys Phe Val Glu Thr Arg Leu Arg Asp
355 360 365

Leu Pro Asp Thr Pro Arg Arg Phe Thr Phe Tyr Pro Cys Val Leu Ala
370 375 380

Thr Glu Gly Phe Thr Ser Gly Arg His Tyr Trp Glu Val Glu Val Gly
385 390 395 400

Asp Lys Thr His Trp Ala Val Gly Val Cys Arg Asp Ser Val Ser Arg
405 410 415

Lys Gly Glu Leu Thr Pro Leu Pro Glu Thr Gly Tyr Trp Arg Val Arg
420 425 430

Leu Trp Asn Gly Asp Lys Tyr Ala Ala Thr Thr Thr Pro Phe Thr Pro
435 440 445

Leu His Ile Lys Val Lys Pro Lys Arg Val Gly Ile Phe Leu Asp Tyr
450 455 460

Glu Ala Gly Thr Leu Ser Phe Tyr Asn Val Thr Asp Arg Ser His Ile
465 470 475 480

Tyr Thr Phe Thr Asp Thr Phe Thr Glu Lys Leu Trp Pro Leu Phe Tyr
485 490 495

Pro Gly Ile Arg Ala Gly Arg Lys Asn Ala Ala Pro Leu Thr Ile Arg
500 505 510

Pro Pro Thr Asp Trp Glu
515

<210> 79

<211> 777

<212> DNA

<213> Homo sapiens

<400> 79

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ctgaagaatg ctggtgactt actgaacagg agtgctccac agaaattaga ggttatttat 720
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<210> 80

<211> 258

<212> PRT

<213> Homo sapiens

<400> 80

Met Ile Pro Leu Gln Lys Asp Asn Gln Glu Glu Gly Val Cys Pro Ile

1 5 10 15

Cys Gln Glu Ser Leu Lys Glu Ala Val Ser Thr Asn Cys Gly His Leu

20 25 30

Phe Cys Arg Val Cys Leu Thr Gln His Val Glu Lys Ala Ser Ala Ser

35 40 45

Gly Val Phe Cys Cys Pro Leu Cys Arg Lys Pro Cys Ser Glu Glu Val

50 55 60

Leu Gly Thr Gly Tyr Ile Cys Pro Asn His Gln Lys Arg Val Cys Arg

65 70 75 80

Phe Cys Glu Glu Ser Arg Leu Leu Leu Cys Val Glu Cys Leu Val Ser

85	90	95
Pro Glu His Met Ser His His Glu Leu Thr Ile Glu Asn Ala Leu Ser		
100	105	110
His Tyr Lys Glu Arg Leu Asn Arg Arg Ser Arg Lys Leu Arg Lys Asp		
115	120	125
Ile Ala Glu Leu Gln Arg Leu Lys Ala Gln Gln Glu Lys Lys Leu Gln		
130	135	140
Ala Leu Gln Phe Gln Val Asp His Gly Asn His Arg Leu Glu Ala Gly		
145	150	155
Pro Glu Ser Gln His Gln Thr Arg Glu Gln Leu Gly Ala Leu Pro Gln		
165	170	175
Gln Trp Leu Gly Gln Leu Glu His Met Pro Ala Glu Ala Ala Arg Ile		
180	185	190
Leu Asp Ile Ser Arg Ala Val Thr Gln Leu Arg Ser Leu Val Ile Asp		
195	200	205
Leu Glu Arg Thr Ala Lys Glu Leu Asp Thr Asn Thr Leu Lys Asn Ala		
210	215	220
Gly Asp Leu Leu Asn Arg Ser Ala Pro Gln Lys Leu Glu Val Ile Tyr		
225	230	235
Pro Gln Leu Glu Lys Gly Val Ser Glu Leu Leu Leu Gln Pro Pro Gln		
245	250	255

Lys Leu

<210> 81
 <211> 1893
 <212> DNA
 <213> Homo sapiens

<400> 81

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<210> 82

<211> 630

<212> PRT

<213> Homo sapiens

<400> 82

Met Ala Ala Val Ala Met Thr Pro Asn Pro Val Gln Thr Leu Gln Glu
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Glu Ala Val Cys Ala Ile Cys Leu Asp Tyr Phe Thr Asp Pro Val Ser
 20 25 30

Ile Gly Cys Gly His Asn Phe Cys Arg Val Cys Val Thr Gln Leu Trp
 35 40 45

Gly Gly Glu Asp Glu Glu Asp Arg Asp Glu Leu Asp Arg Glu Glu Glu
 50 55 60

Glu Glu Asp Gly Glu Glu Glu Val Glu Ala Val Gly Ala Gly Ala
 65 70 75 80

Gly Trp Asp Thr Pro Met Arg Asp Glu Asp Tyr Glu Gly Asp Met Glu
 85 90 95

Glu Glu Val Glu Glu Glu Glu Gly Val Phe Trp Thr Ser Gly Met
 100 105 110

Ser Arg Ser Ser Trp Asp Asn Met Asp Tyr Val Trp Glu Glu Glu Asp
115 120 125

Glu Glu Glu Asp Leu Asp Tyr Tyr Leu Gly Asp Met Glu Glu Glu Asp
130 135 140

Leu Arg Gly Glu Asp Glu Glu Asp Glu Glu Glu Val Leu Glu Glu Val
145 150 155 160

Glu Glu Glu Asp Leu Asp Pro Val Thr Pro Leu Pro Pro Pro Pro Ala
165 170 175

Pro Arg Arg Cys Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Pro Arg
180 185 190

Arg Ser Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Val Ile
195 200 205

Arg Gln Met His Pro Thr Pro Gly Arg Gly Ser Arg Val Thr Asp Gln
210 215 220

Gly Ile Cys Pro Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val
225 230 235 240

Asp Glu Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His Lys
245 250 255

Gln His Ser Val Val Pro Leu Glu Glu Val Val Gln Glu Tyr Lys Ala
260 265 270

Lys Leu Gln Gly His Val Glu Pro Leu Arg Lys His Leu Glu Ala Val
275 280 285

Gln Lys Met Lys Ala Lys Glu Glu Arg Arg Val Thr Glu Leu Lys Ser
290 295 300

Gln Met Lys Ser Glu Leu Ala Ala Val Ala Ser Glu Phe Gly Arg Leu
305 310 315 320

Thr Arg Phe Leu Ala Glu Glu Gln Ala Gly Leu Glu Arg Arg Leu Arg
325 330 335

Glu Met His Glu Ala Gln Leu Gly Arg Ala Gly Ala Ala Ala Ser Arg
340 345 350

Leu Ala Glu Gln Ala Ala Gln Leu Ser Arg Leu Leu Ala Glu Ala Gln
355 360 365

Glu Arg Ser Gln Gln Gly Gly Leu Arg Leu Leu Gln Asp Ile Lys Glu
370 375 380

Thr Phe Asn Arg Cys Glu Glu Val Gln Leu Gln Pro Pro Glu Val Trp
385 390 395 400

Ser Pro Asp Pro Cys Gln Pro His Ser His Asp Phe Leu Thr Asp Ala
405 410 415

Ile Val Arg Lys Met Ser Arg Met Phe Cys Gln Ala Ala Arg Val Asp
420 425 430

Leu Thr Leu Asp Pro Asp Thr Ala His Pro Ala Leu Met Leu Ser Pro
435 440 445

Asp Arg Arg Gly Val Arg Leu Ala Glu Arg Arg Gln Glu Val Ala Asp
450 455 460

His Pro Lys Arg Phe Ser Ala Asp Cys Cys Val Leu Gly Ala Gln Gly
465 470 475 480

Phe Arg Ser Gly Arg His Tyr Trp Glu Val Glu Val Gly Gly Arg Arg
485 490 495

Gly Trp Ala Val Gly Ala Ala Arg Glu Ser Thr His His Lys Glu Lys
500 505 510

Val Gly Pro Gly Gly Ser Ser Val Gly Ser Gly Asp Ala Ser Ser Ser
515 520 525

Arg His His His Arg Arg Arg Arg Leu His Leu Pro Gln Gln Pro Leu
530 535 540

Leu Gln Arg Glu Val Trp Cys Val Gly Thr Asn Gly Lys Arg Tyr Gln
545 550 555 560

Ala Gln Ser Ser Thr Glu Gln Thr Leu Leu Ser Pro Ser Glu Lys Pro
565 570 575

Arg Arg Phe Gly Val Tyr Leu Asp Tyr Glu Ala Gly Arg Leu Gly Phe
580 585 590

Tyr Asn Ala Glu Thr Leu Ala His Val His Thr Phe Ser Ala Ala Phe
595 600 605

Leu Gly Glu Arg Val Phe Pro Phe Phe Arg Val Leu Ser Lys Gly Thr
610 615 620

Arg Ile Lys Leu Cys Pro
625 630

<210> 83

<211> 2172

<212> DNA

<213> Homo sapiens

<400> 83

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cagcaaaatc tggagctgca caacctgacc cccaacacag aatacgtgtt taaagttaga 2040
gccatcaatg ataatgggcc tgggcaatgg agtgatatct gcaagggtgt aacaccagat 2100
ggacatggga agaaccgagc taagtggggc ctgctgaaga atatccagtc tgcctccag 2160
aagcacttct ga 2172

<210> 84
<211> 723
<212> PRT
<213> Homo sapiens

<400> 84

Met Glu Thr Ala Met Cys Val Cys Cys Pro Cys Cys Thr Trp Gln Arg
1 5 10 15

Cys Cys Pro Gln Leu Cys Ser Cys Leu Cys Cys Lys Phe Ile Phe Thr
20 25 30

Ser Glu Arg Asn Cys Thr Cys Phe Pro Cys Pro Tyr Lys Asp Glu Arg
35 40 45

Asn Cys Gln Phe Cys His Cys Thr Cys Ser Glu Ser Pro Asn Cys His
50 55 60

Trp Cys Cys Cys Ser Trp Ala Asn Asp Pro Asn Cys Lys Cys Cys Cys
65 70 75 80

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

Arg Asn Thr Ile Ile Thr Phe His Lys Gly Arg Leu Arg Ser Ile His
100 105 110

Thr Ser Ser Lys Thr Ala Leu Arg Thr Gly Ser Ser Asp Thr Gln Val
115 120 125

Asp Glu Val Lys Ser Ile Pro Ala Asn Ser His Leu Val Asn His Leu
130 135 140

Asn Cys Pro Met Cys Ser Arg Leu Arg Leu His Ser Phe Met Leu Pro
145 150 155 160

Cys Asn His Ser Leu Cys Glu Lys Cys Leu Arg Gln Leu Gln Lys His
165 170 175

Ala Glu Val Thr Glu Asn Phe Phe Ile Leu Ile Cys Pro Val Cys Asp
180 185 190

Arg Ser His Cys Met Pro Tyr Ser Asn Lys Met Gln Leu Pro Glu Asn
195 200 205

Tyr Leu His Gly Arg Leu Thr Lys Arg Tyr Met Gln Glu His Gly Tyr
210 215 220

Leu Lys Trp Arg Phe Asp Arg Ser Ser Gly Pro Ile Leu Cys Gln Val
225 230 235 240

Cys Arg Asn Lys Arg Ile Ala Tyr Lys Arg Cys Ile Thr Cys Arg Leu
245 250 255

Asn Leu Cys Asn Asp Cys Leu Lys Ala Phe His Ser Asp Val Ala Met
260 265 270

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

Ile Cys Ile His His Pro Ser Ser Arg Ile Ile Glu Tyr Cys Arg Asn
290 295 300

Asp Asn Lys Leu Leu Cys Thr Phe Cys Lys Phe Ser Phe His Asn Gly
305 310 315 320

His Asp Thr Ile Ser Leu Ile Asp Ala Cys Ser Glu Arg Ala Ala Ser
325 330 335

Leu Phe Ser Ala Ile Ala Lys Phe Lys Ala Val Arg Tyr Glu Ile Asp
340 345 350

Asn Asp Leu Met Glu Phe Asn Ile Leu Lys Asn Ser Phe Lys Ala Asp
355 360 365

Lys Glu Ala Lys Arg Lys Glu Ile Arg Asn Gly Phe Leu Lys Leu Arg
370 375 380

Ser Ile Leu Gln Glu Lys Glu Lys Ile Ile Met Glu Gln Ile Glu Asn
385 390 395 400

Leu Glu Val Ser Arg Gln Lys Glu Ile Glu Lys Tyr Val Tyr Val Thr
405 410 415

Thr Met Lys Val Asn Glu Met Asp Gly Leu Ile Ala Tyr Ser Lys Glu
420 425 430

Ala Leu Lys Glu Thr Gly Gln Val Ala Phe Leu Gln Ser Ala Lys Ile
435 440 445

Leu Val Asp Gln Ile Glu Asp Gly Ile Gln Thr Thr Tyr Arg Pro Asp
450 455 460

Pro Gln Leu Arg Leu His Ser Ile Asn Tyr Val Pro Leu Asp Phe Val
465 470 475 480

Glu Leu Ser Ser Ala Ile His Glu Leu Phe Pro Thr Gly Pro Lys Lys
485 490 495

Val Arg Ser Ser Gly Asp Ser Leu Pro Ser Pro Tyr Pro Val His Ser
500 505 510

Glu Thr Met Ile Ala Arg Lys Val Thr Phe Ser Thr His Ser Leu Gly
515 520 525

Asn Gln His Ile Tyr Gln Arg Ser Ser Ser Met Leu Ser Phe Ser Asn
530 535 540

Thr Asp Lys Lys Ala Lys Val Gly Leu Glu Ala Cys Gly Arg Ala Gln

545 550 555 560

 Ser Ala Thr Pro Ala Lys Pro Thr Asp Gly Leu Tyr Thr Tyr Trp Ser
 565 570 575

 Ala Gly Ala Asp Ser Gln Ser Val Gln Asn Ser Ser Ser Phe His Asn
 580 585 590

 Trp Tyr Ser Phe Asn Asp Gly Ser Val Lys Thr Pro Gly Pro Ile Val
 595 600 605

 Ile Tyr Gln Thr Leu Val Tyr Pro Arg Ala Ala Lys Val Tyr Trp Thr
 610 615 620

 Cys Pro Ala Glu Asp Val Asp Ser Phe Glu Met Glu Phe Tyr Glu Val
 625 630 635 640

 Ile Thr Ser Pro Pro Asn Asn Val Gln Met Glu Leu Cys Gly Gln Ile
 645 650 655

 Arg Asp Ile Met Gln Gln Asn Leu Glu Leu His Asn Leu Thr Pro Asn
 660 665 670

 Thr Glu Tyr Val Phe Lys Val Arg Ala Ile Asn Asp Asn Gly Pro Gly
 675 680 685

 Gln Trp Ser Asp Ile Cys Lys Val Val Thr Pro Asp Gly His Gly Lys
 690 695 700

 Asn Arg Ala Lys Trp Gly Leu Leu Lys Asn Ile Gln Ser Ala Leu Gln
 705 710 715 720

 Lys His Phe

<210> 85
 <211> 1341
 <212> DNA
 <213> Homo sapiens

<400> 85
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 ctttcgtggg aggaagccca aagtctgca aactgccctg catgcaggga accatcaccg 180
 aaaatggact tcaaaaccaa tattcttctg aagaatttag tgaccattgc cagaaaagcc 240
 agtctctggc aattcctgag ctctgagaaa caaatatgtg ggacccatag gcaaaaaag 300
 aagatgttct gtgacatgga caagagtctc ctctgcttgc tgtgctcaa ctctcaggag 360
 cacggggctc acaaacacca tcccatcgaa gaggcagctg aggaacaccg ggagaaactc 420
 ttaaagcaaa tgaggatttt atggaaaaag attcaagaaa atcagagaaa tctatatgag 480
 gagggaagaa cagccttct ctggaggggc aatgtggttt tacgggcaca gatgatcagg 540
 aatgagtata ggaagctgca tccggttctc cataaggaag aaaaacaaca ttagagaga 600
 ctgaacaagg aataccaaga gatttttcag caactccaga gaagtgggt caaatggat 660
 caaaagagta aacacttgaa agaaatgtat caggaactaa tggaaatgtg tcataaacca 720
 gatgtggagc tgctccagga ttggggagac atcgtggcaa ggagtgagtc cgtgctgctg 780
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 aggctctttg aggatgtgag aagttggatg ttagacgtg gacctttgaa ttctgacaga 960
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 aagaatagca caatggtaa ctctgaggac atatttcttc ttttgtgtct gaaggtggat 1140
 aatcattca atctcttgac cacctccca gtgttctc actacataga gaaacctctg 1200
 ggccgggttg gtgtgtttct tgattttgaa agtggaagtg tgagttttt gaatgcacc 1260
 aagagtccc tcatatggag ttaccagct ggctccttaa ctttctgt caggccttc 1320
 ttttactg gccacagatg a 1341

<210> 86
 <211> 446

<212> PRT

<213> Homo sapiens

<400> 86

Met Asp Ser Asp Phe Ser His Ala Phe Gln Lys Glu Leu Thr Cys Val
1 5 10 15

Ile Cys Leu Asn Tyr Leu Val Asp Pro Val Thr Ile Cys Cys Gly His
20 25 30

Ser Phe Cys Arg Pro Cys Leu Cys Leu Ser Trp Glu Glu Ala Gln Ser
35 40 45

Pro Ala Asn Cys Pro Ala Cys Arg Glu Pro Ser Pro Lys Met Asp Phe
50 55 60

Lys Thr Asn Ile Leu Leu Lys Asn Leu Val Thr Ile Ala Arg Lys Ala
65 70 75 80

Ser Leu Trp Gln Phe Leu Ser Ser Glu Lys Gln Ile Cys Gly Thr His
85 90 95

Arg Gln Thr Lys Lys Met Phe Cys Asp Met Asp Lys Ser Leu Leu Cys
100 105 110

Leu Leu Cys Ser Asn Ser Gln Glu His Gly Ala His Lys His His Pro
115 120 125

Ile Glu Glu Ala Ala Glu Glu His Arg Glu Lys Leu Leu Lys Gln Met
130 135 140

Arg Ile Leu Trp Lys Lys Ile Gln Glu Asn Gln Arg Asn Leu Tyr Glu
145 150 155 160

Glu Gly Arg Thr Ala Phe Leu Trp Arg Gly Asn Val Val Leu Arg Ala
165 170 175

Gln Met Ile Arg Asn Glu Tyr Arg Lys Leu His Pro Val Leu His Lys
180 185 190

Glu Glu Lys Gln His Leu Glu Arg Leu Asn Lys Glu Tyr Gln Glu Ile
195 200 205

Phe Gln Gln Leu Gln Arg Ser Trp Val Lys Met Asp Gln Lys Ser Lys
210 215 220

His Leu Lys Glu Met Tyr Gln Glu Leu Met Glu Met Cys His Lys Pro
225 230 235 240

Asp Val Glu Leu Leu Gln Asp Leu Gly Asp Ile Val Ala Arg Ser Glu
245 250 255

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

Gly Pro Ile Thr Gly Leu Val Tyr Arg Leu Asn Arg Phe Arg Val Glu
275 280 285

Ile Ser Phe His Phe Glu Val Thr Asn His Asn Ile Arg Leu Phe Glu
290 295 300

Asp Val Arg Ser Trp Met Phe Arg Arg Gly Pro Leu Asn Ser Asp Arg
305 310 315 320

Ser Asp Tyr Phe Ala Ala Trp Gly Ala Arg Val Phe Ser Phe Gly Lys
325 330 335

His Tyr Trp Glu Leu Asp Val Asp Asn Ser Cys Asp Trp Ala Leu Gly
340 345 350

Val Cys Asn Asn Ser Trp Ile Arg Lys Asn Ser Thr Met Val Asn Ser
355 360 365

Glu Asp Ile Phe Leu Leu Leu Cys Leu Lys Val Asp Asn His Phe Asn
370 375 380

Leu Leu Thr Thr Ser Pro Val Phe Pro His Tyr Ile Glu Lys Pro Leu

385 390 395 400

Gly Arg Val Gly Val Phe Leu Asp Phe Glu Ser Gly Ser Val Ser Phe

 405 410 415

Leu Asn Val Thr Lys Ser Ser Leu Ile Trp Ser Tyr Pro Ala Gly Ser

 420 425 430

Leu Thr Phe Pro Val Arg Pro Phe Phe Tyr Thr Gly His Arg

 435 440 445

<210> 87
 <211> 1035
 <212> DNA
 <213> Homo sapiens

<400> 87

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tgcgagcccg acgaggctcc gggggccgag gaagtgtgcc gagaatgcgg cttctgctac 120

tgccgccgcc atgccgaggc gcacaggcag aagttcctca gtcacatct ggccgaatac 180

gtccacggct cccaggcctg gaccccgcca gctgacggag agggggcggg gaaggaagaa 240

gcggagggtca aggtggagca ggagaggag atagaaagcg aggcagggga agagagttag 300

tcggaggaag agagcgagtc agaggaagag agcgagacag aggaagagag tgaggatgag 360

agcgatgagg agagtgaaga agacagcgag gaagaaatgg aggatgagca agaaagcgag 420

gccgaagaag acaaccaaga agaaggggaa tccgaggcgg agggagaaac taggcagaa 480

agtgaatttg acccagaaat agaaatggaa gcagagagag tggccaagag gaagtgtccg 540

gacatgggc ttgatttgag tacctattgc caggaagata ggcagctcat ctgtgtcctg 600

tgtccagtca ttggggctca ccagggccac caactctcca ccctagacga agcctttgaa 660

gaattaagaa gcaaagactc aggtggactg aaggccgcta tgatcgaatt ggtggaaagg 720

ttgaagttca agagctcaga ccctaaagta actcgggacc aaatgaagat gtttatacag 780

caggaattta agaaagttca gaaagtatt gctgatgagg agcagaaggc cttcatcta 840

gtggacatcc aagaggcaat ggccacagct catgtgactg agatactggc agacatcaa 900

tcccatatgg ataggttgat gactcagatg gcccaagcca aggaacaact tgatacctct 960
 aatgaatcag ctgagccaaa ggcagagggc gatgaggaag gaccagtgg tgccagtgaa 1020
 gaagaggaca catga 1035

<210> 88
 <211> 344
 <212> PRT
 <213> Homo sapiens

<400> 88

Met Ala Ser Gly Val Gly Ala Ala Phe Glu Glu Leu Pro His Asp Gly
 1 5 10 15

Thr Cys Asp Glu Cys Glu Pro Asp Glu Ala Pro Gly Ala Glu Glu Val
 20 25 30

Cys Arg Glu Cys Gly Phe Cys Tyr Cys Arg Arg His Ala Glu Ala His
 35 40 45

Arg Gln Lys Phe Leu Ser His His Leu Ala Glu Tyr Val His Gly Ser
 50 55 60

Gln Ala Trp Thr Pro Pro Ala Asp Gly Glu Gly Ala Gly Lys Glu Glu
 65 70 75 80

Ala Glu Val Lys Val Glu Gln Glu Arg Glu Ile Glu Ser Glu Ala Gly
 85 90 95

Glu Glu Ser Glu Ser Glu Glu Glu Ser Glu Ser Glu Glu Ser Glu
 100 105 110

Thr Glu Glu Glu Ser Glu Asp Glu Ser Asp Glu Glu Ser Glu Glu Asp
 115 120 125

Ser Glu Glu Glu Met Glu Asp Glu Gln Glu Ser Glu Ala Glu Glu Asp
 130 135 140

Asn Gln Glu Glu Gly Glu Ser Glu Ala Glu Gly Glu Thr Glu Ala Glu

145	150	155	160
Ser Glu Phe Asp Pro Glu Ile Glu Met Glu Ala Glu Arg Val Ala Lys			
	165	170	175
Arg Lys Cys Pro Asp His Gly Leu Asp Leu Ser Thr Tyr Cys Gln Glu			
	180	185	190
Asp Arg Gln Leu Ile Cys Val Leu Cys Pro Val Ile Gly Ala His Gln			
	195	200	205
Gly His Gln Leu Ser Thr Leu Asp Glu Ala Phe Glu Glu Leu Arg Ser			
	210	215	220
Lys Asp Ser Gly Gly Leu Lys Ala Ala Met Ile Glu Leu Val Glu Arg			
	225	230	235
			240
Leu Lys Phe Lys Ser Ser Asp Pro Lys Val Thr Arg Asp Gln Met Lys			
	245	250	255
Met Phe Ile Gln Gln Glu Phe Lys Lys Val Gln Lys Val Ile Ala Asp			
	260	265	270
Glu Glu Gln Lys Ala Leu His Leu Val Asp Ile Gln Glu Ala Met Ala			
	275	280	285
Thr Ala His Val Thr Glu Ile Leu Ala Asp Ile Gln Ser His Met Asp			
	290	295	300
Arg Leu Met Thr Gln Met Ala Gln Ala Lys Glu Gln Leu Asp Thr Ser			
	305	310	315
			320
Asn Glu Ser Ala Glu Pro Lys Ala Glu Gly Asp Glu Glu Gly Pro Ser			
	325	330	335
Gly Ala Ser Glu Glu Glu Asp Thr			
	340		

<210> 89
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 89
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 ctcttgccct gtttcatac agtttgacc acgtgtctgg agcagctgga gcccttctca 180
 gtagtggaca tccgaggggg agactctgac acaagctctg aggggtcaat attccaggaa 240
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 gtgatgctgg agagcctacg tggggaaggc cagggcctgg tgtgtgacct gtgcaacgac 420
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 ctgttctgtg agttctgtga ccggcccgtg tgccaggatt gtgtggtggg ggagcatcgg 660
 gaacaccctt gtgacttcac cagcaatgtc atccacaagc atggggactc tgtgtgggag 720
 ctctcaaag gtactcagcc ccacgtggag gccctggagg aagccctggc tcagatccac 780
 ataataaaca gtgccctcca gaagcgagtg gaggcagtgg cagctgatgt ccggacattc 840
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caccgccac actcaggcgt gtttactgc tgcaccttct gctccagcg gggccagaaa 1560
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cacaaaggcc acccaggtca tccccactgg tcatgctgtg gaaaatttaa tgagaaatct 1680
gaatgcacat ggacaggtgg gcagagcgca ccaggagtc tacttaggac tgtggctctc 1740
tga 1743

<210> 90
<211> 580
<212> PRT
<213> Homo sapiens

<400> 90

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

Ser Gly Thr Ala Leu Gly Asn Ser Gly Lys Thr His Cys Pro Leu Cys
20 25 30

Leu Gly Leu Phe Lys Ala Pro Arg Leu Leu Pro Cys Leu His Thr Val
35 40 45

Cys Thr Thr Cys Leu Glu Gln Leu Glu Pro Phe Ser Val Val Asp Ile
50 55 60

Arg Gly Gly Asp Ser Asp Thr Ser Ser Glu Gly Ser Ile Phe Gln Glu
65 70 75 80

Leu Lys Pro Arg Ser Leu Gln Ser Gln Ile Gly Ile Leu Cys Pro Val
85 90 95

Cys Asp Ala Gln Val Asp Leu Pro Met Gly Gly Val Lys Ala Leu Thr
100 105 110

Ile Asp His Leu Ala Val Asn Asp Val Met Leu Glu Ser Leu Arg Gly
115 120 125

Glu Gly Gln Gly Leu Val Cys Asp Leu Cys Asn Asp Arg Glu Val Glu
130 135 140

Lys Arg Cys Gln Thr Cys Lys Ala Asn Leu Cys His Phe Cys Cys Gln
145 150 155 160

Ala His Arg Arg Gln Lys Lys Thr Thr Tyr His Thr Met Val Asp Leu
165 170 175

Lys Asp Leu Lys Gly Tyr Ser Arg Ile Gly Lys Pro Ile Leu Cys Pro
180 185 190

Val His Pro Ala Glu Glu Leu Arg Leu Phe Cys Glu Phe Cys Asp Arg
195 200 205

Pro Val Cys Gln Asp Cys Val Val Gly Glu His Arg Glu His Pro Cys
210 215 220

Asp Phe Thr Ser Asn Val Ile His Lys His Gly Asp Ser Val Trp Glu
225 230 235 240

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

Ala Gln Ile His Ile Ile Asn Ser Ala Leu Gln Lys Arg Val Glu Ala
260 265 270

Val Ala Ala Asp Val Arg Thr Phe Ser Glu Gly Tyr Ile Lys Ala Ile
275 280 285

Glu Glu His Arg Asp Lys Leu Leu Lys Gln Leu Glu Asp Ile Arg Ala
290 295 300

Gln Lys Glu Asn Ser Leu Gln Leu Gln Lys Ala Gln Leu Glu Gln Leu
305 310 315 320

Leu Ala Asp Met Arg Thr Gly Val Glu Phe Thr Glu His Leu Leu Thr
325 330 335

Ser Gly Ser Asp Leu Glu Ile Leu Ile Thr Lys Arg Val Val Val Glu
340 345 350

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

Asn Asp Lys Ile Arg Phe Cys Pro Gln Glu Lys Ala Gly Gln Cys Arg
370 375 380

Gly Tyr Glu Ile Tyr Gly Thr Ile Asn Thr Lys Glu Val Asp Pro Ala
385 390 395 400

Lys Cys Val Leu Gln Gly Glu Asp Leu His Arg Ala Arg Glu Lys Gln
405 410 415

Thr Ala Ser Phe Thr Leu Leu Cys Lys Asp Ala Ala Gly Glu Ile Met
420 425 430

Gly Arg Gly Gly Asp Asn Val Gln Val Ala Val Val Pro Lys Asp Lys
435 440 445

Lys Asp Ser Pro Val Arg Thr Met Val Gln Asp Asn Lys Asp Gly Thr
450 455 460

Tyr Tyr Ile Ser Tyr Thr Pro Lys Glu Pro Gly Val Tyr Thr Val Trp
465 470 475 480

Val Cys Ile Lys Glu Gln His Val Gln Gly Ser Pro Phe Thr Val Met
485 490 495

Val Arg Arg Lys His Arg Pro His Ser Gly Val Phe His Cys Cys Thr
500 505 510

Phe Cys Ser Ser Gly Gly Gln Lys Thr Ala Arg Cys Ala Cys Gly Gly
515 520 525

Thr Met Pro Gly Gly Tyr Leu Gly Cys Gly His Gly His Lys Gly His
 530 535 540

Pro Gly His Pro His Trp Ser Cys Cys Gly Lys Phe Asn Glu Lys Ser
 545 550 555 560

Glu Cys Thr Trp Thr Gly Gly Gln Ser Ala Pro Arg Ser Leu Leu Arg
 565 570 575

Thr Val Ala Leu
 580

<210> 91
 <211> 2280
 <212> DNA
 <213> Homo sapiens

<400> 91
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 agtaccagca tgaagaacat ggagaaggaa ctgctgtgcc cagtgtgtca agagatgtac 120
 aagcagccac tgggtctgcc ctgtaccac aacgtgtgcc aggcctgtgc ccgagaggtc 180
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 gcctccaccc ctccacccg cagccccgc ctctccgca gaactctccc caagccagac 300
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 gaggccacca agggctgcac agagtccgc gccaccttct gcaatgagtg cttcaagctc 600
 ttccaccctt ggggcaccca gaaggcccag catgagccca ccctgcctac cctctccttc 660
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 cacaccgagg tgagtgggtca gcaggccaag gaggaggtgt cgagctggt gcgggggctg 960
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 gtgcacctgc acacgcccc ggcacctgtc ctgcacttct tcctcgatag ccgtggggc 1620
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<210> 92

<211> 759

<212> PRT

<213> Homo sapiens

<400> 92

Met Ala Glu Gly Glu Asp Met Gln Thr Phe Thr Ser Ile Met Asp Ala
1 5 10 15

Leu Val Arg Ile Ser Thr Ser Met Lys Asn Met Glu Lys Glu Leu Leu
20 25 30

Cys Pro Val Cys Gln Glu Met Tyr Lys Gln Pro Leu Val Leu Pro Cys
35 40 45

Thr His Asn Val Cys Gln Ala Cys Ala Arg Glu Val Leu Gly Gln Gln
50 55 60

Gly Tyr Ile Gly His Gly Gly Asp Pro Ser Ser Glu Pro Thr Ser Pro
65 70 75 80

Ala Ser Thr Pro Ser Thr Arg Ser Pro Arg Leu Ser Arg Arg Thr Leu
85 90 95

Pro Lys Pro Asp Arg Leu Asp Arg Leu Leu Lys Ser Gly Phe Gly Thr
100 105 110

Tyr Pro Gly Arg Lys Arg Gly Ala Leu His Pro Gln Val Ile Met Phe
115 120 125

Pro Cys Pro Ala Cys Gln Gly Asp Val Glu Leu Gly Glu Arg Gly Leu
130 135 140

Ala Gly Leu Phe Arg Asn Leu Thr Leu Glu Arg Val Val Glu Arg Tyr
145 150 155 160

Arg Gln Ser Val Ser Val Gly Gly Ala Ile Leu Cys Gln Leu Cys Lys
165 170 175

Pro Pro Pro Leu Glu Ala Thr Lys Gly Cys Thr Glu Cys Arg Ala Thr

180	185	190
Phe Cys Asn Glu Cys Phe Lys Leu Phe His Pro Trp Gly Thr Gln Lys		
195	200	205
Ala Gln His Glu Pro Thr Leu Pro Thr Leu Ser Phe Arg Pro Lys Gly		
210	215	220
Leu Met Cys Pro Asp His Lys Glu Glu Val Thr His Tyr Cys Lys Thr		
225	230	235 240
Cys Gln Arg Leu Val Cys Gln Leu Cys Arg Val Arg Arg Thr His Ser		
245	250	255
Gly His Lys Ile Thr Pro Val Leu Ser Ala Tyr Gln Ala Leu Lys Asp		
260	265	270
Lys Leu Thr Lys Ser Leu Thr Tyr Ile Leu Gly Asn Gln Asp Thr Val		
275	280	285
Gln Thr Gln Ile Cys Glu Leu Glu Glu Ala Val Arg His Thr Glu Val		
290	295	300
Ser Gly Gln Gln Ala Lys Glu Glu Val Ser Gln Leu Val Arg Gly Leu		
305	310	315 320
Gly Ala Val Leu Glu Glu Lys Arg Ala Ser Leu Leu Gln Ala Ile Glu		
325	330	335
Glu Cys Gln Gln Glu Arg Leu Ala Arg Leu Ser Ala Gln Ile Gln Glu		
340	345	350
His Arg Ser Leu Leu Asp Gly Ser Gly Leu Val Gly Tyr Ala Gln Glu		
355	360	365
Val Leu Lys Glu Thr Asp Gln Pro Cys Phe Val Gln Ala Ala Lys Gln		
370	375	380

Leu His Asn Arg Ile Ala Arg Ala Thr Glu Ala Leu Gln Thr Phe Arg
385 390 395 400

Pro Ala Ala Ser Ser Ser Phe Arg His Cys Gln Leu Asp Val Gly Arg
 405 410 415

Glu Met Lys Leu Leu Thr Glu Leu Asn Phe Leu Arg Val Pro Glu Ala
 420 425 430

Pro Val Ile Asp Thr Gln Arg Thr Phe Ala Tyr Asp Gln Ile Phe Leu
 435 440 445

Cys Trp Arg Leu Pro Pro His Ser Pro Pro Ala Trp His Tyr Thr Val
 450 455 460

Glu Phe Arg Arg Thr Asp Val Pro Ala Gln Pro Gly Pro Thr Arg Trp
465 470 475 480

Gln Arg Arg Glu Glu Val Arg Gly Thr Ser Ala Leu Leu Glu Asn Pro
 485 490 495

Asp Thr Gly Ser Val Tyr Val Leu Arg Val Arg Gly Cys Asn Lys Ala
 500 505 510

Gly Tyr Gly Glu Tyr Ser Glu Asp Val His Leu His Thr Pro Pro Ala
 515 520 525

Pro Val Leu His Phe Phe Leu Asp Ser Arg Trp Gly Ala Ser Arg Glu
 530 535 540

Arg Leu Ala Ile Ser Lys Asp Gln Arg Ala Val Arg Ser Val Pro Gly
545 550 555 560

Leu Pro Leu Leu Leu Ala Ala Asp Arg Leu Leu Thr Gly Cys His Leu
 565 570 575

Ser Val Asp Val Val Leu Gly Asp Val Ala Val Thr Gln Gly Arg Ser
 580 585 590

Tyr Trp Ala Cys Ala Val Asp Pro Ala Ser Tyr Leu Val Lys Val Gly
595 600 605

Val Gly Leu Glu Ser Lys Leu Gln Glu Ser Phe Gln Gly Ala Pro Asp
610 615 620

Val Ile Ser Pro Arg Tyr Asp Pro Asp Ser Gly His Asp Ser Gly Ala
625 630 635 640

Glu Asp Ala Thr Val Glu Ala Ser Pro Pro Phe Ala Phe Leu Thr Ile
645 650 655

Gly Met Gly Lys Ile Leu Leu Gly Ser Gly Ala Ser Ser Asn Ala Gly
660 665 670

Leu Thr Gly Arg Asp Gly Pro Thr Ala Gly Cys Thr Val Pro Leu Pro
675 680 685

Pro Arg Leu Gly Ile Cys Leu Asp Tyr Glu Arg Gly Arg Val Ser Phe
690 695 700

Leu Asp Ala Val Ser Phe Arg Gly Leu Leu Glu Cys Pro Leu Asp Cys
705 710 715 720

Ser Gly Pro Val Cys Pro Ala Phe Cys Phe Ile Gly Gly Gly Ala Val
725 730 735

Gln Leu Gln Glu Pro Val Gly Thr Lys Pro Glu Arg Lys Val Thr Ile
740 745 750

Gly Gly Phe Ala Lys Leu Asp
755

<210> 93

<211> 1917

<212> DNA

<213> Homo sapiens

<400> 93

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 ggcgcgagtg gagccggcgg acccggaggc gcggcccgtg gcccgctgtg ccaggagccc 180
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 cagggctcgg gccccgggtc cggccccggc ccggcccctg ccctggcccc ggagccctcg 300
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 gcgtgtcct gcctctctg cctgcctcc tttgcccc cgacactggg cccgcacgag 480
 cgcagcccc ccctccgagg acaccgcctg gtgcccgcc tgcgccggt agaggagagc 540
 ctgtgccgc gccacctac gccgtcgag cgctactgcc gcgcggagcg cgtgtgtctg 600
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 gacttctccc cacaagagcc ctacaccgc ggccggctgg gccgaacgc cactcctgc 1560

tgcctgcagt ggaatggacg cagcttctcc gtctggttcc atgggctgga ggctcccctg 1620
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 ttgcggggc tctcaccac cagactcaag cctgccttct tctggagag tgtggacgcc 1860
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<210> 94

<211> 638

<212> PRT

<213> Homo sapiens

<400> 94

Met Asp Gly Ser Gly Pro Phe Ser Cys Pro Ile Cys Leu Glu Pro Leu
 1 5 10 15

Arg Glu Pro Val Thr Leu Pro Cys Gly His Asn Phe Cys Leu Ala Cys
 20 25 30

Leu Gly Ala Leu Trp Pro His Arg Gly Ala Ser Gly Ala Gly Gly Pro
 35 40 45

Gly Gly Ala Ala Arg Cys Pro Leu Cys Gln Glu Pro Phe Pro Asp Gly
 50 55 60

Leu Gln Leu Arg Lys Asn His Thr Leu Ser Glu Leu Leu Gln Leu Arg
 65 70 75 80

Gln Gly Ser Gly Pro Gly Ser Gly Pro Gly Pro Ala Pro Ala Leu Ala
 85 90 95

Pro Glu Pro Ser Ala Pro Ser Ala Leu Pro Ser Val Pro Glu Pro Ser
 100 105 110

Ala Pro Cys Ala Pro Glu Pro Trp Pro Ala Gly Glu Glu Pro Val Arg
 115 120 125

Cys Asp Ala Cys Pro Glu Gly Ala Ala Leu Pro Ala Ala Leu Ser Cys
130 135 140

Leu Ser Cys Leu Ala Ser Phe Cys Pro Ala His Leu Gly Pro His Glu
145 150 155 160

Arg Ser Pro Ala Leu Arg Gly His Arg Leu Val Pro Pro Leu Arg Arg
165 170 175

Leu Glu Glu Ser Leu Cys Pro Arg His Leu Arg Pro Leu Glu Arg Tyr
180 185 190

Cys Arg Ala Glu Arg Val Cys Leu Cys Glu Ala Cys Ala Ala Gln Glu
195 200 205

His Arg Gly His Glu Leu Val Pro Leu Glu Gln Glu Arg Ala Leu Gln
210 215 220

Glu Ala Glu Gln Ser Lys Val Leu Ser Ala Val Glu Asp Arg Met Asp
225 230 235 240

Glu Leu Gly Ala Gly Ile Ala Gln Ser Arg Arg Thr Val Ala Leu Ile
245 250 255

Lys Ser Ala Ala Val Ala Glu Arg Glu Arg Val Ser Arg Leu Phe Ala
260 265 270

Asp Ala Ala Ala Ala Leu Gln Gly Phe Gln Thr Gln Val Leu Gly Phe
275 280 285

Ile Glu Glu Gly Glu Ala Ala Met Leu Gly Arg Ser Gln Gly Asp Leu
290 295 300

Arg Arg Gln Glu Glu Gln Arg Ser Arg Leu Ser Arg Ala Arg Gln Asn
305 310 315 320

Leu Ser Gln Val Pro Glu Ala Asp Ser Val Ser Phe Leu Gln Glu Leu

325	330	335
Leu Ala Leu Arg	Leu Ala Leu Glu Asp Gly Cys Gly Pro Gly Pro Gly	
340	345	350
Pro Pro Arg Glu Leu Ser Phe Thr Lys Ser Ser Gln Ala Val Arg Ala		
355	360	365
Val Arg Asp Met Leu Ala Val Ala Cys Val Asn Gln Trp Glu Gln Leu		
370	375	380
Arg Gly Pro Gly Gly Asn Glu Asp Gly Pro Gln Lys Leu Asp Ser Glu		
385	390	395 400
Ala Asp Ala Glu Pro Gln Asp Leu Glu Ser Thr Asn Leu Leu Glu Ser		
405	410	415
Glu Ala Pro Arg Asp Tyr Phe Leu Lys Phe Ala Tyr Ile Val Asp Leu		
420	425	430
Asp Ser Asp Thr Ala Asp Lys Phe Leu Gln Leu Phe Gly Thr Lys Gly		
435	440	445
Val Lys Arg Val Leu Cys Pro Ile Asn Tyr Pro Leu Ser Pro Thr Arg		
450	455	460
Phe Thr His Cys Glu Gln Val Leu Gly Glu Gly Ala Leu Asp Arg Gly		
465	470	475 480
Thr Tyr Tyr Trp Glu Val Glu Ile Ile Glu Gly Trp Val Ser Met Gly		
485	490	495
Val Met Ala Glu Asp Phe Ser Pro Gln Glu Pro Tyr Asp Arg Gly Arg		
500	505	510
Leu Gly Arg Asn Ala His Ser Cys Cys Leu Gln Trp Asn Gly Arg Ser		
515	520	525

Phe Ser Val Trp Phe His Gly Leu Glu Ala Pro Leu Pro His Pro Phe
 530 535 540

Ser Pro Thr Val Gly Val Cys Leu Glu Tyr Ala Asp Arg Ala Leu Ala
 545 550 555 560

Phe Tyr Ala Val Arg Asp Gly Lys Met Ser Leu Leu Arg Arg Leu Lys
 565 570 575

Ala Ser Arg Pro Arg Arg Gly Gly Ile Pro Ala Ser Pro Ile Asp Pro
 580 585 590

Phe Gln Ser Arg Leu Asp Ser His Phe Ala Gly Leu Phe Thr His Arg
 595 600 605

Leu Lys Pro Ala Phe Phe Leu Glu Ser Val Asp Ala His Leu Gln Ile
 610 615 620

Gly Pro Leu Lys Lys Ser Cys Ile Ser Val Leu Lys Arg Arg
 625 630 635

<210> 95

<211> 675

<212> DNA

<213> Homo sapiens

<400> 95

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atctcgcaag tcttcagag ggaactcacc tgcccatct gcatgaacta cttcatagac 120

ccggtcacca tagactgtgg gcacagcttt tgcaggccct gtttctacct caactggcaa 180

gacatcccaa ttctactca gtgctttgaa tgcataaaga caatacagca gagaaacctc 240

aaaactaaca ttcgattgaa gaagatggct tcccttgcca gaaaagccag tctctggcta 300

ttctgagct ctgaggagca aatgtgtggc attcacaggg agacaaagaa gatgttctgt 360

gaagtggaca ggagcctgct ctgtttgctg tgctccagct ctgaggagca ccggtatcac 420

agacactgtc ccgctgagtg ggctgctgag gaacactggg agaagctttt aaagaaaatg 480

cagtctttat gggaaaaagc ttgtgaaaat cagagaaacc tgaatgtgga aaccaccaga 540

atcagccact ggaaggcttt tggagacata ttatacagga gtgagtcgt gctgctgcac 600
 atgccccagc ctctgaatct agcgctcagg gcagggccca tctctggact gagggacagg 660
 ctcaaccaat tctga 675

<210> 96
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 96

Met Ser Arg Arg Ile Ile Val Gly Thr Leu Gln Arg Thr Gln Arg Asn
 1 5 10 15

Met Asn Ser Gly Ile Ser Gln Val Phe Gln Arg Glu Leu Thr Cys Pro
 20 25 30

Ile Cys Met Asn Tyr Phe Ile Asp Pro Val Thr Ile Asp Cys Gly His
 35 40 45

Ser Phe Cys Arg Pro Cys Phe Tyr Leu Asn Trp Gln Asp Ile Pro Ile
 50 55 60

Leu Thr Gln Cys Phe Glu Cys Ile Lys Thr Ile Gln Gln Arg Asn Leu
 65 70 75 80

Lys Thr Asn Ile Arg Leu Lys Lys Met Ala Ser Leu Ala Arg Lys Ala
 85 90 95

Ser Leu Trp Leu Phe Leu Ser Ser Glu Glu Gln Met Cys Gly Ile His
 100 105 110

Arg Glu Thr Lys Lys Met Phe Cys Glu Val Asp Arg Ser Leu Leu Cys
 115 120 125

Leu Leu Cys Ser Ser Ser Gln Glu His Arg Tyr His Arg His Cys Pro
 130 135 140

Ala Glu Trp Ala Ala Glu Glu His Trp Glu Lys Leu Leu Lys Lys Met
 145 150 155 160

Gln Ser Leu Trp Glu Lys Ala Cys Glu Asn Gln Arg Asn Leu Asn Val
 165 170 175

Glu Thr Thr Arg Ile Ser His Trp Lys Ala Phe Gly Asp Ile Leu Tyr
 180 185 190

Arg Ser Glu Ser Val Leu Leu His Met Pro Gln Pro Leu Asn Leu Ala
 195 200 205

Leu Arg Ala Gly Pro Ile Thr Gly Leu Arg Asp Arg Leu Asn Gln Phe
 210 215 220

<210> 97

<211> 1359

<212> DNA

<213> Homo sapiens

<400> 97

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tacttcatag acccggtcac catagactgt gggcacagct ttgcaggcc ttgtttctac 120

ctcaactggc aagacatccc atttctgtc cagtgtctg aatgcacaaa gtcaaccgag 180

cagataaacc tcaaaaccaa cattcattg aagaagatgg cttctcttgc cagaaaagtc 240

agtctctggc tattctgag ctctgaggag caaatgtgtg gcactcacag ggagacaaag 300

aagatattct gtgaagtga caggagcctg ctctgtttgc tgtgtccag ctctcaggag 360

caccggtatc acagacaccg tccattgag tgggctgctg aggaacaccg ggagaagctt 420

ttacagaaaa tgcagtcttt gtgggaaaaa gcttgtgaaa atcacagaaa cctgaatgtg 480

gaaaccacca gaaccagatg ctggaaggat tatgtgaatt taaggctaga agcaattaga 540

gctgagtatc agaagatgcc tgcatttcat catgaagaag aaaaacataa ttggagatg 600

ctgaaaaaga aggggaaaga aatttttcat cgacttcatt taagtaaagc caaaatggct 660

cataggatgg agattttaag aggaatgtat gaggagctga acgaaatgtg ccataaacca 720

gatgtggagc tacttcaggc ttttgagac atattacaca ggagtgagtc cgtgtgtgtg 780

cacatgcccc agcctctgaa tccagagctc agtgcagggc ccatcactgg actgagggac 840
 aggtcaacc aattccgagt gcatattact ctgcatcatg aagaagcaa caatgatatc 900
 tttctgatg aaattttgag aagcatgtgt attggatgtg accatcaaga tgtaccctat 960
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 tataatccaa aacctaccag ccgagtagga ttattcctgg attgtgaggc taagactgtg 1260
 agctttgttg atgttaatca aagctcccta atatacacca tcctaattg ctctttctca 1320
 cctcctctca ggcctatctt ttgctgtatt cacttctga 1359

<210> 98
 <211> 452
 <212> PRT
 <213> Homo sapiens

<400> 98

Met Asn Ser Gly Ile Leu Gln Val Phe Gln Gly Glu Leu Ile Cys Pro
 1 5 10 15

Leu Cys Met Asn Tyr Phe Ile Asp Pro Val Thr Ile Asp Cys Gly His
 20 25 30

Ser Phe Cys Arg Pro Cys Phe Tyr Leu Asn Trp Gln Asp Ile Pro Phe
 35 40 45

Leu Val Gln Cys Ser Glu Cys Thr Lys Ser Thr Glu Gln Ile Asn Leu
 50 55 60

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

Ser Leu Trp Leu Phe Leu Ser Ser Glu Glu Gln Met Cys Gly Thr His
 85 90 95

Arg Glu Thr Lys Lys Ile Phe Cys Glu Val Asp Arg Ser Leu Leu Cys
100 105 110

Leu Leu Cys Ser Ser Ser Gln Glu His Arg Tyr His Arg His Arg Pro
115 120 125

Ile Glu Trp Ala Ala Glu Glu His Arg Glu Lys Leu Leu Gln Lys Met
130 135 140

Gln Ser Leu Trp Glu Lys Ala Cys Glu Asn His Arg Asn Leu Asn Val
145 150 155 160

Glu Thr Thr Arg Thr Arg Cys Trp Lys Asp Tyr Val Asn Leu Arg Leu
165 170 175

Glu Ala Ile Arg Ala Glu Tyr Gln Lys Met Pro Ala Phe His His Glu
180 185 190

Glu Glu Lys His Asn Leu Glu Met Leu Lys Lys Lys Gly Lys Glu Ile
195 200 205

Phe His Arg Leu His Leu Ser Lys Ala Lys Met Ala His Arg Met Glu
210 215 220

Ile Leu Arg Gly Met Tyr Glu Glu Leu Asn Glu Met Cys His Lys Pro
225 230 235 240

Asp Val Glu Leu Leu Gln Ala Phe Gly Asp Ile Leu His Arg Ser Glu
245 250 255

Ser Val Leu Leu His Met Pro Gln Pro Leu Asn Pro Glu Leu Ser Ala
260 265 270

Gly Pro Ile Thr Gly Leu Arg Asp Arg Leu Asn Gln Phe Arg Val His
275 280 285

Ile Thr Leu His His Glu Glu Ala Asn Asn Asp Ile Phe Leu Tyr Glu

290 295 300
 Ile Leu Arg Ser Met Cys Ile Gly Cys Asp His Gln Asp Val Pro Tyr
 305 310 315 320
 Phe Thr Ala Thr Pro Arg Ser Phe Leu Ala Trp Gly Val Gln Thr Phe
 325 330 335
 Thr Ser Gly Lys Tyr Tyr Trp Glu Val His Val Gly Asp Ser Trp Asn
 340 345 350
 Trp Ala Phe Gly Val Cys Asn Met Tyr Arg Lys Glu Lys Asn Gln Asn
 355 360 365
 Glu Lys Ile Asp Gly Lys Ala Gly Leu Phe Leu Leu Gly Cys Val Lys
 370 375 380
 Asn Asp Ile Gln Cys Ser Leu Phe Thr Thr Ser Pro Leu Met Leu Gln
 385 390 395 400
 Tyr Ile Pro Lys Pro Thr Ser Arg Val Gly Leu Phe Leu Asp Cys Glu
 405 410 415
 Ala Lys Thr Val Ser Phe Val Asp Val Asn Gln Ser Ser Leu Ile Tyr
 420 425 430
 Thr Ile Pro Asn Cys Ser Phe Ser Pro Pro Leu Arg Pro Ile Phe Cys
 435 440 445
 Cys Ile His Phe
 450

<210> 99

<211> 1464

<212> DNA

<213> Homo sapiens

<400> 99

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cggacccgaa tcgtcaatga gtcggatgtc ttcagctggg tgatccgccg cgagtccag 540
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aggggcagca actcgtgcc catggtgctg ccccccca gcgggcctgg cccctcagc 1440
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<210> 100

<211> 487

<212> PRT

<213> Homo sapiens

<400> 100

Met Ala Trp Gln Val Ser Leu Pro Glu Leu Glu Asp Arg Leu Gln Cys
1 5 10 15

Pro Ile Cys Leu Glu Val Phe Lys Glu Pro Leu Met Leu Gln Cys Gly
20 25 30

His Ser Tyr Cys Lys Gly Cys Leu Val Ser Leu Ser Cys His Leu Asp
35 40 45

Ala Glu Leu Arg Cys Pro Val Cys Arg Gln Ala Val Asp Gly Ser Ser
50 55 60

Ser Leu Pro Asn Val Ser Leu Ala Arg Val Ile Glu Ala Leu Arg Leu
65 70 75 80

Pro Gly Asp Pro Glu Pro Lys Val Cys Val His His Arg Asn Pro Leu
85 90 95

Ser Leu Phe Cys Glu Lys Asp Gln Glu Leu Ile Cys Gly Leu Cys Gly
100 105 110

Leu Leu Gly Ser His Gln His His Pro Val Thr Pro Val Ser Thr Val
115 120 125

Tyr Ser Arg Met Lys Glu Glu Leu Ala Ala Leu Ile Ser Glu Leu Lys
130 135 140

Gln Glu Gln Lys Lys Val Asp Glu Leu Ile Ala Lys Leu Val Asn Asn
145 150 155 160

Arg Thr Arg Ile Val Asn Glu Ser Asp Val Phe Ser Trp Val Ile Arg
165 170 175

Arg Glu Phe Gln Glu Leu His His Leu Val Asp Glu Glu Lys Ala Arg
180 185 190

Cys Leu Glu Gly Ile Gly Gly His Thr Arg Gly Leu Val Ala Ser Leu
195 200 205

Asp Met Gln Leu Glu Gln Ala Gln Gly Thr Arg Glu Arg Leu Ala Gln
210 215 220

Ala Glu Cys Val Leu Glu Gln Phe Gly Asn Glu Asp His His Lys Phe
225 230 235 240

Ile Arg Lys Phe His Ser Met Ala Ser Arg Ala Glu Met Pro Gln Ala
245 250 255

Arg Pro Leu Glu Gly Ala Phe Ser Pro Ile Ser Phe Lys Pro Gly Leu
260 265 270

His Gln Ala Asp Ile Lys Leu Thr Val Trp Lys Arg Leu Phe Arg Lys
275 280 285

Val Leu Pro Ala Pro Glu Pro Leu Lys Leu Asp Pro Ala Thr Ala His
290 295 300

Pro Leu Leu Glu Leu Ser Lys Gly Asn Thr Val Val Gln Cys Gly Leu
305 310 315 320

Leu Ala Gln Arg Arg Ala Ser Gln Pro Glu Arg Phe Asp Tyr Ser Thr
325 330 335

Cys Val Leu Ala Ser Arg Gly Phe Ser Cys Gly Arg His Tyr Trp Glu
340 345 350

Val Val Val Gly Ser Lys Ser Asp Trp Arg Leu Gly Val Ile Lys Gly
355 360 365

Thr Ala Ser Arg Lys Gly Lys Leu Asn Arg Ser Pro Glu His Gly Val
370 375 380

Trp Leu Ile Gly Leu Lys Glu Gly Arg Val Tyr Glu Ala Phe Ala Cys

385 390 395 400

Pro Arg Val Pro Leu Pro Val Ala Gly His Pro His Arg Ile Gly Leu
 405 410 415

Tyr Leu His Tyr Glu Gln Gly Glu Leu Thr Phe Phe Asp Ala Asp Arg
 420 425 430

Pro Asp Asp Leu Arg Pro Leu Tyr Thr Phe Gln Ala Asp Phe Gln Gly
 435 440 445

Lys Leu Tyr Pro Ile Leu Asp Thr Cys Trp His Glu Arg Gly Ser Asn
 450 455 460

Ser Leu Pro Met Val Leu Pro Pro Pro Ser Gly Pro Gly Pro Leu Ser
465 470 475 480

Pro Glu Gln Pro Thr Lys Leu
 485

<210> 101

<211> 1359

<212> DNA

<213> Homo sapiens

<400> 101

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ctcaactggc aagacacggc agttcttgct cagtgtctg aatgcaagaa gacaacgcgg 180

cagagaaacc tcaactga cattgtttg aagaacatgg ctttcattgc cagaaaagcc 240

agcctccggc aattccttag ctctgaggag caaatatgtg ggatgcacag agagacaaag 300

aagatgttct gtgaagtga caagagcctg ctctgtttgc cgtgctcaa ctctcaggag 360

caccggaatc acatactg tccattgag tgggctgctg aggaacgccg ggaggagctc 420

ctaaaaaaaa tgcagtcttt atgggaaaaa gcttgtaaaa atctcagaaa tctgaacatg 480

gaaaccacaa gaaccagatg ctggaaggat tatgtgagtt taaggataga agcaatcaga 540

gctgaatc agaagatgcc tgcatttctc catgaagaag agcaacatca cttggaaagg 600
 ctgcgaaagg agggcgagga ctttttcag caactcaatg aaagcaaagc cagaatggaa 660
 cattccaggg agcttttaag aggaatgtat gaggatctga agcaaattg ccataaagca 720
 gatgtggagc tactccaggc ttttgagac atattacaca ggtatgagtc tctgctgctg 780
 caagtgtctg agcctgtgaa tccagagctc agtcagggc ccatcactgg actgctggac 840
 agcctcagtg gattcagagt tgattttact ctgcagcctg aaagagccaa tagtcatatc 900
 ttctgtgtg gagatttgag aagcatgaat gttggatgtg accctcaaga tgatcccgat 960
 atcactggaa aatctgaatg ttttctgtg tggggggctc aggctttcac atctggcaaa 1020
 tattattggg aggttcatat gggggactct tggaattggg cttttggtg ctgtaacaat 1080
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 tatgttccaa gacctaccag cacagtagga ttattcctgg attgtgaagg tagaaccgtg 1260
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<210> 102

<211> 452

<212> PRT

<213> Homo sapiens

<400> 102

Met Asn Ser Gly Ile Leu Gln Val Phe Gln Arg Ala Leu Thr Cys Pro

1 5 10 15

Ile Cys Met Asn Tyr Phe Leu Asp Pro Val Thr Ile Asp Cys Gly His

20 25 30

Ser Phe Cys Arg Pro Cys Leu Tyr Leu Asn Trp Gln Asp Thr Ala Val

35 40 45

Leu Ala Gln Cys Ser Glu Cys Lys Lys Thr Thr Arg Gln Arg Asn Leu

50 55 60

Asn Thr Asp Ile Cys Leu Lys Asn Met Ala Phe Ile Ala Arg Lys Ala
65 70 75 80

Ser Leu Arg Gln Phe Leu Ser Ser Glu Glu Gln Ile Cys Gly Met His
 85 90 95

Arg Glu Thr Lys Lys Met Phe Cys Glu Val Asp Lys Ser Leu Leu Cys
 100 105 110

Leu Pro Cys Ser Asn Ser Gln Glu His Arg Asn His Ile His Cys Pro
 115 120 125

Ile Glu Trp Ala Ala Glu Glu Arg Arg Glu Glu Leu Leu Lys Lys Met
 130 135 140

Gln Ser Leu Trp Glu Lys Ala Cys Glu Asn Leu Arg Asn Leu Asn Met
145 150 155 160

Glu Thr Thr Arg Thr Arg Cys Trp Lys Asp Tyr Val Ser Leu Arg Ile
 165 170 175

Glu Ala Ile Arg Ala Glu Tyr Gln Lys Met Pro Ala Phe Leu His Glu
 180 185 190

Glu Glu Gln His His Leu Glu Arg Leu Arg Lys Glu Gly Glu Asp Ile
 195 200 205

Phe Gln Gln Leu Asn Glu Ser Lys Ala Arg Met Glu His Ser Arg Glu
 210 215 220

Leu Leu Arg Gly Met Tyr Glu Asp Leu Lys Gln Met Cys His Lys Ala
225 230 235 240

Asp Val Glu Leu Leu Gln Ala Phe Gly Asp Ile Leu His Arg Tyr Glu
 245 250 255

Ser Leu Leu Leu Gln Val Ser Glu Pro Val Asn Pro Glu Leu Ser Ala
 260 265 270

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

Phe Thr Leu Gln Pro Glu Arg Ala Asn Ser His Ile Phe Leu Cys Gly
290 295 300

Asp Leu Arg Ser Met Asn Val Gly Cys Asp Pro Gln Asp Asp Pro Asp
305 310 315 320

Ile Thr Gly Lys Ser Glu Cys Phe Leu Val Trp Gly Ala Gln Ala Phe
325 330 335

Thr Ser Gly Lys Tyr Tyr Trp Glu Val His Met Gly Asp Ser Trp Asn
340 345 350

Trp Ala Phe Gly Val Cys Asn Asn Tyr Trp Lys Glu Lys Arg Gln Asn
355 360 365

Asp Lys Ile Asp Gly Glu Glu Gly Leu Phe Leu Leu Gly Cys Val Lys
370 375 380

Glu Asp Thr His Cys Ser Leu Phe Thr Thr Ser Pro Leu Val Val Gln
385 390 395 400

Tyr Val Pro Arg Pro Thr Ser Thr Val Gly Leu Phe Leu Asp Cys Glu
405 410 415

Gly Arg Thr Val Ser Phe Val Asp Val Asp Gln Ser Ser Leu Ile Tyr
420 425 430

Thr Ile Pro Asn Cys Ser Phe Ser Pro Pro Leu Arg Pro Ile Phe Cys
435 440 445

Cys Ser His Phe
450

<210> 103

<211> 894
 <212> DNA
 <213> Homo sapiens

<400> 103
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 cgagggtgtg tgacccagct gtggagtaag gaggacgagg aggaccagaa cgaggaggaa 180
 gatgaatggg aggaggagga ggacgaggaa gcggtggggg ccatggatgg atgggacggc 240
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 cctgacctga gaattgatgt ctaccgagaa gaagaaatac tggaagcata cgatgaggac 480
 gaagatgaag agctgtatcc tgacatccac ccgcctcctt ccttgcccct tccagggcag 540
 ttacactgcc cccagtgcc aaagagcttt acacgtcgca gctttctgcc caactgcag 600
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 agtaatgatc agggcatgtg cttaaacac caggaagccc tgaactctt ctgtgaggtg 720
 gacaaagagg ccatctgtgt ggtgtgccga gaatccagga gccacaaaca gcacagcgtg 780
 ctgcctttgg aggaggtggt gcaggagtac caggaaataa agttggaac aactctggtg 840
 ggaatacttc agatagagca agaaagcatt cacagcaagg cctataatca gtaa 894

<210> 104
 <211> 297
 <212> PRT
 <213> Homo sapiens

<400> 104
 Met Ala Gly Tyr Ala Thr Thr Pro Ser Pro Met Gln Thr Leu Gln Glu
 1 5 10 15
 Glu Ala Val Cys Ala Ile Cys Leu Asp Tyr Phe Lys Asp Pro Val Ser
 20 25 30

Ile Ser Cys Gly His Asn Phe Cys Arg Gly Cys Val Thr Gln Leu Trp
35 40 45

Ser Lys Glu Asp Glu Glu Asp Gln Asn Glu Glu Glu Asp Glu Trp Glu
50 55 60

Glu Glu Glu Asp Glu Glu Ala Val Gly Ala Met Asp Gly Trp Asp Gly
65 70 75 80

Ser Ile Arg Glu Val Leu Tyr Arg Gly Asn Ala Asp Glu Glu Leu Phe
85 90 95

Gln Asp Gln Asp Asp Asp Glu Leu Trp Leu Gly Asp Ser Gly Ile Thr
100 105 110

Asn Trp Asp Asn Val Asp Tyr Met Trp Asp Glu Glu Glu Glu Glu
115 120 125

Glu Glu Asp Gln Asp Tyr Tyr Leu Gly Gly Leu Arg Pro Asp Leu Arg
130 135 140

Ile Asp Val Tyr Arg Glu Glu Glu Ile Leu Glu Ala Tyr Asp Glu Asp
145 150 155 160

Glu Asp Glu Glu Leu Tyr Pro Asp Ile His Pro Pro Pro Ser Leu Pro
165 170 175

Leu Pro Gly Gln Phe Thr Cys Pro Gln Cys Arg Lys Ser Phe Thr Arg
180 185 190

Arg Ser Phe Arg Pro Asn Leu Gln Leu Ala Asn Met Val Gln Ile Ile
195 200 205

Arg Gln Met Cys Pro Thr Pro Tyr Arg Gly Asn Arg Ser Asn Asp Gln
210 215 220

Gly Met Cys Phe Lys His Gln Glu Ala Leu Lys Leu Phe Cys Glu Val
225 230 235 240

Asp Lys Glu Ala Ile Cys Val Val Cys Arg Glu Ser Arg Ser His Lys
 245 250 255

Gln His Ser Val Leu Pro Leu Glu Glu Val Val Gln Glu Tyr Gln Glu
 260 265 270

Ile Lys Leu Glu Thr Thr Leu Val Gly Ile Leu Gln Ile Glu Gln Glu
 275 280 285

Ser Ile His Ser Lys Ala Tyr Asn Gln
 290 295

<210> 105
 <211> 1203
 <212> DNA
 <213> Homo sapiens

<400> 105
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 ccctgccaac acaacctgtg ccgcaaatgt gccaacgacg tcttcaggcg ctcgaatcct 180
 ctatggcagt cccggggctc caccactgtg tcttcaggag gccgtttccg ctgccatcg 240
 tgcaggcatg aggttgtcct ggacagacac ggtgtctacg gcctgcagcg aaacctgcta 300
 gtggagaaca ttatcgacat ttacaagcag gagtcatcca ggccgctgca ctccaaggct 360
 gagcagcacc tcattgtcga ggagcatgaa gaagagaaga tcaatattta ctgcctgagc 420
 tgtgaggtgc ccacctgctc tctctgcaag gtcttcggtg cccacaagga ctgtgaggtg 480
 gcccactgc ccaccattta caaacgccag aagaacagg atctcactct gttgccagg 540
 ctggagtga gtggcacaaa cacaacttac tgcagccttg atctcccgag ctcaagtga 600
 cctccatct tagcctcgca gaactaag attatagata gtgagctcag cgatggcatc 660
 gcgatgctgg tggcaggcaa tgaccgctg caagcagtga tcacacagat ggaggaggtg 720
 tgccagacta tcgaggacaa tagccggagg cagaagcagt tgttaaacca gaggtttgag 780
 agcctgtgcg cagtgtgga ggagcgcaag ggtgagctgc tgcaggcgct ggcccgggag 840

caagaggaga agctgcagcg cgtccgcggc ctcatccgtc agtatggcga ccacctggag 900
 gcctcctcta agctggtgga gtctgccatc cagtccatgg aagagccaca aatggcgctg 960
 tatctccagc aggccaagga gctgatcaat aaggtcgggg ccatgtcgaa ggtggagctg 1020
 gcagggcggc cggagccagg ctatgagagc atggagcaat tcaccgtaag ggtggagcac 1080
 gtggccgaaa tgctcgggac catcgacttc cagccaggcg cttccgggga ggaagaggag 1140
 gtggccccag acggagagga gggcagcgcg gggccggagg aagagcggcc ggatgggcct 1200
 taa 1203

<210> 106
 <211> 400
 <212> PRT
 <213> Homo sapiens

<400> 106

Met Asn Phe Thr Val Gly Phe Lys Pro Leu Leu Gly Asp Ala His Ser
 1 5 10 15

Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met
 20 25 30

Phe Ser Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg
 35 40 45

Lys Cys Ala Asn Asp Val Phe Gln Ala Ser Asn Pro Leu Trp Gln Ser
 50 55 60

Arg Gly Ser Thr Thr Val Ser Ser Gly Gly Arg Phe Arg Cys Pro Ser
 65 70 75 80

Cys Arg His Glu Val Val Leu Asp Arg His Gly Val Tyr Gly Leu Gln
 85 90 95

Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Ser
 100 105 110

Ser Arg Pro Leu His Ser Lys Ala Glu Gln His Leu Met Cys Glu Glu

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

Tyr Leu Gln Gln Ala Lys Glu Leu Ile Asn Lys Val Gly Ala Met Ser
 325 330 335

Lys Val Glu Leu Ala Gly Arg Pro Glu Pro Gly Tyr Glu Ser Met Glu
 340 345 350

Gln Phe Thr Val Arg Val Glu His Val Ala Glu Met Leu Arg Thr Ile
 355 360 365

Asp Phe Gln Pro Gly Ala Ser Gly Glu Glu Glu Glu Val Ala Pro Asp
 370 375 380

Gly Glu Glu Gly Ser Ala Gly Pro Glu Glu Glu Arg Pro Asp Gly Pro
 385 390 395 400

<210> 107

<211> 1647

<212> DNA

<213> Homo sapiens

<400> 107

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cctgtcagc						
acaacctgtg	taggaaatgt	gccagtata	tttccaggc	ctctaaccg		180
tatttgccca						
caagaggagg	taccacatg	gcatcagggg	gccgattccg	ctgcccattc		240
ttagacatg						
aagtggtttt	ggatagacat	gggtatatg	gacttcagag	gaacctgtg		300
gtggaaaata						
tcattgacat	ctacaagcag	gagtccacca	ggccagaaaa	gaaatccgac		360
cagcccatgt						
gagaggaaca	tgaagaggag	cgcataca	tctactgtct	gaactgcgaa		420
gtaccacat						
gctctctgtg	caaggtgttt	ggtgcacaca	aagactgcc	ggtggctccc		480
ctcactcatg						
tgttccagag	acagaagtct	gagctcagtg	atggcatcgc	catcctcgtg		540
ggcagcaacg						
atcgagtcca	gggagtgtatc	agccagctgg	aagacacctg	caaaactatc		600
gaggaatgtt						
gcagaaaaca	gaaacaagag	ctttgtgaga	agtttgatta	cctgtatggc		660
atattggagg						
agaggaagaa	tgaatgacc	caagtcatta	cccgaacca	agaggagaaa		720
ctggaacatg						
tccgtgtctt	gatcaaaaag	tattctgatc	atttgagaa	cgctcaaag		780

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 atacgtgaaa ttgactttta cagagaagat gaagatgaag aagaagaaga aggcggagaa 1020
 ggagaaaaag aaggagaagg agaagtggga ggagaagcag tagaagtgga agaggtagaa 1080
 aatgttcaaa cagagtttcc aggagaagat gaaaaccag aaaaagcttc agagctctct 1140
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 agtgcacctg cagctacttc tcagattgga ttgaggctc ctcccctcca gggacaggct 1560
 gcagctccag cgagtggcag tggagctgat tctgagccag ctgccatat cttctcctt 1620
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<210> 108

<211> 548

<212> PRT

<213> Homo sapiens

<400> 108

Met Ser Ala Ser Leu Asn Tyr Lys Ser Phe Ser Lys Glu Gln Gln Thr
 1 5 10 15

Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met
 20 25 30

Phe Thr Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg
 35 40 45

Lys Cys Ala Ser Asp Ile Phe Gln Ala Ser Asn Pro Tyr Leu Pro Thr
50 55 60

Arg Gly Gly Thr Thr Met Ala Ser Gly Gly Arg Phe Arg Cys Pro Ser
65 70 75 80

Cys Arg His Glu Val Val Leu Asp Arg His Gly Val Tyr Gly Leu Gln
85 90 95

Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Ser
100 105 110

Thr Arg Pro Glu Lys Lys Ser Asp Gln Pro Met Cys Glu Glu His Glu
115 120 125

Glu Glu Arg Ile Asn Ile Tyr Cys Leu Asn Cys Glu Val Pro Thr Cys
130 135 140

Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp Cys Gln Val Ala Pro
145 150 155 160

Leu Thr His Val Phe Gln Arg Gln Lys Ser Glu Leu Ser Asp Gly Ile
165 170 175

Ala Ile Leu Val Gly Ser Asn Asp Arg Val Gln Gly Val Ile Ser Gln
180 185 190

Leu Glu Asp Thr Cys Lys Thr Ile Glu Glu Cys Cys Arg Lys Gln Lys
195 200 205

Gln Glu Leu Cys Glu Lys Phe Asp Tyr Leu Tyr Gly Ile Leu Glu Glu
210 215 220

Arg Lys Asn Glu Met Thr Gln Val Ile Thr Arg Thr Gln Glu Glu Lys
225 230 235 240

Leu Glu His Val Arg Ala Leu Ile Lys Lys Tyr Ser Asp His Leu Glu
245 250 255

Asn Val Ser Lys Leu Val Glu Ser Gly Ile Gln Phe Met Asp Glu Pro
260 265 270

Glu Met Ala Val Phe Leu Gln Asn Ala Lys Thr Leu Leu Lys Lys Ile
275 280 285

Ser Glu Ala Ser Lys Ala Phe Gln Met Glu Lys Ile Glu His Gly Tyr
290 295 300

Glu Asn Met Asn His Phe Thr Val Asn Leu Asn Arg Glu Glu Lys Ile
305 310 315 320

Ile Arg Glu Ile Asp Phe Tyr Arg Glu Asp Glu Asp Glu Glu Glu Glu
325 330 335

Glu Gly Gly Glu Gly Glu Lys Glu Gly Glu Gly Glu Val Gly Gly Glu
340 345 350

Ala Val Glu Val Glu Glu Val Glu Asn Val Gln Thr Glu Phe Pro Gly
355 360 365

Glu Asp Glu Asn Pro Glu Lys Ala Ser Glu Leu Ser Gln Val Glu Leu
370 375 380

Gln Ala Ala Pro Gly Ala Leu Pro Val Ser Ser Pro Glu Pro Pro Pro
385 390 395 400

Ala Leu Pro Pro Ala Ala Asp Ala Pro Val Thr Gln Gly Glu Val Val
405 410 415

Pro Thr Gly Ser Glu Gln Thr Thr Glu Ser Glu Thr Pro Val Pro Ala
420 425 430

Ala Ala Glu Thr Ala Asp Pro Leu Phe Tyr Pro Ser Trp Tyr Lys Gly
435 440 445

Gln Thr Arg Lys Ala Thr Thr Asn Pro Pro Cys Thr Pro Gly Ser Glu
450 455 460

Gly Leu Gly Gln Ile Gly Pro Pro Gly Ser Glu Asp Ser Asn Val Arg
 465 470 475 480

Lys Ala Glu Val Ala Ala Ala Ala Ala Ser Glu Arg Ala Ala Val Ser
 485 490 495

Gly Lys Glu Thr Ser Ala Pro Ala Ala Thr Ser Gln Ile Gly Phe Glu
 500 505 510

Ala Pro Pro Leu Gln Gly Gln Ala Ala Ala Pro Ala Ser Gly Ser Gly
 515 520 525

Ala Asp Ser Glu Pro Ala Arg His Ile Phe Ser Phe Ser Trp Leu Asn
 530 535 540

Ser Leu Asn Glu
 545

<210> 109
 <211> 2225
 <212> DNA
 <213> Homo sapiens

<400> 109
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 tgtaaatct gcctggagca gctgcgggca cccaagacac tgccctgcct gcatacctac 120
 tgccaagact gcctggcaca gctggcggat ggcggccgcg tccgtgccc cgagtgccgc 180
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ccctgcctgc ctctggctga agctgtgcgt gcccgaggc cgggcctgga gggactgctg 660
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 aagaactgcc accttctcg gctgtcctt gaggagcagc agccccagaa ggatggtggg 1140
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 cagacacccc acgaggatgg aggaccccag cccacaggg gtggcagacc caacaagaag 1380
 aaaaagtca aaggcaggct caagtcaatt tccgggagc ccagcccagc cctggggccg 1440
 aatctggagc gctctggcct cctcccaga cccatctttt actgcagttt cccacgcgg 1500
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 aagggcaccg tgccggtccc tgagggtgc tcccctgca gcgtggccgc cctgcagagc 1680
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agtaa 2225

<210> 110

<211> 755

<212> PRT

<213> Homo sapiens

<400> 110

Met Val Ser His Gly Ser Ser Pro Ser Leu Leu Glu Ala Leu Ser Ser
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Asp Phe Leu Ala Cys Lys Ile Cys Leu Glu Gln Leu Arg Ala Pro Lys
20 25 30

Thr Leu Pro Cys Leu His Thr Tyr Cys Gln Asp Cys Leu Ala Gln Leu
35 40 45

Ala Asp Gly Gly Arg Val Arg Cys Pro Glu Cys Arg Glu Thr Val Pro
50 55 60

Val Pro Pro Glu Gly Val Ala Ser Phe Lys Thr Asn Phe Phe Val Asn
65 70 75 80

Gly Leu Leu Asp Leu Val Lys Ala Arg Ala Cys Gly Asp Leu Arg Ala
85 90 95

Gly Lys Pro Ala Cys Ala Leu Cys Pro Leu Val Gly Gly Thr Ser Thr
100 105 110

Gly Gly Pro Ala Thr Ala Arg Cys Leu Asp Cys Ala Asp Asp Leu Cys
115 120 125

Gln Ala Cys Ala Asp Gly His Arg Cys Thr Arg Gln Thr His Thr His
130 135 140

Arg Val Val Asp Leu Val Gly Tyr Arg Ala Gly Trp Tyr Asp Glu Glu

145	150	155	160
Ala Arg Glu Arg Gln Ala Ala Gln Cys Pro Gln His Pro Gly Glu Ala			
165	170	175	
Leu Arg Phe Leu Cys Gln Pro Cys Ser Gln Leu Leu Cys Arg Glu Cys			
180	185	190	
Arg Leu Asp Pro His Leu Asp His Pro Cys Leu Pro Leu Ala Glu Ala			
195	200	205	
Val Arg Ala Arg Arg Pro Gly Leu Glu Gly Leu Leu Ala Gly Val Asp			
210	215	220	
Asn Asn Leu Val Glu Leu Glu Ala Ala Arg Arg Val Glu Lys Glu Ala			
225	230	235	240
Leu Ala Arg Leu Arg Glu Gln Ala Ala Arg Val Gly Thr Gln Val Glu			
245	250	255	
Glu Ala Ala Glu Gly Val Leu Arg Ala Leu Leu Ala Gln Lys Gln Glu			
260	265	270	
Val Leu Gly Gln Leu Arg Ala His Val Glu Ala Ala Glu Glu Ala Ala			
275	280	285	
Arg Glu Arg Leu Ala Glu Leu Glu Gly Arg Glu Gln Val Ala Arg Ala			
290	295	300	
Ala Ala Ala Phe Ala Arg Arg Val Leu Ser Leu Gly Arg Glu Ala Glu			
305	310	315	320
Ile Leu Ser Leu Glu Gly Ala Ile Ala Gln Arg Leu Arg Gln Leu Gln			
325	330	335	
Gly Cys Pro Trp Ala Pro Gly Pro Ala Pro Cys Leu Leu Pro Gln Leu			
340	345	350	

Glu Leu His Pro Gly Leu Leu Asp Lys Asn Cys His Leu Leu Arg Leu
355 360 365

Ser Phe Glu Glu Gln Gln Pro Gln Lys Asp Gly Gly Lys Asp Gly Ala
370 375 380

Gly Thr Gln Gly Gly Glu Glu Ser Gln Ser Arg Arg Glu Asp Glu Pro
385 390 395 400

Lys Thr Glu Arg Gln Gly Gly Val Gln Pro Gln Ala Gly Asp Gly Ala
405 410 415

Gln Thr Pro Lys Glu Glu Lys Ala Gln Thr Thr Arg Glu Glu Gly Ala
420 425 430

Gln Thr Leu Glu Glu Asp Arg Ala Gln Thr Pro His Glu Asp Gly Gly
435 440 445

Pro Gln Pro His Arg Gly Gly Arg Pro Asn Lys Lys Lys Lys Phe Lys
450 455 460

Gly Arg Leu Lys Ser Ile Ser Arg Glu Pro Ser Pro Ala Leu Gly Pro
465 470 475 480

Asn Leu Asp Gly Ser Gly Leu Leu Pro Arg Pro Ile Phe Tyr Cys Ser
485 490 495

Phe Pro Thr Arg Met Pro Gly Asp Lys Arg Ser Pro Arg Ile Thr Gly
500 505 510

Leu Cys Pro Phe Gly Pro Arg Glu Ile Leu Val Ala Asp Glu Gln Asn
515 520 525

Arg Ala Leu Lys Arg Phe Ser Leu Asn Gly Asp Tyr Lys Gly Thr Val
530 535 540

Pro Val Pro Glu Gly Cys Ser Pro Cys Ser Val Ala Ala Leu Gln Ser
545 550 555 560

Ala Val Ala Phe Ser Ala Ser Ala Arg Leu Tyr Leu Ile Asn Pro Asn
565 570 575

Gly Glu Val Gln Trp Arg Arg Ala Leu Ser Leu Ser Gln Ala Ser His
580 585 590

Ala Val Ala Ala Leu Pro Ser Gly Asp Arg Val Ala Val Ser Val Ala
595 600 605

Gly His Val Glu Val Tyr Asn Met Glu Gly Ser Leu Ala Thr Arg Phe
610 615 620

Ile Pro Gly Gly Lys Ala Ser Arg Gly Leu Arg Ala Leu Val Phe Leu
625 630 635 640

Thr Thr Ser Pro Gln Gly His Phe Val Gly Ser Asp Trp Gln Gln Asn
645 650 655

Ser Val Val Ile Cys Asp Gly Leu Gly Gln Val Val Gly Glu Tyr Lys
660 665 670

Gly Pro Gly Leu His Gly Cys Gln Pro Gly Ser Val Ser Val Asp Lys
675 680 685

Lys Gly Tyr Ile Phe Leu Thr Leu Arg Glu Val Asn Lys Val Val Ile
690 695 700

Leu Asp Pro Lys Gly Ser Leu Leu Gly Asp Phe Leu Thr Ala Tyr His
705 710 715 720

Gly Leu Glu Lys Pro Arg Val Thr Thr Met Val Asp Gly Arg Tyr Leu
725 730 735

Val Val Ser Leu Ser Asn Gly Thr Ile His Ile Phe Arg Val Arg Ser
740 745 750

Pro Asp Ser
755

<210> 111
 <211> 1461
 <212> DNA
 <213> Homo sapiens

<400> 111
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 tccgagttct gcgagaagtc ggacggcgcg cagggcggcg tctacgcctg tccgcagtgc 180
 cggggcccct tccggccctc gggctttcgc cccaaccggc agctggcggg cctggtggag 240
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 gaggacctga gccgcttctg cgaggaggac gaggcggcg tctgctgggt gtgcgacgcc 360
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 gtaaagctcc agatggctct ggaacttatg aggaaagagt tggaggacgc cttgactcag 480
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 cgcttcagat tggagtttga gaagcatcgt ggctttctgg ccagaggaga gcaacggcag 600
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 gtcacaaggc tggaagcaga gaacatcccc atggaactga agacagcatg ctgcatccct 840
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 caccgagtc tgctcttgac cgccgacctg cgcagtgtgc aggatggaga accatggagg 960
 gatgtcccca acaaccctga gcgatttgac acatggccct gcatcctggg ttgcagagc 1020
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 cctcttctcc aactggaaag tcctcgctgc attgggattt tcttgacta tgaagccggt 1260
 gaaatttcat tctacaatgt cacagatgga tcttatatct acacattcaa ccaactcttc 1320

tctggtcttc ttcggcctta ctttttcac tgtgatgcaa ctcctcttat cttgccaccc 1380

acaacaatag cagggtcagg aaattgggca tccagggatc atttagatcc tgcttctgat 1440

gtaagagatg atcatctcta a 1461

<210> 112

<211> 486

<212> PRT

<213> Homo sapiens

<400> 112

Met Ala Trp Ala Pro Pro Gly Glu Arg Leu Arg Glu Asp Ala Arg Cys
1 5 10 15

Pro Val Cys Leu Asp Phe Leu Gln Glu Pro Val Ser Val Asp Cys Gly
20 25 30

His Ser Phe Cys Leu Arg Cys Ile Ser Glu Phe Cys Glu Lys Ser Asp
35 40 45

Gly Ala Gln Gly Gly Val Tyr Ala Cys Pro Gln Cys Arg Gly Pro Phe
50 55 60

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

Ser Val Arg Arg Leu Gly Leu Gly Ala Gly Pro Gly Ala Arg Arg Cys
85 90 95

Ala Arg His Gly Glu Asp Leu Ser Arg Phe Cys Glu Glu Asp Glu Ala
100 105 110

Ala Leu Cys Trp Val Cys Asp Ala Gly Pro Glu His Arg Thr His Arg
115 120 125

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

Met Ala Leu Glu Leu Met Arg Lys Glu Leu Glu Asp Ala Leu Thr Gln
145 150 155 160

Glu Ala Asn Val Gly Lys Lys Thr Val Ile Trp Lys Glu Lys Val Glu
 165 170 175

Met Gln Arg Gln Arg Phe Arg Leu Glu Phe Glu Lys His Arg Gly Phe
 180 185 190

Leu Ala Gln Glu Glu Gln Arg Gln Leu Arg Arg Leu Glu Ala Glu Glu
 195 200 205

Arg Ala Thr Leu Gln Arg Leu Arg Glu Ser Lys Ser Arg Leu Val Gln
 210 215 220

Gln Ser Lys Ala Leu Lys Glu Leu Ala Asp Glu Leu Gln Glu Arg Cys
225 230 235 240

Gln Arg Pro Ala Leu Gly Leu Leu Glu Gly Val Arg Gly Val Leu Ser
 245 250 255

Arg Ser Lys Ala Val Thr Arg Leu Glu Ala Glu Asn Ile Pro Met Glu
 260 265 270

Leu Lys Thr Ala Cys Cys Ile Pro Gly Arg Arg Glu Leu Leu Arg Lys
 275 280 285

Phe Gln Val Asp Val Lys Leu Asp Pro Ala Thr Ala His Pro Ser Leu
 290 295 300

Leu Leu Thr Ala Asp Leu Arg Ser Val Gln Asp Gly Glu Pro Trp Arg
305 310 315 320

Asp Val Pro Asn Asn Pro Glu Arg Phe Asp Thr Trp Pro Cys Ile Leu
 325 330 335

Gly Leu Gln Ser Phe Ser Ser Gly Arg His Tyr Trp Glu Val Leu Val
 340 345 350

Gly Glu Gly Ala Glu Trp Gly Leu Gly Val Cys Gln Asp Thr Leu Pro
355 360 365

Arg Lys Gly Glu Thr Thr Pro Ser Pro Glu Asn Gly Val Trp Ala Leu
370 375 380

Trp Leu Leu Lys Gly Asn Glu Tyr Met Val Leu Ala Ser Pro Ser Val
385 390 395 400

Pro Leu Leu Gln Leu Glu Ser Pro Arg Cys Ile Gly Ile Phe Leu Asp
405 410 415

Tyr Glu Ala Gly Glu Ile Ser Phe Tyr Asn Val Thr Asp Gly Ser Tyr
420 425 430

Ile Tyr Thr Phe Asn Gln Leu Phe Ser Gly Leu Leu Arg Pro Tyr Phe
435 440 445

Phe Ile Cys Asp Ala Thr Pro Leu Ile Leu Pro Pro Thr Thr Ile Ala
450 455 460

Gly Ser Gly Asn Trp Ala Ser Arg Asp His Leu Asp Pro Ala Ser Asp
465 470 475 480

Val Arg Asp Asp His Leu
485

<210> 113

<211> 1212

<212> DNA

<213> Homo sapiens

<400> 113

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cgtgtactgc catgctctca tacattttgt agaaattgtt tggaaaacat tcttcaggca 120

tctggtaact tttatatatg gagaccttta cgaattccac tcaagtgcc taattgcaga 180

agtattactg aaattgctcc aactggcatt gaatctttac ctgttaattt tgcactaagg 240

gctattattg aaaagtacca gcaagaagac catccagata ttgtcacctg ccctgaacat 300
tacaggcaac cattaatgt ttactgtcta ttagataaaa aattagtttg tggtcattgc 360
cttaccatag gtcaacatca tggatcatct atagatgacc ttcaaagtc ctatttgaat 420
gaaaaggaca ctctcaaaa actgcttgaa cagttgactg acacacactg gacagatctt 480
acccatctta ttgaaaagct gaaagaacaa aaatctcatt ctgagaaaat gatccaaggc 540
gataaggaag ctgttctcca gtattttaag gagcttaatg atacattaga acagaaaaaa 600
aaaagttcc taacggctct ctgtgatgtt ggcaatctaa ttaatcaaga atatactcca 660
caaattgaaa gaatgaagga aatacagag cagcagcttg aattaatggc actgacaata 720
tctttacaag aagagtctcc acttaaattt ctgaaaaag ttgatgatgt acgccagcat 780
gtacagatct tgaacaaaag accacttct gaggttcaac ccgttgaaat ttatcctcga 840
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ctcattccca aatgaaaat ttctcaaaa aggatgtcat gttcctggcc tggtaaggat 960
gaaaaggaag ttgaattttt aaaaatttta aacattgttg tagttacatt aatttcagta 1020
atactgatgt cgatactctt ttcaaccaa cacatcataa cttttttaag tgaatcact 1080
ttaatatgtt ttctgaagc ctctctatct gtttaccaaa gtttatctaa cagtctgcat 1140
aaggtaaaga atatactgtg tcacatttct tattgttga aggaatttgt gtggaaaata 1200
gtttccatt ga 1212

<210> 114

<211> 403

<212> PRT

<213> Homo sapiens

<400> 114

Met His Asn Phe Glu Glu Glu Leu Thr Cys Pro Ile Cys Tyr Ser Ile

1 5 10 15

Phe Glu Asp Pro Arg Val Leu Pro Cys Ser His Thr Phe Cys Arg Asn

20 25 30

Cys Leu Glu Asn Ile Leu Gln Ala Ser Gly Asn Phe Tyr Ile Trp Arg

35 40 45
 Pro Leu Arg Ile Pro Leu Lys Cys Pro Asn Cys Arg Ser Ile Thr Glu
 50 55 60
 Ile Ala Pro Thr Gly Ile Glu Ser Leu Pro Val Asn Phe Ala Leu Arg
 65 70 75 80
 Ala Ile Ile Glu Lys Tyr Gln Gln Glu Asp His Pro Asp Ile Val Thr
 85 90 95
 Cys Pro Glu His Tyr Arg Gln Pro Leu Asn Val Tyr Cys Leu Leu Asp
 100 105 110
 Lys Lys Leu Val Cys Gly His Cys Leu Thr Ile Gly Gln His His Gly
 115 120 125
 His Pro Ile Asp Asp Leu Gln Ser Ala Tyr Leu Lys Glu Lys Asp Thr
 130 135 140
 Pro Gln Lys Leu Leu Glu Gln Leu Thr Asp Thr His Trp Thr Asp Leu
 145 150 155 160
 Thr His Leu Ile Glu Lys Leu Lys Glu Gln Lys Ser His Ser Glu Lys
 165 170 175
 Met Ile Gln Gly Asp Lys Glu Ala Val Leu Gln Tyr Phe Lys Glu Leu
 180 185 190
 Asn Asp Thr Leu Glu Gln Lys Lys Lys Ser Phe Leu Thr Ala Leu Cys
 195 200 205
 Asp Val Gly Asn Leu Ile Asn Gln Glu Tyr Thr Pro Gln Ile Glu Arg
 210 215 220
 Met Lys Glu Ile Arg Glu Gln Gln Leu Glu Leu Met Ala Leu Thr Ile
 225 230 235 240

Ser Leu Gln Glu Glu Ser Pro Leu Lys Phe Leu Glu Lys Val Asp Asp
245 250 255

Val Arg Gln His Val Gln Ile Leu Lys Gln Arg Pro Leu Pro Glu Val
260 265 270

Gln Pro Val Glu Ile Tyr Pro Arg Val Ser Lys Ile Leu Lys Glu Glu
275 280 285

Trp Ser Arg Thr Glu Ile Gly Gln Ile Lys Asn Val Leu Ile Pro Lys
290 295 300

Met Lys Ile Ser Pro Lys Arg Met Ser Cys Ser Trp Pro Gly Lys Asp
305 310 315 320

Glu Lys Glu Val Glu Phe Leu Lys Ile Leu Asn Ile Val Val Val Thr
325 330 335

Leu Ile Ser Val Ile Leu Met Ser Ile Leu Phe Phe Asn Gln His Ile
340 345 350

Ile Thr Phe Leu Ser Glu Ile Thr Leu Ile Trp Phe Ser Glu Ala Ser
355 360 365

Leu Ser Val Tyr Gln Ser Leu Ser Asn Ser Leu His Lys Val Lys Asn
370 375 380

Ile Leu Cys His Ile Phe Tyr Leu Leu Lys Glu Phe Val Trp Lys Ile
385 390 395 400

Val Ser His

<210> 115

<211> 1416

<212> DNA

<213> Homo sapiens

<400> 115

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gagtacttga aagacccagt gaccatcaac tgtgggcaca acttctgtcg ctctgcctc 120
 agtgtatcct ggaaggatct agatgatacc tttccctgtc ctgtctgccg ttttgcttt 180
 ccatacaaga gcttcaggag gaacccccag ctccgtaatt tgactgaaat tgctaaacaa 240
 ctccagatta ggaggagcaa gagaaagagg cagaaagaga atgccatgtg tgaaaaacac 300
 aaccagtttc tgacctctt ctgtgttaaa gatctagaga tcttatgtac acagtgcagt 360
 ttctcacta aacaccagaa gcactacatt tgcctatta agaaagctgc ctcttatcac 420
 agagaaattc tagaaggtag ccttgagccc ttgaggaata atatagaacg agtgaaaaa 480
 gtgataattc tgcaaggcag caaatcagtg gagctgaaaa agaaggtaga atataagagg 540
 gaagaaataa attctgagtt tgagcaaata agattgtttt tacagaatga acaagagatg 600
 attcttaggc agatacaaga tgaagagatg aacatttttag caaaactaaa tgaaaacctt 660
 gtagaacttt cagattatgt ttccacatta aaacatctac tgaggagggt agagggaag 720
 tctgtgcagt caaacctgga attactgaca caagctaaga gtatgcacca caagtatcaa 780
 aacctaaaat gccctgaact ctttcattht agattaacaa aatatggtht cagtcttct 840
 cctcaatatt ctggcttgga cagaattatc aagccatttc aagtagatgt gattctagat 900
 ctcaacacag cacatcctca acttctgtc tctgaggata gaaaagctgt gcgatatgaa 960
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 cctaagacaa cccagcttct gccagtagta aaaccagta aaattggtat ttttctggac 1260
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 aacgattgtt tcacagaagc cgtttgcct tatttctata ctggaacaga ttccgaacct 1380
 cttaaaatct gctcagtatc agattctgaa agataa 1416

<210> 116
 <211> 471
 <212> PRT

<213> Homo sapiens

<400> 116

Met Glu Phe Val Thr Ala Leu Val Asn Leu Gln Glu Glu Ser Ser Cys
1 5 10 15

Pro Ile Cys Leu Glu Tyr Leu Lys Asp Pro Val Thr Ile Asn Cys Gly
20 25 30

His Asn Phe Cys Arg Ser Cys Leu Ser Val Ser Trp Lys Asp Leu Asp
35 40 45

Asp Thr Phe Pro Cys Pro Val Cys Arg Phe Cys Phe Pro Tyr Lys Ser
50 55 60

Phe Arg Arg Asn Pro Gln Leu Arg Asn Leu Thr Glu Ile Ala Lys Gln
65 70 75 80

Leu Gln Ile Arg Arg Ser Lys Arg Lys Arg Gln Lys Glu Asn Ala Met
85 90 95

Cys Glu Lys His Asn Gln Phe Leu Thr Leu Phe Cys Val Lys Asp Leu
100 105 110

Glu Ile Leu Cys Thr Gln Cys Ser Phe Ser Thr Lys His Gln Lys His
115 120 125

Tyr Ile Cys Pro Ile Lys Lys Ala Ala Ser Tyr His Arg Glu Ile Leu
130 135 140

Glu Gly Ser Leu Glu Pro Leu Arg Asn Asn Ile Glu Arg Val Glu Lys
145 150 155 160

Val Ile Ile Leu Gln Gly Ser Lys Ser Val Glu Leu Lys Lys Lys Val
165 170 175

Glu Tyr Lys Arg Glu Glu Ile Asn Ser Glu Phe Glu Gln Ile Arg Leu
180 185 190

Phe Leu Gln Asn Glu Gln Glu Met Ile Leu Arg Gln Ile Gln Asp Glu
195 200 205

Glu Met Asn Ile Leu Ala Lys Leu Asn Glu Asn Leu Val Glu Leu Ser
210 215 220

Asp Tyr Val Ser Thr Leu Lys His Leu Leu Arg Glu Val Glu Gly Lys
225 230 235 240

Ser Val Gln Ser Asn Leu Glu Leu Leu Thr Gln Ala Lys Ser Met His
245 250 255

His Lys Tyr Gln Asn Leu Lys Cys Pro Glu Leu Phe Ser Phe Arg Leu
260 265 270

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

Ile Ile Lys Pro Phe Gln Val Asp Val Ile Leu Asp Leu Asn Thr Ala
290 295 300

His Pro Gln Leu Leu Val Ser Glu Asp Arg Lys Ala Val Arg Tyr Glu
305 310 315 320

Arg Lys Lys Arg Asn Ile Cys Tyr Asp Pro Arg Arg Phe Tyr Val Cys
325 330 335

Pro Ala Val Leu Gly Ser Gln Arg Phe Ser Ser Gly Arg His Tyr Trp
340 345 350

Glu Val Glu Val Gly Asn Lys Pro Lys Trp Ile Leu Gly Val Cys Gln
355 360 365

Asp Cys Leu Leu Arg Asn Trp Gln Asp Gln Pro Ser Val Leu Gly Gly
370 375 380

Phe Trp Ala Ile Gly Arg Tyr Met Lys Ser Gly Tyr Val Ala Ser Gly
385 390 395 400

Pro Lys Thr Thr Gln Leu Leu Pro Val Val Lys Pro Ser Lys Ile Gly
 405 410 415

Ile Phe Leu Asp Tyr Glu Leu Gly Asp Leu Ser Phe Tyr Asn Met Asn
 420 425 430

Asp Arg Ser Ile Leu Tyr Thr Phe Asn Asp Cys Phe Thr Glu Ala Val
 435 440 445

Trp Pro Tyr Phe Tyr Thr Gly Thr Asp Ser Glu Pro Leu Lys Ile Cys
 450 455 460

Ser Val Ser Asp Ser Glu Arg
 465 470

<210> 117
 <211> 630
 <212> DNA
 <213> Homo sapiens

<400> 117
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 attatgtctt ggaaggatct acatgatagt ttcccctgcc cttttgcca cttttgctgt 180
 ccagaaagga aatttataag caatccccag ctgggtagtt tgactgaaat tgctaagcaa 240
 ctccagataa gaagcaagaa gaggaagagg caggaagaga agcatgtgtg taagaagcat 300
 aatcaggttt tgactttctt ctgtcagaaa gacctagagc ttttatgtcc aaggtgcagt 360
 ttgtccactg atcaccagca tcaactgtgt ttggcccataa agaaggctgc ctctatcat 420
 aggaaaaaac tggaggaata caatgcaccg tggaaggaga gagggaact aattgaaaaa 480
 gtcataacta tgcaaccag gaaatcactg gaactgaaga aaaagatgga gtctccttct 540
 gtcaccagcg tggagtgcag ttgcacgacg tcggctcact tcaacctcgg cctcccgga 600
 tcaagcgatt cttctgcctc tggctcctga 630

<210> 118
<211> 209
<212> PRT
<213> Homo sapiens

<400> 118

Met Glu Phe Val Thr Ala Leu Ala Asp Leu Arg Ala Glu Ala Ser Cys
1 5 10 15

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

His Asn Phe Cys Leu Ser Cys Ile Ile Met Ser Trp Lys Asp Leu His
35 40 45

Asp Ser Phe Pro Cys Pro Phe Cys His Phe Cys Cys Pro Glu Arg Lys
50 55 60

Phe Ile Ser Asn Pro Gln Leu Gly Ser Leu Thr Glu Ile Ala Lys Gln
65 70 75 80

Leu Gln Ile Arg Ser Lys Lys Arg Lys Arg Gln Glu Glu Lys His Val
85 90 95

Cys Lys Lys His Asn Gln Val Leu Thr Phe Phe Cys Gln Lys Asp Leu
100 105 110

Glu Leu Leu Cys Pro Arg Cys Ser Leu Ser Thr Asp His Gln His His
115 120 125

Cys Val Trp Pro Ile Lys Lys Ala Ala Ser Tyr His Arg Lys Lys Leu
130 135 140

Glu Glu Tyr Asn Ala Pro Trp Lys Glu Arg Val Glu Leu Ile Glu Lys
145 150 155 160

Val Ile Thr Met Gln Thr Arg Lys Ser Leu Glu Leu Lys Lys Lys Met
165 170 175

Glu Ser Pro Ser Val Thr Arg Leu Glu Cys Ser Cys Thr Ile Ser Ala
 180 185 190

His Phe Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Ser Ala Ser Gly
 195 200 205

Ser

<210> 119

<211> 1428

<212> DNA

<213> Homo sapiens

<400> 119

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 cggcaggagg cgaggggcgc ccgcgactgc cccgagtgcc ggcgcacgtt cgccgagccc 180
 gcgctggcgc ccagcctcaa gctggccaac atcgtggagc gctacagctc cttcccgtg 240
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 ctcttctgcc tcacggaccg cgcgcttctc tgcttcttct gcgacgagcc tgcaactgac 360
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 aagcgacaac tggcggagac caagtcttc accaagagcc tgcggaccac tatcggcgag 540
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 cagctgcgca aggtccagga gggagcccag atcctgcagg agcggctggc tgaaaccgac 720
 cggcacacct tctggctgg ggtggcctca ctgtccgagc ggctcaaggg aaaaatccat 780
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 ccgggcacag cccaccagcg cctgatcctg tcggacgact gcaccattgt ggcttacggc 960
 aactgcacc cacagccact gcaggactcg ccaaagcgct tcgatgtgga ggtgtcgggtg 1020

ctgggttctg aagccttcag tagtggcgtc cactactggg aggtggtggt ggcggagaag 1080
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 ttccgcgaga agttccctgg caagctctgc tcttacttca gccttggcca gagccacgcc 1380
 aatggcaaga acgttcagcc gctgcggatc aacaccgtcc gcatctag 1428

<210> 120

<211> 475

<212> PRT

<213> Homo sapiens

<400> 120

Met Ala Cys Ser Leu Lys Asp Glu Leu Leu Cys Ser Ile Cys Leu Ser
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Ile Tyr Gln Asp Pro Val Ser Leu Gly Cys Glu His Tyr Phe Cys Arg
 20 25 30

Arg Cys Ile Thr Glu His Trp Val Arg Gln Glu Ala Gln Gly Ala Arg
 35 40 45

Asp Cys Pro Glu Cys Arg Arg Thr Phe Ala Glu Pro Ala Leu Ala Pro
 50 55 60

Ser Leu Lys Leu Ala Asn Ile Val Glu Arg Tyr Ser Ser Phe Pro Leu
 65 70 75 80

Asp Ala Ile Leu Asn Ala Arg Arg Ala Ala Arg Pro Cys Gln Ala His
 85 90 95

Asp Lys Val Lys Leu Phe Cys Leu Thr Asp Arg Ala Leu Leu Cys Phe
 100 105 110

Phe Cys Asp Glu Pro Ala Leu His Glu Gln His Gln Val Thr Gly Ile
115 120 125

Asp Asp Ala Phe Asp Glu Leu Gln Arg Glu Leu Lys Asp Gln Leu Gln
130 135 140

Ala Leu Gln Asp Ser Glu Arg Glu His Thr Glu Ala Leu Gln Leu Leu
145 150 155 160

Lys Arg Gln Leu Ala Glu Thr Lys Ser Ser Thr Lys Ser Leu Arg Thr
165 170 175

Thr Ile Gly Glu Ala Phe Glu Arg Leu His Arg Leu Leu Arg Glu Arg
180 185 190

Gln Lys Ala Met Leu Glu Glu Leu Glu Ala Asp Thr Ala Arg Thr Leu
195 200 205

Thr Asp Ile Glu Gln Lys Val Gln Arg Tyr Ser Gln Gln Leu Arg Lys
210 215 220

Val Gln Glu Gly Ala Gln Ile Leu Gln Glu Arg Leu Ala Glu Thr Asp
225 230 235 240

Arg His Thr Phe Leu Ala Gly Val Ala Ser Leu Ser Glu Arg Leu Lys
245 250 255

Gly Lys Ile His Glu Thr Asn Leu Thr Tyr Glu Asp Phe Pro Thr Ser
260 265 270

Lys Tyr Thr Gly Pro Leu Gln Tyr Thr Ile Trp Lys Ser Leu Phe Gln
275 280 285

Asp Ile His Pro Val Pro Ala Ala Leu Thr Leu Asp Pro Gly Thr Ala
290 295 300

His Gln Arg Leu Ile Leu Ser Asp Asp Cys Thr Ile Val Ala Tyr Gly
305 310 315 320

Asn Leu His Pro Gln Pro Leu Gln Asp Ser Pro Lys Arg Phe Asp Val
325 330 335

Glu Val Ser Val Leu Gly Ser Glu Ala Phe Ser Ser Gly Val His Tyr
340 345 350

Trp Glu Val Val Val Ala Glu Lys Thr Gln Trp Val Ile Gly Leu Ala
355 360 365

His Glu Ala Ala Ser Arg Lys Gly Ser Ile Gln Ile Gln Pro Ser Arg
370 375 380

Gly Phe Tyr Cys Ile Val Met His Asp Gly Asn Gln Tyr Ser Ala Cys
385 390 395 400

Thr Glu Pro Trp Thr Arg Leu Asn Val Arg Asp Lys Leu Asp Lys Val
405 410 415

Gly Val Phe Leu Asp Tyr Asp Gln Gly Leu Leu Ile Phe Tyr Asn Ala
420 425 430

Asp Asp Met Ser Trp Leu Tyr Thr Phe Arg Glu Lys Phe Pro Gly Lys
435 440 445

Leu Cys Ser Tyr Phe Ser Pro Gly Gln Ser His Ala Asn Gly Lys Asn
450 455 460

Val Gln Pro Leu Arg Ile Asn Thr Val Arg Ile
465 470 475

<210> 121

<211> 1062

<212> DNA

<213> Homo sapiens

<400> 121

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ctgatctgcc ctatctgcct ggagatgttt accaagccag tggatcatctt gccgtgccag 120

cacaacctgt gccggaagtg tgccaatgac atcttccagg ctgcaaatcc ctactggacc 180
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<210> 122

<211> 353

<212> PRT

<213> Homo sapiens

<400> 122

Met Asp Tyr Lys Ser Ser Leu Ile Gln Asp Gly Asn Pro Met Glu Asn

1 5 10 15

Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met Phe Thr Lys

20 25 30

Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg Lys Cys Ala

35 40 45

Asn Asp Ile Phe Gln Ala Ala Asn Pro Tyr Trp Thr Ser Arg Gly Ser
50 55 60

Ser Val Ser Met Ser Gly Gly Arg Phe Arg Cys Pro Thr Cys Arg His
65 70 75 80

Glu Val Ile Met Asp Arg His Gly Val Tyr Gly Leu Gln Arg Asn Leu
85 90 95

Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Cys Ser Ser Arg
100 105 110

Pro Leu Gln Lys Gly Ser His Pro Met Cys Lys Glu His Glu Asp Glu
115 120 125

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

Cys Lys Val Phe Gly Ile His Lys Ala Cys Glu Val Ala Pro Leu Gln
145 150 155 160

Ser Val Phe Gln Gly Gln Lys Thr Glu Leu Asn Asn Cys Ile Ser Met
165 170 175

Leu Val Ala Gly Asn Asp Arg Val Gln Thr Ile Ile Thr Gln Leu Glu
180 185 190

Asp Ser Arg Arg Val Thr Lys Glu Asn Ser His Gln Val Lys Glu Glu
195 200 205

Leu Ser Gln Lys Phe Asp Thr Leu Tyr Ala Ile Leu Asp Glu Lys Lys
210 215 220

Ser Glu Leu Leu Gln Arg Ile Thr Gln Glu Gln Glu Lys Lys Leu Ser
225 230 235 240

Phe Ile Glu Ala Leu Ile Gln Gln Tyr Gln Glu Gln Leu Asp Lys Ser
245 250 255

Thr Lys Leu Val Glu Thr Ala Ile Gln Ser Leu Asp Glu Pro Gly Gly
 260 265 270

Ala Thr Phe Leu Leu Thr Ala Lys Gln Leu Ile Lys Ser Ile Val Glu
 275 280 285

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

Met Asp Phe Phe Thr Leu Asp Leu Glu His Ile Ala Asp Ala Leu Arg
 305 310 315 320

Ala Ile Asp Phe Gly Thr Asp Glu Glu Glu Glu Glu Phe Ile Glu Glu
 325 330 335

Glu Asp Gln Glu Glu Glu Glu Ser Thr Glu Gly Lys Glu Glu Gly His
 340 345 350

Gln

<210> 123

<211> 1350

<212> DNA

<213> Homo sapiens

<400> 123

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ctctgctcag aagaaggcag agcaccaatg cgctgccctt cgtgcagaaa aatctcagag 180

aagcccaact tcaacaccaa tgtggtactc aaaaagctgt cttccctagc cagacagacc 240

agacctcaga acatcaacag ctgagacaat atctgtgtgc tccatgagga gactaaggag 300

ctcttctgtg aggctgacaa gagattgctc tgtgggccct gctctgagtc accagagcac 360

atggctcaca gccacagccc aataggatgg gctgctgagg aatgcaggga gaaacttata 420

aaggaaatgg actatttatg ggaaatcaat caagagacaa gaaacaatct aaatcaggaa 480

actagaacat ttcatcgtt aaaggactat gtgtcagtaa ggaagaggat aatcactatt 540
 caatatcaaa agatgcctat atttctcat gaggaggagc aacggcatct gcaggcactg 600
 gaaagagaag cagaagagct tttccaacaa ctacaagaca gtcaagttag aatgacccaa 660
 catttagaaa ggatgaaaga catgtacaga gagctgtggg agacatgcca cgtgcctgac 720
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 aggcctttct tttgctttgg ttgtacatga 1350

<210> 124

<211> 449

<212> PRT

<213> Homo sapiens

<400> 124

Met Asp Ser Asp Asp Leu Gln Val Phe Gln Asn Glu Leu Ile Cys Cys

1 5 10 15

Ile Cys Val Asn Tyr Phe Ile Asp Pro Val Thr Ile Asp Cys Gly His

20 25 30

Ser Phe Cys Arg Pro Cys Leu Cys Leu Cys Ser Glu Glu Gly Arg Ala

35 40 45

Pro Met Arg Cys Pro Ser Cys Arg Lys Ile Ser Glu Lys Pro Asn Phe
50 55 60

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

Arg Pro Gln Asn Ile Asn Ser Ser Asp Asn Ile Cys Val Leu His Glu
85 90 95

Glu Thr Lys Glu Leu Phe Cys Glu Ala Asp Lys Arg Leu Leu Cys Gly
100 105 110

Pro Cys Ser Glu Ser Pro Glu His Met Ala His Ser His Ser Pro Ile
115 120 125

Gly Trp Ala Ala Glu Glu Cys Arg Glu Lys Leu Ile Lys Glu Met Asp
130 135 140

Tyr Leu Trp Glu Ile Asn Gln Glu Thr Arg Asn Asn Leu Asn Gln Glu
145 150 155 160

Thr Arg Thr Phe His Ser Leu Lys Asp Tyr Val Ser Val Arg Lys Arg
165 170 175

Ile Ile Thr Ile Gln Tyr Gln Lys Met Pro Ile Phe Leu Asp Glu Glu
180 185 190

Glu Gln Arg His Leu Gln Ala Leu Glu Arg Glu Ala Glu Glu Leu Phe
195 200 205

Gln Gln Leu Gln Asp Ser Gln Val Arg Met Thr Gln His Leu Glu Arg
210 215 220

Met Lys Asp Met Tyr Arg Glu Leu Trp Glu Thr Cys His Val Pro Asp
225 230 235 240

Val Glu Leu Leu Gln Asp Val Arg Asn Val Ser Ala Arg Thr Asp Leu
245 250 255

Ala Gln Met Gln Lys Pro Gln Pro Val Asn Pro Glu Leu Thr Ser Trp
260 265 270

Cys Ile Thr Gly Val Leu Asp Met Leu Asn Asn Phe Arg Val Asp Ser
275 280 285

Ala Leu Ser Thr Glu Met Ile Pro Cys Tyr Ile Ser Leu Ser Glu Asp
290 295 300

Val Arg Tyr Val Ile Phe Gly Asp Asp His Leu Ser Ala Pro Thr Asp
305 310 315 320

Pro Gln Gly Val Asp Ser Phe Ala Val Trp Gly Ala Gln Ala Phe Thr
325 330 335

Ser Gly Lys His Tyr Trp Glu Val Asp Val Thr Leu Ser Ser Asn Trp
340 345 350

Ile Leu Gly Val Cys Gln Asp Ser Arg Thr Ala Asp Ala Asn Phe Val
355 360 365

Ile Asp Ser Asp Glu Arg Phe Phe Leu Ile Ser Ser Lys Arg Ser Asn
370 375 380

His Tyr Ser Leu Ser Thr Asn Ser Pro Pro Leu Ile Gln Tyr Val Gln
385 390 395 400

Arg Pro Leu Gly Gln Val Gly Val Phe Leu Asp Tyr Asp Asn Gly Ser
405 410 415

Val Ser Phe Phe Asp Val Ser Lys Gly Ser Leu Ile Tyr Gly Phe Pro
420 425 430

Pro Ser Ser Phe Ser Ser Pro Leu Arg Pro Phe Phe Cys Phe Gly Cys
435 440 445

Thr

<210> 125

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 125

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gaccgtgctg gaaaggcgtg ccccgagtgc cgggagccct ttccgacgg cgccgagctg 180
cgccgcaacg tggccctcag cggcgtgctg gaggtggtgc gcgccgggcc cgccgggat 240
ccggccccg atcccgcccc cggccccgac cctgccgcgc gctgccccg ccacgggcgg 300
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gagtgtgcc tccacgagcg ggcgtgctg gatgccgagc gcctcaagcg cgaggcccag 420
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gagctgcgca agcaaagcag ccagatccag aactcgcct gcatctggc ctctgggtc 540
tccggcaagt tcagcagcct gctacaggcc ctggaaatac agcacacgac agcactgagg 600
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<210> 126
 <211> 517
 <212> PRT
 <213> Homo sapiens

<400> 126

Met Ala Ala Gln Leu Leu Glu Glu Lys Leu Thr Cys Ala Ile Cys Leu
 1 5 10 15

Gly Leu Tyr Gln Asp Pro Val Thr Leu Pro Cys Gly His Asn Phe Cys
 20 25 30

Gly Ala Cys Ile Arg Asp Trp Trp Asp Arg Cys Gly Lys Ala Cys Pro
 35 40 45

Glu Cys Arg Glu Pro Phe Pro Asp Gly Ala Glu Leu Arg Arg Asn Val
 50 55 60

Ala Leu Ser Gly Val Leu Glu Val Val Arg Ala Gly Pro Ala Arg Asp
 65 70 75 80

Pro Gly Pro Asp Pro Gly Pro Gly Pro Asp Pro Ala Ala Arg Cys Pro
 85 90 95

Arg His Gly Arg Pro Leu Glu Leu Phe Cys Arg Thr Glu Gly Arg Cys
 100 105 110

Val Cys Ser Val Cys Thr Val Arg Glu Cys Arg Leu His Glu Arg Ala
 115 120 125

Leu Leu Asp Ala Glu Arg Leu Lys Arg Glu Ala Gln Leu Arg Ala Ser
 130 135 140

Leu Glu Val Thr Gln Gln Gln Ala Thr Gln Ala Glu Gly Gln Leu Leu
145 150 155 160

Glu Leu Arg Lys Gln Ser Ser Gln Ile Gln Asn Ser Ala Cys Ile Leu
 165 170 175

Ala Ser Trp Val Ser Gly Lys Phe Ser Ser Leu Leu Gln Ala Leu Glu
 180 185 190

Ile Gln His Thr Thr Ala Leu Arg Ser Ile Glu Val Ala Lys Thr Gln
 195 200 205

Ala Leu Ala Gln Ala Arg Asp Glu Glu Gln Arg Leu Arg Val His Leu
 210 215 220

Glu Ala Val Ala Arg His Gly Cys Arg Ile Arg Glu Leu Leu Glu Gln
225 230 235 240

Val Asp Glu Gln Thr Phe Leu Gln Glu Ser Gln Leu Leu Gln Pro Pro
 245 250 255

Gly Pro Leu Gly Pro Leu Thr Pro Leu Gln Trp Asp Glu Asp Gln Gln
 260 265 270

Leu Gly Asp Leu Lys Gln Leu Leu Ser Arg Leu Cys Gly Leu Leu Leu
 275 280 285

Glu Glu Gly Ser His Pro Gly Ala Pro Ala Lys Pro Val Asp Leu Ala
 290 295 300

Pro Val Glu Ala Pro Gly Pro Leu Ala Pro Val Pro Ser Thr Val Cys
305 310 315 320

Pro Leu Arg Arg Lys Leu Trp Gln Asn Tyr Arg Asn Leu Thr Phe Asp
 325 330 335

Pro Val Ser Ala Asn Arg His Phe Tyr Leu Ser Arg Gln Asp Gln Gln

340 345 350

Val Lys His Cys Arg Gln Ser Arg Gly Pro Gly Gly Pro Gly Ser Phe
355 360 365

Glu Leu Trp Gln Val Gln Cys Ala Gln Ser Phe Gln Ala Gly His His
370 375 380

Tyr Trp Glu Val Arg Ala Ser Asp His Ser Val Thr Leu Gly Val Ser
385 390 395 400

Tyr Pro Gln Leu Pro Arg Cys Arg Leu Gly Pro His Thr Asp Asn Ile
405 410 415

Gly Arg Gly Pro Cys Ser Trp Gly Leu Cys Val Gln Glu Asp Ser Leu
420 425 430

Gln Ala Trp His Asn Gly Glu Ala Gln Arg Leu Pro Gly Val Ser Gly
435 440 445

Arg Leu Leu Gly Met Asp Leu Asp Leu Ala Ser Gly Cys Leu Thr Phe
450 455 460

Tyr Ser Leu Glu Pro Gln Thr Gln Pro Leu Tyr Thr Phe His Ala Leu
465 470 475 480

Phe Asn Gln Pro Leu Thr Pro Val Phe Trp Leu Leu Glu Gly Arg Thr
485 490 495

Leu Thr Leu Cys His Gln Pro Gly Ala Val Phe Pro Leu Gly Pro Gln
500 505 510

Glu Glu Val Leu Ser
515

<210> 127

<211> 3651

<212> DNA

<213> Homo sapiens

<400> 127

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ggcccattct ttcctcgggc ccagaaggga tctccaggag tgaatggtgg tcccggagac 180

ttcaccttgt attgtctct acacacacag gaagtactca agctattctg tgagacatgt 240

gatatgtctc ctgccatag ctgcctagt gtggaacaca aagaacacag gtgcagacat 300

gttgagaag ttttgcaaaa ccagaggatg ctctggaag gtgtgactac acaggtggca 360

cataagaaat ccagtctaca gacatctga aagcaaattg aggacaggat tttgaagtg 420

aagcatcagc ataggaaggt ggaaaaccag atcaaatgg ccaagatggt tctgatgaat 480

gagctgaaca aacaggccaa tgggctaata gaggaattag aggggattac taatgagaga 540

aagcgggaagc tggaacagca gttacagagc atcatggttc tcaaccgtca gtttgagcat 600

gtgcagaatt tcatcaactg ggctgtctgc agcaaaacca gtgtcccttt tcttttcagc 660

aaagagctga ttgttttca gatgcagcga ttgctggaga caagttgtaa cacagatcct 720

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 cctccctaca tgcaggaggg catccaaccc aagaggcggc gacgacatat ggagaatgaa 3600
 agagcaaaaa gaatgtcatt tcgcctggcc aacagcatct ctcaggtgtg a 3651

<210> 128

<211> 1216

<212> PRT

<213> Homo sapiens

<400> 128

Met Ala Arg Asn Cys Ser Glu Cys Lys Glu Lys Arg Ala Ala His Ile

1 5 10 15

Leu Cys Thr Tyr Cys Asn Arg Trp Leu Cys Ser Ser Cys Thr Glu Glu

20 25 30

His Arg His Ser Pro Val Pro Gly Gly Pro Phe Phe Pro Arg Ala Gln

35 40 45

Lys Gly Ser Pro Gly Val Asn Gly Gly Pro Gly Asp Phe Thr Leu Tyr

50 55 60

Cys Pro Leu His Thr Gln Glu Val Leu Lys Leu Phe Cys Glu Thr Cys

65 70 75 80

Asp Met Leu Thr Cys His Ser Cys Leu Val Val Glu His Lys Glu His

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

Phe Tyr Gln Ser His Gln Ser Pro Val Ala Gln Gln Glu Ala Leu Ser
290 295 300

His Pro Ser His Lys Phe Gln Ser Pro Ala Val Cys Ser Ser Ser Val
305 310 315 320

Cys Cys Ser His Cys Ser Pro Val Ser Pro Ser Leu Lys Gly Gln Val
325 330 335

Pro Pro Pro Ser Ile His Pro Ala His Ser Phe Arg Gln Pro Pro Glu
340 345 350

Met Val Pro Gln Gln Leu Gly Ser Leu Gln Cys Ser Ala Leu Leu Pro
355 360 365

Arg Glu Lys Glu Leu Ala Cys Ser Pro His Pro Pro Lys Leu Leu Gln
370 375 380

Pro Trp Leu Glu Thr Gln Pro Pro Val Glu Gln Glu Ser Thr Ser Gln
385 390 395 400

Arg Leu Gly Gln Gln Leu Thr Ser Gln Pro Val Cys Ile Val Pro Pro
405 410 415

Gln Asp Val Gln Gln Gly Ala His Ala Gln Pro Thr Leu Gln Thr Pro
420 425 430

Ser Ile Gln Val Gln Phe Gly His His Gln Lys Leu Lys Leu Ser His
435 440 445

Phe Gln Gln Gln Pro Gln Gln Gln Leu Pro Pro Pro Pro Pro Leu
450 455 460

Pro His Pro Pro Pro Pro Leu Pro Pro Pro Pro Gln Gln Pro His Pro
465 470 475 480

Pro Leu Pro Pro Ser Gln His Leu Ala Ser Ser Gln His Glu Ser Pro
485 490 495

Pro Gly Pro Ala Cys Ser Gln Asn Met Asp Ile Met His His Lys Phe
500 505 510

Glu Leu Glu Glu Met Gln Lys Asp Leu Glu Leu Leu Leu Gln Ala Gln
515 520 525

Gln Pro Ser Leu Gln Leu Ser Gln Thr Lys Ser Pro Gln His Leu Gln
530 535 540

Gln Thr Ile Val Gly Gln Ile Asn Tyr Ile Val Arg Gln Pro Ala Pro
545 550 555 560

Val Gln Ser Gln Ser Gln Glu Glu Thr Leu Gln Ala Thr Asp Glu Pro
565 570 575

Pro Ala Ser Gln Gly Ser Lys Pro Ala Leu Pro Leu Asp Lys Asn Thr
580 585 590

Ala Ala Ala Leu Pro Gln Ala Ser Gly Glu Glu Thr Pro Leu Ser Val
595 600 605

Pro Pro Val Asp Ser Thr Ile Gln His Ser Ser Pro Asn Val Val Arg
610 615 620

Lys His Ser Thr Ser Leu Ser Ile Met Gly Phe Ser Asn Thr Leu Glu
625 630 635 640

Met Glu Leu Ser Ser Thr Arg Leu Glu Arg Pro Leu Glu Pro Gln Ile
645 650 655

Gln Ser Val Ser Asn Leu Thr Ala Gly Ala Pro Gln Ala Val Pro Ser
660 665 670

Leu Leu Ser Ala Pro Pro Lys Met Val Ser Ser Leu Thr Ser Val Gln
675 680 685

Asn Gln Ala Met Pro Ser Leu Thr Thr Ser His Leu Gln Thr Val Pro
690 695 700

Ser Leu Val His Ser Thr Phe Gln Ser Met Pro Asn Leu Ile Ser Asp
705 710 715 720

Ser Pro Gln Ala Met Ala Ser Leu Ala Ser Asp His Pro Gln Ala Gly
725 730 735

Pro Ser Leu Met Ser Gly His Thr Gln Ala Val Pro Ser Leu Ala Thr
740 745 750

Cys Pro Leu Gln Ser Ile Pro Pro Val Ser Asp Met Gln Pro Glu Thr
755 760 765

Gly Ser Ser Ser Ser Ser Gly Arg Thr Ser Gly Ser Leu Cys Pro Arg
770 775 780

Asp Gly Ala Asp Pro Ser Leu Glu Asn Ala Leu Cys Lys Val Lys Leu
785 790 795 800

Glu Glu Pro Ile Asn Leu Ser Val Lys Lys Pro Pro Leu Ala Pro Val
805 810 815

Val Ser Thr Ser Thr Ala Leu Gln Gln Tyr Gln Asn Pro Lys Glu Cys
820 825 830

Glu Asn Phe Glu Gln Gly Ala Leu Glu Leu Asp Ala Lys Glu Asn Gln
835 840 845

Ser Ile Arg Ala Phe Asn Ser Glu His Lys Ile Pro Tyr Val Arg Leu
850 855 860

Glu Arg Leu Lys Ile Cys Ala Ala Ser Ser Gly Glu Met Pro Val Phe
865 870 875 880

Lys Leu Lys Pro Gln Lys Asn Asp Gln Asp Gly Ser Phe Leu Leu Ile
885 890 895

Ile Glu Cys Gly Thr Glu Ser Ser Ser Met Ser Ile Lys Val Ser Gln

900	905	910
Asp Arg Leu Ser Glu Ala Thr Gln Ala Pro Gly Leu Glu Gly Arg Lys		
915	920	925
Val Thr Val Thr Ser Leu Ala Gly Gln Arg Pro Pro Glu Val Glu Gly		
930	935	940
Thr Ser Pro Glu Glu His Arg Leu Ile Pro Arg Thr Pro Gly Ala Lys		
945	950	955
		960
Lys Gly Pro Pro Ala Pro Ile Glu Asn Glu Asp Phe Cys Ala Val Cys		
965	970	975
Leu Asn Gly Gly Glu Leu Leu Cys Cys Asp Arg Cys Pro Lys Val Phe		
980	985	990
His Leu Ser Cys His Val Pro Ala Leu Leu Ser Phe Pro Gly Gly Glu		
995	1000	1005
Trp Val Cys Thr Leu Cys Arg Ser Leu Thr Gln Pro Glu Met Glu		
1010	1015	1020
Tyr Asp Cys Glu Asn Ala Cys Tyr Asn Gln Pro Gly Met Arg Ala		
1025	1030	1035
Ser Pro Gly Leu Ser Met Tyr Asp Gln Lys Lys Cys Glu Lys Leu		
1040	1045	1050
Val Leu Ser Leu Cys Cys Asn Asn Leu Ser Leu Pro Phe His Glu		
1055	1060	1065
Pro Val Ser Pro Leu Ala Arg His Tyr Tyr Gln Ile Ile Lys Arg		
1070	1075	1080
Pro Met Asp Leu Ser Ile Ile Arg Arg Lys Leu Gln Lys Lys Asp		
1085	1090	1095

Pro Ala His Tyr Thr Thr Pro Glu Glu Val Val Ser Asp Val Arg
 1100 1105 1110

Leu Met Phe Trp Asn Cys Ala Lys Phe Asn Tyr Pro Asp Ser Glu
 1115 1120 1125

Val Ala Glu Ala Gly Arg Cys Leu Glu Val Phe Phe Glu Gly Trp
 1130 1135 1140

Leu Lys Glu Ile Tyr Pro Glu Lys Arg Phe Ala Gln Pro Arg Gln
 1145 1150 1155

Glu Asp Ser Asp Ser Glu Glu Val Ser Ser Glu Ser Gly Cys Ser
 1160 1165 1170

Thr Pro Gln Gly Phe Pro Trp Pro Pro Tyr Met Gln Glu Gly Ile
 1175 1180 1185

Gln Pro Lys Arg Arg Arg Arg His Met Glu Asn Glu Arg Ala Lys
 1190 1195 1200

Arg Met Ser Phe Arg Leu Ala Asn Ser Ile Ser Gln Val
 1205 1210 1215

<210> 129

<211> 2352

<212> DNA

<213> Homo sapiens

<400> 129

atggaggaag agctgaagtg tcccggtgtgc ggctctctgt ttcgggagcc tatcatcctg 60

ccctgttccc acaatgtctg cctgccttgc gctcgacca tcgcggtgca gaccccggaac 120

ggtgagcagc acctgcccc gccgctcctg ctttccggg gatcggggct gcaggcgggc 180

gccgccgccc ctgcctctct ggagcacgac gctgcggctg gcccggcctg cggcggtgca 240

ggcgggagtg cagctggcgg cctcggcggc ggtgcgggag gtggcggaga ccacgcggac 300

aagctcagct tgtacagcga gacagacagc ggctacgggt cctacacccc gagcctcaag 360

tccccaacg ggggttcgct gctgccatg gtgcccgcac caccggctc ctcggctgcg 420

gcggctcggg gtgccgcctg ctctcgctg tcctcgtctt cgagctccat cacgtgcccg 480
 cagtgccacc gcagcgcctc cctggaccac cgcggcctgc gcggcttcca gcgcaaccgg 540
 ctgctcgagg ccatcgtgca gcggtaccag caggggccgc gggccgtgcc ggggacgtct 600
 gcagccgcgg cggtggccat ctgccagctg tgcgaccgca ccccgccaga gccagcagcc 660
 acgctctcgg agcagtgcca cgtcctctac tgctctgcct gccagctcaa gtgccatcca 720
 tcccggggac ccttcgcaa gcatgcctg gtgcagccgc cgccgcgccc gccgcccgcc 780
 gccgaggcag cctccgggcc cactggcacc gccagggcg ccccgagcgg aggcggcggc 840
 tgcaagagcc cgggaggcgc gggggcgggg gcgactgggg gcagcacggc ccgcaagttc 900
 cccacgtgtc ccgagcatga aatggagaac tacagcatgt actgcgtgag ctgtcgaacc 960
 ccggtgtgtt atctgtgcct ggaggaggcg cggcacgcca agcacaggt gaagccgctg 1020
 ggggccatgt ggaagcagca caaggcaca ctatctcagg cttaatgg agtttcagat 1080
 aaggcaaagg aagcaaagga gtttctggtt cagctaaaga acatattgca gcagatccag 1140
 gaaaacggac tggactacga agcctgcctc gttgctcagt gtgatgcct tgtggatgct 1200
 ttaactcgtc agaaagccaa gctgctcacc aagtgacta aagagaggga acacaagttg 1260
 aagatggttt gggaccagat caatcactgc acattgaagc tgcgtcagtc caccggactg 1320
 atggagtact gcctggaggat gatcaaggag aacgaccct ccgggttctt acagatctca 1380
 gatgctctga tcaagcgcgt ccaggtgtct caggagcagt gggtaaagg cgccctggag 1440
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 caccagctgg acttcattca gatgaaatgt agggtgccac ccgtcccct actgcagctg 1560
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 cacagccccg tggacggcta catcctggag ctggacgacg gtgccggggg acagttccgg 1680
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 gtctgcaga catccgatgt ggctgggtc acatttgacc ccaactctgg gcatcgggac 1860
 atcattttat ccaatgaca ccagacagcc acctgcagca gctatgacga ccgggtggtg 1920

ctgggcacag ctgcgttctc caagggcgtg cactactggg agctgcacgt ggaccggtac 1980
 gacaaccacc cagaccccg cttcgggggtg gccagggcca gcgtgggtcaa ggacatgatg 2040
 ctgggcaagg atgacaaggc ctggggccatg tatgtggaca acaaccgcag ctggttcacg 2100
 cactgcaact cccacaccaa caggacggaa ggtggcgtgt gcaagggggc caccgtgggc 2160
 gtgctgctgg acctgaataa gcacactctc accttttca tcaacgggca gcagcagggc 2220
 cccacagcct tcagccacgt ggacggggtc ttcattgccag ccctcagcct caaccgcaac 2280
 gtgcaggcca ccctgcacac aggattggaa gtgccgacta acctggggcg gccaaagctg 2340
 tcaggcaatt ag 2352

<210> 130
 <211> 783
 <212> PRT
 <213> Homo sapiens

<400> 130

Met Glu Glu Glu Leu Lys Cys Pro Val Cys Gly Ser Leu Phe Arg Glu
 1 5 10 15

Pro Ile Ile Leu Pro Cys Ser His Asn Val Cys Leu Pro Cys Ala Arg
 20 25 30

Thr Ile Ala Val Gln Thr Pro Asp Gly Glu Gln His Leu Pro Gln Pro
 35 40 45

Leu Leu Leu Ser Arg Gly Ser Gly Leu Gln Ala Gly Ala Ala Ala Ala
 50 55 60

Ala Ser Leu Glu His Asp Ala Ala Ala Gly Pro Ala Cys Gly Gly Ala
 65 70 75 80

Gly Gly Ser Ala Ala Gly Gly Leu Gly Gly Gly Ala Gly Gly Gly Gly
 85 90 95

Asp His Ala Asp Lys Leu Ser Leu Tyr Ser Glu Thr Asp Ser Gly Tyr
 100 105 110

Gly Ser Tyr Thr Pro Ser Leu Lys Ser Pro Asn Gly Val Arg Val Leu
115 120 125

Pro Met Val Pro Ala Pro Pro Gly Ser Ser Ala Ala Ala Arg Gly
130 135 140

Ala Ala Cys Ser Ser Leu Ser Ser Ser Ser Ser Ile Thr Cys Pro
145 150 155 160

Gln Cys His Arg Ser Ala Ser Leu Asp His Arg Gly Leu Arg Gly Phe
165 170 175

Gln Arg Asn Arg Leu Leu Glu Ala Ile Val Gln Arg Tyr Gln Gln Gly
180 185 190

Arg Gly Ala Val Pro Gly Thr Ser Ala Ala Ala Val Ala Ile Cys
195 200 205

Gln Leu Cys Asp Arg Thr Pro Pro Glu Pro Ala Ala Thr Leu Cys Glu
210 215 220

Gln Cys Asp Val Leu Tyr Cys Ser Ala Cys Gln Leu Lys Cys His Pro
225 230 235 240

Ser Arg Gly Pro Phe Ala Lys His Arg Leu Val Gln Pro Pro Pro Pro
245 250 255

Pro Pro Pro Pro Ala Glu Ala Ala Ser Gly Pro Thr Gly Thr Ala Gln
260 265 270

Gly Ala Pro Ser Gly Gly Gly Gly Cys Lys Ser Pro Gly Gly Ala Gly
275 280 285

Ala Gly Ala Thr Gly Gly Ser Thr Ala Arg Lys Phe Pro Thr Cys Pro
290 295 300

Glu His Glu Met Glu Asn Tyr Ser Met Tyr Cys Val Ser Cys Arg Thr
305 310 315 320

Pro Val Cys Tyr Leu Cys Leu Glu Glu Gly Arg His Ala Lys His Glu
325 330 335

Val Lys Pro Leu Gly Ala Met Trp Lys Gln His Lys Ala Gln Leu Ser
340 345 350

Gln Ala Leu Asn Gly Val Ser Asp Lys Ala Lys Glu Ala Lys Glu Phe
355 360 365

Leu Val Gln Leu Lys Asn Ile Leu Gln Gln Ile Gln Glu Asn Gly Leu
370 375 380

Asp Tyr Glu Ala Cys Leu Val Ala Gln Cys Asp Ala Leu Val Asp Ala
385 390 395 400

Leu Thr Arg Gln Lys Ala Lys Leu Leu Thr Lys Val Thr Lys Glu Arg
405 410 415

Glu His Lys Leu Lys Met Val Trp Asp Gln Ile Asn His Cys Thr Leu
420 425 430

Lys Leu Arg Gln Ser Thr Gly Leu Met Glu Tyr Cys Leu Glu Val Ile
435 440 445

Lys Glu Asn Asp Pro Ser Gly Phe Leu Gln Ile Ser Asp Ala Leu Ile
450 455 460

Lys Arg Val Gln Val Ser Gln Glu Gln Trp Val Lys Gly Ala Leu Glu
465 470 475 480

Pro Lys Val Ser Ala Glu Phe Asp Leu Thr Leu Asp Ser Glu Pro Leu
485 490 495

Leu Gln Ala Ile His Gln Leu Asp Phe Ile Gln Met Lys Cys Arg Val
500 505 510

Pro Pro Val Pro Leu Leu Gln Leu Glu Lys Cys Cys Thr Arg Asn Asn

515	520	525			
Ser Val Thr Leu Ala Trp Arg Met Pro Pro Phe Thr His Ser Pro Val					
530	535	540			
Asp Gly Tyr Ile Leu Glu Leu Asp Asp Gly Ala Gly Gly Gln Phe Arg					
545	550	555	560		
Glu Val Tyr Val Gly Lys Glu Thr Leu Cys Thr Ile Asp Gly Leu His					
565	570	575			
Phe Asn Ser Thr Tyr Asn Ala Arg Val Lys Ala Phe Asn Ser Ser Gly					
580	585	590			
Val Gly Pro Tyr Ser Lys Thr Val Val Leu Gln Thr Ser Asp Val Ala					
595	600	605			
Trp Phe Thr Phe Asp Pro Asn Ser Gly His Arg Asp Ile Ile Leu Ser					
610	615	620			
Asn Asp Asn Gln Thr Ala Thr Cys Ser Ser Tyr Asp Asp Arg Val Val					
625	630	635	640		
Leu Gly Thr Ala Ala Phe Ser Lys Gly Val His Tyr Trp Glu Leu His					
645	650	655			
Val Asp Arg Tyr Asp Asn His Pro Asp Pro Ala Phe Gly Val Ala Arg					
660	665	670			
Ala Ser Val Val Lys Asp Met Met Leu Gly Lys Asp Asp Lys Ala Trp					
675	680	685			
Ala Met Tyr Val Asp Asn Asn Arg Ser Trp Phe Met His Cys Asn Ser					
690	695	700			
His Thr Asn Arg Thr Glu Gly Gly Val Cys Lys Gly Ala Thr Val Gly					
705	710	715	720		

Val Leu Leu Asp Leu Asn Lys His Thr Leu Thr Phe Phe Ile Asn Gly
725 730 735

Gln Gln Gln Gly Pro Thr Ala Phe Ser His Val Asp Gly Val Phe Met
740 745 750

Pro Ala Leu Ser Leu Asn Arg Asn Val Gln Val Thr Leu His Thr Gly
755 760 765

Leu Glu Val Pro Thr Asn Leu Gly Arg Pro Lys Leu Ser Gly Asn
770 775 780

<210> 131
<211> 1458
<212> DNA
<213> Homo sapiens

<400> 131
atggatccca cagccttggt ggaagccatt gtggaagaag tggcctgtcc catctgtatg 60
accttcctga gggagcccat gagcattgac tgtggccaca gcttctgcca cagctgtctc 120
tctggactct gggagatccc aggagaatcc cagaactggg gttacacctg tcccctctgt 180
cgagctcctg tccagccaag gaacctgcgg cctaattggc agctggccaa tgtttagtaa 240
aaagtccgtc tgctaaggct acatccagga atggggctga agggtagacct gtgtgagcgc 300
catggggaaa agctgaagat gttctgcaaa gaggatgtct tgataatgtg tgaggcctgc 360
agccagtccc cagagcatga ggcccacagt gttgtgcaa tggaggatgt tgcctgggag 420
tacaagtggg aacttcatga ggccctcgaa catctgaaga aagagcaaga agaggcctgg 480
aagcttgaag ttggtgaaag gaaacgaact gccacctgga agatacaggt ggaaaccga 540
aaacagagta ttgtatggga gtttgaataa taccagcgat tactagagaa aaagcagcca 600
ccacatcggc agctgggggc agaggtagca gcagctctgg ccagcctaca gcgggaggca 660
gcggagacca tgcagaaact ggagttgaac catagcgagc tcattccagca gagccaggtc 720
ctgtggagga tgattgcaga gttgaaagag aggtcgaga ggctgtccg ctggatgttg 780
caggatattc aggaagtgtt aaacaggagc aaatcttga gcttgagca gccagaacca 840
atctccctgg agttgaagac agattgccgt gtgctggggc taagagagat cctgaagact 900

tatgcagctg atgtgcgctt ggatccagat actgcttact cccgtctcat cgtgtctgag 960
 gacagaaaac gtgtgcacta tggagacacc aaccagaaac tgccagacaa tcctgagaga 1020
 tttaccgct ataatatcgt cctgggaagc cagtgcattt cctcaggccg gcactactgg 1080
 gaggtggagg tgggagacag gtctgagtgg ggcctgggag tatgtaagca aaatgtagac 1140
 cggaaggagg tggctactt atccccccac tatggattct ggggtataag gctgaggaag 1200
 ggaaatgagt accgagcagg caccgatgag tacccaatcc tgtccttgcc ggtccctcct 1260
 cgccgggtgg gaatcttcgt ggattatgag gcccatgaca tttctttcta caatgtgact 1320
 gactgtggct cccacatctt cactttcccc cgctatccct tccctgggag cctcctgccc 1380
 tattttagtc ctgtctacag cattggaacc aacaacactg ctctctggc catctgctcc 1440
 ctggatgggg aggactaa 1458

<210> 132

<211> 485

<212> PRT

<213> Homo sapiens

<400> 132

Met Asp Pro Thr Ala Leu Val Glu Ala Ile Val Glu Glu Val Ala Cys

1 5 10 15

Pro Ile Cys Met Thr Phe Leu Arg Glu Pro Met Ser Ile Asp Cys Gly

20 25 30

His Ser Phe Cys His Ser Cys Leu Ser Gly Leu Trp Glu Ile Pro Gly

35 40 45

Glu Ser Gln Asn Trp Gly Tyr Thr Cys Pro Leu Cys Arg Ala Pro Val

50 55 60

Gln Pro Arg Asn Leu Arg Pro Asn Trp Gln Leu Ala Asn Val Val Glu

65 70 75 80

Lys Val Arg Leu Leu Arg Leu His Pro Gly Met Gly Leu Lys Gly Asp

85 90 95

Leu Cys Glu Arg His Gly Glu Lys Leu Lys Met Phe Cys Lys Glu Asp
100 105 110

Val Leu Ile Met Cys Glu Ala Cys Ser Gln Ser Pro Glu His Glu Ala
115 120 125

His Ser Val Val Pro Met Glu Asp Val Ala Trp Glu Tyr Lys Trp Glu
130 135 140

Leu His Glu Ala Leu Glu His Leu Lys Lys Glu Gln Glu Glu Ala Trp
145 150 155 160

Lys Leu Glu Val Gly Glu Arg Lys Arg Thr Ala Thr Trp Lys Ile Gln
165 170 175

Val Glu Thr Arg Lys Gln Ser Ile Val Trp Glu Phe Glu Lys Tyr Gln
180 185 190

Arg Leu Leu Glu Lys Lys Gln Pro Pro His Arg Gln Leu Gly Ala Glu
195 200 205

Val Ala Ala Ala Leu Ala Ser Leu Gln Arg Glu Ala Ala Glu Thr Met
210 215 220

Gln Lys Leu Glu Leu Asn His Ser Glu Leu Ile Gln Gln Ser Gln Val
225 230 235 240

Leu Trp Arg Met Ile Ala Glu Leu Lys Glu Arg Ser Gln Arg Pro Val
245 250 255

Arg Trp Met Leu Gln Asp Ile Gln Glu Val Leu Asn Arg Ser Lys Ser
260 265 270

Trp Ser Leu Gln Gln Pro Glu Pro Ile Ser Leu Glu Leu Lys Thr Asp
275 280 285

Cys Arg Val Leu Gly Leu Arg Glu Ile Leu Lys Thr Tyr Ala Ala Asp

290	295	300	
Val Arg Leu Asp Pro Asp Thr Ala Tyr Ser Arg Leu Ile Val Ser Glu			
305	310	315	320
Asp Arg Lys Arg Val His Tyr Gly Asp Thr Asn Gln Lys Leu Pro Asp			
325	330	335	
Asn Pro Glu Arg Phe Tyr Arg Tyr Asn Ile Val Leu Gly Ser Gln Cys			
340	345	350	
Ile Ser Ser Gly Arg His Tyr Trp Glu Val Glu Val Gly Asp Arg Ser			
355	360	365	
Glu Trp Gly Leu Gly Val Cys Lys Gln Asn Val Asp Arg Lys Glu Val			
370	375	380	
Val Tyr Leu Ser Pro His Tyr Gly Phe Trp Val Ile Arg Leu Arg Lys			
385	390	395	400
Gly Asn Glu Tyr Arg Ala Gly Thr Asp Glu Tyr Pro Ile Leu Ser Leu			
405	410	415	
Pro Val Pro Pro Arg Arg Val Gly Ile Phe Val Asp Tyr Glu Ala His			
420	425	430	
Asp Ile Ser Phe Tyr Asn Val Thr Asp Cys Gly Ser His Ile Phe Thr			
435	440	445	
Phe Pro Arg Tyr Pro Phe Pro Gly Arg Leu Leu Pro Tyr Phe Ser Pro			
450	455	460	
Cys Tyr Ser Ile Gly Thr Asn Asn Thr Ala Pro Leu Ala Ile Cys Ser			
465	470	475	480
Leu Asp Gly Glu Asp			
485			

<210> 133
 <211> 1026
 <212> DNA
 <213> Homo sapiens

<400> 133
 atggaggagg agcttgccat ccaacagggt caactggaga caactctgaa ggagcttcag 60
 accctgagga acatgcagaa ggaagctatt gctgctcaca aggaaaacaa gctacatctg 120
 cagcaacatg tgtccatgga gtttctaaag ctgcatcagt tcctgcacag caaagaaaag 180
 gacattttaa ctgagctccg ggaagagggg aaagccttga atgaggagat ggagttgaat 240
 ctgagccagc ttcaggagca atgtctctta gccaaaggata tgttggtgag cattcaggca 300
 aagacggaac aacagaactc cttcgacttt ctcaaagaca tcacaactct cttacatagc 360
 ttggagcaag gaatgaaggt gctggcaacc agagagctta ttccagaaa gctgaacctg 420
 ggccagtaca aaggctctat ccagtacatg gtatggaggg aaatgcagga cactctctgc 480
 ccaggcctgt tccactaac tctggaccct aaaacagctc acccaaactct ggtgctctcc 540
 aaaagccaaa ccagcgtctg gcatgggtgac attaagaaga taatgcctga tgatcctgag 600
 aggtttgact caagtgtggc tgtactgggc tcaagaggct tcacctctgg aaagtggtag 660
 tgggaagtag aagtagcaaa gaagacaaaa tggacagttg gagttgtcag agaattccatc 720
 attcggaagg gcagctgtcc tctaactct gagcaaggat tctggctttt aagactaagg 780
 aaccaaactg atctaaaggc tctggatttg cttctttca gtctgacct gactaacaac 840
 ctcgacaagg tgggcatata cctggattat gaaggaggac agttgtcctt ctacaatgct 900
 aaaaccatga ctcacattta caccttcagt aacactttca tggagaaaact ttatccctac 960
 ttctgccct gccttaatga tggaggagag aataaagaac cattgcacat cttacatcca 1020
 cagtaa 1026

<210> 134
 <211> 341
 <212> PRT
 <213> Homo sapiens

<400> 134
 Met Glu Glu Glu Leu Ala Ile Gln Gln Gly Gln Leu Glu Thr Thr Leu

1	5	10	15
Lys Glu Leu Gln Thr Leu Arg Asn Met Gln Lys Glu Ala Ile Ala Ala			
	20	25	30
His Lys Glu Asn Lys Leu His Leu Gln Gln His Val Ser Met Glu Phe			
	35	40	45
Leu Lys Leu His Gln Phe Leu His Ser Lys Glu Lys Asp Ile Leu Thr			
	50	55	60
Glu Leu Arg Glu Glu Gly Lys Ala Leu Asn Glu Glu Met Glu Leu Asn			
65	70	75	80
Leu Ser Gln Leu Gln Glu Gln Cys Leu Leu Ala Lys Asp Met Leu Val			
	85	90	95
Ser Ile Gln Ala Lys Thr Glu Gln Gln Asn Ser Phe Asp Phe Leu Lys			
	100	105	110
Asp Ile Thr Thr Leu Leu His Ser Leu Glu Gln Gly Met Lys Val Leu			
	115	120	125
Ala Thr Arg Glu Leu Ile Ser Arg Lys Leu Asn Leu Gly Gln Tyr Lys			
	130	135	140
Gly Pro Ile Gln Tyr Met Val Trp Arg Glu Met Gln Asp Thr Leu Cys			
145	150	155	160
Pro Gly Leu Ser Pro Leu Thr Leu Asp Pro Lys Thr Ala His Pro Asn			
	165	170	175
Leu Val Leu Ser Lys Ser Gln Thr Ser Val Trp His Gly Asp Ile Lys			
	180	185	190
Lys Ile Met Pro Asp Asp Pro Glu Arg Phe Asp Ser Ser Val Ala Val			
	195	200	205

Leu Gly Ser Arg Gly Phe Thr Ser Gly Lys Trp Tyr Trp Glu Val Glu
210 215 220

Val Ala Lys Lys Thr Lys Trp Thr Val Gly Val Val Arg Glu Ser Ile
225 230 235 240

Ile Arg Lys Gly Ser Cys Pro Leu Thr Pro Glu Gln Gly Phe Trp Leu
245 250 255

Leu Arg Leu Arg Asn Gln Thr Asp Leu Lys Ala Leu Asp Leu Pro Ser
260 265 270

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

Asp Tyr Glu Gly Gly Gln Leu Ser Phe Tyr Asn Ala Lys Thr Met Thr
290 295 300

His Ile Tyr Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr
305 310 315 320

Phe Cys Pro Cys Leu Asn Asp Gly Gly Glu Asn Lys Glu Pro Leu His
325 330 335

Ile Leu His Pro Gln
340

<210> 135

<211> 1047

<212> DNA

<213> Homo sapiens

<400> 135

atgcagtttg gggaactcct tgctgctgtg aggaaggccc aggccaatgt gatgctcttc 60

ttagaggaga aggagcaagc tgcgctgagc caggccaacg gtatcaaggc ccacctggag 120

tacaggagtg ccgagatgga gaagagtaag caggagctgg agacgatggc ggccatcagc 180

aacctgtcc agttcttgga ggagtactgc aagtttaaga aactgaaga catcaccttc 240

cctagtgttt acatagggct gaaggataaa ctctcgggca tccgcaaagt tatcacggaa 300

tccactgtac acttaatcca gttgctggag aactataaga aaaagctcca ggagttttcc 360
 aaggaagagg agtatgacat cagaactcaa gtgtctgcca ttgttcagcg caaatattgg 420
 acttccaaac ctgagcccag caccagggaa cagttcctcc aatatgtgca tgacatcacg 480
 ttcgaccggg acacagcaca caagtatctc cggctgcagg aggagaaccg caaggtcacc 540
 aacaccacgc cctgggagca tccctaccg gacctccca gcaggttct gactggcgg 600
 caggtgctgt cccagcagag tctgtacctg cacaggtact atttgaggt ggagatcttc 660
 ggggcaggca cctatgttg cctgacctg aaaggcatcg accagaaagg ggaggagcgc 720
 agcagttgca ttccggaaa caacttctcc tggagcctcc aatggaacgg gaaggagttc 780
 acggcctggt acagtgacat ggagaccca ctcaaagctg gccctttctg gaggtctggg 840
 gtctatattg acttcccagg agggatcctt tccttctatg gcgtagagta tgattccatg 900
 actctggttc acaagtttc ctgcaagttt tcagaaccag tctatgctgc cttctggctt 960
 tccaagaagg aaaacgcat cgggattgta gatctgggag aggaaccga gaagccagca 1020
 ccgtccttgg tggggactgc tccctag 1047

<210> 136
 <211> 348
 <212> PRT
 <213> Homo sapiens

<400> 136

Met Gln Phe Gly Glu Leu Leu Ala Ala Val Arg Lys Ala Gln Ala Asn
 1 5 10 15

Val Met Leu Phe Leu Glu Glu Lys Glu Gln Ala Ala Leu Ser Gln Ala
 20 25 30

Asn Gly Ile Lys Ala His Leu Glu Tyr Arg Ser Ala Glu Met Glu Lys
 35 40 45

Ser Lys Gln Glu Leu Glu Thr Met Ala Ala Ile Ser Asn Thr Val Gln
 50 55 60

Phe Leu Glu Glu Tyr Cys Lys Phe Lys Asn Thr Glu Asp Ile Thr Phe
65 70 75 80

Pro Ser Val Tyr Ile Gly Leu Lys Asp Lys Leu Ser Gly Ile Arg Lys
 85 90 95

Val Ile Thr Glu Ser Thr Val His Leu Ile Gln Leu Leu Glu Asn Tyr
 100 105 110

Lys Lys Lys Leu Gln Glu Phe Ser Lys Glu Glu Glu Tyr Asp Ile Arg
 115 120 125

Thr Gln Val Ser Ala Ile Val Gln Arg Lys Tyr Trp Thr Ser Lys Pro
 130 135 140

Glu Pro Ser Thr Arg Glu Gln Phe Leu Gln Tyr Val His Asp Ile Thr
145 150 155 160

Phe Asp Pro Asp Thr Ala His Lys Tyr Leu Arg Leu Gln Glu Glu Asn
 165 170 175

Arg Lys Val Thr Asn Thr Thr Pro Trp Glu His Pro Tyr Pro Asp Leu
 180 185 190

Pro Ser Arg Phe Leu His Trp Arg Gln Val Leu Ser Gln Gln Ser Leu
 195 200 205

Tyr Leu His Arg Tyr Tyr Phe Glu Val Glu Ile Phe Gly Ala Gly Thr
 210 215 220

Tyr Val Gly Leu Thr Cys Lys Gly Ile Asp Gln Lys Gly Glu Glu Arg
225 230 235 240

Ser Ser Cys Ile Ser Gly Asn Asn Phe Ser Trp Ser Leu Gln Trp Asn
 245 250 255

Gly Lys Glu Phe Thr Ala Trp Tyr Ser Asp Met Glu Thr Pro Leu Lys
 260 265 270

Ala Gly Pro Phe Trp Arg Leu Gly Val Tyr Ile Asp Phe Pro Gly Gly
275 280 285

Ile Leu Ser Phe Tyr Gly Val Glu Tyr Asp Ser Met Thr Leu Val His
290 295 300

Lys Phe Ala Cys Lys Phe Ser Glu Pro Val Tyr Ala Ala Phe Trp Leu
305 310 315 320

Ser Lys Lys Glu Asn Ala Ile Arg Ile Val Asp Leu Gly Glu Glu Pro
325 330 335

Glu Lys Pro Ala Pro Ser Leu Val Gly Thr Ala Pro
340 345

<210> 137

<211> 2607

<212> DNA

<213> Homo sapiens

<400> 137

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ggcgcggcgg gagagccgct caagctgcgc tgcccgtgt gcgaccagaa agtagtgcta 300

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<210> 138
 <211> 868
 <212> PRT
 <213> Homo sapiens

<400> 138

Met Ala Ser Phe Pro Glu Thr Asp Phe Gln Ile Cys Leu Leu Cys Lys
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Glu Met Cys Gly Ser Pro Ala Pro Leu Ser Ser Asn Ser Ser Ala Ser
 20 25 30

Ser Ser Ser Ser Gln Thr Ser Thr Ser Ser Gly Gly Gly Gly Gly Gly
 35 40 45

Pro Gly Ala Ala Ala Arg Arg Leu His Val Leu Pro Cys Leu His Ala
 50 55 60

Phe Cys Arg Pro Cys Leu Glu Ala His Arg Leu Pro Ala Ala Gly Gly
 65 70 75 80

Gly Ala Ala Gly Glu Pro Leu Lys Leu Arg Cys Pro Val Cys Asp Gln
 85 90 95

Lys Val Val Leu Ala Glu Ala Ala Gly Met Asp Ala Leu Pro Ser Ser
 100 105 110

Ala Phe Leu Leu Ser Asn Leu Leu Asp Ala Val Val Ala Thr Ala Asp
 115 120 125

Glu Pro Pro Pro Lys Asn Gly Arg Ala Gly Ala Pro Ala Gly Ala Gly
130 135 140

Gly His Ser Asn His Arg His His Ala His His Ala His Pro Arg Ala
145 150 155 160

Ser Ala Ser Ala Pro Pro Leu Pro Gln Ala Pro Gln Pro Pro Ala Pro
165 170 175

Ser Arg Ser Ala Pro Gly Gly Pro Ala Ala Ser Pro Ser Ala Leu Leu
180 185 190

Leu Arg Arg Pro His Gly Cys Ser Ser Cys Asp Glu Gly Asn Ala Ala
195 200 205

Ser Ser Arg Cys Leu Asp Cys Gln Glu His Leu Cys Asp Asn Cys Val
210 215 220

Arg Ala His Gln Arg Val Arg Leu Thr Lys Asp His Tyr Ile Glu Arg
225 230 235 240

Gly Pro Pro Gly Pro Gly Ala Ala Ala Ala Ala Gln Gln Leu Gly Leu
245 250 255

Gly Pro Pro Phe Pro Gly Pro Pro Phe Ser Ile Leu Ser Val Phe Pro
260 265 270

Glu Arg Leu Gly Phe Cys Gln His His Asp Asp Glu Val Leu His Leu
275 280 285

Tyr Cys Asp Thr Cys Ser Val Pro Ile Cys Arg Glu Cys Thr Met Gly
290 295 300

Arg His Gly Gly His Ser Phe Ile Tyr Leu Gln Glu Ala Leu Gln Asp
305 310 315 320

Ser Arg Ala Leu Thr Ile Gln Leu Leu Ala Asp Ala Gln Gln Gly Arg

325	330	335
Gln Ala Ile Gln Leu Ser Ile Glu Gln Ala Gln Thr Val Ala Glu Gln		
340	345	350
Val Glu Met Lys Ala Lys Val Val Gln Ser Glu Val Lys Ala Val Thr		
355	360	365
Ala Arg His Lys Lys Ala Leu Glu Glu Arg Glu Cys Glu Leu Leu Trp		
370	375	380
Lys Val Glu Lys Ile Arg Gln Val Lys Ala Lys Ser Leu Tyr Leu Gln		
385	390	395 400
Val Glu Lys Leu Arg Gln Asn Leu Asn Lys Leu Glu Ser Thr Ile Ser		
405	410	415
Ala Val Gln Gln Val Leu Glu Glu Gly Arg Ala Leu Asp Ile Leu Leu		
420	425	430
Ala Arg Asp Arg Met Leu Ala Gln Val Gln Glu Leu Lys Thr Val Arg		
435	440	445
Ser Leu Leu Gln Pro Gln Glu Asp Asp Arg Val Met Phe Thr Pro Pro		
450	455	460
Asp Gln Ala Leu Tyr Leu Ala Ile Lys Ser Phe Gly Phe Val Ser Ser		
465	470	475 480
Gly Ala Phe Ala Pro Leu Thr Lys Ala Thr Gly Asp Gly Leu Lys Arg		
485	490	495
Ala Leu Gln Gly Lys Val Ala Ser Phe Thr Val Ile Gly Tyr Asp His		
500	505	510
Asp Gly Glu Pro Arg Leu Ser Gly Gly Asp Leu Met Ser Ala Val Val		
515	520	525

Leu Gly Pro Asp Gly Asn Leu Phe Gly Ala Glu Val Ser Asp Gln Gln
530 535 540

Asn Gly Thr Tyr Val Val Ser Tyr Arg Pro Gln Leu Glu Gly Glu His
545 550 555 560

Leu Val Ser Val Thr Leu Cys Asn Gln His Ile Glu Asn Ser Pro Phe
565 570 575

Lys Val Val Val Lys Ser Gly Arg Ser Tyr Val Gly Ile Gly Leu Pro
580 585 590

Gly Leu Ser Phe Gly Ser Glu Gly Asp Ser Asp Gly Lys Leu Cys Arg
595 600 605

Pro Trp Gly Val Ser Val Asp Lys Glu Gly Tyr Ile Ile Val Ala Asp
610 615 620

Arg Ser Asn Asn Arg Ile Gln Val Phe Lys Pro Cys Gly Ala Phe His
625 630 635 640

His Lys Phe Gly Thr Leu Gly Ser Arg Pro Gly Gln Phe Asp Arg Pro
645 650 655

Ala Gly Val Ala Cys Asp Ala Ser Arg Arg Ile Val Val Ala Asp Lys
660 665 670

Asp Asn His Arg Ile Gln Ile Phe Thr Phe Glu Gly Gln Phe Leu Leu
675 680 685

Lys Phe Gly Glu Lys Gly Thr Lys Asn Gly Gln Phe Asn Tyr Pro Trp
690 695 700

Asp Val Ala Val Asn Ser Glu Gly Lys Ile Leu Val Ser Asp Thr Arg
705 710 715 720

Asn His Arg Ile Gln Leu Phe Gly Pro Asp Gly Val Phe Leu Asn Lys
725 730 735

Tyr Gly Phe Glu Gly Ala Leu Trp Lys His Phe Asp Ser Pro Arg Gly
740 745 750

Val Ala Phe Asn His Glu Gly His Leu Val Val Thr Asp Phe Asn Asn
755 760 765

His Arg Leu Leu Val Ile His Pro Asp Cys Gln Ser Ala Arg Phe Leu
770 775 780

Gly Ser Glu Gly Thr Gly Asn Gly Gln Phe Leu Arg Pro Gln Gly Val
785 790 795 800

Ala Val Asp Gln Glu Gly Arg Ile Ile Val Ala Asp Ser Arg Asn His
805 810 815

Arg Val Gln Met Phe Glu Ser Asn Gly Ser Phe Leu Cys Lys Phe Gly
820 825 830

Ala Gln Gly Ser Gly Phe Gly Gln Met Asp Arg Pro Ser Gly Ile Ala
835 840 845

Ile Thr Pro Asp Gly Met Ile Val Val Val Asp Phe Gly Asn Asn Arg
850 855 860

Ile Leu Val Phe
865

<210> 139

<211> 1434

<212> DNA

<213> Homo sapiens

<400> 139

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gtggccgggg agccggcggc ggatggcacc gttctctgcc cctgctgcca ggccccacg 180

cggccgcagg cactcagcac caacctgcag ctggcgcgcc tggaggagg gctggcccag 240

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<210> 140

<211> 477

<212> PRT

<213> Homo sapiens

<400> 140

Met Ser Ala Ala Pro Gly Leu Leu His Gln Glu Leu Ser Cys Pro Leu

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Cys Leu Gln Leu Phe Asp Ala Pro Val Thr Ala Glu Cys Gly His Ser
20 25 30

Phe Cys Arg Ala Cys Leu Gly Arg Val Ala Gly Glu Pro Ala Ala Asp
35 40 45

Gly Thr Val Leu Cys Pro Cys Cys Gln Ala Pro Thr Arg Pro Gln Ala
50 55 60

Leu Ser Thr Asn Leu Gln Leu Ala Arg Leu Val Glu Gly Leu Ala Gln
65 70 75 80

Val Pro Gln Gly His Cys Glu Glu His Leu Asp Pro Leu Ser Ile Tyr
85 90 95

Cys Glu Gln Asp Arg Ala Leu Val Cys Gly Val Cys Ala Ser Leu Gly
100 105 110

Ser His Arg Gly His Arg Leu Leu Pro Ala Ala Glu Ala His Ala Arg
115 120 125

Leu Lys Thr Gln Leu Pro Gln Gln Lys Leu Gln Leu Gln Glu Ala Cys
130 135 140

Met Arg Lys Glu Lys Ser Val Ala Val Leu Glu His Gln Leu Val Glu
145 150 155 160

Val Glu Glu Thr Val Arg Gln Phe Arg Gly Ala Val Gly Glu Gln Leu
165 170 175

Gly Lys Met Arg Val Phe Leu Ala Ala Leu Glu Gly Ser Leu Asp Arg
180 185 190

Glu Ala Glu Arg Val Arg Gly Glu Ala Gly Val Ala Leu Arg Arg Glu
195 200 205

Leu Gly Ser Leu Asn Ser Tyr Leu Glu Gln Leu Arg Gln Met Glu Lys
210 215 220

Val Leu Glu Glu Val Ala Asp Lys Pro Gln Thr Glu Phe Leu Met Lys
225 230 235 240

Tyr Cys Leu Val Thr Ser Arg Leu Gln Lys Ile Leu Ala Glu Ser Pro
 245 250 255

Pro Pro Ala Arg Leu Asp Ile Gln Leu Pro Ile Ile Ser Asp Asp Phe
 260 265 270

Lys Phe Gln Val Trp Arg Lys Met Phe Arg Ala Leu Met Pro Ala Leu
 275 280 285

Glu Glu Leu Thr Phe Asp Pro Ser Ser Ala His Pro Ser Leu Val Val
 290 295 300

Ser Ser Ser Gly Arg Arg Val Glu Cys Ser Glu Gln Lys Ala Pro Pro
305 310 315 320

Ala Gly Glu Asp Pro Arg Gln Phe Asp Lys Ala Val Ala Val Val Ala
 325 330 335

His Gln Gln Leu Ser Glu Gly Glu His Tyr Trp Glu Val Asp Val Gly
 340 345 350

Asp Lys Pro Arg Trp Ala Leu Gly Val Ile Ala Ala Glu Ala Pro Arg
 355 360 365

Arg Gly Arg Leu His Ala Val Pro Ser Gln Gly Leu Trp Leu Leu Gly
 370 375 380

Leu Arg Glu Gly Lys Ile Leu Glu Ala His Val Glu Ala Lys Glu Pro
385 390 395 400

Arg Ala Leu Arg Ser Pro Glu Arg Arg Pro Thr Arg Ile Gly Leu Tyr
 405 410 415

Leu Ser Phe Gly Asp Gly Val Leu Ser Phe Tyr Asp Ala Ser Asp Ala

420	425	430	
Asp Ala Leu Val Pro Leu Phe Ala Phe His Glu Arg Leu Pro Arg Pro			
435	440	445	
Val Tyr Pro Phe Phe Asp Val Cys Trp His Asp Lys Gly Lys Asn Ala			
450	455	460	
Gln Pro Leu Leu Leu Val Gly Pro Glu Gly Ala Glu Ala			
465	470	475	

<210> 141
 <211> 753
 <212> DNA
 <213> Homo sapiens

<400> 141

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<210> 142
 <211> 250
 <212> PRT

<213> Homo sapiens

<400> 142

Met Ala Trp Gln Val Ser Leu Leu Glu Leu Glu Asp Arg Leu Gln Cys
1 5 10 15

Pro Ile Cys Leu Glu Val Phe Lys Glu Ser Leu Met Leu Gln Cys Gly
20 25 30

His Ser Tyr Cys Lys Gly Cys Leu Val Ser Leu Ser Tyr His Leu Asp
35 40 45

Thr Lys Val Arg Cys Pro Met Cys Trp Gln Val Val Asp Gly Ser Ser
50 55 60

Ser Leu Pro Asn Val Ser Leu Ala Trp Val Ile Glu Ala Leu Arg Leu
65 70 75 80

Pro Gly Asp Pro Glu Pro Lys Val Cys Val His His Arg Asn Pro Leu
85 90 95

Ser Leu Phe Cys Glu Lys Asp Gln Glu Leu Ile Cys Gly Leu Cys Gly
100 105 110

Leu Leu Gly Ser His Gln His His Pro Val Thr Pro Val Ser Thr Val
115 120 125

Cys Ser Arg Met Lys Glu Glu Leu Ala Ala Leu Phe Ser Glu Leu Lys
130 135 140

Gln Glu Gln Lys Lys Val Asp Glu Leu Ile Ala Lys Leu Val Lys Asn
145 150 155 160

Arg Thr Arg Ile Val Asn Glu Ser Asp Val Phe Ser Trp Val Ile Arg
165 170 175

Arg Glu Phe Gln Glu Leu Arg His Pro Val Asp Glu Glu Lys Ala Arg
180 185 190

Cys Leu Glu Gly Ile Gly Gly His Thr Arg Gly Leu Val Ala Ser Leu
 195 200 205

Asp Met Gln Leu Glu Gln Ala Gln Gly Thr Arg Glu Arg Leu Ala Gln
 210 215 220

Ala Glu Cys Val Leu Glu Gln Phe Gly Asn Glu Asp His His Glu Phe
 225 230 235 240

Ile Trp Lys Phe His Ser Met Ala Ser Arg
 245 250

<210> 143
 <211> 753
 <212> DNA
 <213> Homo sapiens

<400> 143
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 atctggaagt tccactccat ggcctccagg taa 753

<210> 144

<211> 250

<212> PRT

<213> Homo sapiens

<400> 144

Met Ala Trp Gln Val Ser Leu Leu Glu Leu Glu Asp Trp Leu Gln Cys
1 5 10 15

Pro Ile Cys Leu Glu Val Phe Lys Glu Ser Leu Met Leu Gln Cys Gly
20 25 30

His Ser Tyr Cys Lys Gly Cys Leu Val Ser Leu Ser Tyr His Leu Asp
35 40 45

Thr Lys Val Arg Cys Pro Met Cys Trp Gln Val Val Asp Gly Ser Ser
50 55 60

Ser Leu Pro Asn Val Ser Leu Ala Trp Val Ile Glu Ala Leu Arg Leu
65 70 75 80

Pro Gly Asp Pro Glu Pro Lys Val Cys Val His His Arg Asn Pro Leu
85 90 95

Ser Leu Phe Cys Glu Lys Asp Gln Glu Leu Ile Cys Gly Leu Cys Gly
100 105 110

Leu Leu Gly Ser His Gln His His Pro Val Thr Pro Val Ser Thr Val
115 120 125

Cys Ser Arg Met Lys Glu Glu Leu Ala Ala Leu Phe Ser Glu Leu Lys
130 135 140

Gln Glu Gln Lys Lys Val Asp Glu Leu Ile Ala Lys Leu Val Lys Asn
145 150 155 160

Arg Thr Arg Ile Val Asn Glu Ser Asp Val Phe Ser Trp Val Ile Arg
165 170 175

Arg Glu Phe Gln Glu Leu Arg His Pro Val Asp Glu Glu Lys Ala Arg

180	185	190
Cys Leu Glu Gly Ile Gly Gly His Thr Arg Gly Leu Val Ala Ser Leu		
195	200	205
Asp Met Gln Leu Glu Gln Ala Gln Gly Thr Arg Glu Arg Leu Ala Gln		
210	215	220
Ala Glu Cys Val Leu Glu Gln Phe Gly Asn Glu Asp His His Glu Phe		
225	230	240
Ile Trp Lys Phe His Ser Met Ala Ser Arg		
245	250	
<210> 145		
<211> 1404		
<212> DNA		
<213> Homo sapiens		
<400> 145		
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caacacagga acctcagaag caatgtcccag ctgggaaaca tgattgaaac tgcccagctg	240	
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 cagtattcgg ccctacagaa agttatacag cattttacag acaacgtcac tctagacctg 900
 aagacagccc atcctaacct gctcatttct aaggatagaa cctgcgtaac atttacaag 960
 aaaagacaac gtattcctgg ttcttcaagt ttaccaaga gccctgttgt gttggggatt 1020
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<210> 146

<211> 467

<212> PRT

<213> Homo sapiens

<400> 146

Met Ala His Val Glu Val Leu Ala Arg Leu Gln Lys Glu Thr Lys Cys

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Pro Ile Cys Leu Asp Asp Leu Thr Asp Pro Val Thr Val Glu Cys Gly

20 25 30

His Asn Phe Cys Arg Ser Cys Ile Lys Asp Phe Trp Ala Gly Gln Gln

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Leu Ser Ile Thr Glu Ala Ala Ser Leu His Arg Lys His Leu Gln Asp		
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Tyr Ser Lys Leu Leu Lys Trp Glu Val Lys Glu Ile Gln Gly Leu Met		
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Ser Ala Leu Asn Lys Arg Thr Val Thr Leu Arg Glu Gln Ala Glu Ala		
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Gln Arg Ser Gln Leu Thr Ser Glu Cys Glu Lys Leu Met Arg Phe Leu		
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Asp Gln Glu Glu Arg Ala Ala Phe Ser Arg Leu Glu Asp Glu Glu Met		
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Arg Leu Glu Lys Arg Leu Leu Asp Asn Ile Ala Ala Leu Glu His His		
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Gly Ser Ser Leu Arg Asp Leu Leu Arg His Leu Met Leu Thr Gly Glu		
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		240
Leu Ser Glu Ala Lys Met Leu Ser Thr Val Lys Asp Phe Tyr Leu Asn		
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Cys Arg Arg Gln Leu Ile Ser Pro Ser Ile Phe Pro Val Gln Leu Arg		
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Arg Val Glu Tyr Ser Phe Pro Leu Gln Tyr Ser Ala Leu Gln Lys Val		
275	280	285

Ile Gln His Phe Thr Asp Asn Val Thr Leu Asp Leu Lys Thr Ala His
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Lys Arg Gln Arg Ile Pro Gly Ser Ser Ser Phe Thr Lys Ser Pro Val
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 aggacagcac cctccacccc tgtgatccgc gctgaggact gtactgtgtg ttggaacaca 11460
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 ctctgttga gagaaacagc tcactctgct ctacacattt cctcaagtgg gacagtgatc 11760
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catgtgactg agcgtccagc cagagtgggc atcctgctgg actacaacaa ccagagactt 12060

atcttcatca acgcagagag cgagcagttg ctcttcatca tcaggcacag gtttaatgag 12120

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<211> 4069

<212> PRT

<213> Homo sapiens

<400> 165

Met Ala Ser Arg Asp Ser Asn His Ala Gly Glu Ser Phe Leu Gly Ser
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Asp Gly Asp Glu Glu Ala Thr Arg Glu Leu Glu Thr Glu Glu Glu Ser
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Glu Gly Glu Glu Asp Glu Thr Ala Ala Glu Ser Glu Glu Glu Pro Asp
35 40 45

Ser Arg Leu Ser Asp Gln Asp Glu Glu Gly Lys Ile Lys Gln Glu Tyr
50 55 60

Ile Ile Ser Asp Pro Ser Phe Ser Met Val Thr Val Gln Arg Glu Asp
65 70 75 80

Ser Gly Ile Thr Trp Glu Thr Asn Ser Ser Arg Ser Ser Thr Pro Trp
85 90 95

Ala Ser Glu Glu Ser Gln Thr Ser Gly Val Cys Ser Arg Glu Gly Ser
100 105 110

Thr Val Asn Ser Pro Pro Gly Asn Val Ser Phe Ile Val Asp Glu Val
115 120 125

Lys Lys Val Arg Lys Arg Thr His Lys Ser Lys His Gly Ser Pro Ser
130 135 140

Leu Arg Arg Lys Gly Asn Arg Lys Arg Asn Ser Phe Glu Ser Gln Asp
145 150 155 160

Val Pro Thr Asn Lys Lys Gly Ser Pro Leu Thr Ser Ala Ser Gln Val
 165 170 175

Leu Thr Thr Glu Lys Glu Lys Ser Tyr Thr Gly Ile Tyr Asp Lys Ala
 180 185 190

Arg Lys Lys Lys Thr Thr Ser Asn Thr Pro Pro Ile Thr Gly Ala Ile
 195 200 205

Tyr Lys Glu His Lys Pro Leu Val Leu Arg Pro Val Tyr Ile Gly Thr
 210 215 220

Val Gln Tyr Lys Ile Lys Met Phe Asn Ser Val Lys Glu Glu Leu Ile
225 230 235 240

Pro Leu Gln Phe Tyr Gly Thr Leu Pro Lys Gly Tyr Val Ile Lys Glu
 245 250 255

Ile His Tyr Arg Lys Gly Lys Asp Ala Ser Ile Ser Leu Glu Pro Asp
 260 265 270

Leu Asp Asn Ser Gly Ser Asn Thr Val Ser Lys Thr Arg Lys Leu Val
 275 280 285

Ala Gln Ser Ile Glu Asp Lys Val Lys Glu Val Phe Pro Pro Trp Arg
 290 295 300

Gly Ala Leu Ser Lys Gly Ser Glu Ser Leu Thr Leu Met Phe Ser His
305 310 315 320

Glu Asp Gln Lys Lys Ile Tyr Ala Asp Ser Pro Leu Asn Ala Thr Ser
 325 330 335

Ala Leu Glu His Thr Val Pro Ser Tyr Ser Ser Ser Gly Arg Ala Glu

340	345	350
Gln Gly Ile Gln Leu Arg His Ser Gln Ser Val Pro Gln Gln Pro Glu		
355	360	365
Asp Glu Ala Lys Pro His Glu Val Glu Pro Pro Ser Val Thr Pro Asp		
370	375	380
Thr Pro Ala Thr Met Phe Leu Arg Thr Thr Lys Glu Glu Cys Glu Leu		
385	390	395 400
Ala Ser Pro Gly Thr Ala Ala Ser Glu Asn Asp Ser Ser Val Ser Pro		
405	410	415
Ser Phe Ala Asn Glu Val Lys Lys Glu Asp Val Tyr Ser Ala His His		
420	425	430
Ser Ile Ser Leu Glu Ala Ala Ser Pro Gly Leu Ala Ala Ser Thr Gln		
435	440	445
Asp Gly Leu Asp Pro Asp Gln Glu Gln Pro Asp Leu Thr Ser Ile Glu		
450	455	460
Arg Ala Glu Pro Val Ser Ala Lys Leu Thr Pro Thr His Pro Ser Val		
465	470	475 480
Lys Gly Glu Lys Glu Glu Asn Met Leu Glu Pro Ser Ile Ser Leu Ser		
485	490	495
Glu Pro Leu Met Leu Glu Glu Pro Glu Lys Glu Glu Ile Glu Thr Ser		
500	505	510
Leu Pro Ile Ala Ile Thr Pro Glu Pro Glu Asp Ser Asn Leu Val Glu		
515	520	525
Glu Glu Ile Val Glu Leu Asp Tyr Pro Glu Ser Pro Leu Val Ser Glu		
530	535	540

Lys Pro Phe Pro Pro His Met Ser Pro Glu Val Glu His Lys Glu Glu
545 550 555 560

Glu Leu Ile Leu Pro Leu Leu Ala Ala Ser Ser Pro Glu His Val Ala
565 570 575

Leu Ser Glu Glu Glu Arg Glu Glu Ile Ala Ser Val Ser Thr Gly Ser
580 585 590

Ala Phe Val Ser Glu Tyr Ser Val Pro Gln Asp Leu Asn His Glu Leu
595 600 605

Gln Glu Gln Glu Gly Glu Pro Val Pro Pro Ser Asn Val Glu Ala Ile
610 615 620

Ala Glu His Ala Val Leu Ser Glu Glu Glu Asn Glu Glu Phe Glu Ala
625 630 635 640

Tyr Ser Pro Ala Ala Ala Pro Thr Ser Glu Ser Ser Leu Ser Pro Ser
645 650 655

Thr Thr Glu Lys Thr Ser Glu Asn Gln Ser Pro Leu Phe Ser Thr Val
660 665 670

Thr Pro Glu Tyr Met Val Leu Ser Gly Asp Glu Ala Ser Glu Ser Gly
675 680 685

Cys Tyr Thr Pro Asp Ser Thr Ser Ala Ser Glu Tyr Ser Val Pro Ser
690 695 700

Leu Ala Thr Lys Glu Ser Leu Lys Lys Thr Ile Asp Arg Lys Ser Pro
705 710 715 720

Leu Ile Leu Lys Gly Val Ser Glu Tyr Met Ile Pro Ser Glu Glu Lys
725 730 735

Glu Asp Thr Gly Ser Phe Thr Pro Ala Val Ala Pro Ala Ser Glu Pro
740 745 750

Ser Leu Ser Pro Ser Thr Thr Glu Lys Thr Ser Glu Cys Gln Ser Pro
755 760 765

Leu Pro Ser Thr Ala Thr Ser Glu His Val Val Pro Ser Glu Gly Glu
770 775 780

Asp Leu Gly Ser Glu Arg Phe Thr Pro Asp Ser Lys Leu Ile Ser Lys
785 790 795 800

Tyr Ala Ala Pro Leu Asn Ala Thr Gln Glu Ser Gln Lys Lys Ile Ile
805 810 815

Asn Glu Ala Ser Gln Phe Lys Pro Lys Gly Ile Ser Glu His Thr Val
820 825 830

Leu Ser Val Asp Gly Lys Glu Val Ile Gly Pro Ser Ser Pro Asp Leu
835 840 845

Val Val Ala Ser Glu His Ser Phe Pro Pro His Thr Thr Glu Met Thr
850 855 860

Ser Glu Cys Gln Ala Pro Pro Leu Ser Ala Thr Pro Ser Glu Tyr Val
865 870 875 880

Val Leu Ser Asp Glu Glu Ala Val Glu Leu Glu Arg Tyr Thr Pro Ser
885 890 895

Ser Thr Ser Ala Ser Glu Phe Ser Val Pro Pro Tyr Ala Thr Pro Glu
900 905 910

Ala Gln Glu Glu Glu Ile Val His Arg Ser Leu Asn Leu Lys Gly Ala
915 920 925

Ser Ser Pro Met Asn Leu Ser Glu Glu Asp Gln Glu Asp Ile Gly Pro
930 935 940

Phe Ser Pro Asp Ser Ala Phe Val Ser Glu Phe Ser Phe Pro Pro Tyr
945 950 955 960

Ala Thr Gln Glu Ala Glu Lys Arg Glu Phe Glu Cys Asp Ser Pro Ile
965 970 975

Cys Leu Thr Ser Pro Ser Glu His Thr Ile Leu Ser Asp Glu Asp Thr
980 985 990

Glu Glu Ala Glu Leu Phe Ser Pro Asp Ser Ala Ser Gln Val Ser Ile
995 1000 1005

Pro Pro Phe Arg Ile Ser Glu Thr Glu Lys Asn Glu Leu Glu Pro
1010 1015 1020

Asp Ser Leu Leu Thr Ala Val Ser Ala Ser Gly Tyr Ser Cys Phe
1025 1030 1035

Ser Glu Ala Asp Glu Glu Asp Ile Gly Ser Thr Ala Ala Thr Pro
1040 1045 1050

Val Ser Glu Gln Phe Ser Ser Ser Gln Lys Gln Lys Ala Glu Thr
1055 1060 1065

Phe Pro Leu Met Ser Pro Leu Glu Asp Leu Ser Leu Pro Pro Ser
1070 1075 1080

Thr Asp Lys Ser Glu Lys Ala Glu Ile Lys Pro Glu Ile Pro Thr
1085 1090 1095

Thr Ser Thr Ser Val Ser Glu Tyr Leu Ile Leu Ala Gln Lys Gln
1100 1105 1110

Lys Thr Gln Ala Tyr Leu Glu Pro Glu Ser Glu Asp Leu Ile Pro
1115 1120 1125

Ser His Leu Thr Ser Glu Val Glu Lys Gly Glu Arg Glu Ala Ser
1130 1135 1140

Ser Ser Val Ala Ala Ile Pro Ala Ala Leu Pro Ala Gln Ser Ser

1145	1150	1155
Ile Val Lys Glu Glu Thr Lys	Pro Ala Ser Pro His	Ser Val Leu
1160	1165	1170
Pro Asp Ser Val Pro Ala Ile	Lys Lys Glu Gln Glu	Pro Thr Ala
1175	1180	1185
Ala Leu Thr Leu Lys Ala Ala	Asp Glu Gln Met Ala	Leu Ser Lys
1190	1195	1200
Val Arg Lys Glu Glu Ile Val	Pro Asp Ser Gln Glu	Ala Thr Ala
1205	1210	1215
His Val Ser Gln Asp Gln Lys	Met Glu Pro Gln Pro	Pro Asn Val
1220	1225	1230
Pro Glu Ser Glu Met Lys Tyr	Ser Val Leu Pro Asp	Met Val Asp
1235	1240	1245
Glu Pro Lys Lys Gly Val Lys	Pro Lys Leu Val Leu	Asn Val Thr
1250	1255	1260
Ser Glu Leu Glu Gln Arg Lys	Leu Ser Lys Asn Glu	Pro Glu Val
1265	1270	1275
Ile Lys Pro Tyr Ser Pro Leu	Lys Glu Thr Ser Leu	Ser Gly Pro
1280	1285	1290
Glu Ala Leu Ser Ala Val Lys	Met Glu Met Lys His	Asp Ser Lys
1295	1300	1305
Ile Thr Thr Thr Pro Ile Val	Leu His Ser Ala Ser	Ser Gly Val
1310	1315	1320
Glu Lys Gln Val Glu His Gly	Pro Pro Ala Leu Ala	Phe Ser Ala
1325	1330	1335

Leu Ser Glu Glu Ile Lys Lys Glu Ile Glu Pro Ser Ser Ser Thr
1340 1345 1350

Thr Thr Ala Ser Val Thr Lys Leu Asp Ser Asn Leu Thr Arg Ala
1355 1360 1365

Val Lys Glu Glu Ile Pro Thr Asp Ser Ser Leu Ile Thr Pro Val
1370 1375 1380

Asp Arg Pro Val Leu Thr Lys Val Gly Lys Gly Glu Leu Gly Ser
1385 1390 1395

Gly Leu Pro Pro Leu Val Thr Ser Ala Asp Glu His Ser Val Leu
1400 1405 1410

Ala Glu Glu Asp Lys Val Ala Ile Lys Gly Ala Ser Pro Ile Glu
1415 1420 1425

Thr Ser Ser Lys His Leu Ala Trp Ser Glu Ala Glu Lys Glu Ile
1430 1435 1440

Lys Phe Asp Ser Leu Pro Ser Val Ser Ser Ile Ala Glu His Ser
1445 1450 1455

Val Leu Ser Glu Val Glu Ala Lys Glu Val Lys Ala Gly Leu Pro
1460 1465 1470

Val Ile Lys Thr Ser Ser Ser Gln His Ser Asp Lys Ser Glu Glu
1475 1480 1485

Ala Arg Val Glu Asp Lys Gln Asp Leu Leu Phe Ser Thr Val Cys
1490 1495 1500

Asp Ser Glu Arg Leu Val Ser Ser Gln Lys Lys Ser Leu Met Ser
1505 1510 1515

Thr Ser Glu Val Leu Glu Pro Glu His Glu Leu Pro Leu Ser Leu
1520 1525 1530

Trp Gly Glu Ile Lys Lys Lys Glu Thr Glu Leu Pro Ser Ser Gln
1535 1540 1545

Asn Val Ser Pro Ala Ser Lys His Ile Ile Pro Lys Gly Lys Asp
1550 1555 1560

Glu Glu Thr Ala Ser Ser Ser Pro Glu Leu Glu Asn Leu Ala Ser
1565 1570 1575

Gly Leu Ala Pro Thr Leu Leu Leu Leu Ser Asp Asp Lys Asn Lys
1580 1585 1590

Pro Ala Val Glu Val Ser Ser Thr Ala Gln Gly Asp Phe Pro Ser
1595 1600 1605

Glu Lys Gln Asp Val Ala Leu Ala Glu Leu Ser Leu Glu Pro Glu
1610 1615 1620

Lys Lys Asp Lys Pro His Gln Pro Leu Glu Leu Pro Asn Ala Gly
1625 1630 1635

Ser Glu Phe Ser Ser Asp Leu Gly Arg Gln Ser Gly Ser Ile Gly
1640 1645 1650

Thr Lys Gln Ala Lys Ser Pro Ile Thr Glu Thr Glu Asp Ser Val
1655 1660 1665

Leu Glu Lys Gly Pro Ala Glu Leu Arg Ser Arg Glu Gly Lys Glu
1670 1675 1680

Glu Asn Arg Glu Leu Cys Ala Ser Ser Thr Met Pro Ala Ile Ser
1685 1690 1695

Glu Leu Ser Ser Leu Leu Arg Glu Glu Ser Gln Asn Glu Glu Ile
1700 1705 1710

Lys Pro Phe Ser Pro Lys Ile Ile Ser Leu Glu Ser Lys Glu Pro
1715 1720 1725

Pro Ala Ser Val Ala Glu Gly Gly Asn Pro Glu Glu Phe Gln Pro
1730 1735 1740

Phe Thr Phe Ser Leu Lys Gly Leu Ser Glu Glu Val Ser His Pro
1745 1750 1755

Ala Asp Phe Lys Lys Gly Gly Asn Gln Glu Ile Gly Pro Leu Pro
1760 1765 1770

Pro Thr Gly Asn Leu Lys Ala Gln Val Met Gly Asp Ile Leu Asp
1775 1780 1785

Lys Leu Ser Glu Glu Thr Gly His Pro Asn Ser Ser Gln Val Leu
1790 1795 1800

Gln Ser Ile Thr Glu Pro Ser Lys Ile Ala Pro Ser Asp Leu Leu
1805 1810 1815

Val Glu Gln Lys Lys Thr Glu Lys Ala Leu His Ser Asp Gln Thr
1820 1825 1830

Val Lys Leu Pro Asp Val Ser Thr Ser Ser Glu Asp Lys Gln Asp
1835 1840 1845

Leu Gly Ile Lys Gln Phe Ser Leu Met Arg Glu Asn Leu Pro Leu
1850 1855 1860

Glu Gln Ser Lys Ser Phe Met Thr Thr Lys Pro Ala Asp Val Lys
1865 1870 1875

Glu Thr Lys Met Glu Glu Phe Phe Ile Ser Pro Lys Asp Glu Asn
1880 1885 1890

Trp Met Leu Gly Lys Pro Glu Asn Val Ala Ser Gln His Glu Gln
1895 1900 1905

Arg Ile Ala Gly Ser Val Gln Leu Asp Ser Ser Ser Ser Asn Glu

1910	1915	1920
Leu Arg Pro Gly Gln Leu Lys	Ala Ala Val Ser Ser	Lys Asp His
1925	1930	1935
Thr Cys Glu Val Arg Lys Gln	Val Leu Pro His Ser	Ala Glu Glu
1940	1945	1950
Ser His Leu Ser Ser Gln Glu	Ala Val Ser Ala Leu	Asp Thr Ser
1955	1960	1965
Ser Gly Asn Thr Glu Thr Leu	Ser Ser Lys Ser Tyr	Ser Ser Glu
1970	1975	1980
Glu Val Lys Leu Ala Glu Glu	Pro Lys Ser Leu Val	Leu Ala Gly
1985	1990	1995
Asn Val Glu Arg Asn Ile Ala	Glu Gly Lys Glu Ile	His Ser Leu
2000	2005	2010
Met Glu Ser Glu Ser Leu Leu	Leu Glu Lys Ala Asn	Thr Glu Leu
2015	2020	2025
Ser Trp Pro Ser Lys Glu Asp	Ser Gln Glu Lys Ile	Lys Leu Pro
2030	2035	2040
Pro Glu Arg Phe Phe Gln Lys	Pro Val Ser Gly Leu	Ser Val Glu
2045	2050	2055
Gln Val Lys Ser Glu Thr Ile	Ser Ser Ser Val Lys	Thr Ala His
2060	2065	2070
Phe Pro Ala Glu Gly Val Glu	Pro Ala Leu Gly Asn	Glu Lys Glu
2075	2080	2085
Ala His Arg Ser Thr Pro Pro	Phe Pro Glu Glu Lys	Pro Leu Glu
2090	2095	2100

Glu Ser Lys Met Val Gln Ser Lys Val Ile Asp Asp Ala Asp Glu
2105 2110 2115

Gly Lys Lys Pro Ser Pro Glu Val Lys Ile Pro Thr Gln Arg Lys
2120 2125 2130

Pro Ile Ser Ser Ile His Ala Arg Glu Pro Gln Ser Pro Glu Ser
2135 2140 2145

Pro Glu Val Thr Gln Asn Pro Pro Thr Gln Pro Lys Val Ala Lys
2150 2155 2160

Pro Asp Leu Pro Glu Glu Lys Gly Lys Lys Gly Ile Ser Ser Phe
2165 2170 2175

Lys Ser Trp Met Ser Ser Leu Phe Phe Gly Ser Ser Thr Pro Asp
2180 2185 2190

Asn Lys Val Ala Glu Gln Glu Asp Leu Glu Thr Gln Pro Ser Pro
2195 2200 2205

Ser Val Glu Lys Ala Val Thr Val Ile Asp Pro Glu Gly Thr Ile
2210 2215 2220

Pro Thr Asn Phe Asn Val Ala Glu Lys Pro Ala Asp His Ser Leu
2225 2230 2235

Ser Glu Val Lys Leu Lys Thr Ala Asp Glu Pro Arg Gly Thr Leu
2240 2245 2250

Val Lys Ser Gly Asp Gly Gln Asn Val Lys Glu Lys Ser Met Ile
2255 2260 2265

Leu Ser Asn Val Glu Asp Leu Gln Gln Pro Lys Phe Ile Ser Glu
2270 2275 2280

Val Ser Arg Glu Asp Tyr Gly Lys Lys Glu Ile Ser Gly Asp Ser
2285 2290 2295

Glu Glu Met Asn Ile Asn Ser Val Val Thr Ser Ala Asp Gly Glu
2300 2305 2310

Asn Leu Glu Ile Gln Ser Tyr Ser Leu Ile Gly Glu Lys Leu Val
2315 2320 2325

Met Glu Glu Ala Lys Thr Ile Val Pro Pro His Val Thr Asp Ser
2330 2335 2340

Lys Arg Val Gln Lys Pro Ala Ile Ala Pro Pro Ser Lys Trp Asn
2345 2350 2355

Ile Ser Ile Phe Lys Glu Glu Pro Arg Ser Asp Gln Lys Gln Lys
2360 2365 2370

Ser Leu Leu Ser Phe Asp Val Val Asp Lys Val Pro Gln Gln Pro
2375 2380 2385

Lys Ser Ala Ser Ser Asn Phe Ala Ser Lys Asn Ile Thr Lys Glu
2390 2395 2400

Ser Glu Lys Pro Glu Ser Ile Ile Leu Pro Val Glu Glu Ser Lys
2405 2410 2415

Gly Ser Leu Ile Asp Phe Ser Glu Asp Arg Leu Lys Lys Glu Met
2420 2425 2430

Gln Asn Pro Thr Ser Leu Lys Ile Ser Glu Glu Glu Thr Lys Leu
2435 2440 2445

Arg Ser Val Ser Pro Thr Glu Lys Lys Asp Asn Leu Glu Asn Arg
2450 2455 2460

Ser Tyr Thr Leu Ala Glu Lys Lys Val Leu Ala Glu Lys Gln Asn
2465 2470 2475

Ser Val Ala Pro Leu Glu Leu Arg Asp Ser Asn Glu Ile Gly Lys
2480 2485 2490

Thr Gln Ile Thr Leu Gly Ser Arg Ser Thr Glu Leu Lys Glu Ser
 2495 2500 2505

Lys Ala Asp Ala Met Pro Gln His Phe Tyr Gln Asn Glu Asp Tyr
 2510 2515 2520

Asn Glu Arg Pro Lys Ile Ile Val Gly Ser Glu Lys Glu Lys Gly
 2525 2530 2535

Glu Glu Lys Glu Asn Gln Val Tyr Val Leu Ser Glu Gly Lys Lys
 2540 2545 2550

Gln Gln Glu His Gln Pro Tyr Ser Val Asn Val Ala Glu Ser Met
 2555 2560 2565

Ser Arg Glu Ser Asp Ile Ser Leu Gly His Ser Leu Gly Glu Thr
 2570 2575 2580

Gln Ser Phe Ser Leu Val Lys Ala Thr Ser Val Thr Glu Lys Ser
 2585 2590 2595

Glu Ala Met Leu Ala Glu Ala His Pro Glu Ile Arg Glu Ala Lys
 2600 2605 2610

Ala Val Gly Thr Gln Pro His Pro Leu Glu Glu Ser Lys Val Leu
 2615 2620 2625

Val Glu Lys Thr Lys Thr Phe Leu Pro Val Ala Leu Ser Cys Arg
 2630 2635 2640

Asp Glu Ile Glu Asn His Ser Leu Ser Gln Glu Gly Asn Leu Val
 2645 2650 2655

Leu Glu Lys Ser Ser Arg Asp Met Pro Asp His Ser Glu Glu Lys
 2660 2665 2670

Glu Gln Phe Arg Glu Ser Glu Leu Ser Lys Gly Gly Ser Val Asp

2675	2680	2685
Ile Thr Lys Glu Thr Val Lys	Gln Gly Phe Gln Glu	Lys Ala Val
2690	2695	2700
Gly Thr Gln Pro Arg Pro Leu	Glu Glu Ser Lys Val	Leu Val Glu
2705	2710	2715
Lys Thr Lys Thr Phe Leu Pro	Val Val Leu Ser Cys	His Asp Glu
2720	2725	2730
Ile Glu Asn His Ser Leu Ser	Gln Glu Gly Asn Leu	Val Leu Glu
2735	2740	2745
Lys Ser Ser Arg Asp Met Pro	Asp His Ser Glu Glu	Lys Glu Gln
2750	2755	2760
Phe Lys Glu Ser Glu Leu Trp	Lys Gly Gly Ser Val	Asp Ile Thr
2765	2770	2775
Lys Glu Ser Met Lys Glu Gly	Phe Pro Ser Lys Glu	Ser Glu Arg
2780	2785	2790
Thr Leu Ala Arg Pro Phe Asp	Glu Thr Lys Ser Ser	Glu Thr Pro
2795	2800	2805
Pro Tyr Leu Leu Ser Pro Val	Lys Pro Gln Thr Leu	Ala Ser Gly
2810	2815	2820
Ala Ser Pro Glu Ile Asn Ala	Val Lys Lys Lys Glu	Met Pro Arg
2825	2830	2835
Ser Glu Leu Thr Pro Glu Arg	His Thr Val His Thr	Ile Gln Thr
2840	2845	2850
Ser Lys Asp Asp Thr Ser Asp	Val Pro Lys Gln Ser	Val Leu Val
2855	2860	2865

Ser Lys His His Leu Glu Ala Ala Glu Asp Thr Arg Val Lys Glu
 2870 2875 2880

Pro Leu Ser Ser Ala Lys Ser Asn Tyr Ala Gln Phe Ile Ser Asn
 2885 2890 2895

Thr Ser Ala Ser Asn Ala Asp Lys Met Val Ser Asn Lys Glu Met
 2900 2905 2910

Pro Lys Glu Pro Glu Asp Thr Tyr Ala Lys Gly Glu Asp Phe Thr
 2915 2920 2925

Val Thr Ser Lys Pro Ala Gly Leu Ser Glu Asp Gln Lys Thr Ala
 2930 2935 2940

Phe Ser Ile Ile Ser Glu Gly Cys Glu Ile Leu Asn Ile His Ala
 2945 2950 2955

Pro Ala Phe Ile Ser Ser Ile Asp Gln Glu Glu Ser Glu Gln Met
 2960 2965 2970

Gln Asp Lys Leu Glu Tyr Leu Glu Glu Lys Ala Ser Phe Lys Thr
 2975 2980 2985

Ile Pro Leu Pro Asp Asp Ser Glu Thr Val Ala Cys His Lys Thr
 2990 2995 3000

Leu Lys Ser Arg Leu Glu Asp Glu Lys Val Thr Pro Leu Lys Glu
 3005 3010 3015

Asn Lys Gln Lys Glu Thr His Lys Thr Lys Glu Glu Ile Ser Thr
 3020 3025 3030

Asp Ser Glu Thr Asp Leu Ser Phe Ile Gln Pro Thr Ile Pro Ser
 3035 3040 3045

Glu Glu Asp Tyr Phe Glu Lys Tyr Thr Leu Ile Asp Tyr Asn Ile
 3050 3055 3060

Ser Pro Asp Pro Glu Lys Gln Lys Ala Pro Gln Lys Leu Asn Val
3065 3070 3075

Glu Glu Lys Leu Ser Lys Glu Val Thr Glu Glu Thr Ile Ser Phe
3080 3085 3090

Pro Val Ser Ser Val Glu Ser Ala Leu Glu His Glu Tyr Asp Leu
3095 3100 3105

Val Lys Leu Asp Glu Ser Phe Tyr Gly Pro Glu Lys Gly His Asn
3110 3115 3120

Ile Leu Ser His Pro Glu Thr Gln Ser Gln Asn Ser Ala Asp Arg
3125 3130 3135

Asn Val Ser Lys Asp Thr Lys Arg Asp Val Asp Ser Lys Ser Pro
3140 3145 3150

Gly Met Pro Leu Phe Glu Ala Glu Glu Gly Val Leu Ser Arg Thr
3155 3160 3165

Gln Ile Phe Pro Thr Thr Ile Lys Val Ile Asp Pro Glu Phe Leu
3170 3175 3180

Glu Glu Pro Pro Ala Leu Ala Phe Leu Tyr Lys Asp Leu Tyr Glu
3185 3190 3195

Glu Ala Val Gly Glu Lys Lys Lys Glu Glu Glu Thr Ala Ser Glu
3200 3205 3210

Gly Asp Ser Val Asn Ser Glu Ala Ser Phe Pro Ser Arg Asn Ser
3215 3220 3225

Asp Thr Asp Asp Gly Thr Gly Ile Tyr Phe Glu Lys Tyr Ile Leu
3230 3235 3240

Lys Asp Asp Ile Leu His Asp Thr Ser Leu Thr Gln Lys Asp Gln
3245 3250 3255

Gly Gln Gly Leu Glu Glu Lys Arg Val Gly Lys Asp Asp Ser Tyr
3260 3265 3270

Gln Pro Ile Ala Ala Glu Gly Glu Ile Trp Gly Lys Phe Gly Thr
3275 3280 3285

Ile Cys Arg Glu Lys Ser Leu Glu Glu Gln Lys Gly Val Tyr Gly
3290 3295 3300

Glu Gly Glu Ser Val Asp His Val Glu Thr Val Gly Asn Val Ala
3305 3310 3315

Met Gln Lys Lys Ala Pro Ile Thr Glu Asp Val Arg Val Ala Thr
3320 3325 3330

Gln Lys Ile Ser Tyr Ala Val Pro Phe Glu Asp Thr His His Val
3335 3340 3345

Leu Glu Arg Ala Asp Glu Ala Gly Ser His Gly Asn Glu Val Gly
3350 3355 3360

Asn Ala Ser Pro Glu Val Asn Leu Asn Val Pro Val Gln Val Ser
3365 3370 3375

Phe Pro Glu Glu Glu Phe Ala Ser Gly Ala Thr His Val Gln Glu
3380 3385 3390

Thr Ser Leu Glu Glu Pro Lys Ile Leu Val Pro Pro Glu Pro Ser
3395 3400 3405

Glu Glu Arg Leu Arg Asn Ser Pro Val Gln Asp Glu Tyr Glu Phe
3410 3415 3420

Thr Glu Ser Leu His Asn Glu Val Val Pro Gln Asp Ile Leu Ser
3425 3430 3435

Glu Glu Leu Ser Ser Glu Ser Thr Pro Glu Asp Val Leu Ser Gln

3440	3445	3450
Gly Lys	Glu Ser Phe Glu His	Ile Ser Glu Asn Glu Phe Ala Ser
3455	3460	3465
Glu Ala	Glu Gln Ser Thr Pro	Ala Glu Gln Lys Glu Leu Gly Ser
3470	3475	3480
Glu Arg	Lys Glu Glu Asp Gln	Leu Ser Ser Glu Val Val Thr Glu
3485	3490	3495
Lys Ala	Gln Lys Glu Leu Lys	Lys Ser Gln Ile Asp Thr Tyr Cys
3500	3505	3510
Tyr Thr	Cys Lys Cys Pro Ile	Ser Ala Thr Asp Lys Val Phe Gly
3515	3520	3525
Thr His	Lys Asp His Glu Val	Ser Thr Leu Asp Thr Ala Ile Ser
3530	3535	3540
Ala Val	Lys Val Gln Leu Ala	Glu Phe Leu Glu Asn Leu Gln Glu
3545	3550	3555
Lys Ser	Leu Arg Ile Glu Ala	Phe Val Ser Glu Ile Glu Ser Phe
3560	3565	3570
Phe Asn	Thr Ile Glu Glu Asn	Cys Ser Lys Asn Glu Lys Arg Leu
3575	3580	3585
Glu Glu	Gln Asn Glu Glu Met	Met Lys Lys Val Leu Ala Gln Tyr
3590	3595	3600
Asp Glu	Lys Ala Gln Ser Phe	Glu Glu Val Lys Lys Lys Lys Met
3605	3610	3615
Glu Phe	Leu His Glu Gln Met	Val His Phe Leu Gln Ser Met Asp
3620	3625	3630

Thr Ala	Lys Asp Thr Leu Glu	Thr Ile Val Arg Glu	Ala Glu Glu
3635	3640	3645	
Leu Asp	Glu Ala Val Phe Leu	Thr Ser Phe Glu Glu	Ile Asn Glu
3650	3655	3660	
Arg Leu	Leu Ser Ala Met Glu	Ser Thr Ala Ser Leu	Glu Lys Met
3665	3670	3675	
Pro Ala	Ala Phe Ser Leu Phe	Glu His Tyr Asp Asp	Ser Ser Ala
3680	3685	3690	
Arg Ser	Asp Gln Met Leu Lys	Gln Val Ala Val Pro	Gln Pro Pro
3695	3700	3705	
Arg Leu	Glu Pro Gln Glu Pro	Asn Ser Ala Thr Ser	Thr Thr Ile
3710	3715	3720	
Ala Val	Tyr Trp Ser Met Asn	Lys Glu Asp Val Ile	Asp Ser Phe
3725	3730	3735	
Gln Val	Tyr Cys Met Glu Glu	Pro Gln Asp Asp Gln	Glu Val Asn
3740	3745	3750	
Glu Leu	Val Glu Glu Tyr Arg	Leu Thr Val Lys Glu	Ser Tyr Cys
3755	3760	3765	
Ile Phe	Glu Asp Leu Glu Pro	Asp Arg Cys Tyr Gln	Val Trp Val
3770	3775	3780	
Met Ala	Val Asn Phe Thr Gly	Cys Ser Leu Pro Ser	Glu Arg Ala
3785	3790	3795	
Ile Phe	Arg Thr Ala Pro Ser	Thr Pro Val Ile Arg	Ala Glu Asp
3800	3805	3810	
Cys Thr	Val Cys Trp Asn Thr	Ala Thr Ile Arg Trp	Arg Pro Thr
3815	3820	3825	

Thr Pro Glu Ala Thr Glu Thr Tyr Thr Leu Glu Tyr Cys Arg Gln
 3830 3835 3840

His Ser Pro Glu Gly Glu Gly Leu Arg Ser Phe Ser Gly Ile Lys
 3845 3850 3855

Gly Leu Gln Leu Lys Val Asn Leu Gln Pro Asn Asp Asn Tyr Phe
 3860 3865 3870

Phe Tyr Val Arg Ala Ile Asn Ala Phe Gly Thr Ser Glu Gln Ser
 3875 3880 3885

Glu Ala Ala Leu Ile Ser Thr Arg Gly Thr Arg Phe Leu Leu Leu
 3890 3895 3900

Arg Glu Thr Ala His Pro Ala Leu His Ile Ser Ser Ser Gly Thr
 3905 3910 3915

Val Ile Ser Phe Gly Glu Arg Arg Arg Leu Thr Glu Ile Pro Ser
 3920 3925 3930

Val Leu Gly Glu Glu Leu Pro Ser Cys Gly Gln His Tyr Trp Glu
 3935 3940 3945

Thr Thr Val Thr Asp Cys Pro Ala Tyr Arg Leu Gly Ile Cys Ser
 3950 3955 3960

Ser Ser Ala Val Gln Ala Gly Ala Leu Gly Gln Gly Glu Thr Ser
 3965 3970 3975

Trp Tyr Met His Cys Ser Glu Pro Gln Arg Tyr Thr Phe Phe Tyr
 3980 3985 3990

Ser Gly Ile Val Ser Asp Val His Val Thr Glu Arg Pro Ala Arg
 3995 4000 4005

Val Gly Ile Leu Leu Asp Tyr Asn Asn Gln Arg Leu Ile Phe Ile
 4010 4015 4020

Asn Ala Glu Ser Glu Gln Leu Leu Phe Ile Ile Arg His Arg Phe
 4025 4030 4035

Asn Glu Gly Val His Pro Ala Phe Ala Leu Glu Lys Pro Gly Lys
 4040 4045 4050

Cys Thr Leu His Leu Gly Ile Glu Pro Pro Asp Ser Val Arg His
 4055 4060 4065

Lys

<210> 166
 <211> 1350
 <212> DNA
 <213> Homo sapiens

<400> 166
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 tatttgacag accctgtcac catttgttgt gggcacagat ttgtagtcct ctgtctctgc 120
 ctcttgtagg aagatacact aactcctaatt tgctgccctg tgtgcaggga aatatcacag 180
 caaatgtact tcaaacgcat tatttttgct gagaaacaag ttattcctac aagagaatca 240
 gtccctgcc agttatcaag ctctgccatg ctgatctgta ggagacacca ggaaatcaag 300
 aacctcatct gtgaaactga taggagcctg ctgtgttttc tatgctctca atcccaagg 360
 catgctactc acaaacacta tatgacaagg gaggctgatg aatactatag gaagaaactc 420
 ctgattcaaa tgaagtccat ctggaaaaaa aaacagaaaa atcaaagaaa tctaaacaga 480
 gagaccaaca taatcggaac atgggaagtt ttataaatt tgcggagcat gatgatcagt 540
 gctgaatatc ctaaggtgtg tcaatacctc cgtgaagaag agcaaaagca cgtagagagc 600
 ctggcaagag aaggcaggat aatttttcag caactcaaga gaagtcaaac tagaatggct 660
 aagatgggta tactcctgag agaaatgtat gagaaactga aggaaatgag ctgtaaagca 720
 gatgtgaacc tgcctcagga ttggggagac gtaatgaaaa ggaatgagtt tctgaggctg 780
 gccatgctc agcctgtgaa cccacagctc agtgcagtgga ccatcactgg ggtgtcagaa 840

aggcttaact tcttcagagt gtatatcacc ttggatcgta agatatgcag taatcacaag 900
 cttctgttcg aagacctaag gcatttcgag tgcagccttg atgatacaga catgtcctgt 960
 aatccaacaa gtacacagta tacttctca tggggagctc agatcctcag ctctggcaaa 1020
 cattactggg aggtggatgt gaaagactct tgtaattggg ttataggact ttgcagagaa 1080
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 ctcaaagtg atgaccattt cagtctcttc tctacctccc cactgttacc tcactatatt 1200
 ccaaggcccc aaggctggct aggggtgttc ctggattatg aatgtgggat agtgagcttt 1260
 gttaatgttg cccaaagttc cctcattgt agtttcctct cacgcatctt ctatttcct 1320
 ctcacacctt tcatttgcca cggatctaaa 1350

<210> 167
 <211> 450
 <212> PRT
 <213> Homo sapiens

<400> 167

Met Ala Ser Ala Ile Thr Gln Cys Ser Thr Ser Glu Leu Thr Cys Ser
 1 5 10 15

Ile Cys Thr Asp Tyr Leu Thr Asp Pro Val Thr Ile Cys Cys Gly His
 20 25 30

Arg Phe Cys Ser Pro Cys Leu Cys Leu Trp Glu Asp Thr Leu Thr
 35 40 45

Pro Asn Cys Cys Pro Val Cys Arg Glu Ile Ser Gln Gln Met Tyr Phe
 50 55 60

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

Val Pro Cys Gln Leu Ser Ser Ser Ala Met Leu Ile Cys Arg Arg His
 85 90 95

Gln Glu Ile Lys Asn Leu Ile Cys Glu Thr Asp Arg Ser Leu Leu Cys
100 105 110

Phe Leu Cys Ser Gln Ser Pro Arg His Ala Thr His Lys His Tyr Met
115 120 125

Thr Arg Glu Ala Asp Glu Tyr Tyr Arg Lys Lys Leu Leu Ile Gln Met
130 135 140

Lys Ser Ile Trp Lys Lys Lys Gln Lys Asn Gln Arg Asn Leu Asn Arg
145 150 155 160

Glu Thr Asn Ile Ile Gly Thr Trp Glu Val Phe Ile Asn Leu Arg Ser
165 170 175

Met Met Ile Ser Ala Glu Tyr Pro Lys Val Cys Gln Tyr Leu Arg Glu
180 185 190

Glu Glu Gln Lys His Val Glu Ser Leu Ala Arg Glu Gly Arg Ile Ile
195 200 205

Phe Gln Gln Leu Lys Arg Ser Gln Thr Arg Met Ala Lys Met Gly Ile
210 215 220

Leu Leu Arg Glu Met Tyr Glu Lys Leu Lys Glu Met Ser Cys Lys Ala
225 230 235 240

Asp Val Asn Leu Pro Gln Asp Leu Gly Asp Val Met Lys Arg Asn Glu
245 250 255

Phe Leu Arg Leu Ala Met Pro Gln Pro Val Asn Pro Gln Leu Ser Ala
260 265 270

Trp Thr Ile Thr Gly Val Ser Glu Arg Leu Asn Phe Phe Arg Val Tyr
275 280 285

Ile Thr Leu Asp Arg Lys Ile Cys Ser Asn His Lys Leu Leu Phe Glu
290 295 300

Asp Leu Arg His Leu Gln Cys Ser Leu Asp Asp Thr Asp Met Ser Cys
305 310 315 320

Asn Pro Thr Ser Thr Gln Tyr Thr Ser Ser Trp Gly Ala Gln Ile Leu
 325 330 335

Ser Ser Gly Lys His Tyr Trp Glu Val Asp Val Lys Asp Ser Cys Asn
 340 345 350

Trp Val Ile Gly Leu Cys Arg Glu Ala Trp Thr Lys Arg Asn Asp Met
 355 360 365

Arg Leu Asp Ser Glu Gly Ile Phe Leu Leu Leu Cys Leu Lys Val Asp
 370 375 380

Asp His Phe Ser Leu Phe Ser Thr Ser Pro Leu Leu Pro His Tyr Ile
385 390 395 400

Pro Arg Pro Gln Gly Trp Leu Gly Val Phe Leu Asp Tyr Glu Cys Gly
 405 410 415

Ile Val Ser Phe Val Asn Val Ala Gln Ser Ser Leu Ile Cys Ser Phe
 420 425 430

Leu Ser Arg Ile Phe Tyr Phe Pro Leu Arg Pro Phe Ile Cys His Gly
 435 440 445

Ser Lys
450

<210> 168
<211> 68
<212> PRT
<213> Artificial Sequence

<220>
<223> Leader Sequence

<220>

<221> MISC_FEATURE
<222> (5)..(11)
<223> 6His Tag

<220>
<221> MISC_FEATURE
<222> (40)..(51)
<223> TAT peptide

<220>
<221> MISC_FEATURE
<222> (58)..(67)
<223> HA tag

<400> 168

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Arg Trp Gly Ser Lys Leu Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg
35 40 45

Arg Arg Gly Gly Ser Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp
50 55 60

Tyr Ala Gly Ser
65

<210> 169
<211> 536
<212> PRT
<213> Artificial Sequence

<220>
<223> Leader sequence and TRIM11

<400> 169

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp

20 25 30
 Arg Trp Gly Ser Lys Leu Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg
 35 40 45
 Arg Arg Gly Gly Ser Thr Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp
 50 55 60
 Tyr Ala Gly Ser Met Ala Ala Pro Asp Leu Ser Thr Asn Leu Gln Glu
 65 70 75 80
 Glu Ala Thr Cys Ala Ile Cys Leu Asp Tyr Phe Thr Asp Pro Val Met
 85 90 95
 Thr Asp Cys Gly His Asn Phe Cys Arg Glu Cys Ile Arg Arg Cys Trp
 100 105 110
 Gly Gln Pro Glu Gly Pro Tyr Ala Cys Pro Glu Cys Arg Glu Leu Ser
 115 120 125
 Pro Gln Arg Asn Leu Arg Pro Asn Arg Pro Leu Ala Lys Met Ala Glu
 130 135 140
 Met Ala Arg Arg Leu His Pro Pro Ser Pro Val Pro Gln Gly Val Cys
 145 150 155 160
 Pro Ala His Arg Glu Pro Leu Ala Ala Phe Cys Gly Asp Glu Leu Arg
 165 170 175
 Leu Leu Cys Ala Ala Cys Glu Arg Ser Gly Glu His Trp Ala His Arg
 180 185 190
 Val Arg Pro Leu Gln Asp Ala Ala Glu Asp Leu Lys Ala Lys Leu Glu
 195 200 205
 Lys Ser Leu Glu His Leu Arg Lys Gln Met Gln Asp Ala Leu Leu Phe
 210 215 220

Gln Ala Gln Ala Asp Glu Thr Cys Val Leu Trp Gln Lys Met Val Glu
225 230 235 240

Ser Gln Arg Gln Asn Val Leu Gly Glu Phe Glu Arg Leu Arg Arg Leu
 245 250 255

Leu Ala Glu Glu Glu Gln Gln Leu Leu Gln Arg Leu Glu Glu Glu Glu
 260 265 270

Leu Glu Val Leu Pro Arg Leu Arg Glu Gly Ala Ala His Leu Gly Gln
 275 280 285

Gln Ser Ala His Leu Ala Glu Leu Ile Ala Glu Leu Glu Gly Arg Cys
 290 295 300

Gln Leu Pro Ala Leu Gly Leu Leu Gln Asp Ile Lys Asp Ala Leu Arg
305 310 315 320

Arg Val Gln Asp Val Lys Leu Gln Pro Pro Glu Val Val Pro Met Glu
 325 330 335

Leu Arg Thr Val Cys Arg Val Pro Gly Leu Val Glu Thr Leu Arg Arg
 340 345 350

Phe Arg Gly Asp Val Thr Leu Asp Pro Asp Thr Ala Asn Pro Glu Leu
 355 360 365

Ile Leu Ser Glu Asp Arg Arg Ser Val Gln Arg Gly Asp Leu Arg Gln
 370 375 380

Ala Leu Pro Asp Ser Pro Glu Arg Phe Asp Pro Gly Pro Cys Val Leu
385 390 395 400

Gly Gln Glu Arg Phe Thr Ser Gly Arg His Tyr Trp Glu Val Glu Val
 405 410 415

Gly Asp Arg Thr Ser Trp Ala Leu Gly Val Cys Arg Glu Asn Val Asn
 420 425 430

Arg Lys Glu Lys Gly Glu Leu Ser Ala Gly Asn Gly Phe Trp Ile Leu
435 440 445

Val Phe Leu Gly Ser Tyr Tyr Asn Ser Ser Glu Arg Ala Leu Ala Pro
450 455 460

Leu Arg Asp Pro Pro Arg Arg Val Gly Ile Phe Leu Asp Tyr Glu Ala
465 470 475 480

Gly His Leu Ser Phe Tyr Ser Ala Thr Asp Gly Ser Leu Leu Phe Ile
485 490 495

Phe Pro Glu Ile Pro Phe Ser Gly Thr Leu Arg Pro Leu Phe Ser Pro
500 505 510

Leu Ser Ser Ser Pro Thr Pro Met Thr Ile Cys Arg Pro Lys Gly Gly
515 520 525

Ser Gly Asp Thr Leu Ala Pro Gln
530 535