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 35 40 45

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

Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
 65 70 75 80

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

115 120 125
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 Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
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 Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
 165 170 175
 Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
 180 185 190
 Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
 195 200 205
 Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
 210 215 220
 Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
 225 230 235 240
 Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
 245 250 255
 Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
 260 265 270
 Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
 275 280 285
 Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
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 Gly Leu Pro Tyr Leu Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr
 305 310 315 320
 Asp Lys Glu Ile Glu Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp
 325 330 335
 Ala Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe
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 His Ser Ala Trp Leu Thr Val Leu Pro Ala Pro Gly Arg Glu Lys Glu
 355 360 365
 Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly
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 Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met
 385 390 395 400

Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His
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Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala
420 425 430

Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr
435 440 445

Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser
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Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys
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485 490 495

Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val
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Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu
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Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu
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Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu
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Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg
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Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr
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Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His
610 615 620

Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met
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Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr
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Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro
660 665 670

Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser
675 680 685

Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr
690 695 700

Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His
705 710 715 720

Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met
725 730 735

Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln
740 745 750

Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu
755 760 765

Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro
770 775 780

Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro
785 790 795 800

Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn
805 810 815

Gly Ser Val Lys Thr
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tccggagatg atgaggatga caccgatggt gcggaagatt ttgtcagtga gaacagtaac 180
aacaagagag caccatactg gaccaacaca gaaaagatgg aaaagcggct ccatgctgtg 240
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cgaaaccagc actggagcct cattatggaa agtgtggtcc catctgacaa gggaaattat 420
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25

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Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu Asp Asp Thr
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Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn Lys Arg Ala
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Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg Leu His Ala Val
 65 70 75 80

Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala Gly Gly Asn Pro
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Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu Phe Lys Gln Glu
 100 105 110

His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His Trp Ser Leu Ile
 115 120 125

Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr Thr Cys Val Val
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Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His Leu Asp Val Val
 145 150 155 160

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

Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val Cys Lys Val Tyr
 180 185 190

Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His Val Glu Lys Asn
 195 200 205

Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro Tyr Leu Lys Val Leu Lys
 210 215 220

Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu Val Leu Tyr Ile
 225 230 235 240

Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr Cys Leu Ala Gly
 245 250 255

Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu Thr Val Leu Pro
 260 265 270

Ala Pro Gly Arg Glu Lys Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu
 275 280 285

Ile Ala Ile Tyr Cys Ile Gly Val Phe Leu Ile Ala Cys Met Val Val
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Thr Val Ile Leu Cys Arg Met Lys Asn Thr Thr Lys Lys Pro Asp Phe
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Ser Ser Gln Pro Ala Val His Lys Leu Thr Lys Arg Ile Pro Leu Arg
325 330 335

Arg Gln Val Thr Val Ser Ala Glu Ser Ser Ser Ser Met Asn Ser Asn
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Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr
355 360 365

Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys
370 375 380

Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu
385 390 395 400

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

Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val Lys Met Leu Lys Asp
420 425 430

Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu Met
435 440 445

Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly Ala
450 455 460

Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys
465 470 475 480

Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg Pro Pro Gly Met Glu
485 490 495

Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu Gln Met Thr Phe Lys
500 505 510

Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu
515 520 525

Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu
530 535 540

Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg
545 550 555 560

Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu
565 570 575

Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr
580 585 590

His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Met Trp Glu Ile Phe
595 600 605

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

Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn Cys Thr
625 630 635 640

Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp His Ala Val Pro Ser
645 650 655

Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Ile Leu
660 665 670

Thr Leu Thr Thr Asn Glu Glu Glu Lys Lys Val Ser Gly Ala Val Asp
675 680 685

Cys His Lys Pro Pro Cys Asn Pro Ser His Leu Pro Cys Val Leu Ala
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Val Asp Gln
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<400> 27

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 35 40 45
 Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
 50 55 60
 Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
 65 70 75 80
 Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
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 Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
 100 105 110
 Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
 115 120 125
 Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
 130 135 140
 Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
 145 150 155 160
 Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
 165 170 175
 Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
 180 185 190
 Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
 195 200 205
 Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
 210 215 220
 Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
 225 230 235 240
 Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
 245 250 255
 Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
 260 265 270
 Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
 275 280 285
 Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
 290 295 300

Gly Leu Pro Tyr Leu Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr
305 310 315 320

Asp Lys Glu Ile Glu Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp
325 330 335

Ala Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe
340 345 350

His Ser Ala Trp Leu Thr Val Leu Pro Ala Pro Gly Arg Glu Lys Glu
355 360 365

Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly
370 375 380

Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met
385 390 395 400

Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His
405 410 415

Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Ser Ala Glu Ser
420 425 430

Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg
435 440 445

Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu Tyr
450 455 460

Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr
465 470 475 480

Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala
485 490 495

Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val
500 505 510

Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp
515 520 525

Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn
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Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val
545 550 555 560

Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala
565 570 575

Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro
Page 34

580

585

590

Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu
595 600 605

Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp
610 615 620

Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys Ile
625 630 635 640

Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys
645 650 655

Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala
660 665 670

Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly
675 680 685

Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly
690 695 700

Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met
705 710 715 720

Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp
725 730 735

Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val
740 745 750

Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr Leu
755 760 765

Asp Leu Ser Gln Pro Leu Glu Pro Tyr Ser Pro Cys Tyr Pro Asp Pro
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Arg
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 <211> 1066
 <212> PRT
 <213> Homo sapiens

<400> 33

Met Pro Val Phe His Thr Arg Thr Ile Glu Ser Ile Leu Glu Pro Val
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Ala Gln Gln Ile Ser His Leu Val Ile Met His Glu Glu Gly Glu Val
20 25 30

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

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

Thr Glu Asp Gln Ile Leu Lys Arg Asp Met Pro Pro Ala Phe Ile Lys
65 70 75 80

Val Glu Asn Ala Cys Thr Lys Leu Val Gln Ala Ala Gln Met Leu Gln
85 90 95

Ser Asp Pro Tyr Ser Val Pro Ala Arg Asp Tyr Leu Ile Asp Gly Ser
100 105 110

Arg Gly Ile Leu Ser Gly Thr Ser Asp Leu Leu Leu Thr Phe Asp Glu
115 120 125

Ala Glu Val Arg Lys Ile Ile Arg Val Cys Lys Gly Ile Leu Glu Tyr
130 135 140

Leu Thr Val Ala Glu Val Val Glu Thr Met Glu Asp Leu Val Thr Tyr
145 150 155 160

Thr Lys Asn Leu Gly Pro Gly Met Thr Lys Met Ala Lys Met Ile Asp
165 170 175

Glu Arg Gln Gln Glu Leu Thr His Gln Glu His Arg Val Met Leu Val
180 185 190

Asn Ser Met Asn Thr Val Lys Glu Leu Leu Pro Val Leu Ile Ser Ala
195 200 205

Met Lys Ile Phe Val Thr Thr Lys Asn Ser Lys Asn Gln Gly Ile Glu
210 215 220

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

Ile Asn Glu Ile Ile Arg Val Leu Gln Leu Thr Ser Trp Asp Glu Asp
245 250 255

Ala Trp Ala Ser Lys Asp Thr Glu Ala Met Lys Arg Ala Leu Ala Ser
260 265 270

Ile Asp Ser Lys Leu Asn Gln Ala Lys Gly Trp Leu Arg Asp Pro Ser
275 280 285

Ala Ser Pro Gly Asp Ala Gly Glu Gln Ala Ile Arg Gln Ile Leu Asp
290 295 300

Glu Ala Gly Lys Val Gly Glu Leu Cys Ala Gly Lys Glu Arg Arg Glu
305 310 315 320

Ile Leu Gly Thr Cys Lys Met Leu Gly Gln Met Thr Asp Gln Val Ala
325 330 335

Asp Leu Arg Ala Arg Gly Gln Gly Ser Ser Pro Val Ala Met Gln Lys
340 345 350

Ala Gln Gln Val Ser Gln Gly Leu Asp Val Leu Thr Ala Lys Val Glu
355 360 365

Asn Ala Ala Arg Lys Leu Glu Ala Met Thr Asn Ser Lys Gln Ser Ile
370 375 380

Ala Lys Lys Ile Asp Ala Ala Gln Asn Trp Leu Ala Asp Pro Asn Gly
385 390 395 400

Gly Pro Glu Gly Glu Glu Gln Ile Arg Gly Ala Leu Ala Glu Ala Arg
405 410 415

Lys Ile Ala Glu Leu Cys Asp Asp Pro Lys Glu Arg Asp Asp Ile Leu
420 425 430

Arg Ser Leu Gly Glu Ile Ser Ala Leu Thr Ser Lys Leu Ala Asp Leu
435 440 445

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

Gln Val Ala Thr Ala Leu Gln Asn Leu Gln Thr Lys Thr Asn Arg Ala
465 470 475 480

Val Ala Asn Ser Arg Pro Ala Lys Ala Ala Val His Leu Glu Gly Lys
485 490 495

Ile Glu Gln Ala Gln Arg Trp Ile Asp Asn Pro Thr Val Asp Asp Arg
500 505 510

Gly Val Gly Gln Ala Ala Ile Arg Gly Leu Val Ala Glu Gly His Arg
515 520 525

Leu Ala Asn Val Met Met Gly Pro Tyr Arg Gln Asp Leu Leu Ala Lys
530 535 540

Cys Asp Arg Val Asp Gln Leu Thr Ala Gln Leu Ala Asp Leu Ala Ala
545 550 555 560

Arg Gly Glu Gly Glu Ser Pro Gln Ala Arg Ala Leu Ala Ser Gln Leu
565 570 575

Gln Asp Ser Leu Lys Asp Leu Lys Ala Arg Met Gln Glu Ala Met Thr
580 585 590

Gln Glu Val Ser Asp Val Phe Ser Asp Thr Thr Thr Pro Ile Lys Leu
595 600 605

Leu Ala Val Ala Ala Thr Ala Pro Pro Asp Ala Pro Asn Arg Glu Glu
610 615 620

Val Phe Asp Glu Arg Ala Ala Asn Phe Glu Asn His Ser Gly Lys Leu
625 630 635 640

Gly Ala Thr Ala Glu Lys Ala Ala Ala Val Gly Thr Ala Asn Lys Ser
645 650 655

Thr Val Glu Gly Ile Gln Ala Ser Val Lys Thr Ala Arg Glu Leu Thr
660 665 670

Pro Gln Val Val Ser Ala Ala Arg Ile Leu Leu Arg Asn Pro Gly Asn
Page 49

675 680 685
 Gln Ala Ala Tyr Glu His Phe Glu Thr Met Lys Asn Gln Trp Ile Asp
 690 695 700
 Asn Val Glu Lys Met Thr Gly Leu Val Asp Glu Ala Ile Asp Thr Lys
 705 710 715 720
 Ser Leu Leu Asp Ala Ser Glu Glu Ala Ile Lys Lys Asp Leu Asp Lys
 725 730 735
 Cys Lys Val Ala Met Ala Asn Ile Gln Pro Gln Met Leu Val Ala Gly
 740 745 750
 Ala Thr Ser Ile Ala Arg Arg Ala Asn Arg Ile Leu Leu Val Ala Lys
 755 760 765
 Arg Glu Val Glu Asn Ser Glu Asp Pro Lys Phe Arg Glu Ala Val Lys
 770 775 780
 Ala Ala Ser Asp Glu Leu Ser Lys Thr Ile Ser Pro Met Val Met Asp
 785 790 795 800
 Ala Lys Ala Val Ala Gly Asn Ile Ser Asp Pro Gly Leu Gln Lys Ser
 805 810 815
 Phe Leu Asp Ser Gly Tyr Arg Ile Leu Gly Ala Val Ala Lys Val Arg
 820 825 830
 Glu Ala Phe Gln Pro Gln Glu Pro Asp Phe Pro Pro Pro Pro Pro Asp
 835 840 845
 Leu Glu Gln Leu Arg Leu Thr Asp Glu Leu Ala Pro Pro Lys Pro Pro
 850 855 860
 Leu Pro Glu Gly Glu Val Pro Pro Pro Arg Pro Pro Pro Pro Glu Glu
 865 870 875 880
 Lys Asp Glu Glu Phe Pro Glu Gln Lys Ala Gly Glu Val Ile Asn Gln
 885 890 895
 Pro Met Met Met Ala Ala Arg Gln Leu His Asp Glu Ala Arg Lys Trp
 900 905 910
 Ser Ser Lys Gly Asn Asp Ile Ile Ala Ala Ala Lys Arg Met Ala Leu
 915 920 925
 Leu Met Ala Glu Met Ser Arg Leu Val Arg Gly Gly Ser Gly Thr Lys
 930 935 940
 Arg Ala Leu Ile Gln Cys Ala Lys Asp Ile Ala Lys Ala Ser Asp Glu
 945 950 955 960

Val Thr Arg Leu Ala Lys Glu Val Ala Lys Gln Cys Thr Asp Lys Arg
 965 970 975

Ile Arg Thr Asn Leu Leu Gln Val Cys Glu Arg Ile Pro Thr Ile Ser
 980 985 990

Thr Gln Leu Lys Ile Leu Ser Thr Val Lys Ala Thr Met Leu Gly Arg
 995 1000 1005

Thr Asn Ile Ser Asp Glu Glu Ser Glu Gln Ala Thr Glu Met Leu
 1010 1015 1020

Val His Asn Ala Gln Asn Leu Met Gln Ser Val Lys Glu Thr Val
 1025 1030 1035

Arg Glu Ala Glu Ala Ala Ser Ile Lys Ile Arg Thr Asp Ala Gly
 1040 1045 1050

Phe Thr Leu Arg Trp Val Arg Lys Thr Pro Trp Tyr Gln
 1055 1060 1065

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 <211> 984
 <212> DNA
 <213> Homo sapiens

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 accgcgcccc tggccgccgt gcaggcggcc gtcagcaacc tcgtccgggt tggaaaagag 180
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 gttgagaatg cttgcaccaa gcttgtccag gcagctcaga tgcttcagtc agacccttac 300
 tcagtgcctg ctcgagatta tctaattgat gggtaaggg gcataccttc tggaacatca 360
 gacctgctcc ttaccttcga tgaggctgag gtccctccac ctaggcctcc accaccagag 420
 gaaaaggatg aagagttccc tgagcagaag gccggggagg tgattaacca gccaatgatg 480
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<210> 35
 <211> 327
 <212> PRT
 <213> Homo sapiens

<400> 35

Met Pro Val Phe His Thr Arg Thr Ile Glu Ser Ile Leu Glu Pro Val
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Ala Gln Gln Ile Ser His Leu Val Ile Met His Glu Glu Gly Glu Val
 20 25 30

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

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

Thr Glu Asp Gln Ile Leu Lys Arg Asp Met Pro Pro Ala Phe Ile Lys
 65 70 75 80

Val Glu Asn Ala Cys Thr Lys Leu Val Gln Ala Ala Gln Met Leu Gln
 85 90 95

Ser Asp Pro Tyr Ser Val Pro Ala Arg Asp Tyr Leu Ile Asp Gly Ser
 100 105 110

Arg Gly Ile Leu Ser Gly Thr Ser Asp Leu Leu Leu Thr Phe Asp Glu
 115 120 125

Ala Glu Val Pro Pro Pro Arg Pro Pro Pro Pro Glu Glu Lys Asp Glu
 130 135 140

Glu Phe Pro Glu Gln Lys Ala Gly Glu Val Ile Asn Gln Pro Met Met
 145 150 155 160

Met Ala Ala Arg Gln Leu His Asp Glu Ala Arg Lys Trp Ser Ser Lys
 165 170 175

Gly Asn Asp Ile Ile Ala Ala Ala Lys Arg Met Ala Leu Leu Met Ala
 180 185 190

Glu Met Ser Arg Leu Val Arg Gly Gly Ser Gly Thr Lys Arg Ala Leu
 195 200 205

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

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

Asn Leu Leu Gln Val Cys Glu Arg Ile Pro Thr Ile Ser Thr Gln Leu
245 250 255

Lys Ile Leu Ser Thr Val Lys Ala Thr Met Leu Gly Arg Thr Asn Ile
260 265 270

Ser Asp Glu Glu Ser Glu Gln Ala Thr Glu Met Leu Val His Asn Ala
275 280 285

Gln Asn Leu Met Gln Ser Val Lys Glu Thr Val Arg Glu Ala Glu Ala
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Ala Ser Ile Lys Ile Arg Thr Asp Ala Gly Phe Thr Leu Arg Trp Val
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Arg Lys Thr Pro Trp Tyr Gln
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<212> DNA
<213> Homo sapiens

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attgaatatg agaggcttca tgctgtcatg aaaaagtctt atgacaatga aaagcgtctg 180
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tcaatggacc agcatagcaa catccgagat ttactgaggt tcaaagaaga agtgacaaag 480
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gaacagcagc aggaacaga gcgatcaaaa gaggaggctg aacatgccat cagtcagttc 600
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gccctgcagc agtatgtgca gaagagcaag gaggagcttc agaagctgga gcagcagctg 780
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 <212> PRT
 <213> Homo sapiens

<400> 37

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Asp Lys Ser Leu Glu Lys Phe Arg Ile Glu Tyr Glu Arg Leu His Ala
 35 40 45

Val Met Lys Lys Ser Tyr Asp Asn Glu Lys Arg Leu Met Ala Lys Cys
50 55 60

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

Ala Leu Lys Leu Ser Gln Asp Asp Gln Thr Thr Ile Ala Ser Leu Lys
85 90 95

Lys Glu Ile Glu Lys Ala Trp Lys Met Val Asp Ser Ala Tyr Asp Lys
100 105 110

Glu Gln Lys Ala Lys Glu Thr Ile Leu Ala Leu Lys Glu Glu Ile Val
115 120 125

Asn Leu Thr Lys Leu Val Glu Gln Gly Ser Gly Leu Ser Met Asp Gln
130 135 140

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

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

Ala Gln Thr Thr Glu Gln Gln Gln Glu Thr Glu Arg Ser Lys Glu Glu
180 185 190

Ala Glu His Ala Ile Ser Gln Phe Gln Gln Glu Ile Gln Gln Arg Gln
195 200 205

Asn Glu Ala Ser Arg Glu Phe Arg Lys Lys Glu Lys Leu Glu Lys Glu
210 215 220

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

Ala Leu Gln Gln Tyr Val Gln Lys Ser Lys Glu Glu Leu Gln Lys Leu
245 250 255

Glu Gln Gln Leu Lys Glu Gln Lys Ile Leu Asn Glu Arg Ala Ala Lys
260 265 270

Glu Leu Glu Gln Phe Gln Met Arg Asn Ala Lys Leu Gln Gln Glu Asn
275 280 285

Glu Gln His Ser Leu Val Cys Glu Gln Leu Ser Gln Glu Asn Gln Gln
290 295 300

Lys Ala Leu Glu Leu Lys Ala Lys Glu Glu Glu Val His Gln Met Arg
305 310 315 320

Leu Asp Ile Gly Lys Leu Asn Lys Ile Arg Glu Gln Ile His Lys Lys

325 330 335
 Leu His His Thr Glu Asp Gln Lys Ala Glu Val Glu Gln His Lys Glu
 340 345 350
 Thr Leu Lys Asn Gln Ile Val Gly Leu Glu Arg Glu Val Glu Ala Ser
 355 360 365
 Lys Lys Gln Ala Glu Leu Asp Arg Lys Ala Met Asp Glu Leu Leu Arg
 370 375 380
 Glu Arg Asp Ile Leu Asn Lys Asn Met Leu Lys Ala Val Asn Ala Thr
 385 390 395 400
 Gln Lys Gln Thr Asp Leu Val Lys Leu His Glu Gln Ala Lys Arg Asn
 405 410 415
 Leu Glu Gly Glu Ile Gln Asn Tyr Lys Asp Glu Ala Gln Lys Gln Arg
 420 425 430
 Lys Ile Ile Phe His Leu Glu Lys Glu Arg Asp Arg Tyr Ile Asn Gln
 435 440 445
 Ala Ser Asp Leu Thr Gln Lys Val Leu Met Asn Met Glu Asp Ile Lys
 450 455 460
 Val Arg Glu Thr Gln Ile Phe Asp Tyr Arg Lys Lys Ile Ala Glu Ser
 465 470 475 480
 Glu Ile Lys Leu Lys Gln Gln Gln Asn Leu Tyr Glu Ala Val Arg Ser
 485 490 495
 Asp Arg Asn Leu Tyr Ser Lys Asn Leu Val Glu Ala Gln Asp Glu Ile
 500 505 510
 Thr Asp Met Lys Arg Lys Leu Lys Ile Met Ile His Gln Val Asp Glu
 515 520 525
 Leu Lys Glu Asp Ile Ser Ala Lys Glu Ser Ala Leu Val Lys Leu His
 530 535 540
 Leu Glu Gln Gln Arg Ile Glu Lys Glu Lys Glu Thr Leu Lys Ala Glu
 545 550 555 560
 Leu Gln Lys Leu Arg Gln Gln Ala Leu Glu Thr Lys His Phe Ile Glu
 565 570 575
 Lys Gln Glu Ala Glu Glu Arg Lys Leu Leu Arg Ile Ile Ala Glu Ala
 580 585 590
 Asp Gly Glu Arg Leu Arg Gln Lys Lys Glu Leu Asp Gln Val Ile Ser
 595 600 605

Glu Arg Asp Ile Leu Gly Ser Gln Leu Val Arg Arg Asn Asp Glu Leu
610 615 620

Ala Leu Leu Tyr Glu Lys Ile Lys Ile Gln Gln Ser Val Leu Asn Lys
625 630 635 640

Gly Glu Ser Gln Tyr Asn Gln Arg Leu Glu Asp Met Arg Ile Leu Arg
645 650 655

Leu Glu Ile Lys Lys Leu Arg Arg Glu Lys Gly Ile Leu Ala Arg Ser
660 665 670

Met Ala Asn Val Glu Glu Leu Arg Gln Glu Phe Phe His Met Gln Arg
675 680 685

Glu Leu Leu Lys Glu Arg Thr Arg Cys Arg Ala Leu Glu Glu Glu Leu
690 695 700

Glu Asn Pro Leu Asn Val His Arg Trp Arg Lys Leu Glu Ala Ser Asp
705 710 715 720

Pro Asn Ala Tyr Glu Leu Ile Gln Lys Ile His Thr Leu Gln Lys Arg
725 730 735

Leu Ile Ser Lys Thr Glu Glu Val Val Glu Lys Glu Leu Leu Leu Gln
740 745 750

Glu Lys Glu Lys Leu Tyr Met Glu Leu Lys His Val Leu Ala Arg Gln
755 760 765

Pro Gly Pro Glu Ala Ala Glu Gln Leu Lys Leu Tyr Arg Arg Thr Leu
770 775 780

His Asp Lys Lys Gln Gln Leu Lys Val Leu Ser Ser Glu Leu Asn Met
785 790 795 800

Tyr Glu Val Gln Ser Lys Glu Tyr Lys Tyr Glu Val Glu Lys Leu Thr
805 810 815

Asn Glu Leu Gln Asn Leu Lys Lys Lys Tyr Leu Ala Gln Lys Arg Lys
820 825 830

Glu Gln Leu Gln Lys Asn Lys Asp Thr Ala Pro Met Asp Asn Thr Phe
835 840 845

Leu Met Val Lys Pro Asn Gly Pro Gly Phe Thr Gly Gly Gly Phe Pro
850 855 860

Leu Arg Ser Thr Lys Met Thr Phe
865 870

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 <211> 2469
 <212> DNA
 <213> Homo sapiens

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<210> 39
 <211> 822
 <212> PRT
 <213> Homo sapiens

<400> 39

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Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
35 40 45

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

Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65 70 75 80

Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
85 90 95

Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
100 105 110

Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
115 120 125

Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
130 135 140

Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145 150 155 160

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

Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
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Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
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Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
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Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
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Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
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Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
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Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
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Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
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Gly Leu Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser
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Asn Ala Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly
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Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser
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Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys
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Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg
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His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser
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Ala Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile
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Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val
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Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp
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Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val
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Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala
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Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp
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Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys
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His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro
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Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr
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Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr
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Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile
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His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val
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Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp
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Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala
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Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
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Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu
Page 65

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 Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val
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Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
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Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
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Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
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Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
115 120 125
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145 150 155 160
Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
165 170 175
Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
180 185 190
Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
195 200 205
Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
210 215 220

Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225 230 235 240

Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
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Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
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Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
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Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
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Gly Leu Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser
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325 330 335

Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser
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Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys
355 360 365

Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile
370 375 380

Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg
385 390 395 400

Met Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val
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His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser
420 425 430

Ala Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile
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Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val
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Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp
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Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val
485 490 495

Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala
Page 69

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 aggccacccg ggatggagta ctctatgac attaaccgtg ttcttgagga gcagatgacc 1800
 ttcaaggact tgggtgcatg cacctaccag ctggccagag gcatggagta cttggcttcc 1860

caaaaatgta ttcatcgaga tttagcagcc agaaatgttt tggtaacaga aaacaatgtg 1920
 atgaaaatag cagactttgg actcgccaga gatatcaaca atatagacta ttacaaaaag 1980
 accaccaatg ggcggcttcc agtcaagtgg atggctccag aagccctgtt tgatagagta 2040
 tacactcatc agagtgatgt ctggtccttc ggggtgttaa tgtgggagat cttcacttta 2100
 gggggctcgc cctaccagagg gattcccgtg gaggaacttt ttaagctgct gaaggaagga 2160
 cacagaatgg ataagccagc caactgcacc aacgaactgt acatgatgat gagggactgt 2220
 tggcatgcag tgccctccca gagaccaacg ttcaagcagt tggtagaaga cttggatcga 2280
 attctcactc tcacaaccaa tgag 2304

<210> 45
 <211> 768
 <212> PRT
 <213> Homo sapiens

<400> 45

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

Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
 35 40 45

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

Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
 65 70 75 80

Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
 85 90 95

Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
 100 105 110

Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
 115 120 125

Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
 130 135 140

Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
 145 150 155 160

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

Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
 180 185 190
 Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
 195 200 205
 Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
 210 215 220
 Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
 225 230 235 240
 Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
 245 250 255
 Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
 260 265 270
 Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
 275 280 285
 Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
 290 295 300
 Gly Leu Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser
 305 310 315 320
 Asn Ala Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly
 325 330 335
 Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser
 340 345 350
 Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys
 355 360 365
 Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile
 370 375 380
 Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg
 385 390 395 400
 Met Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val
 405 410 415
 His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser
 420 425 430
 Ala Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile
 435 440 445
 Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val

450

455

460

Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp
465 470 475 480

Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val
485 490 495

Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala
500 505 510

Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp
515 520 525

Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys
530 535 540

His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro
545 550 555 560

Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr
565 570 575

Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn
580 585 590

Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr
595 600 605

Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile
610 615 620

His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val
625 630 635 640

Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp
645 650 655

Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala
660 665 670

Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp
675 680 685

Ser Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro
690 695 700

Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly
705 710 715 720

His Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met
725 730 735

Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys
 740 745 750

Gln Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu
 755 760 765

<210> 46
 <211> 2130
 <212> DNA
 <213> Homo sapiens

<400> 46
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 gcccggccct ccttcagttt agttgaggat accacattag agccagaaga gccaccaacc 120
 aaataccaaa tctctcaacc agaagtgtac gtggctgcgc caggggagtc gctagagggtg 180
 cgctgcctgt tgaaagatgc cgccgtgatc agttggacta aggatggggg gcacttgggg 240
 cccaacaata ggacagtgtt tattggggag tacttgcaga taaagggcgc cagcctaga 300
 gactccggcc tctatgcttg tactgccagt aggactgtag acagtgaac ttggtacttc 360
 atggtgaatg tcacagatgc catctcatcc ggagatgatg aggatgacac cgatgggtgcg 420
 gaagattttg tcagtgagaa cagtaacaac aagagagcac catactggac caacacagaa 480
 aagatggaaa agcggctcca tgctgtgcct gcggccaaca ctgtcaagtt tcgctgcca 540
 gccgggggga acccaatgcc aaccatgcgg tggctgaaaa acgggaagga gtttaagcag 600
 gagcatcgca ttggaggcta caaggtagca aaccagcact ggagcctcat tatggaaagt 660
 gtggtcccat ctgacaaggg aaattatacc tgtgtagtgg agaataaata cgggtccatc 720
 aatcacacgt accacctgga tggtgtggcg cctggaagag aaaaggagat tacagcttcc 780
 ccagactacc tggagatagc catttactgc ataggggtct tcttaatcgc ctgtatggtg 840
 gtaacagtca tcctgtgccg aatgaagaac acgaccaaga agccagactt cagcagccag 900
 ccggctgtgc acaagctgac caaacgtatc cccctgcgga gacaggtaac agtttcgggt 960
 gagtccagct cctccatgaa ctccaacacc ccgctgggtga ggataacaac acgcctctct 1020
 tcaacggcag acacccccat gctggcaggg gtctccgagt atgaacttcc agaggacca 1080
 aaatgggagt ttccaagaga taagctgaca ctgggcaagc ccctgggaga aggttgcttt 1140
 gggcaagtgg tcatggcgga agcagtggga attgacaaag acaagcccaa ggaggcggtc 1200
 accgtggccg tgaagatgtt gaaagatgat gccacagaga aagaccttct tgatctggtg 1260
 tcagagatgg agatgatgaa gatgattggg aaacacaaga atatcataaa tcttcttgga 1320
 gcctgcacac aggatgggccc tctctatgtc atagttgagt atgcctctaa aggcaacctc 1380
 cgagaatacc tccgagcccc gagggcaccg gggatggagt actcctatga cattaaccgt 1440
 gttcctgagg agcagatgac cttcaaggac ttggtgtcat gcacctacca gctggccaga 1500
 ggcattggagt acttggtctt ccaaaaatgt attcatcgag atttagcagc cagaaatgtt 1560
 ttggtaacag aaaacaatgt gatgaaaata gcagactttg gactcgccag agatatcaac 1620

aatatagact attacaaaaa gaccaccaat gggcggttc cagtcaagtg gatggctcca 1680
 gaagccctgt ttgatagagt atacactcat cagagtgatg tctggtcctt cggggtgta 1740
 atgtgggaga tcttcacttt agggggctcg ccctaccag ggattcccgt ggaggaaactt 1800
 ttttaagctgc tgaággaagg acacagaatg gataagccag ccaactgcac caacgaactg 1860
 tacatgatga tgagggactg ttggcatgca gtgccctccc agagaccaac gttcaagcag 1920
 ttggtagaag acttggatcg aattctcact ctcacaacca atgaggaata cttggacctc 1980
 agccaacctc tcgaacagta ttcacctagt taccctgaca caagaagttc ttgttcttca 2040
 ggagatgatt ctgttttttc tccagacccc atgccttacg aaccatgcct tcctcagtat 2100
 ccacacataa acggcagtgt taaaacatga 2130

<210> 47
 <211> 709
 <212> PRT
 <213> Homo sapiens

<400> 47

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

Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
35 40 45

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

Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65 70 75 80

Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
85 90 95

Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
100 105 110

Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
115 120 125

Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
130 135 140

Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145 150 155 160

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

Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
 180 185 190
 Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
 195 200 205
 Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
 210 215 220
 Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
 225 230 235 240
 Asn His Thr Tyr His Leu Asp Val Val Ala Pro Gly Arg Glu Lys Glu
 245 250 255
 Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly
 260 265 270
 Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met
 275 280 285
 Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His
 290 295 300
 Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala
 305 310 315 320
 Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr
 325 330 335
 Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser
 340 345 350
 Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys
 355 360 365
 Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val
 370 375 380
 Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val
 385 390 395 400
 Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu
 405 410 415
 Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His
 420 425 430
 Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu
 435 440 445

Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu
 450 455 460
 Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg
 465 470 475 480
 Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr
 485 490 495
 Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His
 500 505 510
 Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met
 515 520 525
 Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr
 530 535 540
 Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro
 545 550 555 560
 Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser
 565 570 575
 Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr
 580 585 590
 Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His
 595 600 605
 Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met
 610 615 620
 Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln
 625 630 635 640
 Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu
 645 650 655
 Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro
 660 665 670
 Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro
 675 680 685
 Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn
 690 695 700
 Gly Ser Val Lys Thr
 705

<210> 48
 <211> 2124
 <212> DNA
 <213> Homo sapiens

<400> 48
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 gcccgccct ccttcagttt agttgaggat accacattag agccagaagg agcaccatac 120
 tggaccaaca cagaaaagat ggaaaagcgg ctccatgctg tgcctgcggc caacactgtc 180
 aagtttcgct gcccgccgg ggggaaccca atgccaaacca tgcggtggct gaaaaacggg 240
 aaggagtta agcaggagca tcgcattgga ggctacaagg tacgaaacca gcactggagc 300
 ct cattatgg aaagtgtggt cccatctgac aagggaaatt atacctgtgt agtgagaat 360
 gaatacgggt ccatcaatca cacgtaccac ctggatgttg tggagcgatc gcctcaccgg 420
 cccatcctcc aagccggact gccggcaaat gcctccacag tggtcggagg agacgtagag 480
 tttgtctgca aggtttacag tgatgccag ccccatcc agtgatcaa gcacgtggaa 540
 aagaacggca gtaaatcagg gcccgacggg ctgccctacc tcaaggttct caagcactcg 600
 gggataaata gttccaatgc agaagtgtg gctctgttca atgtgaccga ggcggatgct 660
 ggggaatata tatgtaagg ctccaattat atagggcagg ccaaccagtc tgcctggctc 720
 actgtcctgc caaacagca agcgcctgga agagaaaagg agattacagc ttccccagac 780
 tacctggaga tagccattta ctgcatagg gtcttcttaa tcgcctgtat ggtggaaca 840
 gtcacctgt gccgaatgaa gaacacgacc aagaagccag acttcagcag ccagccggct 900
 gtgcacaagc tgaccaaacg tatccccctg cggagacagg taacagtttc ggctgagtcc 960
 agtcctcca tgaactcaa cccccgctg gtgaggataa caacacgcct ctcttcaacg 1020
 gcagacaccc ccatgctggc aggggtctcc gagtatgaac ttccagagga cccaaaatgg 1080
 gagtttcaa gagataagct gacactgggc aagcccctgg gagaagggtg ctttgggcaa 1140
 gtggtcatgg cggaagcagt ggggaattgac aaagacaagc ccaaggaggc ggtcaccgtg 1200
 gccgtgaaga tggtgaaaga tgatgccaca gagaaagacc tttctgatct ggtgtcagag 1260
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 acacaggatg ggcctctcta tgtcatagtt gagtatgcct ctaaaggcaa cctccgagaa 1380
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 gaggagcaga tgaccttcaa ggacttggtg tcatgcacct accagctggc cagaggcatg 1500
 gagtacttgg cttcccaaaa atgtattcat cgagatttag cagccagaaa tgttttggta 1560
 acagaaaaca atgtgatgaa aatagcagac tttggactcg ccagagatat caacaatata 1620
 gactattaca aaaagaccac caatgggcgg cttccagtca agtggatggc tccagaagcc 1680
 ctgtttgata gagtatacac tcatcagagt gatgtctggt ccttcggggg gttaatgtgg 1740
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 ctgctgaagg aaggacacag aatggataag ccagccaact gcaccaacga actgtacatg 1860
 atgatgaggg actgttggca tgcagtgcc tcccagagac caacgttcaa gcagttggta 1920

gaagacttgg atcgaattct cactctcaca accaatgagg aatacttggga cctcagccaa 1980
 cctctcgaac agtattcacc tagttaccct gacacaagaa gttcttggtc ttcaggagat 2040
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 ataaacggca gtgttaaaac atga 2124

<210> 49
 <211> 707
 <212> PRT
 <213> Homo sapiens
 <400> 49

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

Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
 20 25 30

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

Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys
 50 55 60

Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly
 65 70 75 80

Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn
 85 90 95

Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly
 100 105 110

Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr
 115 120 125

Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln
 130 135 140

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

Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile
 165 170 175

Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro
 180 185 190

Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser Asn Ala Glu
 195 200 205

Val₂₁₀ Leu Ala Leu Phe Asn Val₂₁₅ Thr Glu Ala Asp Ala₂₂₀ Gly Glu Tyr Ile

Cys₂₂₅ Lys Val Ser Asn₂₃₀ Tyr Ile Gly Gln Ala Asn₂₃₅ Gln Ser Ala Trp Leu₂₄₀

Thr Val Leu Pro Lys₂₄₅ Gln Gln Ala Pro Gly₂₅₀ Arg Glu Lys Glu Ile₂₅₅ Thr

Ala Ser Pro Asp₂₆₀ Tyr Leu Glu Ile Ala₂₆₅ Ile Tyr Cys Ile Gly₂₇₀ Val Phe

Leu Ile Ala₂₇₅ Cys Met Val Val Thr₂₈₀ Val Ile Leu Cys Arg₂₈₅ Met Lys Asn

Thr Thr₂₉₀ Lys Lys Pro Asp Phe₂₉₅ Ser Ser Gln Pro Ala₃₀₀ Val His Lys Leu

Thr₃₀₅ Lys Arg Ile Pro Leu₃₁₀ Arg Arg Gln Val Thr₃₁₅ Val Ser Ala Glu Ser₃₂₀

Ser Ser Ser Met₃₂₅ Asn Ser Asn Thr Pro Leu₃₃₀ Val Arg Ile Thr Thr₃₃₅ Arg

Leu Ser Ser Thr₃₄₀ Ala Asp Thr Pro Met₃₄₅ Leu Ala Gly Val Ser₃₅₀ Glu Tyr

Glu Leu Pro₃₅₅ Glu Asp Pro Lys Trp₃₆₀ Glu Phe Pro Arg Asp₃₆₅ Lys Leu Thr

Leu Gly₃₇₀ Lys Pro Leu Gly Glu₃₇₅ Gly Cys Phe Gly Gln₃₈₀ Val Val Met Ala

Glu₃₈₅ Ala Val Gly Ile Asp₃₉₀ Lys Asp Lys Pro Lys₃₉₅ Glu Ala Val Thr₄₀₀ Val

Ala Val Lys Met₄₀₅ Leu Lys Asp Asp Ala Thr₄₁₀ Glu Lys Asp Leu Ser₄₁₅ Asp

Leu Val Ser₄₂₀ Glu Met Glu Met Met Lys₄₂₅ Met Ile Gly Lys His₄₃₀ Lys Asn

Ile Ile Asn₄₃₅ Leu Leu Gly Ala Cys₄₄₀ Thr Gln Asp Gly₄₄₅ Pro Leu Tyr Val

Ile Val₄₅₀ Glu Tyr Ala Ser Lys₄₅₅ Gly Asn Leu Arg Glu₄₆₀ Tyr Leu Arg Ala

Arg Arg Pro Pro Gly Met₄₇₀ Glu Tyr Ser Tyr Asp₄₇₅ Ile Asn Arg Val Pro₄₈₀

Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu

485

490

495

Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp
 500 505 510

Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys Ile
 515 520 525

Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys
 530 535 540

Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala
 545 550 555 560

Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly
 565 570 575

Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly
 580 585 590

Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met
 595 600 605

Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp
 610 615 620

Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val
 625 630 635 640

Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr Leu
 645 650 655

Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp Thr
 660 665 670

Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro
 675 680 685

Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser
 690 695 700

Val Lys Thr
 705

<210> 50
 <211> 2118
 <212> DNA
 <213> Homo sapiens

<400> 50
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aaataccaaa tctctcaacc agaagtgtac gtggctgctc caggggagtc gctagaggtg	180
cgctgcctgt tgaaagatgc cgccgtgata agttggacta aggatggggg gcacttgggg	240
cccaacaata ggacagtgtt tattggggag tacttgacaga taaagggcgc cacgcctaga	300
gactccggcc tctatgcttg tactgccagt aggactgtag acagtgaaac ttggtacttc	360
atggtgaatg tcacagatgc catctcatcc ggagatgatg aggatgacac cgatggtgctg	420
gaagattttg tcagtggaga cagtaacaac aagagagcac catactggac caacacagaa	480
aagatggaaa agcgggtcca tgctgtgcct gcggccaaca ctgtcaagtt tcgctgcccc	540
gccgggggga acccaatgcc aaccatgcgg tggctgaaaa acgggaagga gtttaagcag	600
gagcatcgca ttggaggcta caaggtagca aaccagcact ggagcctcat tatggaaagt	660
gtggtcccat ctgacaaggg aaattatacc tgtgtagtgg agaataaata cgggtccatc	720
aatcacacgt accacctgga tgttggtggg cgatcgctc accggcccat cctccaagcc	780
ggactgccgg caaatgcctc cacagtggtc ggaggagacg tagagtttgt ctgcaaggtt	840
tacagtgatg cccagcccca catccagtgg atcaagcacg tggaaaagaa cggcagtaaa	900
tacgggcccc acgggctgcc ctacctcaag gttctcaagg tttcggtga gtccagctcc	960
tccatgaact ccaacacccc gctggtgagg ataacaacac gcctctcttc aacggcagac	1020
accccatgc tggcaggggt ctccgagtat gaacttccag aggacccaaa atgggagttt	1080
ccaagagata agctgacact gggcaagccc ctgggagaag gttgctttgg gcaagtggtc	1140
atggcggaag cagtgggaat tgacaaagac aagcccaagg aggcggtcac cgtggccgtg	1200
aagatgttga aagatgatgc cacagagaaa gacctttctg atctggtgtc agagatggag	1260
atgatgaaga tgattgggaa acacaagaat atcataaatc ttcttgagac ctgcacacag	1320
gatgggcctc tctatgtcat agttgagtat gcctctaaag gcaacctccg agaatactc	1380
cgagcccgga ggccacccgg gatggagtac tcctatgaca ttaaccgtgt tcctgaggag	1440
cagatgacct tcaaggactt ggtgtcatgc acctaccagc tggccagagg catggagtac	1500
ttggcttccc aaaaatgtat tcatcgagat ttagcagcca gaaatgtttt ggtaacagaa	1560
aacaatgtga tgaaaatagc agactttgga ctgcagagag atatcaaaa tatagactat	1620
tacaaaaaga ccaccaatgg gcggcttcca gtcaagtgga tggctccaga agccctgttt	1680
gatagagtat acactcatca gagtgatgtc tggctcctcg ggggtgtaat gtgggagatc	1740
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aaggaaggac acagaatgga taagccagcc aactgcacca acgaactgta catgatgatg	1860
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gaacagtatt cacctagtta ccctgacaca agaagtctt gttcttcagg agatgattct	2040
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<400> 51

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Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
 35 40 45

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

Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
 65 70 75 80

Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
 85 90 95

Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
 100 105 110

Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
 115 120 125

Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
 130 135 140

Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
 145 150 155 160

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

Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
 180 185 190

Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
 195 200 205

Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
 210 215 220

Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
 225 230 235 240

Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
 245 250 255

Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
260 265 270

Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
275 280 285

Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
290 295 300

Gly Leu Pro Tyr Leu Lys Val Leu Lys Val Ser Ala Glu Ser Ser Ser
305 310 315 320

Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser
325 330 335

Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu
340 345 350

Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly
355 360 365

Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala
370 375 380

Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val
385 390 395 400

Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val
405 410 415

Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile
420 425 430

Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val
435 440 445

Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg
450 455 460

Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu
465 470 475 480

Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg
485 490 495

Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala
500 505 510

Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp
515 520 525

Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr
530 535 540

Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe
545 550 555 560

Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu
565 570 575

Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro
580 585 590

Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys
595 600 605

Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp
610 615 620

His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp
625 630 635 640

Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr Leu Asp Leu
645 650 655

Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp Thr Arg Ser
660 665 670

Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro Met Pro
675 680 685

Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser Val Lys
690 695 700

Thr
705

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<212> DNA
<213> Homo sapiens

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tggaccaaca cagaaaagat ggaaaagcgg ctccatgctg tgcctgcggc caacactgtc 180
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ctcattatgg aaagtgtggt cccatctgac aagggaaatt atacctgtgt agtggagaat 360
gaatacgggt ccatcaatca cacgtaccac ctggatgttg tggagcgatc gcctcaccgg 420

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cagtattcac ctagttaacc tgacacaaga agttcttgtt cttcaggaga tgattctggt     2040
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<210> 53
<211> 704
<212> PRT
<213> Homo sapiens

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<400> 53
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Leu Glu Pro Glu Gly Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu
35 40 45

Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys
50 55 60

Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly
65 70 75 80

Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn
85 90 95

Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly
100 105 110

Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr
115 120 125

Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln
130 135 140

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

Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile
165 170 175

Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro
180 185 190

Tyr Leu Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu
195 200 205

Ile Glu Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu
210 215 220

Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala
225 230 235 240

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

Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly Val Phe Leu
260 265 270

Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met Lys Asn Thr
275 280 285

Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His Lys Leu Thr
 290 295 300
 Lys Arg Ile Pro Leu Arg Arg Gln Val Ser Ala Glu Ser Ser Ser Ser
 305 310 315 320
 Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser Ser
 325 330 335
 Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu Pro
 340 345 350
 Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly Lys
 355 360 365
 Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Val
 370 375 380
 Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val Lys
 385 390 395 400
 Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val Ser
 405 410 415
 Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn
 420 425 430
 Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu
 435 440 445
 Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg Pro
 450 455 460
 Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu Gln
 465 470 475 480
 Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg Gly
 485 490 495
 Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala
 500 505 510
 Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp Phe
 515 520 525
 Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr Thr
 530 535 540
 Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp
 545 550 555 560
 Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Met

565

570

575

Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val
 580 585 590

Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro
 595 600 605

Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp His
 610 615 620

Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu
 625 630 635 640

Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr Leu Asp Leu Ser
 645 650 655

Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp Thr Arg Ser Ser
 660 665 670

Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro Met Pro Tyr
 675 680 685

Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser Val Lys Thr
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 <211> 2008
 <212> DNA
 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

<400> 55

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 20 25 30

Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu Asp Asp Thr
 35 40 45

Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn Lys Arg Ala
 50 55 60

Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg Leu His Ala Val
 65 70 75 80

Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala Gly Gly Asn Pro

85										90				95			
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His	Arg	Ile 115	Gly	Gly	Tyr	Lys	Val 120	Arg	Asn	Gln	His	Trp 125	Ser	Leu	Ile		
Met	Glu 130	Ser	Val	Val	Pro	Ser 135	Asp	Lys	Gly	Asn	Tyr 140	Thr	Cys	Val	Val		
Glu 145	Asn	Glu	Tyr	Gly	Ser 150	Ile	Asn	His	Thr	Tyr 155	His	Leu	Asp	Val	Val		
Glu	Arg	Ser	Pro	His 165	Arg	Pro	Ile	Leu	Gln 170	Ala	Gly	Leu	Pro	Ala 175	Asn		
Ala	Ser	Thr	Val 180	Val	Gly	Gly	Asp	Val 185	Glu	Phe	Val	Cys	Lys 190	Val	Tyr		
Ser	Asp	Ala 195	Gln	Pro	His	Ile	Gln 200	Trp	Ile	Lys	His	Val 205	Glu	Lys	Asn		
Gly	Ser 210	Lys	Tyr	Gly	Pro	Asp 215	Gly	Leu	Pro	Tyr	Leu 220	Lys	Val	Leu	Lys		
Ala 225	Ala	Gly	Val	Asn	Thr 230	Thr	Asp	Lys	Glu	Ile 235	Glu	Val	Leu	Tyr	Ile 240		
Arg	Asn	Val	Thr	Phe 245	Glu	Asp	Ala	Gly	Glu 250	Tyr	Thr	Cys	Leu	Ala 255	Gly		
Asn	Ser	Ile	Gly 260	Ile	Ser	Phe	His	Ser 265	Ala	Trp	Leu	Thr	Val 270	Leu	Pro		
Ala	Pro	Gly 275	Arg	Glu	Lys	Glu	Ile 280	Thr	Ala	Ser	Pro	Asp 285	Tyr	Leu	Glu		
Ile	Ala 290	Ile	Tyr	Cys	Ile	Gly 295	Val	Phe	Leu	Ile	Ala 300	Cys	Met	Val	Val		
Thr 305	Val	Ile	Leu	Cys	Arg 310	Met	Lys	Asn	Thr	Thr 315	Lys	Lys	Pro	Asp	Phe 320		
Ser	Ser	Gln	Pro	Ala 325	Val	His	Lys	Leu	Thr 330	Lys	Arg	Ile	Pro	Leu 335	Arg		
Arg	Gln	Val	Ser 340	Ala	Glu	Ser	Ser	Ser 345	Ser	Met	Asn	Ser	Asn 350	Thr	Pro		
Leu	Val	Arg 355	Ile	Thr	Thr	Arg	Leu 360	Ser	Ser	Thr	Ala	Asp 365	Thr	Pro	Met		

Leu Ala Gly Val Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu
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Phe Pro Arg Asp Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys
 385 390 395 400

Phe Gly Gln Val Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys
 405 410 415

Pro Lys Glu Ala Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala
 420 425 430

Thr Glu Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys
 435 440 445

Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr
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Gln Asp Gly Pro Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn
 465 470 475 480

Leu Arg Glu Tyr Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser
 485 490 495

Tyr Asp Ile Asn Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu
 500 505 510

Val Ser Cys Thr Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser
 515 520 525

Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr
 530 535 540

Glu Asn Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile
 545 550 555 560

Asn Asn Ile Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val
 565 570 575

Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln
 580 585 590

Ser Asp Val Trp Ser Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu
 595 600 605

Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu
 610 615 620

Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu
 625 630 635 640

Leu Tyr Met Met Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg
645 650 655

Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Ile
660 665

<210> 56
<211> 1782
<212> DNA
<213> Homo sapiens

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tacttggacc tcagccaacc tctcgaacag tattcaccta gttaccctga cacaagaagt 1680
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 cttcctcagt atccacacat aaacggcagt gttaaaacat ga 1782

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 <211> 593
 <212> PRT
 <213> Homo sapiens

<400> 57

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Pro Phe Trp Arg Lys Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala
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Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe
 35 40 45

Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys
 50 55 60

His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro Tyr
 65 70 75 80

Leu Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile
 85 90 95

Glu Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr
 100 105 110

Thr Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp
 115 120 125

Leu Thr Val Leu Pro Ala Pro Gly Arg Glu Lys Glu Ile Thr Ala Ser
 130 135 140

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

Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met Lys Asn Thr Thr
 165 170 175

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

Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Glu Ser Ser Ser
 195 200 205

Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser
 210 215 220

Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu
225 230 235 240

Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly
245 250 255

Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala
260 265 270

Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val
275 280 285

Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val
290 295 300

Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile
305 310 315 320

Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val
325 330 335

Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg
340 345 350

Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu
355 360 365

Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg
370 375 380

Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala
385 390 395 400

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

Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr
420 425 430

Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe
435 440 445

Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu
450 455 460

Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro
465 470 475 480

Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys
485 490 495

Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp
 500 505 510

His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp
 515 520 525

Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr Leu Asp Leu
 530 535 540

Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp Thr Arg Ser
 545 550 555 560

Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro Met Pro
 565 570 575

Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser Val Lys
 580 585 590

Thr

<210> 58
 <211> 1116
 <212> DNA
 <213> Homo sapiens

<400> 58
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 acagtttcgg ctgagttccag ctctccatg aactccaaca ccccgctggt gaggataaca 120
 acacgcctct cttcaacggc agacaccccc atgctggcag gggctctccga gtatgaactt 180
 ccagaggacc caaaatggga gtttccaaga gataagctga cactgggcaa gcccctggga 240
 gaagggttgc ttgggcaagt ggtcatggcg gaagcagtgga gaattgacaa agacaagccc 300
 aaggaggcgg tcaccgtggc cgtgaagatg ttgaaagatg atgccacaga gaaagacctt 360
 tctgatctgg tgtcagagat ggagatgatg aagatgattg ggaaacacaa gaatatcata 420
 aatcttcttg gagcctgcac acaggatggg cctctctatg tcatagttga gtatgcctct 480
 aaaggcaacc tccgagaata cctccgagcc cggaggccac ccgggatgga gtactcctat 540
 gacattaacc gtgttcctga ggagcagatg accttcaagg acttggtgtc atgcacctac 600
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 agagatatca acaatataga ctattacaaa aagaccacca atgggcggct tccagtcaag 780
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 gtggaggaac tttttaagct gctgaaggaa ggacacagaa tggataagcc agccaactgc 960
 accaacgaac tgaatacttg gacctcagcc aacctctcga acagtattca cctagttacc 1020
 ctgacacaag aagttcttgt tcttcaggag atgattctgt tttttctcca gaccccatgc 1080

cttacgaacc atgccttcct cagtatccac acataa

1116

<210> 59
 <211> 371
 <212> PRT
 <213> Homo sapiens

<400> 59

Phe Ser Ser Gln Pro Ala Val His Lys Leu Thr Lys Arg Ile Pro Leu
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Arg Arg Gln Val Thr Val Ser Ala Glu Ser Ser Ser Ser Met Asn Ser
 20 25 30

Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser Ser Thr Ala Asp
 35 40 45

Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu Pro Glu Asp Pro
 50 55 60

Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly Lys Pro Leu Gly
 65 70 75 80

Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Val Gly Ile Asp
 85 90 95

Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val Lys Met Leu Lys
 100 105 110

Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu
 115 120 125

Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly
 130 135 140

Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu Tyr Ala Ser
 145 150 155 160

Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg Pro Pro Gly Met
 165 170 175

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

Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg Gly Met Glu Tyr
 195 200 205

Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val
 210 215 220

Leu Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala
 225 230 235 240

Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg
245 250 255

Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr
260 265 270

Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Met Trp Glu Ile
275 280 285

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

Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn Cys
305 310 315 320

Thr Asn Glu Leu Asn Thr Trp Thr Ser Ala Asn Leu Ser Asn Ser Ile
325 330 335

His Leu Val Thr Leu Thr Gln Glu Val Leu Val Leu Gln Glu Met Ile
340 345 350

Leu Phe Phe Leu Gln Thr Pro Cys Leu Thr Asn His Ala Phe Leu Ser
355 360 365

Ile His Thr
370

<210> 60
<211> 2421
<212> DNA
<213> Homo sapiens

<220>
<221> variation
<222> (1404)..(1404)
<223> R = A or G (dbSNP entry rs767809)

<220>
<221> variation
<222> (1830)..(1830)
<223> S = C or G (dbSNP entry rs2131956)

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gccatgcaga aagctcagca ggtatctcag ggtctggatg tgctcacagc aaaagtggaa 120
aatgcagctc gcaagctgga agccatgacc aactcaaagc agagcattgc aaagaagatc 180
gatgctgctc agaactggct tgcagatcca aatggtggac cggaaggaga agagcagatt 240
cgaggtgctt tggctgaagc tcggaaaata gcagaattat gtgatgatcc taaagaaaga 300
gatgacattc tacgttcctt tggggaaata tctgctctga cttctaaatt agcagatcta 360
cgaagacagg ggaaaggaga ttctccagag gctcgagcct tggccaaaca ggtggccacg 420

gccctgcaga acctgcagac caaaaccaac cgggctgtgg ccaacagcag accggccaaa	480
gcagctgtac accttgaggg caagattgag caagcacagc ggtggattga taatcccaca	540
gtggatgacc gtggagtcgg tcaggctgcc atccgggggc ttgtggccga agggcatcgt	600
ctggctaatt ttatgatggg gccttatcgg caagatcttc tcgccaagtg tgaccgagtg	660
gaccagctga cagcccagct ggctgacctg gctgccagag ggggaagggga gagtcctcag	720
gcacgagcac ttgcatctca gctccaagac tccttaaagg atctaaaagc tcggatgcag	780
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ttggcagtgg cagccacggc gcctcctgat gcgcctaaca ggggaagagg atttgatgag	900
agggcagcta actttgaaaa ccattcagga aagcttggtg ctacggccga gaaggcggct	960
gcggttggtg ctgctaataa atcaacagtg gaaggcattc aggcctcagt gaagacggcc	1020
cgagaactca caccacaggt ggtctcggct gctcgtatct tacttaggaa ccctggaaat	1080
caagctgctt atgaacattt tgagaccatg aagaaccagt ggatcgataa tgttgaaaaa	1140
atgacagggc tggtgagcga agccattgat accaaatctc tgttgatgc ttcagaagaa	1200
gcaattaaaa aagacctgga caagtgaag gtagctatgg ccaacattca gcctcagatg	1260
ctggttgctg gggcaaccag tattgctcgt cgggccaacc ggatcctgct ggtggctaag	1320
agggaggtgg agaattccga ggatcccaag ttccgtgagg ctgtgaaagc tgcctctgat	1380
gaattgagca aaaccatctc cccratggtg atggatgcaa aagctgtggc tggaaacatt	1440
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gccaaagtca gagaagcctt ccaacctcag gagcctgact tcccggccgc tccaccagac	1560
cttgaacaac tccgactaac agatgagctt gtcctccca aaccacctct gcctgaaggt	1620
gaggtccctc cacctaggcc tccaccacca gaggaaaagg atgaagagtt ccctgagcag	1680
aaggccgggg aggtgattaa ccagccaatg atgatggctg ccagacagct ccatgatgaa	1740
gctcgcaaat ggtccagcaa gccgggcata ccagccgctg aggtgggtat aggtgttgta	1800
gctgaggcag atgcggccga tgctgctggs ttccctgtcc cccctgacat ggaagacgat	1860
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gcagcagcca agcgcattgg tctgctgatg gctgagatgt ctcggctggg aagagggggc	2040
agtggtagca agcgggcact cattcagtgt gccaaaggac tcgccaaggc ctgagatgag	2100
gtgactcggg tggccaagga ggttgccaag cagtgcacag ataaacggat tagaaccaac	2160
ctcttacagg tatgtgagcg aatcccaacc ataagcacc agctcaaaaat cctgtccaca	2220
gtgaaggcca ccatgctggg ccggaccaac atcagtgatg aggagtctga gcaggccaca	2280
gagatgctgg ttcacaatgc ccagaacctc atgcagtctg tgaaggagac tgtgcgggaa	2340
gctgaagctg cttcaatcaa aattcgaaca gatgctggat ttacactgcg ctgggttaga	2400
aagactccct ggtaccagta g	2421

<210> 61
 <211> 806
 <212> PRT
 <213> Homo sapiens

<400> 61

Gly Gln Met Thr Asp Gln Val Ala Asp Leu Arg Ala Arg Gly Gln Gly
 1 5 10 15

Ser Ser Pro Val Ala Met Gln Lys Ala Gln Gln Val Ser Gln Gly Leu
 20 25 30

Asp Val Leu Thr Ala Lys Val Glu Asn Ala Ala Arg Lys Leu Glu Ala
 35 40 45

Met Thr Asn Ser Lys Gln Ser Ile Ala Lys Lys Ile Asp Ala Ala Gln
 50 55 60

Asn Trp Leu Ala Asp Pro Asn Gly Gly Pro Glu Gly Glu Glu Gln Ile
 65 70 75 80

Arg Gly Ala Leu Ala Glu Ala Arg Lys Ile Ala Glu Leu Cys Asp Asp
 85 90 95

Pro Lys Glu Arg Asp Asp Ile Leu Arg Ser Leu Gly Glu Ile Ser Ala
 100 105 110

Leu Thr Ser Lys Leu Ala Asp Leu Arg Arg Gln Gly Lys Gly Asp Ser
 115 120 125

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

Leu Gln Thr Lys Thr Asn Arg Ala Val Ala Asn Ser Arg Pro Ala Lys
 145 150 155 160

Ala Ala Val His Leu Glu Gly Lys Ile Glu Gln Ala Gln Arg Trp Ile
 165 170 175

Asp Asn Pro Thr Val Asp Asp Arg Gly Val Gly Gln Ala Ala Ile Arg
 180 185 190

Gly Leu Val Ala Glu Gly His Arg Leu Ala Asn Val Met Met Gly Pro
 195 200 205

Tyr Arg Gln Asp Leu Leu Ala Lys Cys Asp Arg Val Asp Gln Leu Thr
 210 215 220

Ala Gln Leu Ala Asp Leu Ala Ala Arg Gly Glu Gly Glu Ser Pro Gln
 225 230 235 240

Ala Arg Ala Leu Ala Ser Gln Leu Gln Asp Ser Leu Lys Asp Leu Lys
 245 250 255

Ala Arg Met Gln Glu Ala Met Thr Gln Glu Val Ser Asp Val Phe Ser
260 265 270

Asp Thr Thr Thr Pro Ile Lys Leu Leu Ala Val Ala Ala Thr Ala Pro
275 280 285

Pro Asp Ala Pro Asn Arg Glu Glu Val Phe Asp Glu Arg Ala Ala Asn
290 295 300

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

Ala Val Gly Thr Ala Asn Lys Ser Thr Val Glu Gly Ile Gln Ala Ser
325 330 335

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

Ile Leu Leu Arg Asn Pro Gly Asn Gln Ala Ala Tyr Glu His Phe Glu
355 360 365

Thr Met Lys Asn Gln Trp Ile Asp Asn Val Glu Lys Met Thr Gly Leu
370 375 380

Val Asp Glu Ala Ile Asp Thr Lys Ser Leu Leu Asp Ala Ser Glu Glu
385 390 395 400

Ala Ile Lys Lys Asp Leu Asp Lys Cys Lys Val Ala Met Ala Asn Ile
405 410 415

Gln Pro Gln Met Leu Val Ala Gly Ala Thr Ser Ile Ala Arg Arg Ala
420 425 430

Asn Arg Ile Leu Leu Val Ala Lys Arg Glu Val Glu Asn Ser Glu Asp
435 440 445

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

Thr Ile Ser Pro Met Val Met Asp Ala Lys Ala Val Ala Gly Asn Ile
465 470 475 480

Ser Asp Pro Gly Leu Gln Lys Ser Phe Leu Asp Ser Gly Tyr Arg Ile
485 490 495

Leu Gly Ala Val Ala Lys Val Arg Glu Ala Phe Gln Pro Gln Glu Pro
500 505 510

Asp Phe Pro Pro Pro Pro Pro Asp Leu Glu Gln Leu Arg Leu Thr Asp
515 520 525

Glu Leu Ala Pro Pro Lys Pro Pro Leu Pro Glu Gly Glu Val Pro Pro
 530 535 540

Pro Arg Pro Pro Pro Pro Glu Glu Lys Asp Glu Glu Phe Pro Glu Gln
 545 550 555 560

Lys Ala Gly Glu Val Ile Asn Gln Pro Met Met Met Ala Ala Arg Gln
 565 570 575

Leu His Asp Glu Ala Arg Lys Trp Ser Ser Lys Pro Gly Ile Pro Ala
 580 585 590

Ala Glu Val Gly Ile Gly Val Val Ala Glu Ala Asp Ala Ala Asp Ala
 595 600 605

Ala Gly Phe Pro Val Pro Pro Asp Met Glu Asp Asp Tyr Glu Pro Glu
 610 615 620

Leu Leu Leu Met Pro Ser Asn Gln Pro Val Asn Gln Pro Ile Leu Ala
 625 630 635 640

Ala Ala Gln Ser Leu His Arg Glu Ala Thr Lys Trp Ser Ser Lys Gly
 645 650 655

Asn Asp Ile Ile Ala Ala Ala Lys Arg Met Ala Leu Leu Met Ala Glu
 660 665 670

Met Ser Arg Leu Val Arg Gly Gly Ser Gly Thr Lys Arg Ala Leu Ile
 675 680 685

Gln Cys Ala Lys Asp Ile Ala Lys Ala Ser Asp Glu Val Thr Arg Leu
 690 695 700

Ala Lys Glu Val Ala Lys Gln Cys Thr Asp Lys Arg Ile Arg Thr Asn
 705 710 715 720

Leu Leu Gln Val Cys Glu Arg Ile Pro Thr Ile Ser Thr Gln Leu Lys
 725 730 735

Ile Leu Ser Thr Val Lys Ala Thr Met Leu Gly Arg Thr Asn Ile Ser
 740 745 750

Asp Glu Glu Ser Glu Gln Ala Thr Glu Met Leu Val His Asn Ala Gln
 755 760 765

Asn Leu Met Gln Ser Val Lys Glu Thr Val Arg Glu Ala Glu Ala Ala
 770 775 780

Ser Ile Lys Ile Arg Thr Asp Ala Gly Phe Thr Leu Arg Trp Val Arg
 785 790 795 800

Lys Thr Pro Trp Tyr Gln
805

<210> 62
<211> 279
<212> DNA
<213> Homo sapiens

<400> 62
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gcgacccaga agcagacaga cttggtaaag ctccatgaac aagccaagag gaacctggag 120
ggagaaatcc agaactacaa ggatgaggct cagaagcaga gaaagatcat ctttcatctg 180
gaaaaggagc gtgaccggtg catcaaccaa gccagtgacc ttacgcaaaa ggctgactct 240
gtcaggatgc cctggcctct ggacaaaggg aaatggtga 279

<210> 63
<211> 92
<212> PRT
<213> Homo sapiens

<400> 63

Met Asp Glu Leu Leu Arg Glu Arg Asp Ile Leu Asn Lys Asn Met Leu
1 5 10 15

Lys Ala Val Asn Ala Thr Gln Lys Gln Thr Asp Leu Val Lys Leu His
20 25 30

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

Glu Ala Gln Lys Gln Arg Lys Ile Ile Phe His Leu Glu Lys Glu Arg
50 55 60

Asp Arg Tyr Ile Asn Gln Ala Ser Asp Leu Thr Gln Lys Ala Asp Ser
65 70 75 80

Val Arg Met Pro Trp Pro Leu Asp Lys Gly Lys Trp
85 90

<210> 64
<211> 187
<212> DNA
<213> Homo sapiens

<400> 64
tctcactctc acaaccaatg aggaataactt ggacctcagc caacctctcg aacagtattc 60
acctagttac cctgacacaa gaagttcttg ttcttcagga gatgattctg tttttctcc 120
agaccccatg ccttacgaac catgccttcc tcagtatcca cacataaacg gcagtgttaa 180
aacatga 187

<210> 65
<211> 139

<212> DNA
<213> Homo sapiens

<220>
<221> variation
<222> (112)..(112)
<223> Y = C or T (dbSNP entry rs1047057)

<400> 65
gcagttggta gaagacttgg atcgaattct cactctcaca accaatgagg aggagaagaa 60
ggtttctgga gcagtggaact gccacaagcc accatgtaac ccctctcacc tgccgtgcgt 120
aytggtctgtg gaccagtag 139

<210> 66
<211> 85
<212> DNA
<213> Homo sapiens

<400> 66
tctcactctc acaaccaatg aggaatactt ggacctcagt cagcctctcg aaccgtattc 60
accttggttat cctgacccaa gatga 85

<210> 67
<211> 55
<212> DNA
<213> Homo sapiens

<400> 67
gcagttggta gaagacttgg atcgaattct cactctcaca accaatgaga tctga 55

<210> 68
<211> 3304
<212> DNA
<213> Homo sapiens

<220>
<221> variation
<222> (2388)..(2388)
<223> R = G or A (dbSNP entry rs767809)

<220>
<221> variation
<222> (2814)..(2814)
<223> S = C or G (dbSNP entry rs2131956)

<400> 68
atgccagtgt ttcatacgcg cacgatcgag agcatcctgg agccggtggc acagcagatc 60
tcccacctgg tgataatgca cgaggagggc gaggtggacg gcaaagccat tcctgacctc 120
accgcgcccc tggccgccgt gcaggcggcc gtcagcaacc tcgtccgggt tggaaaagag 180
actgttcaaa cactgagga tcagattttg aagagagata tgccaccagc atttattaag 240
gttgagaatg cttgcaccaa gcttgctcag gcagctcaga tgcttcagtc agacccttac 300
tcagtgcctg ctcgagatta tctaattgat ggggtcaagg gcacccctctc tggaacatca 360
gacctgctcc ttaccttcga tgaggctgag gtccgtaaaa ttattagagt ttgcaaagga 420
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acaaagaatc ttgggccagg aatgactaag atggccaaga tgattgacga gagacagcag	540
gagctcactc accaggagca ccgagtgatg ttggtgaact cgatgaacac cgtgaaagag	600
ttgctgccag ttctcatttc agctatgaag atttttgtaa caactaaaaa ctcaaaaaac	660
caaggcatag aggaagcttt aaaaaatcgc aattttactg tagaaaaaat gagtgtgaa	720
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gataccacaa ctcccatcaa gctgttggca gtggcagcca cggcgctcc tgatgctcct	1860
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attcaggcct cagtgaagac ggcccagaaa ctcacacccc aggtgggtctc ggctgctcgt	2040
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tctctgttgg atgcttcaga agaagcaatt aaaaaagacc tggacaagtg caaggtagct	2220
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ggatatcgga tcctgggagc tgtggccaag gtcagagaag ccttccaacc tcaggagcct	2520

gacttcccgc cgcctccacc agaccttgaa caactccgac taacagatga gcttgctcct	2580
cccaaaccac ctctgcctga aggtgaggtc cctccaccta ggcctccacc accagaggaa	2640
aaggatgaag agttccctga gcagaaggcc ggggaggtga ttaaccagcc aatgatgatg	2700
gctgccagac agctccatga tgaagctcgc aaatggtcca gcaagccggg catcccagcc	2760
gctgaggtgg gtataggtgt thtagctgag gcagatgcgg ccgatgctgc tggsttcctt	2820
gtccccctg acatggaaga cgattacgaa cctgagctgc tgttaatgcc atccaatcag	2880
ccggtcaacc agcccattct ggccgcggct cagtccttgc atcggaagc taccaagtgg	2940
tctagtaagg gcaatgacat cattgcagca gccaagcgca tggctctgct gatggctgag	3000
atgtctcggc tggtaagagg gggcagtgg accaagcggg cactcattca gtgtgccaag	3060
gacatcgcca aggcctcaga tgaggtgact cggttggcca aggaggttgc caagcagtgc	3120
acagataaac ggattagaac caacctctta caggtatgtg agcgaatccc aaccataagc	3180
accagctca aaatcctgtc cacagtgaag gccaccatgc tgggccggac caacatcagt	3240
gatgaggagt ctgagcaggc cacagagatg ctggttcaca atgccagaa cctcatgcag	3300
tctg	3304

<210> 69
 <211> 3100
 <212> DNA
 <213> Homo sapiens

<220>
 <221> variation
 <222> (2388)..(2388)
 <223> R = A or G (dbSNP entry rs767809)

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 <212> DNA
 <213> Homo sapiens

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 <213> Homo sapiens

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<210> 72
 <211> 32
 <212> DNA
 <213> Homo sapiens

<400> 72

caagcagttg gtagaagact tggatcgaat tc 32

<210> 73
 <211> 61
 <212> DNA
 <213> Homo sapiens

<400> 73
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 a 61

<210> 74
 <211> 67
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (66)..(66)
 <223> n means ambiguous base calling

<400> 74
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<210> 75
 <211> 78
 <212> DNA
 <213> Homo sapiens

<400> 75
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<210> 76
 <211> 60
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (13)..(13)
 <223> n means ambiguous base calling

<400> 76
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<210> 77
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 <212> DNA
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<220>
 <221> misc_feature
 <222> (71)..(71)
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<400> 77

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acaagaagaa n 71

<210> 78
<211> 73
<212> DNA
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<400> 78
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tggtctctga aca 73

<210> 79
<211> 100
<212> DNA
<213> Homo sapiens

<400> 79
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<210> 80
<211> 100
<212> DNA
<213> Homo sapiens

<400> 80
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