

GENENLAW-#306717-v1-P4190R1_SequenceListing_as_filed.TXT
SEQUENCE LISTING

<110> GENENTECH, INC.
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
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WOODRUFF, Prescott

<120> COMPOSITIONS AND METHODS FOR TREATING AND DIAGNOSING ASTHMA

<130> P4190R1

<140>
<141>

<150> 61/205,392
<151> 2009-01-16

<150> 61/128,383
<151> 2008-05-20

<150> 61/041,480
<151> 2008-04-01

<150> 61/072,572
<151> 2008-03-31

<160> 261

<170> PatentIn version 3.5

<210> 1
<211> 836
<212> PRT
<213> Homo sapiens

<400> 1
Met Ile Pro Phe Leu Pro Met Phe Ser Leu Leu Leu Leu Ile Val
1 5 10 15

Asn Pro Ile Asn Ala Asn Asn His Tyr Asp Lys Ile Leu Ala His Ser
20 25 30

Arg Ile Arg Gly Arg Asp Gln Gly Pro Asn Val Cys Ala Leu Gln Gln
35 40 45

Ile Leu Gly Thr Lys Lys Lys Tyr Phe Ser Thr Cys Lys Asn Trp Tyr
50 55 60

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

Pro Gly Tyr Met Arg Met Glu Gly Met Lys Gly Cys Pro Ala Val Leu
85 90 95

Pro Ile Asp His Val Tyr Gly Thr Leu Gly Ile Val Gly Ala Thr Thr
100 105 110

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

GENENLAW-#306717-v1-P4190R1_SequenceListing_as_filed.TXT

Lys Gly Ser Phe Thr Tyr Phe Ala Pro Ser Asn Glu Ala Trp Asp Asn
130 135 140

Leu Asp Ser Asp Ile Arg Arg Gly Leu Glu Ser Asn Val Asn Val Glu
145 150 155 160

Leu Leu Asn Ala Leu His Ser His Met Ile Asn Lys Arg Met Leu Thr
165 170 175

Lys Asp Leu Lys Asn Gly Met Ile Ile Pro Ser Met Tyr Asn Asn Leu
180 185 190

Gly Leu Phe Ile Asn His Tyr Pro Asn Gly Val Val Thr Val Asn Cys
195 200 205

Ala Arg Ile Ile His Gly Asn Gln Ile Ala Thr Asn Gly Val Val His
210 215 220

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

Ile Glu Ala Glu Asp Asp Leu Ser Ser Phe Arg Ala Ala Ala Ile Thr
245 250 255

Ser Asp Ile Leu Glu Ala Leu Gly Arg Asp Gly His Phe Thr Leu Phe
260 265 270

Ala Pro Thr Asn Glu Ala Phe Glu Lys Leu Pro Arg Gly Val Leu Glu
275 280 285

Arg Ile Met Gly Asp Lys Val Ala Ser Glu Ala Leu Met Lys Tyr His
290 295 300

Ile Leu Asn Thr Leu Gln Cys Ser Glu Ser Ile Met Gly Gly Ala Val
305 310 315 320

Phe Glu Thr Leu Glu Gly Asn Thr Ile Glu Ile Gly Cys Asp Gly Asp
325 330 335

Ser Ile Thr Val Asn Gly Ile Lys Met Val Asn Lys Lys Asp Ile Val
340 345 350

Thr Asn Asn Gly Val Ile His Leu Ile Asp Gln Val Leu Ile Pro Asp
355 360 365

Ser Ala Lys Gln Val Ile Glu Leu Ala Gly Lys Gln Gln Thr Thr Phe
370 375 380

Thr Asp Leu Val Ala Gln Leu Gly Leu Ala Ser Ala Leu Arg Pro Asp
385 390 395 400

GENENLAW-#306717-v1-P4190R1_SequenceListing_as_filed.TXT

Gly Glu Tyr Thr Leu Leu Ala Pro Val Asn Asn Ala Phe Ser Asp Asp
405 410 415

Thr Leu Ser Met Asp Gln Arg Leu Leu Lys Leu Ile Leu Gln Asn His
420 425 430

Ile Leu Lys Val Lys Val Gly Leu Asn Glu Leu Tyr Asn Gly Gln Ile
435 440 445

Leu Glu Thr Ile Gly Gly Lys Gln Leu Arg Val Phe Val Tyr Arg Thr
450 455 460

Ala Val Cys Ile Glu Asn Ser Cys Met Glu Lys Gly Ser Lys Gln Gly
465 470 475 480

Arg Asn Gly Ala Ile His Ile Phe Arg Glu Ile Ile Lys Pro Ala Glu
485 490 495

Lys Ser Leu His Glu Lys Leu Lys Gln Asp Lys Arg Phe Ser Thr Phe
500 505 510

Leu Ser Leu Leu Glu Ala Ala Asp Leu Lys Glu Leu Leu Thr Gln Pro
515 520 525

Gly Asp Trp Thr Leu Phe Val Pro Thr Asn Asp Ala Phe Lys Gly Met
530 535 540

Thr Ser Glu Glu Lys Glu Ile Leu Ile Arg Asp Lys Asn Ala Leu Gln
545 550 555 560

Asn Ile Ile Leu Tyr His Leu Thr Pro Gly Val Phe Ile Gly Lys Gly
565 570 575

Phe Glu Pro Gly Val Thr Asn Ile Leu Lys Thr Thr Gln Gly Ser Lys
580 585 590

Ile Phe Leu Lys Glu Val Asn Asp Thr Leu Leu Val Asn Glu Leu Lys
595 600 605

Ser Lys Glu Ser Asp Ile Met Thr Thr Asn Gly Val Ile His Val Val
610 615 620

Asp Lys Leu Leu Tyr Pro Ala Asp Thr Pro Val Gly Asn Asp Gln Leu
625 630 635 640

Leu Glu Ile Leu Asn Lys Leu Ile Lys Tyr Ile Gln Ile Lys Phe Val
645 650 655

Arg Gly Ser Thr Phe Lys Glu Ile Pro Val Thr Val Tyr Thr Thr Lys
660 665 670

Ile Ile Thr Lys Val Val Glu Pro Lys Ile Lys Val Ile Glu Gly Ser
675 680 685

Leu Gln Pro Ile Ile Lys Thr Glu Gly Pro Thr Leu Thr Lys Val Lys
690 695 700

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

Thr Glu Val Ile His Gly Glu Pro Ile Ile Lys Lys Tyr Thr Lys Ile
725 730 735

Ile Asp Gly Val Pro Val Glu Ile Thr Glu Lys Glu Thr Arg Glu Glu
740 745 750

Arg Ile Ile Thr Gly Pro Glu Ile Lys Tyr Thr Arg Ile Ser Thr Gly
755 760 765

Gly Gly Glu Thr Glu Glu Thr Leu Lys Lys Leu Leu Gln Glu Glu Val
770 775 780

Thr Lys Val Thr Lys Phe Ile Glu Gly Gly Asp Gly His Leu Phe Glu
785 790 795 800

Asp Glu Glu Ile Lys Arg Leu Leu Gln Gly Asp Thr Pro Val Arg Lys
805 810 815

Leu Gln Ala Asn Lys Lys Val Gln Gly Ser Arg Arg Arg Leu Arg Glu
820 825 830

Gly Arg Ser Gln
835

<210> 2
<211> 141
<212> PRT
<213> Homo sapiens

<400> 2
Met Ala Gln His Leu Ser Thr Leu Leu Leu Leu Ala Thr Leu Ala
1 5 10 15

Val Ala Leu Ala Trp Ser Pro Lys Glu Glu Asp Arg Ile Ile Pro Gly
20 25 30

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

His Phe Ala Ile Ser Glu Tyr Asn Lys Ala Thr Lys Asp Asp Tyr Tyr
50 55 60

GENENLAW-#306717-v1-P4190R1_SequenceListing_as_filed.TXT

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

Val Asn Tyr Phe Phe Asp Val Glu Val Gly Arg Thr Ile Cys Thr Lys
85 90 95

Ser Gln Pro Asn Leu Asp Thr Cys Ala Phe His Glu Gln Pro Glu Leu
100 105 110

Gln Lys Lys Gln Leu Cys Ser Phe Glu Ile Tyr Glu Val Pro Trp Glu
115 120 125

Asn Arg Arg Ser Leu Val Lys Ser Arg Cys Gln Glu Ser
130 135 140

<210> 3
<211> 94
<212> PRT
<213> Homo sapiens

<400> 3
Met Met Gly Leu Ser Leu Ala Ser Ala Val Leu Leu Ala Ser Leu Leu
1 5 10 15

Ser Leu His Leu Gly Thr Ala Thr Arg Gly Ser Asp Ile Ser Lys Thr
20 25 30

Cys Cys Phe Gln Tyr Ser His Lys Pro Leu Pro Trp Thr Trp Val Arg
35 40 45

Ser Tyr Glu Phe Thr Ser Asn Ser Cys Ser Gln Arg Ala Val Ile Phe
50 55 60

Thr Thr Lys Arg Gly Lys Lys Val Cys Thr His Pro Arg Lys Lys Trp
65 70 75 80

Val Gln Lys Tyr Ile Ser Leu Leu Lys Thr Pro Lys Gln Leu
85 90

<210> 4
<211> 914
<212> PRT
<213> Homo sapiens

<400> 4
Met Gly Pro Phe Lys Ser Ser Val Phe Ile Leu Ile Leu His Leu Leu
1 5 10 15

Glu Gly Ala Leu Ser Asn Ser Leu Ile Gln Leu Asn Asn Asn Gly Tyr
20 25 30

Glu Gly Ile Val Val Ala Ile Asp Pro Asn Val Pro Glu Asp Glu Thr
35 40 45

GENENLAW-#306717-v1-P4190R1_SequenceListing_as_filed.TXT

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

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

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

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

Gly Asn Asp Glu Pro Tyr Thr Glu Gln Met Gly Asn Cys Gly Glu Lys
115 120 125

Gly Glu Arg Ile His Leu Thr Pro Asp Phe Ile Ala Gly Lys Lys Leu
130 135 140

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

Leu Arg Trp Gly Val Phe Asp Glu Tyr Asn Asn Asp Glu Lys Phe Tyr
165 170 175

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

Gly Thr Asn Val Val Lys Lys Cys Gln Gly Gly Ser Cys Tyr Thr Lys
195 200 205

Arg Cys Thr Phe Asn Lys Val Thr Gly Leu Tyr Glu Lys Gly Cys Glu
210 215 220

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

Gln His Val Asp Ser Ile Val Glu Phe Cys Thr Glu Gln Asn His Asn
245 250 255

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

Trp Glu Val Ile Arg Asp Ser Glu Asp Phe Lys Lys Thr Thr Pro Met
275 280 285

Thr Thr Gln Pro Pro Asn Pro Thr Phe Ser Leu Leu Gln Ile Gly Gln
290 295 300

Arg Ile Val Cys Leu Val Leu Asp Lys Ser Gly Ser Met Ala Thr Gly
305 310 315 320

GENENLAW-#306717-v1-P4190R1_SequenceListing_as_filed.TXT

Asn Arg Leu Asn Arg Leu Asn Gln Ala Gly Gln Leu Phe Leu Leu Gln
325 330 335

Thr Val Glu Leu Gly Ser Trp Val Gly Met Val Thr Phe Asp Ser Ala
340 345 350

Ala His Val Gln Ser Glu Leu Ile Gln Ile Asn Ser Gly Ser Asp Arg
355 360 365

Asp Thr Leu Ala Lys Arg Leu Pro Ala Ala Ala Ser Gly Gly Thr Ser
370 375 380

Ile Cys Ser Gly Leu Arg Ser Ala Phe Thr Val Ile Arg Lys Lys Tyr
385 390 395 400

Pro Thr Asp Gly Ser Glu Ile Val Leu Leu Thr Asp Gly Glu Asp Asn
405 410 415

Thr Ile Ser Gly Cys Phe Asn Glu Val Lys Gln Ser Gly Ala Ile Ile
420 425 430

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

Ser Lys Met Thr Gly Gly Leu Gln Thr Tyr Ala Ser Asp Gln Val Gln
450 455 460

Asn Asn Gly Leu Ile Asp Ala Phe Gly Ala Leu Ser Ser Gly Asn Gly
465 470 475 480

Ala Val Ser Gln Arg Ser Ile Gln Leu Glu Ser Lys Gly Leu Thr Leu
485 490 495

Gln Asn Ser Gln Trp Met Asn Gly Thr Val Ile Val Asp Ser Thr Val
500 505 510

Gly Lys Asp Thr Leu Phe Leu Ile Thr Trp Thr Thr Gln Pro Pro Gln
515 520 525

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

Asp Lys Asn Thr Lys Met Ala Tyr Leu Gln Ile Pro Gly Ile Ala Lys
545 550 555 560

Val Gly Thr Trp Lys Tyr Ser Leu Gln Ala Ser Ser Gln Thr Leu Thr
565 570 575

Leu Thr Val Thr Ser Arg Ala Ser Asn Ala Thr Leu Pro Pro Ile Thr
580 585 590

GENENLAW-#306717-v1-P4190R1_SequenceListing_as_filed.TXT

Val Thr Ser Lys Thr Asn Lys Asp Thr Ser Lys Phe Pro Ser Pro Leu
595 600 605

Val Val Tyr Ala Asn Ile Arg Gln Gly Ala Ser Pro Ile Leu Arg Ala
610 615 620

Ser Val Thr Ala Leu Ile Glu Ser Val Asn Gly Lys Thr Val Thr Leu
625 630 635 640

Glu Leu Leu Asp Asn Gly Ala Gly Ala Asp Ala Thr Lys Asp Asp Gly
645 650 655

Val Tyr Ser Arg Tyr Phe Thr Thr Tyr Asp Thr Asn Gly Arg Tyr Ser
660 665 670

Val Lys Val Arg Ala Leu Gly Gly Val Asn Ala Ala Arg Arg Arg Val
675 680 685

Ile Pro Gln Gln Ser Gly Ala Leu Tyr Ile Pro Gly Trp Ile Glu Asn
690 695 700

Asp Glu Ile Gln Trp Asn Pro Pro Arg Pro Glu Ile Asn Lys Asp Asp
705 710 715 720

Val Gln His Lys Gln Val Cys Phe Ser Arg Thr Ser Ser Gly Gly Ser
725 730 735

Phe Val Ala Ser Asp Val Pro Asn Ala Pro Ile Pro Asp Leu Phe Pro
740 745 750

Pro Gly Gln Ile Thr Asp Leu Lys Ala Glu Ile His Gly Gly Ser Leu
755 760 765

Ile Asn Leu Thr Trp Thr Ala Pro Gly Asp Asp Tyr Asp His Gly Thr
770 775 780

Ala His Lys Tyr Ile Ile Arg Ile Ser Thr Ser Ile Leu Asp Leu Arg
785 790 795 800

Asp Lys Phe Asn Glu Ser Leu Gln Val Asn Thr Thr Ala Leu Ile Pro
805 810 815

Lys Glu Ala Asn Ser Glu Glu Val Phe Leu Phe Lys Pro Glu Asn Ile
820 825 830

Thr Phe Glu Asn Gly Thr Asp Leu Phe Ile Ala Ile Gln Ala Val Asp
835 840 845

Lys Val Asp Leu Lys Ser Glu Ile Ser Asn Ile Ala Arg Val Ser Leu
850 855 860

GENENLAW-#306717-v1-P4190R1_SequenceListing_as_filed.TXT

Phe Ile Pro Pro Gln Thr Pro Pro Glu Thr Pro Ser Pro Asp Glu Thr
865 870 875 880

Ser Ala Pro Cys Pro Asn Ile His Ile Asn Ser Thr Ile Pro Gly Ile
885 890 895

His Ile Leu Lys Ile Met Trp Lys Trp Ile Gly Glu Leu Gln Leu Ser
900 905 910

Ile Ala

<210> 5
<211> 141
<212> PRT
<213> Homo sapiens

<400> 5
Met Ala Trp Pro Leu Cys Thr Leu Leu Leu Leu Ala Thr Gln Ala
1 5 10 15

Val Ala Leu Ala Trp Ser Pro Gln Glu Glu Asp Arg Ile Ile Glu Gly
20 25 30

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

His Phe Val Ile Ser Glu Tyr Asn Lys Ala Thr Glu Asp Glu Tyr Tyr
50 55 60

Arg Arg Leu Leu Arg Val Leu Arg Ala Arg Glu Gln Ile Val Gly Gly
65 70 75 80

Val Asn Tyr Phe Phe Asp Ile Glu Val Gly Arg Thr Ile Cys Thr Lys
85 90 95

Ser Gln Pro Asn Leu Asp Thr Cys Ala Phe His Glu Gln Pro Glu Leu
100 105 110

Gln Lys Lys Gln Leu Cys Ser Phe Gln Ile Tyr Glu Val Pro Trp Glu
115 120 125

Asp Arg Met Ser Leu Val Asn Ser Arg Cys Gln Glu Ala
130 135 140

<210> 6
<211> 134
<212> PRT
<213> Homo sapiens

<400> 6
Met Leu Leu Val Leu Leu Ser Val Val Leu Leu Ala Leu Ser Ser Ala
1 5 10 15

Gln Ser Thr Asp Asn Asp Val Asn Tyr Glu Asp Phe Thr Phe Thr Ile
20 25 30

Pro Asp Val Glu Asp Ser Ser Gln Arg Pro Asp Gln Gly Pro Gln Arg
35 40 45

Pro Pro Pro Glu Gly Leu Leu Pro Arg Pro Pro Gly Asp Ser Gly Asn
50 55 60

Gln Asp Asp Gly Pro Gln Gln Arg Pro Pro Lys Pro Gly Gly His His
65 70 75 80

Arg His Pro Pro Pro Pro Phe Gln Asn Gln Gln Arg Pro Pro Arg
85 90 95

Arg Gly His Arg Gln Leu Ser Leu Pro Arg Phe Pro Ser Val Ser Leu
100 105 110

Gln Glu Ala Ser Ser Phe Phe Arg Arg Asp Arg Pro Ala Arg His Pro
115 120 125

Gln Glu Gln Pro Leu Trp
130

<210> 7
<211> 415
<212> PRT
<213> Homo sapiens

<400> 7
Met Glu Asp Leu Cys Val Ala Asn Thr Leu Phe Ala Leu Asn Leu Phe
1 5 10 15

Lys His Leu Ala Lys Ala Ser Pro Thr Gln Asn Leu Phe Leu Ser Pro
20 25 30

Trp Ser Ile Ser Ser Thr Met Ala Met Val Tyr Met Gly Ser Arg Gly
35 40 45

Ser Thr Glu Asp Gln Met Ala Lys Val Leu Gln Phe Asn Glu Val Gly
50 55 60

Ala Asn Ala Val Thr Pro Met Thr Pro Glu Asn Phe Thr Ser Cys Gly
65 70 75 80

Phe Met Gln Gln Ile Gln Lys Gly Ser Tyr Pro Asp Ala Ile Leu Gln
85 90 95

Ala Gln Ala Ala Asp Lys Ile His Ser Ser Phe Arg Ser Leu Ser Ser
100 105 110

Ala Ile Asn Ala Ser Thr Gly Asn Tyr Leu Leu Glu Ser Val Asn Lys
115 120 125

GENENLAW-#306717-v1-P4190R1_SequenceListing_as_filed.TXT

Leu Phe Gly Glu Lys Ser Ala Ser Phe Arg Glu Glu Tyr Ile Arg Leu
130 135 140

Cys Gln Lys Tyr Tyr Ser Ser Glu Pro Gln Ala Val Asp Phe Leu Glu
145 150 155 160

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

Thr Lys Gly Lys Ile Pro Asn Leu Leu Pro Glu Gly Ser Val Asp Gly
180 185 190

Asp Thr Arg Met Val Leu Val Asn Ala Val Tyr Phe Lys Gly Lys Trp
195 200 205

Lys Thr Pro Phe Glu Lys Lys Leu Asn Gly Leu Tyr Pro Phe Arg Val
210 215 220

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

Leu Asn Ile Gly Tyr Ile Glu Asp Leu Lys Ala Gln Ile Leu Glu Leu
245 250 255

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

Ala Asp Val Ser Thr Gly Leu Glu Leu Leu Glu Ser Glu Ile Thr Tyr
275 280 285

Asp Lys Leu Asn Lys Trp Thr Ser Lys Asp Lys Met Ala Glu Asp Glu
290 295 300

Val Glu Val Tyr Ile Pro Gln Phe Lys Leu Glu Glu His Tyr Glu Leu
305 310 315 320

Arg Ser Ile Leu Arg Ser Met Gly Met Glu Asp Ala Phe Asn Lys Gly
325 330 335

Arg Ala Asn Phe Ser Gly Met Ser Glu Arg Asn Asp Leu Phe Leu Ser
340 345 350

Glu Val Phe His Gln Ala Met Val Asp Val Asn Glu Glu Gly Thr Glu
355 360 365

Ala Ala Ala Gly Thr Gly Gly Val Met Thr Gly Arg Thr Gly His Gly
370 375 380

Gly Pro Gln Phe Val Ala Asp His Pro Phe Leu Phe Leu Ile Met His
385 390 395 400

Lys Ile Thr Asn Cys Ile Leu Phe Phe Gly Arg Phe Ser Ser Pro
405 410 415

<210> 8
<211> 702
<212> PRT
<213> Homo sapiens

<400> 8
Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1 5 10 15

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
20 25 30

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

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
50 55 60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65 70 75 80

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
85 90 95

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

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
115 120 125

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

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

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
165 170 175

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
180 185 190

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
195 200 205

Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
210 215 220

GENENLAW-#306717-v1-P4190R1_SequenceListing_as_filed.TXT

Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225 230 235 240

Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
245 250 255

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
260 265 270

Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
275 280 285

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
290 295 300

Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305 310 315 320

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

Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
340 345 350

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
355 360 365

Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
370 375 380

Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
385 390 395 400

Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
405 410 415

Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
420 425 430

Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
435 440 445

Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
450 455 460

Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
465 470 475 480

Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
485 490 495

Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
500 505 510

Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
515 520 525

Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
530 535 540

Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
545 550 555 560

Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
565 570 575

Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
580 585 590

Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
595 600 605

Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
610 615 620

Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
625 630 635 640

Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
645 650 655

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

Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala Gly Ala Thr
675 680 685

Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile
690 695 700

<210> 9

<211> 1153

<212> PRT

<213> Homo sapiens

<400> 9

Met Ala Cys Pro Trp Lys Phe Leu Phe Lys Thr Lys Phe His Gln Tyr
1 5 10 15

Ala Met Asn Gly Glu Lys Asp Ile Asn Asn Asn Val Glu Lys Ala Pro
20 25 30

Cys Ala Thr Ser Ser Pro Val Thr Gln Asp Asp Leu Gln Tyr His Asn
35 40 45

Leu Ser Lys Gln Gln Asn Glu Ser Pro Gln Pro Leu Val Glu Thr Gly
 50 55 60
 Lys Lys Ser Pro Glu Ser Leu Val Lys Leu Asp Ala Thr Pro Leu Ser
 65 70 75 80
 Ser Pro Arg His Val Arg Ile Lys Asn Trp Gly Ser Gly Met Thr Phe
 85 90 95
 Gln Asp Thr Leu His His Lys Ala Lys Gly Ile Leu Thr Cys Arg Ser
 100 105 110
 Lys Ser Cys Leu Gly Ser Ile Met Thr Pro Lys Ser Leu Thr Arg Gly
 115 120 125
 Pro Arg Asp Lys Pro Thr Pro Pro Asp Glu Leu Leu Pro Gln Ala Ile
 130 135 140
 Glu Phe Val Asn Gln Tyr Tyr Gly Ser Phe Lys Glu Ala Lys Ile Glu
 145 150 155 160
 Glu His Leu Ala Arg Val Glu Ala Val Thr Lys Glu Ile Glu Thr Thr
 165 170 175
 Gly Thr Tyr Gln Leu Thr Gly Asp Glu Leu Ile Phe Ala Thr Lys Gln
 180 185 190
 Ala Trp Arg Asn Ala Pro Arg Cys Ile Gly Arg Ile Gln Trp Ser Asn
 195 200 205
 Leu Gln Val Phe Asp Ala Arg Ser Cys Ser Thr Ala Arg Glu Met Phe
 210 215 220
 Glu His Ile Cys Arg His Val Arg Tyr Ser Thr Asn Asn Gly Asn Ile
 225 230 235 240
 Arg Ser Ala Ile Thr Val Phe Pro Gln Arg Ser Asp Gly Lys His Asp
 245 250 255
 Phe Arg Val Trp Asn Ala Gln Leu Ile Arg Tyr Ala Gly Tyr Gln Met
 260 265 270
 Pro Asp Gly Ser Ile Arg Gly Asp Pro Ala Asn Val Glu Phe Thr Gln
 275 280 285
 Leu Cys Ile Asp Leu Gly Trp Lys Pro Lys Tyr Gly Arg Phe Asp Val
 290 295 300
 Val Pro Leu Val Leu Gln Ala Asn Gly Arg Asp Pro Glu Leu Phe Glu
 305 310 315 320

Ile Pro Pro Asp Leu Val Leu Glu Val Ala Met Glu His Pro Lys Tyr
325 330 335

Glu Trp Phe Arg Glu Leu Glu Leu Lys Trp Tyr Ala Leu Pro Ala Val
340 345 350

Ala Asn Met Leu Leu Glu Val Gly Gly Leu Glu Phe Pro Gly Cys Pro
355 360 365

Phe Asn Gly Trp Tyr Met Gly Thr Glu Ile Gly Val Arg Asp Phe Cys
370 375 380

Asp Val Gln Arg Tyr Asn Ile Leu Glu Glu Val Gly Arg Arg Met Gly
385 390 395 400

Leu Glu Thr His Lys Leu Ala Ser Leu Trp Lys Asp Gln Ala Val Val
405 410 415

Glu Ile Asn Ile Ala Val Leu His Ser Phe Gln Lys Gln Asn Val Thr
420 425 430

Ile Met Asp His His Ser Ala Ala Glu Ser Phe Met Lys Tyr Met Gln
435 440 445

Asn Glu Tyr Arg Ser Arg Gly Gly Cys Pro Ala Asp Trp Ile Trp Leu
450 455 460

Val Pro Pro Met Ser Gly Ser Ile Thr Pro Val Phe His Gln Glu Met
465 470 475 480

Leu Asn Tyr Val Leu Ser Pro Phe Tyr Tyr Tyr Gln Val Glu Ala Trp
485 490 495

Lys Thr His Val Trp Gln Asp Glu Lys Arg Arg Pro Lys Arg Arg Glu
500 505 510

Ile Pro Leu Lys Val Leu Val Lys Ala Val Leu Phe Ala Cys Met Leu
515 520 525

Met Arg Lys Thr Met Ala Ser Arg Val Arg Val Thr Ile Leu Phe Ala
530 535 540

Thr Glu Thr Gly Lys Ser Glu Ala Leu Ala Trp Asp Leu Gly Ala Leu
545 550 555 560

Phe Ser Cys Ala Phe Asn Pro Lys Val Val Cys Met Asp Lys Tyr Arg
565 570 575

Leu Ser Cys Leu Glu Glu Glu Arg Leu Leu Leu Val Val Thr Ser Thr
580 585 590

GENENLAW-#306717-v1-P4190R1_SequenceListing_as_filed.TXT

Phe Gly Asn Gly Asp Cys Pro Gly Asn Gly Glu Lys Leu Lys Lys Ser
595 600 605

Leu Phe Met Leu Lys Glu Leu Asn Asn Lys Phe Arg Tyr Ala Val Phe
610 615 620

Gly Leu Gly Ser Ser Met Tyr Pro Arg Phe Cys Ala Phe Ala His Asp
625 630 635 640

Ile Asp Gln Lys Leu Ser His Leu Gly Ala Ser Gln Leu Thr Pro Met
645 650 655

Gly Glu Gly Asp Glu Leu Ser Gly Gln Glu Asp Ala Phe Arg Ser Trp
660 665 670

Ala Val Gln Thr Phe Lys Ala Ala Cys Glu Thr Phe Asp Val Arg Gly
675 680 685

Lys Gln His Ile Gln Ile Pro Lys Leu Tyr Thr Ser Asn Val Thr Trp
690 695 700

Asp Pro His His Tyr Arg Leu Val Gln Asp Ser Gln Pro Leu Asp Leu
705 710 715 720

Ser Lys Ala Leu Ser Ser Met His Ala Lys Asn Val Phe Thr Met Arg
725 730 735

Leu Lys Ser Arg Gln Asn Leu Gln Ser Pro Thr Ser Ser Arg Ala Thr
740 745 750

Ile Leu Val Glu Leu Ser Cys Glu Asp Gly Gln Gly Leu Asn Tyr Leu
755 760 765

Pro Gly Glu His Leu Gly Val Cys Pro Gly Asn Gln Pro Ala Leu Val
770 775 780

Gln Gly Ile Leu Glu Arg Val Val Asp Gly Pro Thr Pro His Gln Thr
785 790 795 800

Val Arg Leu Glu Ala Leu Asp Glu Ser Gly Ser Tyr Trp Val Ser Asp
805 810 815

Lys Arg Leu Pro Pro Cys Ser Leu Ser Gln Ala Leu Thr Tyr Phe Leu
820 825 830

Asp Ile Thr Thr Pro Pro Thr Gln Leu Leu Leu Gln Lys Leu Ala Gln
835 840 845

Val Ala Thr Glu Glu Pro Glu Arg Gln Arg Leu Glu Ala Leu Cys Gln
850 855 860

Pro Ser Glu Tyr Ser Lys Trp Lys Phe Thr Asn Ser Pro Thr Phe Leu
865 870 875 880

Glu Val Leu Glu Glu Phe Pro Ser Leu Arg Val Ser Ala Gly Phe Leu
885 890 895

Leu Ser Gln Leu Pro Ile Leu Lys Pro Arg Phe Tyr Ser Ile Ser Ser
900 905 910

Ser Arg Asp His Thr Pro Thr Glu Ile His Leu Thr Val Ala Val Val
915 920 925

Thr Tyr His Thr Arg Asp Gly Gln Gly Pro Leu His His Gly Val Cys
930 935 940

Ser Thr Trp Leu Asn Ser Leu Lys Pro Gln Asp Pro Val Pro Cys Phe
945 950 955 960

Val Arg Asn Ala Ser Gly Phe His Leu Pro Glu Asp Pro Ser His Pro
965 970 975

Cys Ile Leu Ile Gly Pro Gly Thr Gly Ile Ala Pro Phe Arg Ser Phe
980 985 990

Trp Gln Gln Arg Leu His Asp Ser Gln His Lys Gly Val Arg Gly Gly
995 1000 1005

Arg Met Thr Leu Val Phe Gly Cys Arg Arg Pro Asp Glu Asp His
1010 1015 1020

Ile Tyr Gln Glu Glu Met Leu Glu Met Ala Gln Lys Gly Val Leu
1025 1030 1035

His Ala Val His Thr Ala Tyr Ser Arg Leu Pro Gly Lys Pro Lys
1040 1045 1050

Val Tyr Val Gln Asp Ile Leu Arg Gln Gln Leu Ala Ser Glu Val
1055 1060 1065

Leu Arg Val Leu His Lys Glu Pro Gly His Leu Tyr Val Cys Gly
1070 1075 1080

Asp Val Arg Met Ala Arg Asp Val Ala His Thr Leu Lys Gln Leu
1085 1090 1095

Val Ala Ala Lys Leu Lys Leu Asn Glu Glu Gln Val Glu Asp Tyr
1100 1105 1110

Phe Phe Gln Leu Lys Ser Gln Lys Arg Tyr His Glu Asp Ile Phe
1115 1120 1125

Gly Ala Val Phe Pro Tyr Glu Ala Lys Lys Asp Arg Val Ala Val
1130 1135 1140

Gln Pro Ser Ser Leu Glu Met Ser Ala Leu
1145 1150

<210> 10
<211> 390
<212> PRT
<213> Homo sapiens

<400> 10
Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
1 5 10 15

Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
20 25 30

Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
35 40 45

Thr Ala Gln Gln Ile Ser Lys Val Leu His Phe Asp Gln Val Thr Glu
50 55 60

Asn Thr Thr Glu Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
65 70 75 80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
85 90 95

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

Tyr Gln Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
115 120 125

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

Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
145 150 155 160

Asn Leu Phe Pro Asp Gly Thr Ile Gly Asn Asp Thr Thr Leu Val Leu
165 170 175

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Asn Lys Phe Lys Lys
180 185 190

Glu Asn Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
195 200 205

GENENLAW-#306717-v1-P4190R1_SequenceListing_as_filed.TXT

Ser Val Gln Met Met Arg Gln Tyr Asn Ser Phe Asn Phe Ala Leu Leu
210 215 220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
225 230 235 240

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

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

Gln Asn Met Arg Glu Thr Cys Val Asp Leu His Leu Pro Arg Phe Lys
275 280 285

Met Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
290 295 300

Val Asn Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Trp Ser
305 310 315 320

His Gly Leu Ser Val Ser Lys Val Leu His Lys Ala Phe Val Glu Val
325 330 335

Thr Glu Glu Gly Val Glu Ala Ala Ala Ala Thr Ala Val Val Val Val
340 345 350

Glu Leu Ser Ser Pro Ser Thr Asn Glu Glu Phe Cys Cys Asn His Pro
355 360 365

Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
370 375 380

Gly Arg Phe Ser Ser Pro
385 390

<210> 11
<211> 141
<212> PRT
<213> Homo sapiens

<400> 11
Met Ala Arg Pro Leu Cys Thr Leu Leu Leu Leu Met Ala Thr Leu Ala
1 5 10 15

Gly Ala Leu Ala Ser Ser Ser Lys Glu Glu Asn Arg Ile Ile Pro Gly
20 25 30

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

His Phe Ala Ile Ser Glu Tyr Asn Lys Ala Thr Glu Asp Glu Tyr Tyr
50 55 60

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

Val Asn Tyr Phe Phe Asp Val Glu Val Gly Arg Thr Ile Cys Thr Lys
85 90 95

Ser Gln Pro Asn Leu Asp Thr Cys Ala Phe His Glu Gln Pro Glu Leu
100 105 110

Gln Lys Lys Gln Leu Cys Ser Phe Glu Ile Tyr Glu Val Pro Trp Glu
115 120 125

Asp Arg Met Ser Leu Val Asn Ser Arg Cys Gln Glu Ala
130 135 140

<210> 12

<211> 393

<212> PRT

<213> Homo sapiens

<400> 12

Met Leu Leu Ile Leu Leu Ser Val Ala Leu Leu Ala Leu Ser Ser Ala
1 5 10 15

Gln Asn Leu Asn Glu Asp Val Ser Gln Glu Glu Ser Pro Ser Leu Ile
20 25 30

Ala Gly Lys Pro Gln Gly Pro Pro Pro Gln Gly Gly Asn Gln Pro Gln
35 40 45

Gly Pro Pro Pro Pro Pro Gly Lys Pro Gln Gly Pro Pro Pro Gln Gly
50 55 60

Gly Asn Lys Pro Gln Gly Pro Pro Pro Pro Gly Lys Pro Gln Gly Pro
65 70 75 80

Pro Pro Gln Gly Asp Lys Ser Arg Ser Pro Arg Ser Pro Pro Gly Lys
85 90 95

Pro Gln Gly Pro Pro Pro Gln Gly Gly Asn Gln Pro Gln Gly Pro Pro
100 105 110

Pro Pro Pro Gly Lys Pro Gln Gly Pro Pro Pro Gln Gly Gly Asn Lys
115 120 125

Pro Gln Gly Pro Pro Pro Pro Gly Lys Pro Gln Gly Pro Pro Pro Gln
130 135 140

Gly Asp Asn Lys Ser Arg Ser Ser Arg Ser Pro Pro Gly Lys Pro Gln
145 150 155 160

GENENLAW-#306717-v1-P4190R1_SequenceListing_as_filed.TXT

Gly Pro Pro Pro Gln Gly Gly Asn Gln Pro Gln Gly Pro Pro Pro Pro
165 170 175

Pro Gly Lys Pro Gln Gly Pro Pro Pro Gln Gly Gly Asn Lys Pro Gln
180 185 190

Gly Pro Pro Pro Pro Gly Lys Pro Gln Gly Pro Pro Pro Gln Gly Asp
195 200 205

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

Pro Gln Gly Gly Asn Gln Pro Gln Gly Pro Pro Pro Pro Gly Lys
225 230 235 240

Pro Gln Gly Pro Pro Pro Gln Gly Gly Asn Arg Pro Gln Gly Pro Pro
245 250 255

Pro Pro Gly Lys Pro Gln Gly Pro Pro Pro Gln Gly Asp Lys Ser Arg
260 265 270

Ser Ser Gln Ser Pro Pro Gly Lys Pro Gln Gly Pro Pro Pro Gln Gly
275 280 285

Gly Asn Gln Pro Gln Gly Pro Pro Pro Pro Gly Lys Pro Gln Gly
290 295 300

Pro Pro Pro Gln Gly Gly Asn Lys Pro Gln Gly Pro Pro Pro Gly
305 310 315 320

Lys Pro Gln Gly Pro Pro Ala Gln Gly Gly Ser Lys Ser Gln Ser Ala
325 330 335

Arg Ser Pro Pro Gly Lys Pro Gln Gly Pro Pro Gln Gln Glu Gly Asn
340 345 350

Asn Pro Gln Gly Pro Pro Pro Pro Ala Gly Gly Asn Pro Gln Gln Pro
355 360 365

Gln Ala Pro Pro Ala Gly Gln Pro Gln Gly Pro Pro Arg Pro Pro Gln
370 375 380

Gly Gly Arg Pro Ser Arg Pro Pro Gln
385 390

<210> 13
<211> 235
<212> PRT
<213> Homo sapiens

<400> 13
Met Leu Ser Leu Leu Leu Leu Ala Leu Pro Val Leu Ala Ser Pro Ala
1 5 10 15

Tyr Val Ala Pro Ala Pro Gly Gln Ala Leu Gln Gln Thr Gly Ile Val
20 25 30

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

Arg Val Arg Gly Pro Tyr Trp Met His Phe Cys Gly Gly Ser Leu Ile
50 55 60

His Pro Gln Trp Val Leu Thr Ala Ala His Cys Val Glu Pro Asp Ile
65 70 75 80

Lys Asp Leu Ala Ala Leu Arg Val Gln Leu Arg Glu Gln His Leu Tyr
85 90 95

Tyr Gln Asp Gln Leu Leu Pro Val Ser Arg Ile Ile Val His Pro Gln
100 105 110

Phe Tyr Ile Ile Gln Thr Gly Ala Asp Ile Ala Leu Leu Glu Leu Glu
115 120 125

Glu Pro Val Asn Ile Ser Ser His Ile His Thr Val Thr Leu Pro Pro
130 135 140

Ala Ser Glu Thr Phe Pro Pro Gly Met Pro Cys Trp Val Thr Gly Trp
145 150 155 160

Gly Asp Val Asp Asn Asn Val His Leu Pro Pro Pro Tyr Pro Leu Lys
165 170 175

Glu Val Glu Val Pro Val Val Glu Asn His Leu Cys Asn Ala Glu Tyr
180 185 190

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

Met Leu Cys Ala Gly Ser Glu Asn His Asp Ser Cys Gln Gly Asp Ser
210 215 220

Gly Gly Pro Leu Val Cys Lys Val Asn Gly Thr
225 230 235

<210> 14
<211> 321
<212> PRT
<213> Homo sapiens

<400> 14
Met Ala Leu Gly Ala Cys Gly Leu Leu Leu Leu Ala Val Pro Gly
1 5 10 15

Val Ser Leu Arg Thr Leu Gln Pro Gly Cys Gly Arg Pro Gln Val Ser
20 25 30

Asp Ala Gly Gly Arg Ile Val Gly Gly His Ala Ala Pro Ala Gly Ala
35 40 45

Trp Pro Trp Gln Ala Ser Leu Arg Leu Arg Arg Met His Val Cys Gly
50 55 60

Gly Ser Leu Leu Ser Pro Gln Trp Val Leu Thr Ala Ala His Cys Phe
65 70 75 80

Ser Gly Ser Leu Asn Ser Ser Asp Tyr Gln Val His Leu Gly Glu Leu
85 90 95

Glu Ile Thr Leu Ser Pro His Phe Ser Thr Val Arg Gln Ile Ile Leu
100 105 110

His Ser Ser Pro Ser Gly Gln Pro Gly Thr Ser Gly Asp Ile Ala Leu
115 120 125

Val Glu Leu Ser Val Pro Val Thr Leu Ser Ser Arg Ile Leu Pro Val
130 135 140

Cys Leu Pro Glu Ala Ser Asp Asp Phe Cys Pro Gly Ile Arg Cys Trp
145 150 155 160

Val Thr Gly Trp Gly Tyr Thr Arg Glu Gly Glu Pro Leu Pro Pro Pro
165 170 175

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

Arg Arg Asp Tyr Pro Gly Pro Gly Gly Ser Ile Leu Gln Pro Asp Met
195 200 205

Leu Cys Ala Arg Gly Pro Gly Asp Ala Cys Gln Asp Asp Ser Gly Gly
210 215 220

Pro Leu Val Cys Gln Val Asn Gly Ala Trp Val Gln Ala Gly Ile Val
225 230 235 240

Ser Trp Gly Glu Gly Cys Gly Arg Pro Asn Arg Pro Gly Val Tyr Thr
245 250 255

Arg Val Pro Ala Tyr Val Asn Trp Ile Arg Arg His Ile Thr Ala Ser
260 265 270

Gly Gly Ser Glu Ser Gly Tyr Pro Arg Leu Pro Leu Leu Ala Gly Leu
275 280 285

GENENLAW-#306717-v1-P4190R1_SequenceListing_as_filed.TXT

Phe Leu Pro Gly Leu Phe Leu Leu Val Ser Cys Val Leu Leu Ala
290 295 300

Lys Cys Leu Leu His Pro Ser Ala Asp Gly Thr Pro Phe Pro Ala Pro
305 310 315 320

Asp

<210> 15
<211> 540
<212> PRT
<213> Homo sapiens

<400> 15
Met Ala Lys Gly Glu Gly Ala Glu Ser Gly Ser Ala Ala Gly Leu Leu
1 5 10 15

Pro Thr Ser Ile Leu Gln Ser Thr Glu Arg Pro Ala Gln Val Lys Lys
20 25 30

Glu Pro Lys Lys Lys Lys Gln Gln Leu Ser Val Cys Asn Lys Leu Cys
35 40 45

Tyr Ala Leu Gly Gly Ala Pro Tyr Gln Val Thr Gly Cys Ala Leu Gly
50 55 60

Phe Phe Leu Gln Ile Tyr Leu Leu Asp Val Ala Gln Lys Asp Glu Glu
65 70 75 80

Val Val Phe Cys Phe Ser Ser Phe Gln Val Gly Pro Phe Ser Ala Ser
85 90 95

Ile Ile Leu Phe Val Gly Arg Ala Trp Asp Ala Ile Thr Asp Pro Leu
100 105 110

Val Gly Leu Cys Ile Ser Lys Ser Pro Trp Thr Cys Leu Gly Arg Leu
115 120 125

Met Pro Trp Ile Ile Phe Ser Thr Pro Leu Ala Val Ile Ala Tyr Phe
130 135 140

Leu Ile Trp Phe Val Pro Asp Phe Pro His Gly Gln Thr Tyr Trp Tyr
145 150 155 160

Leu Leu Phe Tyr Cys Leu Phe Glu Thr Met Val Thr Cys Phe His Val
165 170 175

Pro Tyr Ser Ala Leu Thr Met Phe Ile Ser Thr Glu Gln Thr Glu Arg
180 185 190

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

Leu Gly Thr Ala Ile Gln Gly Gln Ile Val Gly Gln Ala Asp Thr Pro
210 215 220

Cys Phe Gln Asp Leu Asn Ser Ser Thr Val Ala Ser Gln Ser Ala Asn
225 230 235 240

His Thr His Gly Thr Thr Ser His Arg Glu Thr Gln Lys Ala Tyr Leu
245 250 255

Leu Ala Ala Gly Val Ile Val Cys Ile Tyr Ile Ile Cys Ala Val Ile
260 265 270

Leu Ile Leu Gly Val Arg Glu Gln Arg Glu Pro Tyr Glu Ala Gln Gln
275 280 285

Ser Glu Pro Ile Ala Tyr Phe Arg Gly Leu Arg Leu Val Met Ser His
290 295 300

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

Phe Met Leu Val Glu Gly Asn Phe Val Leu Phe Cys Thr Tyr Thr Leu
325 330 335

Gly Phe Arg Asn Glu Phe Gln Asn Leu Leu Leu Ala Ile Met Leu Ser
340 345 350

Ala Thr Leu Thr Ile Pro Ile Trp Gln Trp Phe Leu Thr Arg Phe Gly
355 360 365

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

Ile Leu Val Ala Leu Met Glu Ser Asn Leu Ile Ile Thr Tyr Ala Val
385 390 395 400

Ala Val Ala Ala Gly Ile Ser Val Ala Ala Ala Phe Leu Leu Pro Trp
405 410 415

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

Phe His Gly Thr Glu Pro Ile Phe Phe Ser Phe Tyr Val Phe Phe Thr
435 440 445

Lys Phe Ala Ser Gly Val Ser Leu Gly Ile Ser Thr Leu Ser Leu Asp
450 455 460

Phe Ala Gly Tyr Gln Thr Arg Gly Cys Ser Gln Pro Glu Arg Val Lys
465 470 475 480

Phe Thr Leu Asn Met Leu Val Thr Met Ala Pro Ile Val Leu Ile Leu
485 490 495

Leu Gly Leu Leu Leu Phe Lys Met Tyr Pro Ile Asp Glu Glu Arg Arg
500 505 510

Arg Gln Asn Lys Lys Ala Leu Gln Ala Leu Arg Asp Glu Ala Ser Ser
515 520 525

Ser Gly Cys Ser Glu Thr Asp Ser Thr Glu Leu Ala
530 535 540

<210> 16
<211> 417
<212> PRT
<213> Homo sapiens

<400> 16
Met Arg Leu Ile Leu Pro Val Gly Leu Ile Ala Thr Thr Leu Ala Ile
1 5 10 15

Ala Pro Val Arg Phe Asp Arg Glu Lys Val Phe Arg Val Lys Pro Gln
20 25 30

Asp Glu Lys Gln Ala Asp Ile Ile Lys Asp Leu Ala Lys Thr Asn Glu
35 40 45

Leu Asp Phe Trp Tyr Pro Gly Ala Thr His His Val Ala Ala Asn Met
50 55 60

Met Val Asp Phe Arg Val Ser Glu Lys Glu Ser Gln Ala Ile Gln Ser
65 70 75 80

Ala Leu Asp Gln Asn Lys Met His Tyr Glu Ile Leu Ile His Asp Leu
85 90 95

Gln Glu Glu Ile Glu Lys Gln Phe Asp Val Lys Glu Asp Ile Pro Gly
100 105 110

Arg His Ser Tyr Ala Lys Tyr Asn Asn Trp Glu Lys Ile Val Ala Trp
115 120 125

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

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

Glu Lys Asn Glu Arg Arg Lys Ala Ile Phe Met Asp Cys Gly Ile His
165 170 175

Ala Arg Glu Trp Val Ser Pro Ala Phe Cys Gln Trp Phe Val Tyr Gln
180 185 190

Ala Thr Lys Thr Tyr Gly Arg Asn Lys Ile Met Thr Lys Leu Leu Asp
195 200 205

Arg Met Asn Phe Tyr Ile Leu Pro Val Phe Asn Val Asp Gly Tyr Ile
210 215 220

Trp Ser Trp Thr Lys Asn Arg Met Trp Arg Lys Asn Arg Ser Lys Asn
225 230 235 240

Gln Asn Ser Lys Cys Ile Gly Thr Asp Leu Asn Arg Asn Phe Asn Ala
245 250 255

Ser Trp Asn Ser Ile Pro Asn Thr Asn Asp Pro Cys Ala Asp Asn Tyr
260 265 270

Arg Gly Ser Ala Pro Glu Ser Glu Lys Glu Thr Lys Ala Val Thr Asn
275 280 285

Phe Ile Arg Ser His Leu Asn Glu Ile Lys Val Tyr Ile Thr Phe His
290 295 300

Ser Tyr Ser Gln Met Leu Leu Phe Pro Tyr Gly Tyr Thr Ser Lys Leu
305 310 315 320

Pro Pro Asn His Glu Asp Leu Ala Lys Val Ala Lys Ile Gly Thr Asp
325 330 335

Val Leu Ser Thr Arg Tyr Glu Thr Arg Tyr Ile Tyr Gly Pro Ile Glu
340 345 350

Ser Thr Ile Tyr Pro Ile Ser Gly Ser Ser Leu Asp Trp Ala Tyr Asp
355 360 365

Leu Gly Ile Lys His Thr Phe Ala Phe Glu Leu Arg Asp Lys Gly Lys
370 375 380

Phe Gly Phe Leu Leu Pro Glu Ser Arg Ile Lys Pro Thr Cys Arg Glu
385 390 395 400

Thr Met Leu Ala Val Lys Phe Ile Ala Lys Tyr Ile Leu Lys His Thr
405 410 415

Ser

<210> 17
<211> 338
<212> PRT
<213> Homo sapiens

<400> 17

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

Asn Leu Leu Ile Thr Gln Gln Ile Ile Pro Val Leu Tyr Cys Met Val
20 25 30

Phe Ile Ala Gly Ile Leu Leu Asn Gly Val Ser Gly Trp Ile Phe Phe
35 40 45

Tyr Val Pro Ser Ser Lys Ser Phe Ile Ile Tyr Leu Lys Asn Ile Val
50 55 60

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

Asp Ser Gly Leu Gly Pro Trp Gln Leu Asn Val Phe Val Cys Arg Val
85 90 95

Ser Ala Val Leu Phe Tyr Val Asn Met Tyr Val Ser Ile Val Phe Phe
100 105 110

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

Thr Ser Phe Ile Gln Ser Val Ser Tyr Ser Lys Leu Leu Ser Val Ile
130 135 140

Val Trp Met Leu Met Leu Leu Leu Ala Val Pro Asn Ile Ile Leu Thr
145 150 155 160

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

Ser Glu Leu Gly Arg Lys Trp His Lys Ala Ser Asn Tyr Ile Phe Val
180 185 190

Ala Ile Phe Trp Ile Val Phe Leu Leu Leu Ile Val Phe Tyr Thr Ala
195 200 205

Ile Thr Lys Lys Ile Phe Lys Ser His Leu Lys Ser Ser Arg Asn Ser
210 215 220

Thr Ser Val Lys Lys Lys Ser Ser Arg Asn Ile Phe Ser Ile Val Phe
225 230 235 240

Val Phe Phe Val Cys Phe Val Pro Tyr His Ile Ala Arg Ile Pro Tyr
245 250 255

Thr Lys Ser Gln Thr Glu Ala His Tyr Ser Cys Gln Ser Lys Glu Ile
260 265 270

Leu Arg Tyr Met Lys Glu Phe Thr Leu Leu Leu Ser Ala Ala Asn Val
275 280 285

Cys Leu Asp Pro Ile Ile Tyr Phe Phe Leu Cys Gln Pro Phe Arg Glu
290 295 300

Ile Leu Cys Lys Lys Leu His Ile Pro Leu Lys Ala Gln Asn Asp Leu
305 310 315 320

Asp Ile Ser Arg Ile Lys Arg Gly Asn Thr Thr Leu Glu Ser Thr Asp
325 330 335

Thr Leu

<210> 18
<211> 852
<212> PRT
<213> Homo sapiens

<400> 18
Met Ala Met Arg Ser Gly Arg His Pro Ser Leu Leu Leu Leu Leu Val
1 5 10 15

Leu Leu Leu Trp Leu Leu Gln Val Ser Ile Ile Asp Ser Val Gln Gln
20 25 30

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

Leu Arg Arg Ser Lys Arg Arg Trp Val Ile Thr Thr Leu Glu Leu Glu
50 55 60

Glu Glu Asp Pro Gly Pro Phe Pro Lys Leu Ile Gly Glu Leu Phe Asn
65 70 75 80

Asn Met Ser Tyr Asn Met Ser Leu Met Tyr Leu Ile Ser Gly Pro Gly
85 90 95

Val Asp Glu Tyr Pro Glu Ile Gly Leu Phe Ser Leu Glu Asp His Glu
100 105 110

Asn Gly Arg Ile Tyr Val His Arg Pro Val Asp Arg Glu Met Thr Pro
115 120 125

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

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

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

Asn Gln Ser Ala Gly Gln Pro Ile Phe Gln Met Leu Ala Val Asp Leu
180 185 190

Asp Glu Glu Asn Thr Pro Asn Ser Gln Val Leu Tyr Phe Leu Ile Ser
195 200 205

Gln Thr Pro Leu Leu Lys Glu Ser Gly Phe Arg Val Asp Arg Leu Ser
210 215 220

Gly Glu Ile Arg Leu Ser Gly Cys Leu Asp Tyr Glu Thr Ala Pro Gln
225 230 235 240

Phe Thr Leu Leu Ile Arg Ala Arg Asp Cys Gly Glu Pro Ser Leu Ser
245 250 255

Ser Thr Thr Thr Val His Val Asp Val Gln Glu Gly Asn Asn His Arg
260 265 270

Pro Ala Phe Thr Gln Glu Asn Tyr Lys Val Gln Ile Pro Glu Gly Arg
275 280 285

Ala Ser Gln Gly Val Leu Arg Leu Leu Val Gln Asp Arg Asp Ser Pro
290 295 300

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

Glu Gly His Phe Asp Ile Ser Thr Asp Pro Glu Thr Asn Glu Gly Ile
325 330 335

Leu Asn Val Ile Lys Pro Leu Asp Tyr Glu Thr Arg Pro Ala Gln Ser
340 345 350

Leu Ile Ile Val Val Glu Asn Glu Glu Arg Leu Val Phe Cys Glu Arg
355 360 365

Gly Lys Leu Gln Pro Pro Arg Lys Ala Ala Ala Ser Ala Thr Val Ser
370 375 380

Val Gln Val Thr Asp Ala Asn Asp Pro Pro Ala Phe His Pro Gln Ser
385 390 395 400

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

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

His Asp Pro Ala Asn Trp Val Ser Val Asp Lys Asn Ser Gly Val Val
435 440 445

Ile Thr Val Glu Pro Ile Asp Arg Glu Ser Pro His Val Asn Asn Ser
450 455 460

Phe Tyr Val Ile Ile Ile His Ala Val Asp Asp Gly Phe Pro Pro Gln
465 470 475 480

Thr Ala Thr Gly Thr Leu Met Leu Phe Leu Ser Asp Ile Asn Asp Asn
485 490 495

Val Pro Thr Leu Arg Pro Arg Ser Arg Tyr Met Glu Val Cys Glu Ser
500 505 510

Ala Val His Glu Pro Leu His Ile Glu Ala Glu Asp Pro Asp Leu Glu
515 520 525

Pro Phe Ser Asp Pro Phe Thr Phe Glu Leu Asp Asn Thr Trp Gly Asn
530 535 540

Ala Glu Asp Thr Trp Lys Leu Gly Arg Asn Trp Gly Gln Ser Val Glu
545 550 555 560

Leu Leu Thr Leu Arg Ser Leu Pro Arg Gly Asn Tyr Leu Val Pro Leu
565 570 575

Phe Ile Gly Asp Lys Gln Gly Leu Ser Gln Lys Gln Thr Val His Val
580 585 590

Arg Ile Cys Pro Cys Ala Ser Gly Leu Thr Cys Val Glu Leu Ala Asp
595 600 605

Ala Glu Val Gly Leu His Val Gly Ala Leu Phe Pro Val Cys Ala Ala
610 615 620

Phe Val Ala Leu Ala Val Ala Leu Leu Phe Leu Leu Arg Cys Tyr Phe
625 630 635 640

Val Leu Glu Pro Lys Arg His Gly Cys Ser Val Ser Asn Asp Glu Gly
645 650 655

His Gln Thr Leu Val Met Tyr Asn Ala Glu Ser Lys Gly Thr Ser Ala
660 665 670

Gln Thr Trp Ser Asp Val Glu Gly Gln Arg Pro Ala Leu Leu Ile Cys
675 680 685

Thr Ala Ala Ala Gly Pro Thr Gln Gly Val Lys Ala Tyr Pro Asp Ala
690 695 700

Thr Met His Arg Gln Leu Leu Ala Pro Val Glu Gly Arg Met Ala Glu
705 710 715 720

Thr Leu Asn Gln Ser Lys Glu Arg Asn Arg Phe Ser Leu Ser Arg Gly
725 730 735

Cys Ile Ile Pro Gln Gly Arg Ala Thr Ala Gly Arg Gly Leu Pro Gln
740 745 750

Asp Ile Tyr Lys Glu Met Met Pro Arg Arg Leu Thr Gln Thr Gly Lys
755 760 765

Arg Lys His Gly Ala Leu Ala Arg Thr Pro Ser Phe Lys Lys Val Val
770 775 780

Tyr Asp His Lys Glu Asp Glu Glu Asn Lys Ala Gly Arg Lys Gln Arg
785 790 795 800

Ser His Leu Phe Lys Val Met Gln Leu Arg Asn Glu Gln Gly Gly Val
805 810 815

Arg Val Gln Ser Ala His Ser Pro Ser Pro Leu Asn Lys Lys Ala Cys
820 825 830

Phe Pro Gly Asp Tyr Arg Gly Glu Ser Ala Gly Gly His Asn Cys Arg
835 840 845

Ala Val Ser Gly
850

<210> 19
<211> 782
<212> PRT
<213> Homo sapiens

<400> 19
Met Ala Pro His Arg Pro Ala Pro Ala Leu Leu Cys Ala Leu Ser Leu
1 5 10 15

Ala Leu Cys Ala Leu Ser Leu Pro Val Arg Ala Ala Thr Ala Ser Arg
20 25 30

Gly Ala Ser Gln Ala Gly Ala Pro Gln Gly Arg Val Pro Glu Ala Arg
35 40 45

Pro Asn Ser Met Val Val Glu His Pro Glu Phe Leu Lys Ala Gly Lys
50 55 60

Glu Pro Gly Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro
65 70 75 80

Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val
85 90 95

Ile Leu Lys Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu
100 105 110

His Tyr Trp Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala
115 120 125

Ala Ile Phe Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val
130 135 140

Gln His Arg Glu Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr
145 150 155 160

Phe Lys Ser Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe
165 170 175

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

Lys Gly Arg Arg Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Glu
195 200 205

Ser Phe Asn Asn Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile
210 215 220

His Gln Trp Cys Gly Ser Asn Ser Asn Arg Tyr Glu Arg Leu Lys Ala
225 230 235 240

Thr Gln Val Ser Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala
245 250 255

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

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

Lys Glu Asp Ala Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser
290 295 300

Asn Gly Ala Gly Thr Met Ser Val Ser Leu Val Ala Asp Glu Asn Pro
305 310 315 320

Phe Ala Gln Gly Ala Leu Lys Ser Glu Asp Cys Phe Ile Leu Asp His
325 330 335

Gly Lys Asp Gly Lys Ile Phe Val Trp Lys Gly Lys Gln Ala Asn Thr
340 345 350

Glu Glu Arg Lys Ala Ala Leu Lys Thr Ala Ser Asp Phe Ile Thr Lys
355 360 365

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

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

Gln Thr Asp Gly Leu Gly Leu Ser Tyr Leu Ser Ser His Ile Ala Asn
405 410 415

Val Glu Arg Val Pro Phe Asp Ala Ala Thr Leu His Thr Ser Thr Ala
420 425 430

Met Ala Ala Gln His Gly Met Asp Asp Asp Gly Thr Gly Gln Lys Gln
435 440 445

Ile Trp Arg Ile Glu Gly Ser Asn Lys Val Pro Val Asp Pro Ala Thr
450 455 460

Tyr Gly Gln Phe Tyr Gly Gly Asp Ser Tyr Ile Ile Leu Tyr Asn Tyr
465 470 475 480

Arg His Gly Gly Arg Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala
485 490 495

Gln Ser Thr Gln Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln
500 505 510

Leu Asp Glu Glu Leu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln
515 520 525

Gly Lys Glu Pro Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met
530 535 540

Ile Ile Tyr Lys Gly Gly Thr Ser Arg Glu Gly Gly Gln Thr Ala Pro
545 550 555 560

Ala Ser Thr Arg Leu Phe Gln Val Arg Ala Asn Ser Ala Gly Ala Thr
565 570 575

Arg Ala Val Glu Val Leu Pro Lys Ala Gly Ala Leu Asn Ser Asn Asp
580 585 590

Ala Phe Val Leu Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Thr
595 600 605

Gly Ala Ser Glu Ala Glu Lys Thr Gly Ala Gln Glu Leu Leu Arg Val
610 615 620

Leu Arg Ala Gln Pro Val Gln Val Ala Glu Gly Ser Glu Pro Asp Gly
625 630 635 640

Phe Trp Glu Ala Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg
645 650 655

Leu Lys Asp Lys Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys
660 665 670

Ser Asn Lys Ile Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu
675 680 685

Met Gln Glu Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp
690 695 700

Asp Gln Val Phe Val Trp Val Gly Lys Asp Ser Gln Glu Glu Glu Lys
705 710 715 720

Thr Glu Ala Leu Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala
725 730 735

Asn Arg Asp Arg Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu
740 745 750

Pro Pro Ser Phe Val Gly Trp Phe Leu Gly Trp Asp Asp Asp Tyr Trp
755 760 765

Ser Val Asp Pro Leu Asp Arg Ala Met Ala Glu Leu Ala Ala
770 775 780

<210> 20
<211> 164
<212> PRT
<213> Homo sapiens

<400> 20
Met Gly Asp Leu Pro Gly Leu Val Arg Leu Ser Ile Ala Leu Arg Ile
1 5 10 15

Gln Pro Asn Asp Gly Pro Val Phe Tyr Lys Val Asp Gly Gln Arg Phe
20 25 30

Gly Gln Asn Arg Thr Ile Lys Leu Leu Thr Gly Ser Ser Tyr Lys Val
35 40 45

Glu Val Lys Ile Lys Pro Ser Thr Leu Gln Val Glu Asn Ile Ser Ile
50 55 60

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

Asp Arg Val Val Tyr Thr Gly Thr Tyr Asp Thr Glu Gly Val Thr Pro
85 90 95

Thr Lys Ser Gly Glu Arg Gln Pro Ile Gln Ile Thr Met Pro Phe Thr
100 105 110

Asp Ile Gly Thr Phe Glu Thr Val Trp Gln Val Lys Phe Tyr Asn Tyr
115 120 125

His Lys Arg Asp His Cys Gln Trp Gly Ser Pro Phe Ser Val Ile Glu
130 135 140

Tyr Glu Cys Lys Pro Asn Glu Thr Arg Ser Leu Met Trp Val Asn Lys
145 150 155 160

Glu Ser Phe Leu

<210> 21

<211> 295

<212> PRT

<213> Homo sapiens

<400> 21

Met Tyr Arg Ile Ser Gln Leu Met Ser Thr Pro Val Ala Ser Ser Ser
1 5 10 15

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

Pro Ser Phe Thr Cys Asp Ser Leu Asp Gly Tyr His Ser Phe Glu Cys
35 40 45

Gly Ser Ile Asp Pro Leu Thr Gly Ser His Tyr Thr Cys Arg Arg Ser
50 55 60

Pro Arg Leu Leu Thr Asn Gly Tyr Tyr Ile Trp Thr Glu Asp Ser Phe
65 70 75 80

Leu Cys Asp Lys Asp Gly Asn Ile Thr Leu Asn Pro Ser Gln Thr Ser
85 90 95

Val Met Tyr Lys Glu Asn Leu Val Arg Ile Phe Arg Lys Lys Lys Arg
100 105 110

Ile Cys His Ser Phe Ser Ser Leu Phe Asn Leu Ser Thr Ser Lys Ser
115 120 125

Trp Leu His Gly Ser Ile Phe Gly Asp Ile Asn Ser Ser Pro Ser Glu
130 135 140

Asp Asn Trp Leu Lys Gly Thr Arg Arg Leu Asp Thr Asp His Cys Asn
145 150 155 160

Gly Asn Ala Asp Asp Leu Asp Cys Ser Ser Leu Thr Asp Asp Trp Glu
165 170 175

Ser Gly Lys Met Asn Ala Glu Ser Val Ile Thr Ser Ser Ser Ser His
180 185 190

Ile Ile Ser Gln Pro Pro Gly Gly Asn Ser His Ser Leu Ser Leu Gln
195 200 205

Ser Gln Leu Thr Ala Ser Glu Arg Phe Gln Glu Asn Ser Ser Asp His
210 215 220

Ser Glu Thr Arg Leu Leu Gln Glu Val Phe Phe Gln Ala Ile Leu Leu
225 230 235 240

Ala Val Cys Leu Ile Ile Ser Ala Cys Ala Arg Trp Phe Met Gly Glu
245 250 255

Ile Leu Ala Ser Val Phe Thr Cys Ser Leu Met Ile Thr Val Ala Tyr
260 265 270

Val Lys Ser Leu Phe Leu Ser Leu Ala Ser Tyr Phe Lys Thr Thr Ala
275 280 285

Cys Ala Arg Phe Val Lys Ile
290 295

<210> 22
<211> 198
<212> PRT
<213> Homo sapiens

<400> 22
Met Asp Ala Ile Leu Asn Tyr Arg Ser Glu Asp Thr Glu Asp Tyr Tyr
1 5 10 15

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

Glu Phe Lys Val Arg Ala Leu Glu Cys His Pro Asp Lys His Pro Glu
35 40 45

Asn Pro Lys Ala Val Glu Thr Phe Gln Lys Leu Gln Lys Ala Lys Glu
50 55 60

Ile Leu Thr Asn Glu Glu Ser Arg Ala Arg Tyr Asp His Trp Arg Arg
65 70 75 80

Ser Gln Met Ser Met Pro Phe Gln Gln Trp Glu Ala Leu Asn Asp Ser
85 90 95

Val Lys Thr Ser Met His Trp Val Val Arg Gly Lys Lys Asp Leu Met
100 105 110

Leu Glu Glu Ser Asp Lys Thr His Thr Thr Lys Met Glu Asn Glu Glu
115 120 125

Cys Asn Glu Gln Arg Glu Arg Lys Lys Glu Glu Leu Ala Ser Thr Ala
130 135 140

Glu Lys Thr Glu Gln Lys Glu Pro Lys Pro Leu Glu Lys Ser Val Ser
145 150 155 160

Pro Gln Asn Ser Asp Ser Ser Gly Phe Ala Asp Val Asn Gly Trp His
165 170 175

Leu Arg Phe Arg Trp Ser Lys Asp Ala Pro Ser Glu Leu Leu Arg Lys
180 185 190

Phe Arg Asn Tyr Glu Ile
195

<210> 23
<211> 159
<212> PRT
<213> Homo sapiens

<400> 23
Met Ser Arg Arg Asn Cys Trp Ile Cys Lys Met Cys Arg Asp Glu Ser
1 5 10 15

Lys Arg Pro Pro Ser Asn Leu Thr Leu Glu Glu Val Leu Gln Trp Ala
20 25 30

Gln Ser Phe Glu Asn Leu Met Ala Thr Lys Tyr Gly Pro Val Val Tyr
35 40 45

Ala Ala Tyr Leu Lys Met Glu His Ser Asp Glu Asn Ile Gln Phe Trp
50 55 60

Met Ala Cys Glu Thr Tyr Lys Lys Ile Ala Ser Arg Trp Ser Arg Ile
65 70 75 80

Ser Arg Ala Lys Lys Leu Tyr Lys Ile Tyr Ile Gln Pro Gln Ser Pro
85 90 95

Arg Glu Ile Asn Ile Asp Ser Ser Thr Arg Glu Thr Ile Ile Arg Asn
100 105 110

Ile Gln Glu Pro Thr Glu Thr Cys Phe Glu Glu Ala Gln Lys Ile Val
115 120 125

Tyr Met His Met Glu Arg Asp Ser Tyr Pro Arg Phe Leu Lys Ser Glu
130 135 140

Met Tyr Gln Lys Leu Leu Lys Thr Met Gln Ser Asn Asn Ser Phe
145 150 155

<210> 24
 <211> 514
 <212> PRT
 <213> Homo sapiens

<400> 24

Met Ala Leu Ser Glu Leu Ala Leu Val Arg Trp Leu Gln Glu Ser Arg
 1 5 10 15

Arg Ser Arg Lys Leu Ile Leu Phe Ile Val Phe Leu Ala Leu Leu Leu
 20 25 30

Asp Asn Met Leu Leu Thr Val Val Val Pro Ile Ile Pro Ser Tyr Leu
 35 40 45

Tyr Ser Ile Lys His Glu Lys Asn Ala Thr Glu Ile Gln Thr Ala Arg
 50 55 60

Pro Val His Thr Ala Ser Ile Ser Asp Ser Phe Gln Ser Ile Phe Ser
 65 70 75 80

Tyr Tyr Asp Asn Ser Thr Met Val Thr Gly Asn Ala Thr Arg Asp Leu
 85 90 95

Thr Leu His Gln Thr Ala Thr Gln His Met Val Thr Asn Ala Ser Ala
 100 105 110

Val Pro Ser Asp Cys Pro Ser Glu Asp Lys Asp Leu Leu Asn Glu Asn
 115 120 125

Val Gln Val Gly Leu Leu Phe Ala Ser Lys Ala Thr Val Gln Leu Ile
 130 135 140

Thr Asn Pro Phe Ile Gly Leu Leu Thr Asn Arg Ile Gly Tyr Pro Ile
 145 150 155 160

Pro Ile Phe Ala Gly Phe Cys Ile Met Phe Val Ser Thr Ile Met Phe
 165 170 175

Ala Phe Ser Ser Ser Tyr Ala Phe Leu Leu Ile Ala Arg Ser Leu Gln
 180 185 190

Gly Ile Gly Ser Ser Cys Ser Ser Val Ala Gly Met Gly Met Leu Ala
 195 200 205

Ser Val Tyr Thr Asp Asp Glu Glu Arg Gly Asn Val Met Gly Ile Ala
 210 215 220

Leu Gly Gly Leu Ala Met Gly Val Leu Val Gly Pro Pro Phe Gly Ser
 225 230 235 240

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

Ala Leu Val Leu Leu Asp Gly Ala Ile Gln Leu Phe Val Leu Gln Pro
260 265 270

Ser Arg Val Gln Pro Glu Ser Gln Lys Gly Thr Pro Leu Thr Thr Leu
275 280 285

Leu Lys Asp Pro Tyr Ile Leu Ile Ala Ala Gly Ser Ile Cys Phe Ala
290 295 300

Asn Met Gly Ile Ala Met Leu Glu Pro Ala Leu Pro Ile Trp Met Met
305 310 315 320

Glu Thr Met Cys Ser Arg Lys Trp Gln Leu Gly Val Ala Phe Leu Pro
325 330 335

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

His Lys Met Gly Arg Trp Leu Cys Ala Leu Leu Gly Met Ile Ile Val
355 360 365

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

Ile Ala Pro Asn Phe Gly Val Gly Phe Ala Ile Gly Met Val Asp Ser
385 390 395 400

Ser Met Met Pro Ile Met Gly Tyr Leu Val Asp Leu Arg His Val Ser
405 410 415

Val Tyr Gly Ser Val Tyr Ala Ile Ala Asp Val Ala Phe Cys Met Gly
420 425 430

Tyr Ala Ile Gly Pro Ser Ala Gly Gly Ala Ile Ala Lys Ala Ile Gly
435 440 445

Phe Pro Trp Leu Met Thr Ile Ile Gly Ile Ile Asp Ile Leu Phe Ala
450 455 460

Pro Leu Cys Phe Phe Leu Arg Ser Pro Pro Ala Lys Glu Glu Lys Met
465 470 475 480

Ala Ile Leu Met Asp His Asn Cys Pro Ile Lys Thr Lys Met Tyr Thr
485 490 495

Gln Asn Asn Ile Gln Ser Tyr Pro Ile Gly Glu Asp Glu Glu Ser Glu
500 505 510

Ser Asp

<210> 25
 <211> 397
 <212> PRT
 <213> Homo sapiens

<400> 25
 Met Asp Ser Leu Ala Thr Ser Ile Asn Gln Phe Ala Leu Glu Leu Ser
 1 5 10 15

Lys Lys Leu Ala Glu Ser Ala Gln Gly Lys Asn Ile Phe Phe Ser Ser
 20 25 30

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

Thr Thr Ala Ala Gln Met Ala Gln Val Leu Gln Phe Asn Arg Asp Gln
 50 55 60

Gly Val Lys Cys Asp Pro Glu Ser Glu Lys Lys Arg Lys Met Glu Phe
 65 70 75 80

Asn Leu Ser Asn Ser Glu Glu Ile His Ser Asp Phe Gln Thr Leu Ile
 85 90 95

Ser Glu Ile Leu Lys Pro Asn Asp Asp Tyr Leu Leu Lys Thr Ala Asn
 100 105 110

Ala Ile Tyr Gly Glu Lys Thr Tyr Ala Phe His Asn Lys Tyr Leu Glu
 115 120 125

Asp Met Lys Thr Tyr Phe Gly Ala Glu Pro Gln Pro Val Asn Phe Val
 130 135 140

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

Gln Thr Glu Gly Lys Ile Gln Asn Leu Leu Pro Asp Asp Ser Val Asp
 165 170 175

Ser Thr Thr Arg Met Ile Leu Val Asn Ala Leu Tyr Phe Lys Gly Ile
 180 185 190

Trp Glu His Gln Phe Leu Val Gln Asn Thr Thr Glu Lys Pro Phe Arg
 195 200 205

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

Lys Leu His Ile Phe His Ile Glu Lys Pro Lys Ala Val Gly Leu Gln
 225 230 235 240

Leu Tyr Tyr Lys Ser Arg Asp Leu Ser Leu Leu Ile Leu Leu Pro Glu
245 250 255

Asp Ile Asn Gly Leu Glu Gln Leu Glu Lys Ala Ile Thr Tyr Glu Lys
260 265 270

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

Leu His Leu Pro Lys Phe Lys Leu Glu Asp Ser Tyr Asp Leu Lys Ser
290 295 300

Thr Leu Ser Ser Met Gly Met Ser Asp Ala Phe Ser Gln Ser Lys Ala
305 310 315 320

Asp Phe Ser Gly Met Ser Ser Ala Arg Asn Leu Phe Leu Ser Asn Val
325 330 335

Phe His Lys Ala Phe Val Glu Ile Asn Glu Gln Gly Thr Glu Ala Ala
340 345 350

Ala Gly Ser Gly Ser Glu Ile Asp Ile Arg Ile Arg Val Pro Ser Ile
355 360 365

Glu Phe Asn Ala Asn His Pro Phe Leu Phe Phe Ile Arg His Asn Lys
370 375 380

Thr Asn Thr Ile Leu Phe Tyr Gly Arg Leu Cys Ser Pro
385 390 395

<210> 26
<211> 729
<212> PRT
<213> Homo sapiens

<400> 26
Met Asp Asp Leu Thr Leu Leu Asp Leu Leu Glu Cys Pro Val Cys Phe
1 5 10 15

Glu Lys Leu Asp Val Thr Ala Lys Val Leu Pro Cys Gln His Thr Phe
20 25 30

Cys Lys Pro Cys Leu Gln Arg Val Phe Lys Ala His Lys Glu Leu Arg
35 40 45

Cys Pro Glu Cys Arg Thr Pro Val Phe Ser Asn Ile Glu Ala Leu Pro
50 55 60

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

Ser Ser Gly Arg Gly Gly Ser Phe Arg Arg Pro Gly Thr Met Thr Leu
85 90 95

Gln Asp Gly Arg Lys Ser Arg Thr Asn Pro Arg Arg Leu Gln Ala Ser
100 105 110

Pro Phe Arg Leu Val Pro Asn Val Arg Ile His Met Asp Gly Val Pro
115 120 125

Arg Ala Lys Ala Leu Cys Asn Tyr Arg Gly Gln Asn Pro Gly Asp Leu
130 135 140

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

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

Ser Ser Val Glu Val Ile Lys Gln Leu Pro Gln Pro Pro Pro Leu Cys
180 185 190

Arg Ala Leu Tyr Asn Phe Asp Leu Arg Gly Lys Asp Lys Ser Glu Asn
195 200 205

Gln Asp Cys Leu Thr Phe Leu Lys Asp Asp Ile Ile Thr Val Ile Ser
210 215 220

Arg Val Asp Glu Asn Trp Ala Glu Gly Lys Leu Gly Asp Lys Val Gly
225 230 235 240

Ile Phe Pro Ile Leu Phe Val Glu Pro Asn Leu Thr Ala Arg His Leu
245 250 255

Leu Glu Lys Asn Lys Gly Arg Gln Ser Ser Cys Thr Lys Asn Leu Ser
260 265 270

Leu Val Ser Ser Ser Ser Arg Gly Asn Thr Ser Thr Leu Arg Arg Gly
275 280 285

Pro Gly Ser Arg Arg Lys Val Pro Gly Gln Phe Ser Ile Thr Thr Ala
290 295 300

Leu Asn Thr Leu Asn Arg Met Val His Ser Pro Ser Gly Arg His Met
305 310 315 320

Val Glu Ile Ser Thr Pro Val Leu Ile Ser Ser Ser Asn Pro Ser Val
325 330 335

Ile Thr Gln Pro Met Glu Lys Ala Asp Val Pro Ser Ser Cys Val Gly
340 345 350

Gln Val Ser Thr Tyr His Pro Ala Pro Val Ser Pro Gly His Ser Thr
355 360 365

Ala Val Val Ser Leu Pro Gly Ser Gln Gln His Leu Ser Ala Asn Met
370 375 380

Phe Val Ala Leu His Ser Tyr Ser Ala His Gly Pro Asp Glu Leu Asp
385 390 395 400

Leu Gln Lys Gly Glu Gly Val Arg Val Leu Gly Lys Cys Gln Asp Gly
405 410 415

Trp Leu Arg Gly Val Ser Leu Val Thr Gly Arg Val Gly Ile Phe Pro
420 425 430

Asn Asn Tyr Val Ile Pro Ile Phe Arg Lys Thr Ser Ser Phe Pro Asp
435 440 445

Ser Arg Ser Pro Gly Leu Tyr Thr Thr Trp Thr Leu Ser Thr Ser Ser
450 455 460

Val Ser Ser Gln Gly Ser Ile Ser Glu Gly Asp Pro Arg Gln Ser Arg
465 470 475 480

Pro Phe Lys Ser Val Phe Val Pro Thr Ala Ile Val Asn Pro Val Arg
485 490 495

Ser Thr Ala Gly Pro Gly Thr Leu Gly Gln Gly Ser Leu Arg Lys Gly
500 505 510

Arg Ser Ser Met Arg Lys Asn Gly Ser Leu Gln Arg Pro Leu Gln Ser
515 520 525

Gly Ile Pro Thr Leu Val Val Gly Ser Leu Arg Arg Ser Pro Thr Met
530 535 540

Val Leu Arg Pro Gln Gln Phe Gln Phe Tyr Gln Pro Gln Gly Ile Pro
545 550 555 560

Ser Ser Pro Ser Ala Val Val Val Glu Met Gly Ser Lys Pro Ala Leu
565 570 575

Thr Gly Glu Pro Ala Leu Thr Cys Ile Ser Arg Gly Ser Glu Ala Arg
580 585 590

Ile His Ser Ala Ala Ser Ser Leu Ile Met Glu Asp Lys Glu Ile Pro
595 600 605

Ile Lys Ser Glu Pro Leu Pro Lys Pro Pro Ala Ser Ala Pro Pro Ser
610 615 620

Ile Leu Val Lys Pro Glu Asn Ser Arg Asn Gly Ile Glu Lys Gln Val
625 630 635 640

Lys Thr Val Arg Phe Gln Asn Tyr Ser Pro Pro Pro Thr Lys His Tyr
645 650 655

Thr Ser His Pro Thr Ser Gly Lys Pro Glu Gln Pro Ala Thr Leu Lys
660 665 670

Ala Ser Gln Pro Glu Ala Ala Ser Leu Gly Pro Glu Met Thr Val Leu
675 680 685

Phe Ala His Arg Ser Gly Cys His Ser Gly Gln Gln Thr Asp Leu Arg
690 695 700

Arg Lys Ser Ala Leu Ala Lys Ala Thr Thr Leu Val Ser Thr Ala Ser
705 710 715 720

Gly Thr Gln Thr Val Phe Pro Ser Lys
725

<210> 27
<211> 240
<212> PRT
<213> Homo sapiens

<400> 27
Met Asp Thr Glu Ser Asn Arg Arg Ala Asn Leu Ala Leu Pro Gln Glu
1 5 10 15

Pro Ser Ser Val Pro Ala Phe Glu Val Leu Glu Ile Ser Pro Gln Glu
20 25 30

Val Ser Ser Gly Arg Leu Leu Lys Ser Ala Ser Ser Pro Pro Leu His
35 40 45

Thr Trp Leu Thr Val Leu Lys Lys Glu Gln Glu Phe Leu Gly Val Thr
50 55 60

Gln Ile Leu Thr Ala Met Ile Cys Leu Cys Phe Gly Thr Val Val Cys
65 70 75 80

Ser Val Leu Asp Ile Ser His Ile Glu Gly Asp Ile Phe Ser Ser Phe
85 90 95

Lys Ala Gly Tyr Pro Phe Trp Gly Ala Ile Phe Phe Ser Ile Ser Gly
100 105 110

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

Gly Ser Leu Gly Ala Asn Thr Ala Ser Ser Ile Ala Gly Gly Thr Gly
130 135 140

Ile Thr Ile Leu Ile Ile Asn Leu Lys Lys Ser Leu Ala Tyr Ile His
145 150 155 160

Ile His Ser Cys Gln Lys Phe Phe Glu Thr Lys Cys Phe Met Ala Ser
165 170 175

Phe Ser Thr Glu Ile Val Val Met Met Leu Phe Leu Thr Ile Leu Gly
180 185 190

Leu Gly Ser Ala Val Ser Leu Thr Ile Cys Gly Ala Gly Glu Glu Leu
195 200 205

Lys Gly Asn Lys Val Pro Glu Asp Arg Val Tyr Glu Glu Leu Asn Ile
210 215 220

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

<210> 28
<211> 521
<212> PRT
<213> Homo sapiens

<400> 28
Met Ala Ser Asn Ser Leu Phe Ser Thr Val Thr Pro Cys Gln Gln Asn
1 5 10 15

Phe Phe Trp Asp Pro Ser Thr Ser Arg Arg Phe Ser Pro Pro Ser Ser
20 25 30

Ser Leu Gln Pro Gly Lys Met Ser Asp Val Ser Pro Val Val Ala Ala
35 40 45

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
50 55 60

Gln Gln Gln Gln Gln Gln Gln Gln Glu Ala Ala Ala Ala Ala Ala Ala
65 70 75 80

Ala Ala Ala Ala Ala Ala Ala Ala Ala Val Pro Arg Leu Arg Pro Pro
85 90 95

His Asp Asn Arg Thr Met Val Glu Ile Ile Ala Asp His Pro Ala Glu
100 105 110

Leu Val Arg Thr Asp Ser Pro Asn Phe Leu Cys Ser Val Leu Pro Ser
115 120 125

His Trp Arg Cys Asn Lys Thr Leu Pro Val Ala Phe Lys Val Val Ala
130 135 140

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

Asp Glu Asn Tyr Ser Ala Glu Leu Arg Asn Ala Ser Ala Val Met Lys
165 170 175

Asn Gln Val Ala Arg Phe Asn Asp Leu Arg Phe Val Gly Arg Ser Gly
180 185 190

Arg Gly Lys Ser Phe Thr Leu Thr Ile Thr Val Phe Thr Asn Pro Pro
195 200 205

Gln Val Ala Thr Tyr His Arg Ala Ile Lys Val Thr Val Asp Gly Pro
210 215 220

Arg Glu Pro Arg Arg His Arg Gln Lys Leu Asp Asp Ser Lys Pro Ser
225 230 235 240

Leu Phe Ser Asp Arg Leu Ser Asp Leu Gly Arg Ile Pro His Pro Ser
245 250 255

Met Arg Val Gly Val Pro Pro Gln Asn Pro Arg Pro Ser Leu Asn Ser
260 265 270

Ala Pro Ser Pro Phe Asn Pro Gln Gly Gln Ser Gln Ile Thr Asp Pro
275 280 285

Arg Gln Ala Gln Ser Ser Pro Pro Trp Ser Tyr Asp Gln Ser Tyr Pro
290 295 300

Ser Tyr Leu Ser Gln Met Thr Ser Pro Ser Ile His Ser Thr Thr Pro
305 310 315 320

Leu Ser Ser Thr Arg Gly Thr Gly Leu Pro Ala Ile Thr Asp Val Pro
325 330 335

Arg Arg Ile Ser Asp Asp Asp Thr Ala Thr Ser Asp Phe Cys Leu Trp
340 345 350

Pro Ser Thr Leu Ser Lys Lys Ser Gln Ala Gly Ala Ser Glu Leu Gly
355 360 365

Pro Phe Ser Asp Pro Arg Gln Phe Pro Ser Ile Ser Ser Leu Thr Glu
370 375 380

Ser Arg Phe Ser Asn Pro Arg Met His Tyr Pro Ala Thr Phe Thr Tyr
385 390 395 400

Thr Pro Pro Val Thr Ser Gly Met Ser Leu Gly Met Ser Ala Thr Thr
405 410 415

His Tyr His Thr Tyr Leu Pro Pro Pro Tyr Pro Gly Ser Ser Gln Ser
420 425 430

Gln Ser Gly Pro Phe Gln Thr Ser Ser Thr Pro Tyr Leu Tyr Tyr Gly
435 440 445

Thr Ser Ser Gly Ser Tyr Gln Phe Pro Met Val Pro Gly Gly Asp Arg
450 455 460

Ser Pro Ser Arg Met Leu Pro Pro Cys Thr Thr Thr Ser Asn Gly Ser
465 470 475 480

Thr Leu Leu Asn Pro Asn Leu Pro Asn Gln Asn Asp Gly Val Asp Ala
485 490 495

Asp Gly Ser His Ser Ser Ser Pro Thr Val Leu Asn Ser Ser Gly Arg
500 505 510

Met Asp Glu Ser Val Trp Arg Pro Tyr
515 520

<210> 29

<211> 599

<212> PRT

<213> Homo sapiens

<400> 29

Met Ser Arg Ser Leu Leu Leu Arg Phe Leu Leu Phe Leu Leu Leu Leu
1 5 10 15

Pro Pro Leu Pro Val Leu Leu Ala Asp Pro Gly Ala Pro Thr Pro Val
20 25 30

Asn Pro Cys Cys Tyr Tyr Pro Cys Gln His Gln Gly Ile Cys Val Arg
35 40 45

Phe Gly Leu Asp Arg Tyr Gln Cys Asp Cys Thr Arg Thr Gly Tyr Ser
50 55 60

Gly Pro Asn Cys Thr Ile Pro Gly Leu Trp Thr Trp Leu Arg Asn Ser
65 70 75 80

Leu Arg Pro Ser Pro Ser Phe Thr His Phe Leu Leu Thr His Gly Arg
85 90 95

Trp Phe Trp Glu Phe Val Asn Ala Thr Phe Ile Arg Glu Met Leu Met
100 105 110

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

Tyr Asn Ser Ala His Asp Tyr Ile Ser Trp Glu Ser Phe Ser Asn Val
130 135 140

Ser Tyr Tyr Thr Arg Ile Leu Pro Ser Val Pro Lys Asp Cys Pro Thr
145 150 155 160

Pro Met Gly Thr Lys Gly Lys Lys Gln Leu Pro Asp Ala Gln Leu Leu
165 170 175

Ala Arg Arg Phe Leu Leu Arg Arg Lys Phe Ile Pro Asp Pro Gln Gly
180 185 190

Thr Asn Leu Met Phe Ala Phe Phe Ala Gln His Phe Thr His Gln Phe
195 200 205

Phe Lys Thr Ser Gly Lys Met Gly Pro Gly Phe Thr Lys Ala Leu Gly
210 215 220

His Gly Val Asp Leu Gly His Ile Tyr Gly Asp Asn Leu Glu Arg Gln
225 230 235 240

Tyr Gln Leu Arg Leu Phe Lys Asp Gly Lys Leu Lys Tyr Gln Val Leu
245 250 255

Asp Gly Glu Met Tyr Pro Pro Ser Val Glu Glu Ala Pro Val Leu Met
260 265 270

His Tyr Pro Arg Gly Ile Pro Pro Gln Ser Gln Met Ala Val Gly Gln
275 280 285

Glu Val Phe Gly Leu Leu Pro Gly Leu Met Leu Tyr Ala Thr Leu Trp
290 295 300

Leu Arg Glu His Asn Arg Val Cys Asp Leu Leu Lys Ala Glu His Pro
305 310 315 320

Thr Trp Gly Asp Glu Gln Leu Phe Gln Thr Thr Arg Leu Ile Leu Ile
325 330 335

Gly Glu Thr Ile Lys Ile Val Ile Glu Glu Tyr Val Gln Gln Leu Ser
340 345 350

Gly Tyr Phe Leu Gln Leu Lys Phe Asp Pro Glu Leu Leu Phe Gly Val
355 360 365

Gln Phe Gln Tyr Arg Asn Arg Ile Ala Met Glu Phe Asn His Leu Tyr
370 375 380

His Trp His Pro Leu Met Pro Asp Ser Phe Lys Val Gly Ser Gln Glu
385 390 395 400

Tyr Ser Tyr Glu Gln Phe Leu Phe Asn Thr Ser Met Leu Val Asp Tyr
405 410 415

Gly Val Glu Ala Leu Val Asp Ala Phe Ser Arg Gln Ile Ala Gly Arg
420 425 430

Ile Gly Gly Gly Arg Asn Met Asp His His Ile Leu His Val Ala Val
435 440 445

Asp Val Ile Arg Glu Ser Arg Glu Met Arg Leu Gln Pro Phe Asn Glu
450 455 460

Tyr Arg Lys Arg Phe Gly Met Lys Pro Tyr Thr Ser Phe Gln Glu Leu
465 470 475 480

Val Gly Glu Lys Glu Met Ala Ala Glu Leu Glu Glu Leu Tyr Gly Asp
485 490 495

Ile Asp Ala Leu Glu Phe Tyr Pro Gly Leu Leu Leu Glu Lys Cys His
500 505 510

Pro Asn Ser Ile Phe Gly Glu Ser Met Ile Glu Ile Gly Ala Pro Phe
515 520 525

Ser Leu Lys Gly Leu Leu Gly Asn Pro Ile Cys Ser Pro Glu Tyr Trp
530 535 540

Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Asn Ile Val Lys Thr
545 550 555 560

Ala Thr Leu Lys Lys Leu Val Cys Leu Asn Thr Lys Thr Cys Pro Tyr
565 570 575

Val Ser Phe Arg Val Pro Asp Ala Ser Gln Asp Asp Gly Pro Ala Val
580 585 590

Glu Arg Pro Ser Thr Glu Leu
595

<210> 30
<211> 662
<212> PRT
<213> Homo sapiens

<400> 30
Met Gly Leu Tyr Arg Ile Arg Val Ser Thr Gly Ala Ser Leu Tyr Ala
1 5 10 15

Gly Ser Asn Asn Gln Val Gln Leu Trp Leu Val Gly Gln His Gly Glu
20 25 30

Ala Ala Leu Gly Lys Arg Leu Trp Pro Ala Arg Gly Lys Glu Thr Glu
35 40 45

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Leu Lys Val Glu Val Pro Glu Tyr Leu Gly Pro Leu Leu Phe Val Lys
50 55 60

Leu Arg Lys Arg His Leu Leu Lys Asp Asp Ala Trp Phe Cys Asn Trp
65 70 75 80

Ile Ser Val Gln Gly Pro Gly Ala Gly Asp Glu Val Arg Phe Pro Cys
85 90 95

Tyr Arg Trp Val Glu Gly Asn Gly Val Leu Ser Leu Pro Glu Gly Thr
100 105 110

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

Glu Glu Glu Leu Glu Glu Arg Arg Lys Leu Tyr Arg Trp Gly Asn Trp
130 135 140

Lys Asp Gly Leu Ile Leu Asn Met Ala Gly Ala Lys Leu Tyr Asp Leu
145 150 155 160

Pro Val Asp Glu Arg Phe Leu Glu Asp Lys Arg Val Asp Phe Glu Val
165 170 175

Ser Leu Ala Lys Gly Leu Ala Asp Leu Ala Ile Lys Asp Ser Leu Asn
180 185 190

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

Cys Gly Gln Ser Lys Leu Ala Glu Arg Val Arg Asp Ser Trp Lys Glu
210 215 220

Asp Ala Leu Phe Gly Tyr Gln Phe Leu Asn Gly Ala Asn Pro Val Val
225 230 235 240

Leu Arg Arg Ser Ala His Leu Pro Ala Arg Leu Val Phe Pro Pro Gly
245 250 255

Met Glu Glu Leu Gln Ala Gln Leu Glu Lys Glu Leu Glu Gly Gly Thr
260 265 270

Leu Phe Glu Ala Asp Phe Ser Leu Leu Asp Gly Ile Lys Ala Asn Val
275 280 285

Ile Leu Cys Ser Gln Gln His Leu Ala Ala Pro Leu Val Met Leu Lys
290 295 300

Leu Gln Pro Asp Gly Lys Leu Leu Pro Met Val Ile Gln Leu Gln Leu
305 310 315 320

Pro Arg Thr Gly Ser Pro Pro Pro Pro Leu Phe Leu Pro Thr Asp Pro
325 330 335

Pro Met Ala Trp Leu Leu Ala Lys Cys Trp Val Arg Ser Ser Asp Phe
340 345 350

Gln Leu His Glu Leu Gln Ser His Leu Leu Arg Gly His Leu Met Ala
355 360 365

Glu Val Ile Val Val Ala Thr Met Arg Cys Leu Pro Ser Ile His Pro
370 375 380

Ile Phe Lys Leu Ile Ile Pro His Leu Arg Tyr Thr Leu Glu Ile Asn
385 390 395 400

Val Arg Ala Arg Thr Gly Leu Val Ser Asp Met Gly Ile Phe Asp Gln
405 410 415

Ile Met Ser Thr Gly Gly Gly Gly His Val Gln Leu Leu Lys Gln Ala
420 425 430

Gly Ala Phe Leu Thr Tyr Ser Ser Phe Cys Pro Pro Asp Asp Leu Ala
435 440 445

Asp Arg Gly Leu Leu Gly Val Lys Ser Ser Phe Tyr Ala Gln Asp Ala
450 455 460

Leu Arg Leu Trp Glu Ile Ile Tyr Arg Tyr Val Glu Gly Ile Val Ser
465 470 475 480

Leu His Tyr Lys Thr Asp Val Ala Val Lys Asp Asp Pro Glu Leu Gln
485 490 495

Thr Trp Cys Arg Glu Ile Thr Glu Ile Gly Leu Gln Gly Ala Gln Asp
500 505 510

Arg Gly Phe Pro Val Ser Leu Gln Ala Arg Asp Gln Val Cys His Phe
515 520 525

Val Thr Met Cys Ile Phe Thr Cys Thr Gly Gln His Ala Ser Val His
530 535 540

Leu Gly Gln Leu Asp Trp Tyr Ser Trp Val Pro Asn Ala Pro Cys Thr
545 550 555 560

Met Arg Leu Pro Pro Pro Thr Thr Lys Asp Ala Thr Leu Glu Thr Val
565 570 575

Met Ala Thr Leu Pro Asn Phe His Gln Ala Ser Leu Gln Met Ser Ile
580 585 590

Thr Trp Gln Leu Gly Arg Arg Gln Pro Val Met Val Ala Val Gly Gln
595 600 605

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

Lys Phe Arg Glu Glu Leu Ala Ala Leu Asp Lys Glu Ile Glu Ile Arg
625 630 635 640

Asn Ala Lys Leu Asp Met Pro Tyr Glu Tyr Leu Arg Pro Ser Val Val
645 650 655

Glu Asn Ser Val Ala Ile
660

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tacaatccaaa ttaagtttgg tcgtggtagc accttcaaag aaatccccgt gactgtctat 180
agaccacac taacaaaagt caaaattgaa ggtgaacctg aattcagact gattaaagaa 240
ggtgaaacaa taactgaagt gatccatgga gagccaatta ttaaaaaata caccaaaatc 300
attgatggag tgcctgtgga aataactgaa aaagagacac gagaagaacg aatcattaca 360
ggtcctgaaa taaaatacac taggatttct actggagggtg gagaaacaga agaaactctg 420
aagaaattgt tacaagaaga agacacaccc gtgaggaagt tgcaagccaa caaaaaagtt 480
caanggatct agaagacgat taagggaagg tcgttctcag tgaaaatcca 530

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<212> DNA
<213> Homo sapiens

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ttagagaaaa atccttgtca ccagattcat tacaattcaa atcgaagagt tgtgaactgt 180
tatcccattg aaaagaccga gccttgtatg tatgttatgg atacataaaa tgcacgcaag 240
ccattatctc tccatgggaa gctaagttat aaaaataggt gcttgggtgta caaaactttt 300
tatatcaaaa ggctttgcac atttctatat gagtgggttt actggtaaata tatgttattt 360

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<210> 33
<211> 493
<212> DNA
<213> Homo sapiens

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tatgtaccaa gtcccagccc aacttggaca cctgtgcctt ccatgaacag ccagaactgc 180
agaagaaaca gttatgctct ttcgagatct acgaagtcc ctgggaggac agaatgtccc 240
tggtgaattc caggtgtcaa gaagcctagg ggtctgtgcc aggccagtca caccgaccac 300
caccactcc caccctctgt agtgctcca cccctggact ggtggcccc accctgcggg 360
aggcctcccc atgtgcctgt gccaaagagac agacagagaa ggctgcagga gtcctttgtt 420
gctcagcagg gcgctctgcc ctccctcctt cttcttgct tctaataagac ctggtacatg 480
gtacacacac ccc 493

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<212> DNA
<213> Homo sapiens

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acgtccgctg cgggtactaa gagccaggca acagaccgtt gggggggtga attacttctt 180
cgacgtagag gtggggccgaa ccatatgtac caagtcccag cccaacttgg acacctgtgc 240
cttccatgaa cagccagaac tgcagaagaa acagttgtgc tctttcgaga tctacgaagt 300
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gccag 365

<210> 35
<211> 410
<212> DNA
<213> Homo sapiens

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gcctccctcc tgagtctcca ccttggaaact gccacacgtg ggagtgacat atccaagacc 120
tgctgcttcc aatacagcca caagcccctt ccctggacct ggggtgcgaag ctatgaattc 180
accagtaaca gctgctcca gcgggctgtg atattcacta caaaagagg caagaaagtc 240
tgtacccatc caaggaaaaa atgggtgcaa aaatacattt ctttactgaa aactccgaaa 300
caattgtgac tcagctgaat tttcatccga ggacgcttgg accccgctct tggctctgca 360

gccctctggg gagcctgcgg aatcttttct gaaggctaca tggacccgct 410

<210> 36
<211> 489
<212> DNA
<213> Homo sapiens

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acaagtattc ttgatctcag agacaagttc aatgaatctc ttcaagtga tactactgct 180
ctcatcccaa aggaagccaa ctctgaggaa gtctttttgt ttaaaccaga aaacattact 240
tttgaaaatg gcacagatct tttcattgct attcaggctg ttgataaggc cgatctgaaa 300
tcagaaatat ccaacattgc acgagtatct ttgtttattc ctccacagac tccgccagag 360
acacctagtc ctgatgaaac gtctgctcct tgtcctaata ttcatatcaa cagcaccatt 420
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gcctagggc 489

<210> 37
<211> 324
<212> DNA
<213> Homo sapiens

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tgagtactac agacgcctgc tgcgggtgct acgagccagg gagcagatcg tgggcggggc 180
gaattacttc ttcgacatag aggtgggccg aaccatatgt accaagtccc agcccaactt 240
ggacacctgt gccttccatg aacagccaga actgcagaag aaacagttgt gctctttcca 300
gatctacgaa gttccctggg agga 324

<210> 38
<211> 310
<212> DNA
<213> Homo sapiens

<400> 38
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cccagagacc tcctcctgaa ggactcctac ctagaccccc tggatgtagt ggtaaccaag 120
atgatgggtc tcagcagaga ccacaaaac caggaggcca tcaccgcat cctccccac 180
ctccttttca aaatcagcaa cgaccacccc aacgaggaca ccgtcaactc tctctacccc 240
gatttccttc tgctcgcctg caggaagcat catcattctt ccggagggac agaccagcaa 300
gacatcccca 310

<210> 39
<211> 465

<212> DNA

<213> Homo sapiens

<400> 39

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gcctcagaat	tgctatttca	aattgccaaa	aatttagaga	tgttttctac	atatttctgc	120
tcttctgaac	aacttctgct	accactaaa	taaaaacaca	gaaataatta	gacaattgtc	180
tattataaca	tgacaaccct	attaatcatt	tggtcttcta	aaatgggatc	atgcccattt	240
agattttcct	tactatcagt	ttatttttat	aacattaact	tttactttgt	tatttattat	300
tttatataat	ggtgagtttt	taaattattg	ctcactgcct	atttaatgta	gctaataaag	360
ttatagaagc	agatgatctg	ttaatttcct	atctaataaa	tgcccttaat	tgttctcata	420
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<210> 40

<211> 323

<212> DNA

<213> Homo sapiens

<400> 40

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gagaaaataa	ttaatttcac	gggactaaat	gaactaatga	ggattgctga	ttctttaaat	180
gtcttgtttc	ccagatttca	ggaaactttt	tttcttttaa	gctatccact	cttacagcaa	240
tttgataaaa	tatacttttg	tgaacaaaaa	ttgagacatt	tacattttct	ccctatgtgg	300
tcgctccaga	cttgggaaac	tat				323

<210> 41

<211> 500

<212> DNA

<213> Homo sapiens

<400> 41

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cagatgagga	ccacatctac	caggaggaga	tgctggagat	ggcccagaag	ggggtgctgc	180
atgcggtgca	cacagcctat	tcccgcctgc	ctggcaagcc	caaggtctat	gttcaggaca	240
tcctgcggca	gcagctggcc	agcgagggtg	tccgtgtgct	ccacaaggag	ccaggccacc	300
tctatgtttg	cggggatgtg	cgcatggccc	gggacgtggc	ccacaccctg	aagcagctgg	360
tggtgccaa	gctgaaattg	aatgaggagc	aggtcgagga	ctatttcttt	cagctcaaga	420
gccagaagcg	ctatcacgaa	gatatctttg	gtgctgtatt	tccttacgag	gcgaagaagg	480
acaggggtggc	ggtgcagccc					500

<210> 42

<211> 363

<212> DNA

<213> Homo sapiens

<400> 42

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agaaccatgg gaatggtgaa tatcttcaat ggggatgcag acctctcagg catgacctgg	120
agccacggtc tctcagtatc taaagtccta cacaaggcct ttgtggaggt cactgaggag	180
ggagtggaaag ctgcagctgc caccgctgta gtagtagtcg aattatcatc tccttcaact	240
aatgaagagt tctgttgtaa tcaccctttc ctattcttca taaggcaaaa taagaccaac	300
agcatcctct tctatggcag attctcatcc ccatagatgc aattagtctg tctactccatt	360
tag	363

<210> 43

<211> 508

<212> DNA

<213> Homo sapiens

<400> 43

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aaaaaagaaa acactaaaga ggaaaaattt tggccaaaca aggatgtaca ggccaagggtc	120
ctggaaatac catacaaagg caaagatcta agcatgattg tgctgctgcc aaatgaaatc	180
gatggtctgc agaagcttga agagaaactc actgctgaga aattgatgga atggacaagt	240
ttgcagaata tgagagagac atgtgtcgat ttacacttac ctcggttcaa aatggaagag	300
agctatgacc tcaaggacac gttgagaacc atgggaatgg tgaatatctt caatggggat	360
gcagacctct caggcatgac ctggagccac ggtctctcag tatctaaagt cctacacaag	420
gcctttgttg aggtcactga ggagggagtg gaagctgcag ctgccaccgc ttagtagta	480
gtcgaattat catctccttc aactaatg	508

<210> 44

<211> 493

<212> DNA

<213> Homo sapiens

<400> 44

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ccagggagca gacctttggg ggggtgaatt acttcttcga cgtagagggtg ggccgcacca	120
tatgtaccaa gtcccagccc aacttggaca cctgtgcctt ccatgaacag ccagaactgc	180
agaagaaaca gttatgctct ttcgagatct acgaagttcc ctgggaggac agaattgtccc	240
tggtgaattc cagggtgtcaa gaagcctagg ggtctgtgcc aggccagtca caccgaccac	300
cacccactcc caccctctgt agtgctccca cccctggact ggtggccccc accctgcggg	360
aggcctcccc atgtgcctgt gccaagagac agacagagaa ggctgcagga gtcctttgtt	420
gctcagcagg gcgctctgcc ctccctcctt ccttcttgct tctaataagac ctggtacatg	480
gtacacacac ccc	493

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<211> 447
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caaggtcccc cacctccttg aaagccacaa ggcccccccc cagcaggagg caatccccag 240
cagcctcagg cacctcctgc tggaaagccc caggggccac ctccacctcc tcaagggggc 300
aggccacca gacctgccc gggacaacag cctccccagt aatctaggat tcaatgacag 360
gaagtgaata agaagatatc agtgaattca aataattcaa ttgctacaaa tgccgtgaca 420
ttggaacaag gtcacatag ctctaac 447

<210> 46
<211> 304
<212> DNA
<213> Homo sapiens

<400> 46
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ggtgtgcaag gtgaatggca cctggctaca ggcgggcgtg gtcagctggg acgagggctg 180
tgcccagccc aaccggcctg gcatctacac ccgtgtcacc tactacttgg actggatcca 240
ccactatgtc ccaaaaagc cgtgagtcag gcctgggtgt gccacctggg tccactggagg 300
acca 304

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<211> 358
<212> DNA
<213> Homo sapiens

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aaataaccacc ttggcgccca cacgggagac gacgtccgca tcgtccgtga cgacatgctg 120
tgtgccggga acacccggag ggactcatgc cagggcgact ccggagggcc cctggtgtgc 180
aagggtgaatg gcacctggct gcaggcgggc gtggtcagct ggggcgaggg ctgtgcccag 240
cccaaccggc ctggcatcta caccgtgtc acctactact tggactggat ccaccactat 300
gtccccaaaa agccgtgagt caggcctggg ttggccacct gggtcactgg aggaccaa 358

<210> 48
<211> 542
<212> DNA
<213> Homo sapiens

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ccactatgtc cccaaaaagc cgtgagtcag gcctgggttg gccacctggg tcaactggagg	300
accaaccct gctgtccaaa acaccactgc ttctaccca ggtggcgact gccccccaca	360
ccttcctgc cccgtcctga gtgccccttc ctgtcctaag cccctgctc tcttctgagc	420
ccctccct gtcctgagga cccttcccta tctgagccc ccttcctgt cctaagcctg	480
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ct	542

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ggtgtgcaag gtgaatggca cctggctgca ggcgggctg gtcagctggg gcgagggctg	180
tgcccagccc aaccggcctg gcatctacac ccgtgtcacc tactacttgg actggatcca	240
ccactatgtc cccaaaaagc cgtgagtcag gcctgggttg gccacctggg tcaactggagg	300
accaaccct gctgtccaaa acaccactgc ttctaccca ggtggcgact gccccccaca	360
ccttcctgc cccgtcctga gtgccccttc ctgtcctaag cccctgctc tcttctgagc	420
ccctccct gtcctgagga cccttcccta tctgagccc ccttcctgt cctaagcctg	480
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<400> 50	
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ccccctgcct cggagacctt ccccccgggg atgccgtgct gggtcactgg ctggggcgat	180
gtggacaatg atgagccct cccaccgcca ttctccctga agcaggtgaa ggtccccata	240
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cgcatcatcc gtgacgacat gctgtgtgcc gggaacaccc ggagggactc atgccagggc	360
gactctggag ggcccctggt gtgcaagggt aatggcacct ggctacaggc gggcgtggtc	420
agctgggacg agggctgtgc ccagcccaac cggcctggca tctacaccg tgtcacctac	480
tacttggact ggatccacca ctatgtcccc aaaaagccgt gagtcaggcc tgggggtgt	538

<210> 51
 <211> 366
 <212> DNA
 <213> Homo sapiens

<400> 51
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 cccctgcct cagagacctt ccccccgagg atgccgtgct gggtcactgg ctggggcgat 180
 gtggacaatg atgagcgcct cccaccgcca tttcctctga agcaggtgaa ggtccccata 240
 atggaaaacc acatttgtga cgaaaatac caccttggcg cctacacggg agacgacgtc 300
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 gcgact 366

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 <211> 496
 <212> DNA
 <213> Homo sapiens

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 <222> (345)..(345)
 <223> a, c, g, t, unknown or other

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 <222> (347)..(348)
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 <222> (366)..(366)
 <223> a, c, g, t, unknown or other

<220>
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 <222> (405)..(405)
 <223> a, c, g, t, unknown or other

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 <223> a, c, g, t, unknown or other

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 cccctgcct cggagacctt ccccccgagn ntgccgtgct gggtcactgg ctggggcgat 180
 gtggacaatg atgagcccct cccaccgcca tttcccttga agcaggtgaa ggtccccata 240

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gactcnggag ggcccctggt gtgcaaggtg aatggcacct ggctncaggc gggcgtggtc	420
agctgggncg agggctgtgc ccagcccaac cggcctggca tctacacccg tgtcacctac	480
tacttggact ggatcc	496

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 <211> 408
 <212> DNA
 <213> Homo sapiens

<400> 53	
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acaaatgtgg ttttccatta tggggacctt cacctgcttc agaggaaatg gcggtgggag	120
gcgctcatca ttgtccacat cgccccagcc agtgacccag cacggcatcc ccggggggaa	180
ggtctctgag gcagggggca gggtgaccgt gtggacgtgg ctggagacgt tcaccggctc	240
ctccagctcc agcagggcga tgtccgctcc gatctgggcg gtgtagaact gtgggtgcac	300
gatgatcctg ctgaccggca gcagctggtc ctggtagtag aggtgctgct cccgcagttg	360
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<210> 54
 <211> 520
 <212> DNA
 <213> Homo sapiens

<400> 54	
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ctccgggggg cctctggtct gccagggtgaa cggtgcctgg gtgcaggctg gcattgtgag	180
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cgtgaactgg atccgccgcc acatcacagc atcagggggc tcagagtctg ggtaccccag	300
gctccccctc ctggctggct tattcctccc cggcctcttc cttctgctag tctcctgtgt	360
cctgctggcc aagtgcctgc tgcacccatc tgcggatggt actcccttcc ccgcccctga	420
ctgatggcag gaatccaagt gcatttctta aataagttac tatttattcc gtcgccccc	480
ctccctctcc cttgagaagc tgagtcttct gcatcagatt	520

<210> 55
 <211> 508
 <212> DNA
 <213> Homo sapiens

<400> 55	
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tcgtactcca ctctgttttg gcagtaaatac gtgtaggcct ctgcttgagc tgggtcttgg	120
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ttgaaaagca tccgtagttt aaacaagcct ctttcccacg gagtcccttt ctttcctgga	360
atggcgcaact cccagttcat gaggttcatc gtgccatcgg gattttttgt tgggacagcc	420
acgaaaccaa atgggtgggtc tttcctccat gctttcctct cctgggcgag tctgctgagg	480
gcgatccccg acatgttcaa agtccctc	508

<210> 56
 <211> 510
 <212> DNA
 <213> Homo sapiens

<400> 56	
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gtccacctgg tcaggggcca tggtagccgc gcggtaaagc accgtgtaca gggcctcctc	180
gtagagcatc tccacctcct ctggggccag ggctctcagg ccgaggctgg gatccacagg	240
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gccttcccc ttcttcagca tgaggcgcat gtgggcaaag aactccacgc catccccggg	360
tttcaggcc cccgtggcag gctcctgcgg gtcggcgctg gcactccctg ggtcctgctc	420
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<210> 57
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 57	
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tgcaggcact gagggacgag gccagcagct ctggctgctc agaaacagac tccacagagc	120
tggctagcat cctctagggc ccgccacgtt gcccgaagcc accatgcaga agggcacaga	180
agggatcagg acctgtctgc cggcttgctg agcagctgga ctgcagggtg taggaaggga	240
actgaagact caaggaggtg gcccaggaca cttgctgtgc tcaactgtgg gccggctgct	300
ctgtggcctc ctgcctcccc tctgcctgcc tgtggggcca agccctgggg ctgccactgt	360
gaatatgccca aggactgata gggcctagcc cggaacacta atgtaga	407

<210> 58
 <211> 565
 <212> DNA
 <213> Homo sapiens

<400> 58	
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aaaggcaaat ttggttttct ccttccagaa tcccggataa agccaacgtg cagagagacc	180
atgctagctg tcaaatttat tgccaagtat atcctcaagc atacttccta aagaactgcc	240
ctctgttttg aataagccaa ttaatccttt tttgtgcctt tcatcagaaa gtcaatcttc	300
agttatcccc aaatgcagct tctatttcac ctgaatcctt ctcttgctca ttttaagtccc	360
atgttactgc tgtttgcttt tactttacttt cagtagcacc ataacgaagt agctttaagt	420
gaaacctttt aactaccttt ctttgctcca agtgaagttt ggaccagca gaaagcatta	480
ttttgaaagg tgatatacag tggggcacag aaaacaaatg aaaaccctca gtttctcaca	540
gattttcacc atgtggcttc atcaa	565

<210> 59
 <211> 459
 <212> DNA
 <213> Homo sapiens

<400> 59	
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attggcatac gttatcagca acttccccctg ttcaatagta tgggaaaaat aagatgactg	120
ggaaaaagac acacccacac cgtagaacat atattaatct actggcgaat gggaaaggag	180
accattttct tagaaagcaa ataaacttga tttttttaa tctaaaattt acattaatga	240
gtgcaaaaata acacataaaa tgaaaattca cacatcacat ttttctggaa aacagacgga	300
ttttacttct ggagacatgg catacgggta ctgacttatg agctaccaa actaaattct	360
ttctctgcta ttaactggct agaagacatt catctattht tcaaagttht tttcaaaaca	420
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 <211> 430
 <212> DNA
 <213> Homo sapiens

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 <223> a, c, g, t, unknown or other

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 <223> a, c, g, t, unknown or other

<220>
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 <222> (349)..(352)
 <223> a, c, g, t, unknown or other

<400> 60	
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ttaccttcta gtcctaggat gaggacacac tattagtttg aattaaatgc tttgatattc	120

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tcagatcagc catcttgaac caaagcaaaa ccacaagtta cactttctta aaatttgatt	180
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ctagctttga gggtaaatga aaatataacc catagattac ccagccactt gggaacagca	300
ggtaatactg aagaaaaata aaaatagatt ttgaaaacgt tannnanann nntatgatta	360
tgattctgtt ccatttaagg gaaaacttag gtaaatagag aaattttttc tataacattg	420
tgtagtcagt	430

<210> 61
 <211> 358
 <212> DNA
 <213> Homo sapiens

<400> 61	
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aaaagacaga agccttgact tctgctaagc ggtacatcga gacggaccca gccaatcggg	120
atcggcggac gcccatcacc gtggtgaagc aaggctttga gcctccctcc ttgtgtggct	180
ggttccttggt ctgggatgat gattactggt ctgtggaccc cttggacagg gccatggctg	240
agctggctgc ctgaggaggg gcagggccca cccatgtcac cggtcagtgc cttttggaac	300
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<210> 62
 <211> 506
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (86)..(86)
 <223> a, c, g, t, unknown or other

<220>
 <221> modified_base
 <222> (118)..(118)
 <223> a, c, g, t, unknown or other

<400> 62	
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attccactga ctaacttttg tgtttngttt ccaagttaag tgattcctcc ttttttngt	120
tcaatgttaa atttaaaaat aacaatgtgt atgggtcctc ccatgtgtaa tatggtaaca	180
tgtaacttgc agtgtttgcc agctttcaaa gcaggctttg tgaaaatgta atacaaacag	240
cagtgaatgg gactcaaatg ttgtgcttcc tataaacagc tccgctcttt caggggaagga	300
tggtaacaaa ctagaaggac aaatatgtac gtatttataa cgtattaaaa ctcttttaag	360
tagcttaagg tattgtgcaa tggcctagcc tagtagaaat gggggaaaag cattgctgtg	420
gaccattgtt aaagtgcag gagttgtagg gttaccctt tgacaagctt ccatagtctt	480
cagacacgca cattgatggc atccct	506

<210> 63
 <211> 496
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (60)..(60)
 <223> a, c, g, t, unknown or other

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 <222> (75)..(75)
 <223> a, c, g, t, unknown or other

<220>
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 <222> (114)..(114)
 <223> a, c, g, t, unknown or other

<220>
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 <222> (131)..(131)
 <223> a, c, g, t, unknown or other

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 <223> a, c, g, t, unknown or other

<220>
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 <223> a, c, g, t, unknown or other

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 <223> a, c, g, t, unknown or other

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 <223> a, c, g, t, unknown or other

<220>
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 <222> (203)..(203)
 <223> a, c, g, t, unknown or other

<220>
 <221> modified_base
 <222> (207)..(207)
 <223> a, c, g, t, unknown or other

<400> 63	
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gatgatgggt natatganaa ntggacagga aagaagcant ttctgaaagt tatantcttt	180
tgaaccacgt tctaaaccaa gnttttnatc ttcttggggc tcgtaattac ctttcacttt	240
aatgtcactt aaagatatata cacagaaaaa tgccttgagg gcaaaatata ggcaaaacac	300
caatgcgctt tcaaatgcat gaaaatggtg cagttgtacc cttgagcctt gactcaaggg	360

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ctgtagatgt tccctttcca cccccacac ttggtgcgtg ttcacaaagc aaatatggcc	420
tgtaattcaa atttgttcta tgtgatactc tctgagtaaa aactcataca tgcagaaaat	480
tgtctttgct cgaaat	496

<210> 64
 <211> 560
 <212> DNA
 <213> Homo sapiens

<400> 64 cccaagcccc tagagaagtc agtctccccg caaaattcag attcttcagg ttttcagat	60
gtgaatggtt ggcaccttcg tttccgctgg tccaaggatg ctccctcaga actcctgagg	120
aagttcagaa actatgaaat atgaaatata tctgcttcaa aaaatgagga agagcaagac	180
tgtcccctat gctgccaaca tgcagtcttt gtttatgtct taaaaatgtc atgtttatgt	240
catgtctgtg aattgctgag tactaattga ttctccatc cttgaatcag ttctcataat	300
gcttttttaa taagaaaaat tcagaagatg aatttcttcc aatatttgaa taaattaaag	360
ctcttagata cagagtagat tgtattatat gctttttcct attaatacta cttatagaaa	420
tccattaaaa agcaatctct gtacagtgtt tttaaataatt tcattgacat actgtgatct	480
ctattagtga tggatgtaca aaaaatgttt tcttaccctt gacttacaat gaaatgtgaa	540
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<210> 65
 <211> 512
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (443)..(443)
 <223> a, c, g, t, unknown or other

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ttttgtgtca taatttacia attagttctt taaaaattgt tgttatatga attgtgtttc	180
tagcatgaat gttctataga gtactctaaa taacttgaat ttatagacaa atgctactca	240
cagtacaatc aattgtatta taccatgaga aaatcaaaaa ggtgttcttc agagacattt	300
tatctataaa attttctac tattatgttc attaacaaac ttctttatca catgtatctt	360
ctacgtgtaa aacatttctg atgatttttt aacaaaaaat atatgaattt cttcatttgc	420
tcttgcattc acattgctat aanggatata aaatgtgggt tctatatttt gagatgtttt	480
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<210> 66
 <211> 551

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (114)..(114)

<223> a, c, g, t, unknown or other

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<222> (119)..(120)

<223> a, c, g, t, unknown or other

<220>

<221> modified_base

<222> (127)..(127)

<223> a, c, g, t, unknown or other

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<222> (129)..(129)

<223> a, c, g, t, unknown or other

<220>

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<222> (149)..(149)

<223> a, c, g, t, unknown or other

<220>

<221> modified_base

<222> (152)..(152)

<223> a, c, g, t, unknown or other

<220>

<221> modified_base

<222> (163)..(163)

<223> a, c, g, t, unknown or other

<220>

<221> modified_base

<222> (167)..(168)

<223> a, c, g, t, unknown or other

<220>

<221> modified_base

<222> (189)..(189)

<223> a, c, g, t, unknown or other

<220>

<221> modified_base

<222> (243)..(243)

<223> a, c, g, t, unknown or other

<400> 66

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aggggttneng gttctccctg cccccaatnc cnatatactt tantgcnntt ttatTTTTgc 180

ctttacggnc tctgtgtctt tctgcaagaa ggcctggcaa aggtatgcct gctgttggtc 240

ccntcgggat aagataaaat ataaataaaa ccttcagaac tgTTTTggag caaaagatag 300

cttgtacttg gggaaaaaaa ttctaagttc ttttatatga ctaatatctt tggtttagcaa 360

gactggaaag aggtgttttt ttaaaatgta cataccagaa caaagaacat acagctctct 420

gaacatttat tttttgaaca gaggtggttt ttatgttttg acctggtaat acagatacaa	480
aaactttaat gaggtagcaa tgaatattca actgtttgac tgctaagtgt atctgtccat	540
atttttagcaa g	551

<210> 67
 <211> 474
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (365)..(365)
 <223> a, c, g, t, unknown or other

<220>
 <221> modified_base
 <222> (429)..(429)
 <223> a, c, g, t, unknown or other

<400> 67	
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gaacagctgg aaaaggccat cacctatgag aagctgaatg agtggaccag tgcagacatg	120
atggagttgt atgaagtgc gctacacctt cccaagttca agctggaaga cagttatgat	180
ctcaagtcaa ccttgagcag tatggggatg agtgcagcct tcagccaaag caaagctgat	240
ttctcaggaa tgtcttcagc aagaaacctt tttttgtcca atgttttcca taaggctttt	300
gtggaaataa atgaacaagg tactgaagct gcagctggca gtgggagtga gatagatata	360
cgaantagag tcccatccat tgaattcaat gcaaatcacc cattcctctt cttcatcagg	420
cacaataana accaacacca ttctttttta tggaagatta tgctccccct aatc	474

<210> 68
 <211> 287
 <212> DNA
 <213> Homo sapiens

<400> 68	
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atgaagtgct aaatttgctc ttaccgcga gactgatcag aagaagcaaa aggggaaagg	120
gggctagagg tccactcgca ctttttacat cagacaagag gaggactgtg ccagaaatct	180
gtgcatgaaa caccatctgc ttttcatgca gggaggggtc aaccgtgtga acgtgcagag	240
attactcgag ctttctttgc caaaaatatg cattcttccc agctgta	287

<210> 69
 <211> 545
 <212> DNA
 <213> Homo sapiens

<400> 69	
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ggacctctag gagtggatcc aatctatatc ttacagttg tatagtatat gatattctct	120

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tacgcccacc tcaggcagac acagagcaca atgctggggg tctcttcaca ctatcactgc	300
cccaaattgt ctttctaaat ttcaacttca atgtcatctt ctccatgaag accactgaat	360
gaacaccttt tcatccagcc ttaatttctt gctccataac tactctatcc cacgatgcag	420
tattgtatca ttaattatta gtgtgcttgt gacctcctta tgtattctca attacctgta	480
tttgtgcaat aaattggaat aatgtaactt gatttcttat ctgtgtttgt gttggcatgc	540
aagat	545

<210> 70
 <211> 420
 <212> DNA
 <213> Homo sapiens

<400> 70	
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ttttctatgt gagaattttt tagatgtgtg tttacttcat gtttaciaat aactgtttgc	120
tttttaatgc agtactttga aatatatcag ccaaaccat aacttacaat aatttcttag	180
gtattctgaa taaaattcca tttcttttgg atatgcttta ccattcttag gtttctgtgg	240
aacaaaaata tttgtagcat tttgtgtaa tacaagcttt cttttttatt ttttccaatt	300
gctattgccc aagaattgct ttccatgcac atattgtaa aattccgctt tgtgccacag	360
gtcatgattg tggatgagtt tactcttaac ttcaaaggga ctatttgtat tgtatgttgc	420

<210> 71
 <211> 534
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (486)..(493)
 <223> a, c, g, t, unknown or other

<400> 71	
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atttggtgga tgtgatgggt gggttttatt gtcagtttgg ttgggctata gcacacagtt	180
atttaaatcaa acagtaatct aggtgtggct gtgaaggat tttgtagatg tgattaacat	240
ctacaatcag ttgactttta gtgaaagaga ttacttaaat aatttggttg agctgcacct	300
gattagttga aaggcctcaa gaacaaacac tgcagtttcc tggaaaagaa gaaactttgc	360
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tttgaagttt gccaacccca acaattgtgt gaattaattt ctaaaaataa agctatatac	480
agccannnnn nnntatttgt gggggatttg tttcaggatc tctacagata ccaa	534

<210> 72
 <211> 478
 <212> DNA
 <213> Homo sapiens

<400> 72
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 ctcttcctct ttcttcattc agatctatat ggcaaatagc cacaattata taaatcattt 180
 caagactaga atagggggat ataatacata ttactccaca ctttttatga atcaaatatg 240
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 gccatcacca cggctcactg cagcctcagc gtcctgggct caaatgatcc tcccacctca 360
 gcctcctgag tagctgggac tacaggctca tgccatcatg ccagctaata atttttttat 420
 tttcgtggag acggggcctc actatgttgc ctaggctgga aataggattt tgaaccca 478

<210> 73
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 73
 ggatgctgag cggattctg 19

<210> 74
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 74
 ccctcgcgaa aaagtttctt 20

<210> 75
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 75
 aaggtctcag ctgggcagtt t 21

<210> 76

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

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 primer"

 <400> 76
 aaactgggcc acctcgatt 19

 <210> 77
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 probe"

 <400> 77
 ccagcttgca tgtccgagac acca 24

 <210> 78
 <211> 20
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 <213> Artificial Sequence

 <220>
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 <223> /note="Description of Artificial Sequence: Synthetic
 primer"

 <400> 78
 ggggtctcacc tcccaactgc 20

 <210> 79
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 primer"

 <400> 79
 tgtctgttac ggtcaactcg gt 22

 <210> 80
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 primer"

 <400> 80
 gcttccccct ctgttcttcc t 21

<210> 81
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
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 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"

 <400> 185
 tgagaacagc tgcacccact t 21

 <210> 186
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic primer"

 <400> 186
 gctgaaggca tctcggagat 20

 <210> 187
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic probe"

 <400> 187

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caggcaacct gcctaacatg cttcg

<210> 188
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 188
actgctactg ctgctgagcc t 21

<210> 189
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 189
ggtgaggtgg atcggttgta gt 22

<210> 190
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 190
caatcccacg aaatccagga 20

<210> 191
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 191
ttcaggttga ccatcacagt cc 22

<210> 192
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
probe"

<400> 192
cccaaattct gaggacaaga acttcccc

28

<210> 193
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 193
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

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

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

Ala Met Ile Trp Gly Asp Gly Lys Ile Val Tyr Asn Ser Ala Leu Lys
50 55 60

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

Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Gly Asp Gly Tyr Tyr Pro Tyr Ala Met Asp Asn Trp Gly Gln Gly Ser
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 194
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 194
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ser Val Ser Leu Gly
1 5 10 15

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

Gly Asn Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
Page 96

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Asp
50 55 60

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

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

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

<210> 195
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 195
Arg Ala Ser Lys Ser Val Asp Ser Tyr Gly Asn Ser Phe Met His
1 5 10 15

<210> 196
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 196
Leu Ala Ser Asn Leu Glu Ser
1 5

<210> 197
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 197
Gln Gln Asn Asn Glu Asp Pro Arg Thr
1 5

<210> 198
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 198
 Ala Tyr Ser Val Asn
 1 5

<210> 199
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 199
 Met Ile Trp Gly Asp Gly Lys Ile Val Tyr Asn Ser Ala Leu Lys Ser
 1 5 10 15

<210> 200
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 200
 Asp Gly Tyr Tyr Pro Tyr Ala Met Asp Asn
 1 5 10

<210> 201
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 201
 Arg Ser Ser Gln Ser Pro Val His Ser Asn Gly Asn Thr Tyr Leu His
 1 5 10 15

<210> 202
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 202
 Lys Val Ser Asn Arg Phe Ser

1

5

<210> 203
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 203
Ser Gln Ser Thr His Ile Pro Trp Thr
1 5

<210> 204
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 204
Ser Tyr Trp Met His
1 5

<210> 205
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 205
Glu Ile Asp Pro Ser Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ser

<210> 206
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 206
Glu Arg Ser Pro Arg Tyr Phe Asp Val
1 5

<210> 207

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

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

 <400> 207
 Arg Ser Ser Gln Ser Ile Val His Gly Asn Gly Asn Thr Tyr Leu Glu
 1 5 10 15

<210> 208
 <211> 7
 <212> PRT
 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

 <400> 208
 Arg Val Ser Asn Arg Phe Ser
 1 5

<210> 209
 <211> 9
 <212> PRT
 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

 <400> 209
 Phe Gln Gly Ser His Val Pro Tyr Thr
 1 5

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

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

 <400> 210
 Ser Tyr Trp Leu Asn
 1 5

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

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 211

Met Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Val Phe Lys
1 5 10 15

Asp

<210> 212

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 212

Gly Arg Gly Asn Phe Tyr Gly Gly Ser His Ala Met Glu Tyr
1 5 10

<210> 213

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic E25 light chain variable sequence"

<400> 213

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

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

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

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

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

Thr Val

<210> 214
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 E25 heavy chain variable sequence"

<400> 214
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

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

Val Ala Ser Ile Thr Tyr Asp Gly Ser Thr Asn Tyr Asn Pro Ser Val
 50 55 60

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

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

Ala Arg Gly Ser His Tyr Phe Gly His Trp His Phe Ala Val Trp Gly
 100 105 110

Gln Gly

<210> 215
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 peptide"

<400> 215
 Ser Tyr Thr Met His
 1 5

<210> 216
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 peptide"

<400> 216

Ser Tyr Ala Met Ser
1 5

<210> 217

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 217

Asn Phe Gly Met His
1 5

<210> 218

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 218

Asn Tyr Gly Met His
1 5

<210> 219

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 219

Ile Ile Ser Gly Ser Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 220

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 220

Ala Ile Trp Tyr Asp Gly His Asp Lys Tyr Tyr Ser Tyr Tyr Val Lys
1 5 10 15

Gly

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<210> 221
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 221
Ala Ile Trp Tyr Asp Gly His Asp Lys Tyr Tyr Ala Tyr Tyr Val Lys
1           5           10           15
```

Gly

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<210> 222
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 222
Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Val Asp Ser Val Lys
1           5           10           15
```

Gly

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<210> 223
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 223
Val Ile Trp Asn Asp Gly Ser Asn Lys Tyr Tyr Val Asp Ser Val Lys
1           5           10           15
```

Gly

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<210> 224
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 224
Asp Ser Ser Ser Trp Tyr Arg Tyr Phe Asp Tyr
1 5 10

<210> 225
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 225
Asp Arg Leu Val Ala Pro Gly Thr Phe Asp Tyr
1 5 10

<210> 226
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 226
Lys Asn Trp Ser Phe Asp Phe
1 5

<210> 227
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 227
Asp Arg Met Gly Ile Tyr Tyr Tyr Gly Met Asp Val
1 5 10

<210> 228
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 228
Arg Ala Ser Gln Gly Ile Ser Ser Trp Leu Ala
1 5 10

<210> 229
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 229
 Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
 1 5 10

<210> 230
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 230
 Arg Ala Ser Gln Ser Val Ser Ser Asn Tyr Leu Ala
 1 5 10

<210> 231
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 231
 Arg Ala Ser Gln Gly Val Ser Arg Tyr Leu Ala
 1 5 10

<210> 232
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 232
 Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
 1 5 10

<210> 233
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 233

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 234

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 234

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 235

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 235

Met Pro Pro Val Trp Lys Val
1 5

<210> 236

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 236

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 237

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 237

Leu His Pro Leu Cys Lys Val
1 5

<210> 238
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 238
 Asn Ser Leu Ile Val Thr Leu Thr
 1 5

<210> 239
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 239
 Gln Gln Tyr Asn Ser Tyr Pro Tyr Thr
 1 5

<210> 240
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 240
 Gln Gln Tyr Gly Ser Ser Phe Thr
 1 5

<210> 241
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 241
 Gln Gln Arg Ser Asn Trp Gln Tyr Thr
 1 5

<210> 242
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

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peptide"

<400> 242
Gln Gln Arg Ser Asn Trp Thr
1 5

<210> 243
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 243
Asn Ser Ile Ile Val Ser Leu Thr
1 5

<210> 244
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 244
Arg Ser Ser Gln Ser Leu Val His Asn Asn Ala Asn Thr Tyr Leu His
1 5 10 15

<210> 245
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 245
Lys Val Ser Asn Arg Phe Ser
1 5

<210> 246
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 246
Ser Gln Asn Thr Leu Val Pro Trp Thr
1 5

<210> 247
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 247
 Gly Phe Thr Phe Ser Asp Tyr Gly Ile Ala
 1 5 10

<210> 248
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 248
 Ala Phe Ile Ser Asp Leu Ala Tyr Thr Ile Tyr Tyr Ala Asp Thr Val
 1 5 10 15

Thr Gly

<210> 249
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 249
 Ala Arg Asp Asn Trp Asp Ala Met Asp Tyr
 1 5 10

<210> 250
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic Humanized 47H4 V.5 heavy chain variable sequence"

<400> 250
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

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

Ala Phe Ile Ser Asp Leu Ala Tyr Thr Ile Tyr Tyr Ala Asp Thr Val
50 55 60

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

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

Ala Arg Asp Asn Trp Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 251

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
Humanized 47H4 V.24-6 light chain variable sequence"

<400> 251

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

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

Asn Ala Asn Thr Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Thr Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg

<210> 252

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<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        Humanized 47H4 V.1,2 heavy chain variable sequence"

<400> 252
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15

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

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

Ala Phe Ile Ser Asp Leu Ala Tyr Thr Ile Tyr Tyr Ala Asp Thr Val
          50          55          60

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

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

Ala Arg Asp Asn Trp Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
          100         105         110

Val Thr Val Ser Ser
          115

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<210> 253
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        Humanized 47H4 V.1,3 light chain variable sequence"

<400> 253
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1          5          10          15

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

Asn Gly Asn Thr Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
          35          40          45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
          50          55          60

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

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

Thr Leu Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg

<210> 254
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 254
Arg Ser Ser Gln Asp Ile Ser Asn Ser Leu Asn
1 5 10

<210> 255
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 255
Ser Thr Ser Arg Leu His Ser
1 5

<210> 256
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 256
Gln Gln Gly His Thr Leu Pro Trp Thr
1 5

<210> 257
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 257
Gly Tyr Thr Phe Thr Asp Tyr Tyr Met Met
1 5 10

<210> 258
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 258
Gly Asp Asn Ile Asp Pro Asn Asn Tyr Asp Thr Ser Tyr Asn Gln Lys
1 5 10 15

Phe Lys Gly

<210> 259
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 259
Ala Ser Lys Ala Tyr
1 5

<210> 260
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 260
Arg Ser Ser Gln Asp Ile Ser Asn Ala Leu Asn
1 5 10

<210> 261
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 261

Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile Met
1 5 10