

SEQUENCE LISTING

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<120> Binding molecules that inhibit cancer growth.

<130> P108305PC00

<140> PCT/NL2016/050726
<141> 2016-10-21

<150> EP 15191343.1
<151> 2015-10-23

<150> 16168647.2
<151> 2016-05-06

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<170> PatentIn version 3.5

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35 40 45

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

Ser Val Phe Thr Ser Tyr Leu Asp Leu Ser Met Asn Asn Ile Ser Gln
65 70 75 80

Leu Leu Pro Asn Pro Leu Pro Ser Leu Arg Phe Leu Glu Glu Leu Arg
85 90 95

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

Leu Tyr Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg His
115 120 125

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

Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly
145 150 155 160

Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu
165 170 175

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

Leu Ala Leu Asn Lys Ile His His Ile Pro Asp Tyr Ala Phe Gly Asn
195 200 205

Leu Ser Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile His Ser
210 215 220

Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp
225 230 235 240

Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu
245 250 255

Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile
260 265 270

Pro Glu Lys Ala Phe Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe
275 280 285

Tyr Asp Asn Pro Ile Gln Phe Val Gly Arg Ser Ala Phe Gln His Leu
290 295 300

Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu
305 310 315 320

Phe Pro Asp Leu Thr Gly Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr
325 330 335

Gly Ala Gln Ile Ser Ser Leu Pro Gln Thr Val Cys Asn Gln Leu Pro
340 345 350

Asn Leu Gln Val Leu Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro
355 360 365

Ser Phe Ser Val Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn
370 375 380

Glu Ile Tyr Glu Ile Lys Val Asp Thr Phe Gln Gln Leu Leu Ser Leu
385 390 395 400

Arg Ser Leu Asn Leu Ala Trp Asn Lys Ile Ala Ile Ile His Pro Asn
405 410 415

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

Ala Phe Gly Val Cys Glu Asn Ala Tyr Lys Ile Ser Asn Gln Trp Asn
485 490 495

Lys Gly Asp Asn Ser Ser Met Asp Asp Leu His Lys Lys Asp Ala Gly
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Met Phe Gln Ala Gln Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp
515 520 525

Phe Glu Glu Asp Leu Lys Ala Leu His Ser Val Gln Cys Ser Pro Ser
530 535 540

Pro Gly Pro Phe Lys Pro Cys Glu His Leu Leu Asp Gly Trp Leu Ile
545 550 555 560

Arg Ile Gly Val Trp Thr Ile Ala Val Leu Ala Leu Thr Cys Asn Ala
565 570 575

Leu Val Thr Ser Thr Val Phe Arg Ser Pro Leu Tyr Ile Ser Pro Ile
580 585 590

Lys Leu Leu Ile Gly Val Ile Ala Ala Val Asn Met Leu Thr Gly Val
595 600 605

Ser Ser Ala Val Leu Ala Gly Val Asp Ala Phe Thr Phe Gly Ser Phe
610 615 620

Ala Arg His Gly Ala Trp Trp Glu Asn Gly Val Gly Cys His Val Ile
625 630 635 640

Gly Phe Leu Ser Ile Phe Ala Ser Glu Ser Ser Val Phe Leu Leu Thr
645 650 655

Leu Ala Ala Leu Glu Arg Gly Phe Ser Val Lys Tyr Ser Ala Lys Phe
660 665 670

Glu Thr Lys Ala Pro Phe Ser Ser Leu Lys Val Ile Ile Leu Leu Cys
675 680 685

Ala Leu Leu Ala Leu Thr Met Ala Ala Val Pro Leu Leu Gly Gly Ser
690 695 700

Lys Tyr Gly Ala Ser Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro
705 710 715 720

Ser Thr Met Gly Tyr Met Val Ala Leu Ile Leu Leu Asn Ser Leu Cys
725 730 735

Phe Leu Met Met Thr Ile Ala Tyr Thr Lys Leu Tyr Cys Asn Leu Asp
740 745 750

Lys Gly Asp Leu Glu Asn Ile Trp Asp Cys Ser Met Val Lys His Ile
755 760 765

Ala Leu Leu Leu Phe Thr Asn Cys Ile Leu Asn Cys Pro Val Ala Phe
770 775 780

Leu Ser Phe Ser Ser Leu Ile Asn Leu Thr Phe Ile Ser Pro Glu Val
785 790 795 800

Ile Lys Phe Ile Leu Leu Val Val Val Pro Leu Pro Ala Cys Leu Asn
805 810 815

Pro Leu Leu Tyr Ile Leu Phe Asn Pro His Phe Lys Glu Asp Leu Val
820 825 830

Ser Leu Arg Lys Gln Thr Tyr Val Trp Thr Arg Ser Lys His Pro Ser
835 840 845

Leu Met Ser Ile Asn Ser Asp Asp Val Glu Lys Gln Ser Cys Asp Ser
850 855 860

Thr Gln Ala Leu Val Thr Phe Thr Ser Ser Ser Ile Thr Tyr Asp Leu
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Pro Pro Ser Ser Val Pro Ser Pro Ala Tyr Pro Val Thr Glu Ser Cys
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His Leu Ser Ser Val Ala Phe Val Pro Cys Leu
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35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65 70 75 80

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

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

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195 200 205

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

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

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

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260 265 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His

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295

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Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
 305 310 315 320

Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
 325 330 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
 340 345 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
 355 360 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
 370 375 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
 385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
 405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
 420 425 430

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

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
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Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
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Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
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Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625 630 635 640

Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
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Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
660 665 670

Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
675 680 685

Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu

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695

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Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
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Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
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Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
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Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
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Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
 770 775 780

Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
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Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
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Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
 820 825 830

Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
 835 840 845

Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
 850 855 860

Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
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Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
 885 890 895

Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
900 905 910

Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
915 920 925

Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
930 935 940

Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
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Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
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Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
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995 1000 1005

Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe
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Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu
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Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn
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Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg
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1070 1075 1080

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

1085

1090

1095

Lys Arg Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln
1100 1105 1110

Pro Leu Asn Pro Ala Pro Ser Arg Asp Pro His Tyr Gln Asp Pro
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His Ser Thr Ala Val Gly Asn Pro Glu Tyr Leu Asn Thr Val Gln
1130 1135 1140

Pro Thr Cys Val Asn Ser Thr Phe Asp Ser Pro Ala His Trp Ala
1145 1150 1155

Gln Lys Gly Ser His Gln Ile Ser Leu Asp Asn Pro Asp Tyr Gln
1160 1165 1170

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

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

Pro Phe Leu Glu Glu Leu Gln Leu Ala Gly Asn Asp Leu Ser Phe Ile
85 90 95

His Pro Lys Ala Leu Ser Gly Leu Lys Glu Leu Lys Val Leu Thr Leu
100 105 110

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

Ser Ala Leu Gln Ser Leu Arg Leu Asp Ala Asn His Ile Thr Ser Val
130 135 140

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

Asp Asp Asn Ser Leu Thr Glu Val Pro Val His Pro Leu Ser Asn Leu
165 170 175

Pro Thr Leu Gln Ala Leu Thr Leu Ala Leu Asn Lys Ile Ser Ser Ile
180 185 190

Pro Asp Phe Ala Phe Thr Asn Leu Ser Ser Leu Val Val Leu His Leu
195 200 205

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

Asp Asn Leu Glu Thr Leu Asp Leu Asn Tyr Asn Asn Leu Gly Glu Phe
225 230 235 240

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

Ser Asn Ser Ile Ser Val Ile Pro Asp Gly Ala Phe Asp Gly Asn Pro
260 265 270

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

Asn Ser Ala Phe His Asn Leu Ser Asp Leu His Ser Leu Val Ile Arg
290 295 300

Gly Ala Ser Met Val Gln Gln Phe Pro Asn Leu Thr Gly Thr Val His
305 310 315 320

Leu Glu Ser Leu Thr Leu Thr Gly Thr Lys Ile Ser Ser Ile Pro Asn
325 330 335

Asn Leu Cys Gln Glu Gln Lys Met Leu Arg Thr Leu Asp Leu Ser Tyr
340 345 350

Asn Asn Ile Arg Asp Leu Pro Ser Phe Asn Gly Cys His Ala Leu Glu
355 360 365

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

Phe Gln Gly Leu Ile Ser Leu Arg Ile Leu Asp Leu Ser Arg Asn Leu
385 390 395 400

Ile His Glu Ile His Ser Arg Ala Phe Ala Thr Leu Gly Pro Ile Thr
405 410 415

Asn Leu Asp Val Ser Phe Asn Glu Leu Thr Ser Phe Pro Thr Glu Gly
420 425 430

Leu Asn Gly Leu Asn Gln Leu Lys Leu Val Gly Asn Phe Lys Leu Lys
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Glu Ala Leu Ala Ala Lys Asp Phe Val Asn Leu Arg Ser Leu Ser Val
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Asn Leu Asn Thr Glu Asp Asn Ser Leu Gln Asp His Ser Val Ala Gln
485 490 495

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

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

Leu Thr Thr Phe Ala Ser Cys Thr Ser Leu Pro Ser Ser Lys Leu Phe
565 570 575

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580 585 590

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

Gly Ile Trp Trp Glu Thr Gly Ser Gly Cys Lys Val Ala Gly Phe Leu
610 615 620

Ala Val Phe Ser Ser Glu Ser Ala Ile Phe Leu Leu Met Leu Ala Thr
625 630 635 640

Val Glu Arg Ser Leu Ser Ala Lys Asp Ile Met Lys Asn Gly Lys Ser
645 650 655

Asn His Leu Lys Gln Phe Arg Val Ala Ala Leu Leu Ala Phe Leu Gly
660 665 670

Ala Thr Val Ala Gly Cys Phe Pro Leu Phe His Arg Gly Glu Tyr Ser
675 680 685

Ala Ser Pro Leu Cys Leu Pro Phe Pro Thr Gly Glu Thr Pro Ser Leu
690 695 700

Gly Phe Thr Val Thr Leu Val Leu Leu Asn Ser Leu Ala Phe Leu Leu
705 710 715 720

Met Ala Val Ile Tyr Thr Lys Leu Tyr Cys Asn Leu Glu Lys Glu Asp
725 730 735

Leu Ser Glu Asn Ser Gln Ser Ser Met Ile Lys His Val Ala Trp Leu
740 745 750

Ile Phe Thr Asn Cys Ile Phe Phe Cys Pro Val Ala Phe Phe Ser Phe
755 760 765

Ala Pro Leu Ile Thr Ala Ile Ser Ile Ser Pro Glu Ile Met Lys Ser
770 775 780

Val Thr Leu Ile Phe Phe Pro Leu Pro Ala Cys Leu Asn Pro Val Leu
785 790 795 800

Tyr Val Phe Phe Asn Pro Lys Phe Lys Glu Asp Trp Lys Leu Leu Lys
805 810 815

Arg Arg Val Thr Lys Lys Ser Gly Ser Val Ser Val Ser Ile Ser Ser
820 825 830

Gln Gly Gly Cys Leu Glu Gln Asp Phe Tyr Tyr Asp Cys Gly Met Tyr
835 840 845

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

Leu Leu Thr Lys Pro Val Ser Cys Lys His Leu Ile Lys Ser His Ser
865 870 875 880

Cys Pro Ala Leu Ala Val Ala Ser Cys Gln Arg Pro Glu Gly Tyr Trp
885 890 895

Ser Asp Cys Gly Thr Gln Ser Ala His Ser Asp Tyr Ala Asp Glu Glu
900 905 910

Asp Ser Phe Val Ser Asp Ser Ser Asp Gln Val Gln Ala Cys Gly Arg
915 920 925

Ala Cys Phe Tyr Gln Ser Arg Gly Phe Pro Leu Val Arg Tyr Ala Tyr
930 935 940

Asn Leu Pro Arg Val Lys Asp Ser Arg Asp Tyr Lys Asp Asp Asp Asp
945 950 955 960

Lys Ala Gly Ala Asp Tyr Lys Asp Asp Asp Asp Lys Leu Asp Gly Gly
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Val Pro Asp Tyr Ala
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35 40 45

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

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

Pro Phe Leu Glu Glu Leu Gln Leu Ala Gly Asn Asp Leu Ser Phe Ile
85 90 95

His Pro Lys Ala Leu Ser Gly Leu Lys Glu Leu Lys Val Leu Thr Leu
100 105 110

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

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

130

135

140

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

Asp Asp Asn Ser Leu Thr Glu Val Pro Val His Pro Leu Ser Asn Leu
 165 170 175

Pro Thr Leu Gln Ala Leu Thr Leu Ala Leu Asn Lys Ile Ser Ser Ile
 180 185 190

Pro Asp Phe Ala Phe Thr Asn Leu Ser Ser Leu Val Val Leu His Leu
 195 200 205

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

Asp Asn Leu Glu Thr Leu Asp Leu Asn Tyr Asn Asn Leu Gly Glu Phe
 225 230 235 240

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

Ser Asn Ser Ile Ser Val Ile Pro Asp Gly Ala Phe Asp Gly Asn Pro
 260 265 270

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

Asn Ser Ala Phe His Asn Leu Ser Asp Leu His Ser Leu Val Ile Arg
 290 295 300

Gly Ala Ser Met Val Gln Gln Phe Pro Asn Leu Thr Gly Thr Val His
 305 310 315 320

Leu Glu Ser Leu Thr Leu Thr Gly Thr Lys Ile Ser Ser Ile Pro Asn
 325 330 335

Asn Leu Cys Gln Glu Gln Lys Met Leu Arg Thr Leu Asp Leu Ser Tyr
340 345 350

Asn Asn Ile Arg Asp Leu Pro Ser Phe Asn Gly Cys His Ala Leu Glu
355 360 365

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

Phe Gln Gly Leu Ile Ser Leu Arg Ile Leu Asp Leu Ser Arg Asn Leu
385 390 395 400

Ile His Glu Ile His Ser Arg Ala Phe Ala Thr Leu Gly Pro Ile Thr
405 410 415

Asn Leu Asp Val Ser Phe Asn Glu Leu Thr Ser Phe Pro Thr Glu Gly
420 425 430

Leu Asn Gly Leu Asn Gln Leu Lys Leu Val Gly Asn Phe Lys Leu Lys
435 440 445

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

Pro Tyr Ala Tyr Gln Cys Cys Ala Phe Trp Gly Cys Asp Ser Tyr Ala
465 470 475 480

Asn Leu Asn Thr Glu Asp Asn Ser Leu Gln Asp His Ser Val Ala Gln
485 490 495

Glu Lys Gly Thr Ala Asp Ala Ala Asn Val Thr Ser Thr Leu Glu Asn
500 505 510

Glu Glu His Ser Gln Ile Ile Ile His Cys Thr Pro Ser Thr Gly Ala
515 520 525

Phe Lys Pro Cys Glu Tyr Leu Leu Gly Ser Trp Met Ile Arg Val Ala

530

535

540

Leu Tyr Val Gly Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile Ile
545 550 555 560

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

Glu Asp Lys Glu Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu Pro
580 585 590

Pro Glu Gln Leu Arg Glu Leu Ser Arg Glu Arg Glu Glu Glu Asp Asp
595 600 605

Tyr Arg Gln Glu Glu Gln Arg Ser Thr Gly Arg Glu Ser Pro Asp His
610 615 620

Leu Asp Gln Asp Tyr Lys Asp Asp Asp Asp Lys
625 630 635

<210> 5

<211> 953

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence full length hLGR5-FLAG-HA insert (

<220>

<221> SIGNAL

<222> (1)..(21)

<220>

<221> MISC_FEATURE

<222> (908)..(909)

<223> linker

<220>

<221> MISC_FEATURE

<222> (910)..(918)

<223> FLAG tag

<220>
<221> MISC_FEATURE
<222> (919)..(921)
<223> linker

<220>
<221> MISC_FEATURE
<222> (922)..(929)
<223> FLAG tag

<220>
<221> MISC_FEATURE
<222> (930)..(933)
<223> linker

<220>
<221> MISC_FEATURE
<222> (934)..(942)
<223> HA tag

<220>
<221> MISC_FEATURE
<222> (943)..(945)
<223> linker

<220>
<221> MISC_FEATURE
<222> (946)..(953)
<223> HA tag

<400> 5

Met Asp Thr Ser Arg Leu Gly Val Leu Leu Ser Leu Pro Val Leu Leu
1 5 10 15

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

Gly Cys Pro Thr His Cys His Cys Glu Pro Asp Gly Arg Met Leu Leu
35 40 45

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

Ser Val Phe Thr Ser Tyr Leu Asp Leu Ser Met Asn Asn Ile Ser Gln
65 70 75 80

Leu Leu Pro Asn Pro Leu Pro Ser Leu Arg Phe Leu Glu Glu Leu Arg
85 90 95

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

Leu Tyr Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg His
115 120 125

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

Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly
145 150 155 160

Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu
165 170 175

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

Leu Ala Leu Asn Lys Ile His His Ile Pro Asp Tyr Ala Phe Gly Asn
195 200 205

Leu Ser Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile His Ser
210 215 220

Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp
225 230 235 240

Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu
245 250 255

Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile
260 265 270

Pro Glu Lys Ala Phe Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe
275 280 285

Tyr Asp Asn Pro Ile Gln Phe Val Gly Arg Ser Ala Phe Gln His Leu
290 295 300

Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu
305 310 315 320

Phe Pro Asp Leu Thr Gly Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr
325 330 335

Gly Ala Gln Ile Ser Ser Leu Pro Gln Thr Val Cys Asn Gln Leu Pro
340 345 350

Asn Leu Gln Val Leu Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro
355 360 365

Ser Phe Ser Val Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn
370 375 380

Glu Ile Tyr Glu Ile Lys Val Asp Thr Phe Gln Gln Leu Leu Ser Leu
385 390 395 400

Arg Ser Leu Asn Leu Ala Trp Asn Lys Ile Ala Ile Ile His Pro Asn
405 410 415

Ala Phe Ser Thr Leu Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn
420 425 430

Leu Leu Ser Ser Phe Pro Ile Thr Gly Leu His Gly Leu Thr His Leu
435 440 445

Lys Leu Thr Gly Asn His Ala Leu Gln Ser Leu Ile Ser Ser Glu Asn
450 455 460

Phe Pro Glu Leu Lys Val Ile Glu Met Pro Tyr Ala Tyr Gln Cys Cys
465 470 475 480

Ala Phe Gly Val Cys Glu Asn Ala Tyr Lys Ile Ser Asn Gln Trp Asn
485 490 495

Lys Gly Asp Asn Ser Ser Met Asp Asp Leu His Lys Lys Asp Ala Gly
500 505 510

Met Phe Gln Ala Gln Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp
515 520 525

Phe Glu Glu Asp Leu Lys Ala Leu His Ser Val Gln Cys Ser Pro Ser
530 535 540

Pro Gly Pro Phe Lys Pro Cys Glu His Leu Leu Asp Gly Trp Leu Ile
545 550 555 560

Arg Ile Gly Val Trp Thr Ile Ala Val Leu Ala Leu Thr Cys Asn Ala
565 570 575

Leu Val Thr Ser Thr Val Phe Arg Ser Pro Leu Tyr Ile Ser Pro Ile
580 585 590

Lys Leu Leu Ile Gly Val Ile Ala Ala Val Asn Met Leu Thr Gly Val
595 600 605

Ser Ser Ala Val Leu Ala Gly Val Asp Ala Phe Thr Phe Gly Ser Phe
610 615 620

Ala Arg His Gly Ala Trp Trp Glu Asn Gly Val Gly Cys His Val Ile
625 630 635 640

Gly Phe Leu Ser Ile Phe Ala Ser Glu Ser Ser Val Phe Leu Leu Thr
645 650 655

Leu Ala Ala Leu Glu Arg Gly Phe Ser Ala Lys Tyr Ser Ala Lys Phe
660 665 670

Glu Thr Lys Ala Pro Phe Ser Ser Leu Lys Val Ile Ile Leu Leu Cys
675 680 685

Ala Leu Leu Ala Leu Thr Met Ala Ala Val Pro Leu Leu Gly Gly Ser
690 695 700

Lys Tyr Gly Ala Ser Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro
705 710 715 720

Ser Thr Met Gly Tyr Met Val Ala Leu Ile Leu Leu Asn Ser Leu Cys
725 730 735

Phe Leu Met Met Thr Ile Ala Tyr Thr Lys Leu Tyr Cys Asn Leu Asp
740 745 750

Lys Gly Asp Leu Glu Asn Ile Trp Asp Cys Ser Met Val Lys His Ile
755 760 765

Ala Leu Leu Leu Phe Thr Asn Cys Ile Leu Asn Cys Pro Val Ala Phe
770 775 780

Leu Ser Phe Ser Ser Leu Ile Asn Leu Thr Phe Ile Ser Pro Glu Val
785 790 795 800

Ile Lys Phe Ile Leu Leu Val Val Val Pro Leu Pro Ala Cys Leu Asn
805 810 815

Pro Leu Leu Tyr Ile Leu Phe Asn Pro His Phe Lys Glu Asp Leu Val
820 825 830

Ser Leu Arg Lys Gln Thr Tyr Val Trp Thr Arg Ser Lys His Pro Ser
835 840 845

Leu Met Ser Ile Asn Ser Asp Asp Val Glu Lys Gln Ser Cys Asp Ser
850 855 860

Thr Gln Ala Leu Val Thr Phe Thr Ser Ser Ser Ile Thr Tyr Asp Leu
865 870 875 880

Pro Pro Ser Ser Val Pro Ser Pro Ala Tyr Pro Val Thr Glu Ser Cys
885 890 895

His Leu Ser Ser Val Ala Phe Val Pro Cys Leu Ala Arg Asp Tyr Lys
900 905 910

Asp Asp Asp Asp Lys Ala Gly Ala Asp Tyr Lys Asp Asp Asp Asp Lys
915 920 925

Leu Asp Gly Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ala Gly Ala
930 935 940

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
945 950

<210> 6
<211> 654
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence hLGR5(ECD)-GPA33(TM)-FLAG insert in pVax1

<220>
<221> SIGNAL
<222> (1)..(21)

<220>
<221> MISC_FEATURE
<222> (563)..(646)
<223> GPA33

<220>
<221> MISC_FEATURE
<222> (647)..(654)
<223> FLAG tag

<400> 6

Met Asp Thr Ser Arg Leu Gly Val Leu Leu Ser Leu Pro Val Leu Leu
1 5 10 15

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

Gly Cys Pro Thr His Cys His Cys Glu Pro Asp Gly Arg Met Leu Leu
35 40 45

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

Ser Val Phe Thr Ser Tyr Leu Asp Leu Ser Met Asn Asn Ile Ser Gln
65 70 75 80

Leu Leu Pro Asn Pro Leu Pro Ser Leu Arg Phe Leu Glu Glu Leu Arg
85 90 95

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

Leu Tyr Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg His
115 120 125

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

Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly
145 150 155 160

Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu
165 170 175

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

Leu Ala Leu Asn Lys Ile His His Ile Pro Asp Tyr Ala Phe Gly Asn
195 200 205

Leu Ser Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile His Ser

210

215

220

Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp
 225 230 235 240

Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu
 245 250 255

Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile
 260 265 270

Pro Glu Lys Ala Phe Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe
 275 280 285

Tyr Asp Asn Pro Ile Gln Phe Val Gly Arg Ser Ala Phe Gln His Leu
 290 295 300

Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu
 305 310 315 320

Phe Pro Asp Leu Thr Gly Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr
 325 330 335

Gly Ala Gln Ile Ser Ser Leu Pro Gln Thr Val Cys Asn Gln Leu Pro
 340 345 350

Asn Leu Gln Val Leu Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro
 355 360 365

Ser Phe Ser Val Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn
 370 375 380

Glu Ile Tyr Glu Ile Lys Val Asp Thr Phe Gln Gln Leu Leu Ser Leu
 385 390 395 400

Arg Ser Leu Asn Leu Ala Trp Asn Lys Ile Ala Ile Ile His Pro Asn
 405 410 415

Ala Phe Ser Thr Leu Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn
420 425 430

Leu Leu Ser Ser Phe Pro Ile Thr Gly Leu His Gly Leu Thr His Leu
435 440 445

Lys Leu Thr Gly Asn His Ala Leu Gln Ser Leu Ile Ser Ser Glu Asn
450 455 460

Phe Pro Glu Leu Lys Val Ile Glu Met Pro Tyr Ala Tyr Gln Cys Cys
465 470 475 480

Ala Phe Gly Val Cys Glu Asn Ala Tyr Lys Ile Ser Asn Gln Trp Asn
485 490 495

Lys Gly Asp Asn Ser Ser Met Asp Asp Leu His Lys Lys Asp Ala Gly
500 505 510

Met Phe Gln Ala Gln Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp
515 520 525

Phe Glu Glu Asp Leu Lys Ala Leu His Ser Val Gln Cys Ser Pro Ser
530 535 540

Pro Gly Pro Phe Lys Pro Cys Glu His Leu Leu Asp Gly Trp Leu Ile
545 550 555 560

Arg Val Ala Leu Tyr Val Gly Ile Ala Val Gly Val Val Ala Ala Leu
565 570 575

Ile Ile Ile Gly Ile Ile Ile Tyr Cys Cys Cys Cys Arg Gly Lys Asp
580 585 590

Asp Asn Thr Glu Asp Lys Glu Asp Ala Arg Pro Asn Arg Glu Ala Tyr
595 600 605

Glu Glu Pro Pro Glu Gln Leu Arg Glu Leu Ser Arg Glu Arg Glu Glu

610

615

620

Glu Asp Asp Tyr Arg Gln Glu Glu Gln Arg Ser Thr Gly Arg Glu Ser
 625 630 635 640

Pro Asp His Leu Asp Gln Asp Tyr Lys Asp Asp Asp Asp Lys
 645 650

<210> 7
 <211> 936
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence full length mouse (m)Lgr5-Myc-HIS insert in
 pEF1_Myc/His

<220>
 <221> SIGNAL
 <222> (1)..(21)

<220>
 <221> MISC_FEATURE
 <222> (908)..(915)
 <223> linker

<220>
 <221> MISC_FEATURE
 <222> (916)..(925)
 <223> cMyc-tag

<220>
 <221> MISC_FEATURE
 <222> (926)..(930)
 <223> linker

<220>
 <221> MISC_FEATURE
 <222> (931)..(936)
 <223> His tag

<400> 7

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

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

Gly Cys Pro Ser His Cys His Cys Glu Leu Asp Gly Arg Met Leu Leu
35 40 45

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

Ser Val Phe Thr Ser Tyr Leu Asp Leu Ser Met Asn Asn Ile Ser Gln
65 70 75 80

Leu Pro Ala Ser Leu Leu His Arg Leu Cys Phe Leu Glu Glu Leu Arg
85 90 95

Leu Ala Gly Asn Ala Leu Thr His Ile Pro Lys Gly Ala Phe Thr Gly
100 105 110

Leu His Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg Gln
115 120 125

Val Pro Glu Glu Ala Leu Gln Asn Leu Arg Ser Leu Gln Ser Leu Arg
130 135 140

Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly
145 150 155 160

Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Asp
165 170 175

Val Pro Val Gln Ala Phe Arg Ser Leu Ser Ala Leu Gln Ala Met Thr
180 185 190

Leu Ala Leu Asn Lys Ile His His Ile Ala Asp Tyr Ala Phe Gly Asn
195 200 205

Leu Ser Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile His Ser

210

215

220

Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp
 225 230 235 240

Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Lys Thr Leu
 245 250 255

Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile
 260 265 270

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

Tyr Asp Asn Pro Ile Gln Phe Val Gly Val Ser Ala Phe Gln His Leu
 290 295 300

Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser His Ile Thr Glu
 305 310 315 320

Phe Pro His Leu Thr Gly Thr Ala Thr Leu Glu Ser Leu Thr Leu Thr
 325 330 335

Gly Ala Lys Ile Ser Ser Leu Pro Gln Ala Val Cys Asp Gln Leu Pro
 340 345 350

Asn Leu Gln Val Leu Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro
 355 360 365

Ser Leu Ser Gly Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn
 370 375 380

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

Arg Ser Leu Asn Leu Ala Trp Asn Lys Ile Ala Ile Ile His Pro Asn
 405 410 415

Ala Phe Ser Thr Leu Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn
420 425 430

Leu Leu Ser Ser Phe Pro Val Thr Gly Leu His Gly Leu Thr His Leu
435 440 445

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

Phe Pro Glu Leu Lys Ile Ile Glu Met Pro Ser Ala Tyr Gln Cys Cys
465 470 475 480

Ala Phe Gly Gly Cys Glu Asn Val Tyr Lys Ile Ser Asn Gln Trp Asn
485 490 495

Lys Asp Asp Gly Asn Ser Val Asp Asp Leu His Lys Lys Asp Ala Gly
500 505 510

Leu Phe Gln Val Gln Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp
515 520 525

Phe Glu Glu Asp Leu Lys Ala Leu His Ser Val Gln Cys Ser Pro Ser
530 535 540

Pro Gly Pro Phe Lys Pro Cys Glu His Leu Phe Gly Ser Trp Leu Ile
545 550 555 560

Arg Ile Gly Val Trp Thr Thr Ala Val Leu Ala Leu Ser Cys Asn Ala
565 570 575

Leu Val Ala Leu Thr Val Phe Arg Thr Pro Leu Tyr Ile Ser Ser Ile
580 585 590

Lys Leu Leu Ile Gly Val Ile Ala Val Val Asp Ile Leu Met Gly Val
595 600 605

Ser Ser Ala Val Leu Ala Ala Val Asp Ala Phe Thr Phe Gly Arg Phe

610

615

620

Ala Gln His Gly Ala Trp Trp Glu Asp Gly Ile Gly Cys Gln Ile Val
 625 630 635 640

Gly Phe Leu Ser Ile Phe Ala Ser Glu Ser Ser Ile Phe Leu Leu Thr
 645 650 655

Leu Ala Ala Leu Glu Arg Gly Phe Ser Val Lys Cys Ser Ser Lys Phe
 660 665 670

Glu Val Lys Ala Pro Leu Phe Ser Leu Arg Ala Ile Val Leu Leu Cys
 675 680 685

Val Leu Leu Ala Leu Thr Ile Ala Thr Ile Pro Leu Leu Gly Gly Ser
 690 695 700

Lys Tyr Asn Ala Ser Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro
 705 710 715 720

Ser Thr Thr Gly Tyr Met Val Ala Leu Val Leu Leu Asn Ser Leu Cys
 725 730 735

Phe Leu Ile Met Thr Ile Ala Tyr Thr Lys Leu Tyr Cys Ser Leu Glu
 740 745 750

Lys Gly Glu Leu Glu Asn Leu Trp Asp Cys Ser Met Val Lys His Ile
 755 760 765

Ala Leu Leu Leu Phe Ala Asn Cys Ile Leu Tyr Cys Pro Val Ala Phe
 770 775 780

Leu Ser Phe Ser Ser Leu Leu Asn Leu Thr Phe Ile Ser Pro Asp Val
 785 790 795 800

Ile Lys Phe Ile Leu Leu Val Ile Val Pro Leu Pro Ser Cys Leu Asn
 805 810 815

Pro Leu Leu Tyr Ile Val Phe Asn Pro His Phe Lys Glu Asp Met Gly
820 825 830

Ser Leu Gly Lys His Thr Arg Phe Trp Met Arg Ser Lys His Ala Ser
835 840 845

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

Thr Gln Ala Leu Val Ser Phe Thr His Ala Ser Ile Ala Tyr Asp Leu
865 870 875 880

Pro Ser Thr Ser Gly Ala Ser Pro Ala Tyr Pro Met Thr Glu Ser Cys
885 890 895

His Leu Ser Ser Val Ala Phe Val Pro Cys Leu Ala Ala Ala Arg Gly
900 905 910

His Pro Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His
915 920 925

Thr Gly His His His His His His
930 935

<210> 8
<211> 281
<212> PRT
<213> Artificial Sequence

<220>
<223> Human ZNRF3(ECD) in pDisplay

<220>
<221> SIGNAL
<222> (1)..(55)

<220>
<221> MISC_FEATURE
<222> (222)..(231)
<223> cMyc-tag

<220>

<221> MISC_FEATURE

<222> (232)..(281)

<223> PDGFR

<400> 8

Met Arg Pro Arg Ser Gly Gly Arg Pro Gly Ala Thr Gly Arg Arg Arg
1 5 10 15

Arg Arg Leu Arg Arg Arg Pro Arg Gly Leu Arg Cys Ser Arg Leu Pro
20 25 30

Pro Pro Pro Pro Leu Pro Leu Leu Leu Gly Leu Leu Leu Ala Ala Ala
35 40 45

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

Leu Phe Glu Ser Ser Pro Ser Gly Asp Tyr Thr Thr Tyr Thr Thr Gly
65 70 75 80

Leu Thr Gly Arg Phe Ser Arg Ala Gly Ala Thr Leu Ser Ala Glu Gly
85 90 95

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

Glu Asp Leu Tyr Glu Tyr Gly Trp Val Gly Val Val Lys Leu Glu Gln
115 120 125

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

Arg Ala Val Gln Arg Gly Ala Thr Ala Val Ile Phe Asp Val Ser Glu
145 150 155 160

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

Lys Arg Pro Val Val Tyr Val Lys Gly Ala Asp Ala Ile Lys Leu Met
180 185 190

Asn Ile Val Asn Lys Gln Lys Val Ala Arg Ala Arg Ile Gln His Arg
195 200 205

Pro Pro Arg Gln Pro Thr Glu Tyr Phe Asp Met Val Asp Glu Gln Lys
210 215 220

Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly Gln Asp Thr Gln Glu
225 230 235 240

Val Ile Val Val Pro His Ser Leu Pro Phe Lys Val Val Val Ile Ser
245 250 255

Ala Ile Leu Ala Leu Val Val Leu Thr Ile Ile Ser Leu Ile Ile Leu
260 265 270

Ile Met Leu Trp Gln Lys Lys Pro Arg
275 280

<210> 9
<211> 256
<212> PRT
<213> Artificial Sequence

<220>
<223> Human ZNRF3 truncation mutant

<220>
<221> SIGNAL
<222> (1)..(55)

<220>
<221> MISC_FEATURE
<222> (218)..(232)
<223> predicted TM region

<220>
<221> MISC_FEATURE

<222> (233)..(256)

<223> intracellular tail

<400> 9

Met Arg Pro Arg Ser Gly Gly Arg Pro Gly Ala Thr Gly Arg Arg Arg
1 5 10 15

Arg Arg Leu Arg Arg Arg Pro Arg Gly Leu Arg Cys Ser Arg Leu Pro
20 25 30

Pro Pro Pro Pro Leu Pro Leu Leu Leu Gly Leu Leu Leu Ala Ala Ala
35 40 45

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

Leu Phe Glu Ser Ser Pro Ser Gly Asp Tyr Thr Thr Tyr Thr Thr Gly
65 70 75 80

Leu Thr Gly Arg Phe Ser Arg Ala Gly Ala Thr Leu Ser Ala Glu Gly
85 90 95

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

Glu Asp Leu Tyr Glu Tyr Gly Trp Val Gly Val Val Lys Leu Glu Gln
115 120 125

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

Arg Ala Val Gln Arg Gly Ala Thr Ala Val Ile Phe Asp Val Ser Glu
145 150 155 160

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

Lys Arg Pro Val Val Tyr Val Lys Gly Ala Asp Ala Ile Lys Leu Met

180

185

190

Asn Ile Val Asn Lys Gln Lys Val Ala Arg Ala Arg Ile Gln His Arg
 195 200 205

Pro Pro Arg Gln Pro Thr Glu Tyr Phe Asp Met Gly Ile Phe Leu Ala
 210 215 220

Phe Phe Val Val Val Ser Leu Val Cys Leu Ile Leu Leu Val Lys Ile
 225 230 235 240

Lys Leu Lys Gln Arg Arg Ser Gln Asn Ser Met Asn Arg Pro Ala Val
 245 250 255

<210> 10
 <211> 164
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mouse ZNRF3 ECD-His in pUPE

<220>
 <221> MISC_FEATURE
 <222> (1)..(2)
 <223> amino acids encoded by cloning sites

<220>
 <221> MISC_FEATURE
 <222> (155)..(157)
 <223> amino acids encoded by cloning sites

<220>
 <221> MISC_FEATURE
 <222> (158)..(164)
 <223> His tag

<400> 10

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

Pro Ser Gly Asp Tyr Thr Thr His Thr Thr Gly Leu Thr Gly Arg Phe

20

25

30

Ser Arg Ala Gly Ala Met Leu Ser Ala Glu Gly Glu Ile Val Gln Met
 35 40 45

His Pro Leu Gly Leu Cys Asn Asn Asp Glu Glu Asp Leu Tyr Glu
 50 55 60

Tyr Gly Trp Val Gly Val Val Lys Leu Glu Gln Pro Glu Leu Asp Pro
 65 70 75 80

Lys Pro Cys Leu Thr Val Leu Gly Lys Ala Lys Arg Ala Val Gln Arg
 85 90 95

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

Asp Gln Leu Asn Gln Gly Ser Glu Asp Pro Leu Lys Arg Pro Val Val
 115 120 125

Tyr Val Lys Gly Ala Asp Ala Ile Lys Leu Met Asn Ile Val Asn Lys
 130 135 140

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

His His His His

<210> 11

<211> 278

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse (m)ZNRF3 sequence in pDisplay

<220>

<221> SIGNAL

<222> (1)..(52)

<220>

<221> MISC_FEATURE

<222> (217)..(218)

<223> amino acids that are encoded by cloning sites

<220>

<221> MISC_FEATURE

<222> (219)..(228)

<223> cMyc-tag

<220>

<221> MISC_FEATURE

<222> (229)..(278)

<223> PDGFR

<400> 11

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

Arg Arg Leu Arg Arg Gly Pro Arg Gly Arg Arg Leu Pro Pro Pro Pro
20 25 30

Pro Leu Pro Leu Leu Leu Gly Leu Leu Leu Ala Ala Ala Gly Pro Gly
35 40 45

Ala Ala Arg Ala Lys Glu Thr Ala Phe Val Glu Val Val Leu Phe Glu
50 55 60

Ser Ser Pro Ser Gly Asp Tyr Thr Thr His Thr Thr Gly Leu Thr Gly
65 70 75 80

Arg Phe Ser Arg Ala Gly Ala Met Leu Ser Ala Glu Gly Glu Ile Val
85 90 95

Gln Met His Pro Leu Gly Leu Cys Asn Asn Asn Asp Glu Glu Asp Leu
100 105 110

Tyr Glu Tyr Gly Trp Val Gly Val Val Lys Leu Glu Gln Pro Glu Leu
115 120 125

Asp Pro Lys Pro Cys Leu Thr Val Leu Gly Lys Ala Lys Arg Ala Val
130 135 140

Gln Arg Gly Ala Thr Ala Val Ile Phe Asp Val Ser Glu Asn Pro Glu
145 150 155 160

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

Val Val Tyr Val Lys Gly Ala Asp Ala Ile Lys Leu Met Asn Ile Val
180 185 190

Asn Lys Gln Lys Val Ala Arg Ala Arg Ile Gln His Leu Pro Pro Arg
195 200 205

Gln Pro Thr Glu Tyr Phe Asp Met Val Asp Glu Gln Lys Leu Ile Ser
210 215 220

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

Val Pro His Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu
245 250 255

Ala Leu Val Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu
260 265 270

Trp Gln Lys Lys Pro Arg
275

<210> 12
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> Human RNF43 in pDisplay

<220>
<221> SIGNAL
<222> (1)..(42)

<220>
<221> MISC_FEATURE
<222> (200)..(201)
<223> amino acids encoded by cloning sites

<220>
<221> MISC_FEATURE
<222> (202)..(211)
<223> cMyc-tag

<220>
<221> MISC_FEATURE
<222> (212)..(261)
<223> PDGFR

<400> 12

Met Ser Gly Gly His Gln Leu Gln Leu Ala Ala Leu Trp Pro Trp Leu
1 5 10 15

Leu Met Ala Thr Leu Gln Ala Gly Phe Gly Arg Thr Gly Leu Val Leu
20 25 30

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

Arg Val Ile Pro Leu Lys Met Asp Pro Thr Gly Lys Leu Asn Leu Thr
50 55 60

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

Lys Leu Met Gln Ser His Pro Leu Tyr Leu Cys Asn Ala Ser Asp Asp
85 90 95

Asp Asn Leu Glu Pro Gly Phe Ile Ser Ile Val Lys Leu Glu Ser Pro
100 105 110

Arg Arg Ala Pro Arg Pro Cys Leu Ser Leu Ala Ser Lys Ala Arg Met

115

120

125

Ala Gly Glu Arg Gly Ala Ser Ala Val Leu Phe Asp Ile Thr Glu Asp
130 135 140

Arg Ala Ala Ala Glu Gln Leu Gln Gln Pro Leu Gly Leu Thr Trp Pro
145 150 155 160

Val Val Leu Ile Trp Gly Asn Asp Ala Glu Lys Leu Met Glu Phe Val
165 170 175

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

Ala Trp Pro Asp Tyr Asp Val Val Asp Glu Gln Lys Leu Ile Ser Glu
195 200 205

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

Pro His Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala
225 230 235 240

Leu Val Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp
245 250 255

Gln Lys Lys Pro Arg
260

<210> 13

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse RNF43 in pDisplay

<220>

<221> MISC_FEATURE

<222> (200)..(201)
<223> amino acids encoded by cloning site

<220>
<221> MISC_FEATURE
<222> (202)..(211)
<223> cMyc-tag

<220>
<221> MISC_FEATURE
<222> (212)..(261)
<223> PDGFR

<400> 13

Met Ser Gly Gly His Gln Leu Gln Leu Ala Val Leu Trp Pro Trp Leu
1 5 10 15

Leu Met Ala Thr Leu His Ala Gly Phe Gly His Thr Gly Arg Val Leu
20 25 30

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

Arg Val Ile Pro Leu Lys Met Asp Pro Thr Gly Lys Leu Asn Leu Thr
50 55 60

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

Lys Leu Met Gln Ser His Pro Leu Tyr Leu Cys Asn Ala Ser Asp Asp
85 90 95

Asp Asn Leu Glu Pro Gly Phe Ile Ser Ile Val Lys Leu Glu Ser Pro
100 105 110

Arg Arg Ala Pro Arg Pro Cys Leu Ser Leu Ala Ser Lys Ala Arg Met
115 120 125

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

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

Val Val Leu Ile Trp Gly Ser Asp Ala Ala Lys Leu Met Glu Phe Val
165 170 175

Tyr Lys Asn Arg Lys Ala Tyr Val Trp Ile Glu Leu Lys Glu Pro Pro
180 185 190

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

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

Pro His Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala
225 230 235 240

Leu Val Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp
245 250 255

Gln Lys Lys Pro Arg
260

<210> 14
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 14
ccagcaggat ccgccgccac catggacacc tcccggctcg gtg

43

<210> 15
<211> 38
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 15

ccagcagcgg ccgcttagag acatgggaca aatgccac

38

<210> 16

<211> 907

<212> PRT

<213> Macaca fascicularis

<220>

<221> SIGNAL

<222> (1)..(21)

<400> 16

Met Asp Thr Ser Arg Leu Gly Val Leu Leu Ser Leu Pro Val Leu Leu
1 5 10 15

Gln Leu Ala Ala Gly Ser Ser Ser Pro Arg Ser Gly Ala Leu Leu Arg
20 25 30

Gly Cys Pro Thr His Cys His Cys Glu Pro Asp Gly Arg Met Leu Leu
35 40 45

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

Ser Val Phe Thr Ser Tyr Leu Asp Leu Ser Met Asn Asn Ile Ser Gln
65 70 75 80

Leu Leu Pro Asn Pro Leu Pro Ser Leu Arg Phe Leu Glu Glu Leu Arg
85 90 95

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

Leu Tyr Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg Gln
115 120 125

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

Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly
145 150 155 160

Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu
165 170 175

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

Leu Ala Leu Asn Lys Ile His His Ile Pro Asp Tyr Ala Phe Gly Asn
195 200 205

Leu Ser Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile His Ser
210 215 220

Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp
225 230 235 240

Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu
245 250 255

Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile
260 265 270

Pro Glu Lys Ala Phe Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe
275 280 285

Tyr Asp Asn Pro Ile Gln Phe Val Gly Arg Ser Ala Phe Gln His Leu
290 295 300

Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu
305 310 315 320

Phe Pro Asp Leu Thr Gly Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr

325

330

335

Gly Ala Gln Ile Ser Ser Leu Pro Gln Thr Val Cys Asn Gln Leu Pro
 340 345 350

Asn Leu Gln Val Leu Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro
 355 360 365

Ser Phe Ser Val Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn
 370 375 380

Glu Ile Tyr Glu Ile Lys Val Asp Thr Phe Gln Gln Leu Leu Ser Leu
 385 390 395 400

Arg Ser Leu Asn Leu Ala Trp Asn Lys Ile Ala Ile Ile His Pro Asn
 405 410 415

Ala Phe Ser Thr Leu Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn
 420 425 430

Leu Leu Ser Ser Phe Pro Val Thr Gly Leu His Gly Leu Thr His Leu
 435 440 445

Lys Leu Thr Gly Asn His Ala Leu Gln Ser Leu Ile Ser Ser Glu Asn
 450 455 460

Phe Pro Glu Leu Lys Ile Ile Glu Met Pro Tyr Ala Tyr Gln Cys Cys
 465 470 475 480

Ala Phe Gly Val Cys Glu Asn Ala Tyr Lys Ile Ser Asn Gln Trp Asn
 485 490 495

Lys Gly Asp Asn Ser Ser Met Asp Asp Leu His Lys Lys Asp Ala Gly
 500 505 510

Met Phe Gln Val Gln Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp
 515 520 525

Phe Glu Glu Asp Leu Lys Ala Leu His Ser Val Gln Cys Ser Pro Ser
530 535 540

Pro Gly Pro Phe Lys Pro Cys Glu His Leu Leu Asp Gly Trp Leu Ile
545 550 555 560

Arg Ile Gly Val Trp Thr Ile Ala Val Leu Ala Leu Thr Cys Asn Ala
565 570 575

Leu Val Thr Ser Thr Val Phe Arg Ser Pro Leu Tyr Ile Ser Pro Ile
580 585 590

Lys Leu Leu Ile Gly Val Ile Ala Val Val Asn Met Leu Thr Gly Val
595 600 605

Ser Ser Ala Val Leu Ala Gly Val Asp Ala Phe Thr Phe Gly Ser Phe
610 615 620

Ala Arg His Gly Ala Trp Trp Glu Asn Gly Val Gly Cys Gln Val Ile
625 630 635 640

Gly Phe Leu Ser Ile Phe Ala Ser Glu Ser Ser Val Phe Leu Leu Thr
645 650 655

Leu Ala Ala Leu Glu Arg Gly Phe Ser Val Lys Cys Ser Ala Lys Phe
660 665 670

Glu Thr Lys Ala Pro Phe Ser Ser Leu Lys Val Ile Ile Leu Leu Cys
675 680 685

Ala Leu Leu Ala Leu Thr Met Ala Ala Val Pro Leu Leu Gly Gly Ser
690 695 700

Glu Tyr Gly Ala Ser Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro
705 710 715 720

Ser Thr Thr Gly Tyr Met Val Ala Leu Ile Leu Leu Asn Ser Leu Cys

725

730

735

Phe Leu Met Met Thr Ile Ala Tyr Thr Lys Leu Tyr Cys Asn Leu Asp
740 745 750

Lys Gly Asp Leu Glu Asn Ile Trp Asp Cys Ser Met Val Lys His Ile
755 760 765

Ala Leu Leu Leu Phe Thr Asn Cys Ile Leu Tyr Cys Pro Val Ala Phe
770 775 780

Leu Ser Phe Ser Ser Leu Leu Asn Leu Thr Phe Ile Ser Pro Glu Val
785 790 795 800

Ile Lys Phe Ile Leu Leu Val Ile Val Pro Leu Pro Ala Cys Leu Asn
805 810 815

Pro Leu Leu Tyr Ile Leu Phe Asn Pro His Phe Lys Glu Asp Leu Val
820 825 830

Ser Leu Gly Lys Gln Thr Tyr Phe Trp Thr Arg Ser Lys His Pro Ser
835 840 845

Leu Met Ser Ile Asn Ser Asp Asp Val Glu Lys Gln Ser Cys Asp Ser
850 855 860

Thr Gln Ala Leu Val Thr Phe Thr Ser Ser Ser Ile Ala Tyr Asp Leu
865 870 875 880

Pro Pro Ser Ser Val Pro Ser Pro Ala Tyr Pro Val Thr Glu Ser Cys
885 890 895

His Leu Ser Ser Val Ala Phe Val Pro Cys Leu
900 905

<210> 17
<211> 381
<212> DNA

<213> Artificial Sequence

<220>

<223> MF1337

<220>

<221> CDS

<222> (1)..(381)

<400> 17

gag	gtg	cag	ctg	gtg	gag	act	ggg	gct	gag	gtg	aag	aag	ccg	ggg	gcc	48
Glu	Val	Gln	Leu	Val	Glu	Thr	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	
1				5					10					15		

tca	gtg	aag	gtc	tcc	tgc	aag	gct	tct	gac	tac	atc	ttc	acc	aaa	tat	96
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Asp	Tyr	Ile	Phe	Thr	Lys	Tyr	
			20					25					30			

gac	atc	aac	tgg	gtg	cgc	cag	gcc	cct	gga	caa	ggg	ctt	gaa	tgg	atg	144
Asp	Ile	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
		35					40					45				

gga	tgg	atg	agc	gct	aac	act	gga	aac	acg	ggc	tat	gca	cag	aag	ttc	192
Gly	Trp	Met	Ser	Ala	Asn	Thr	Gly	Asn	Thr	Gly	Tyr	Ala	Gln	Lys	Phe	
	50					55					60					

cag	ggc	aga	gtc	acc	atg	acc	agg	gac	acg	tcc	ata	aac	aca	gcc	tac	240
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Ile	Asn	Thr	Ala	Tyr	
65					70					75				80		

atg	gag	ctg	agc	agc	ctg	aca	tct	ggg	gac	acg	gcc	gtt	tat	ttc	tgt	288
Met	Glu	Leu	Ser	Ser	Leu	Thr	Ser	Gly	Asp	Thr	Ala	Val	Tyr	Phe	Cys	
				85					90					95		

gcg	agg	agt	agt	ctt	ttc	aag	aca	gag	acg	gcg	ccc	tac	tat	cac	ttc	336
Ala	Arg	Ser	Ser	Leu	Phe	Lys	Thr	Glu	Thr	Ala	Pro	Tyr	Tyr	His	Phe	
			100					105					110			

gct	ctg	gac	gtc	tgg	ggc	caa	ggg	acc	acg	gtc	acc	gtc	tcc	agt		381
Ala	Leu	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser		
		115					120					125				

<210> 18

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 18

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

Ser Val Lys Val Ser Cys Lys Ala Ser Asp Tyr Ile Phe Thr Lys Tyr
20 25 30

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

Gly Trp Met Ser Ala Asn Thr Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Thr Ser Gly Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Ser Ser Leu Phe Lys Thr Glu Thr Ala Pro Tyr Tyr His Phe
100 105 110

Ala Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 19

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> MF3755

<220>

<221> CDS

<222> (1)..(360)

<400> 19

cag	gtg	cag	ctg	gtg	cag	tct	ggg	tct	gag	ttg	aag	aag	cct	ggg	gcc	48
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ser	Glu	Leu	Lys	Lys	Pro	Gly	Ala	
1				5					10					15		

tca	gtg	aag	att	tcc	tgc	aag	gct	tct	gga	tac	gac	ttc	act	aac	tat	96
Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Asp	Phe	Thr	Asn	Tyr	
			20					25					30			

gct	atg	aat	tgg	gtg	cga	cag	gcc	cct	gga	cac	ggg	ctt	gag	tgg	atg	144
Ala	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	His	Gly	Leu	Glu	Trp	Met	
		35					40					45				

gga	tgg	atc	aac	gcc	aac	act	ggg	gac	cca	acg	tat	gcc	cag	ggc	ttc	192
Gly	Trp	Ile	Asn	Ala	Asn	Thr	Gly	Asp	Pro	Thr	Tyr	Ala	Gln	Gly	Phe	
	50					55					60					

aca	gga	cgg	ttt	gtc	ttc	tcc	ttg	gac	acc	tct	gtc	agc	acg	gca	tat	240
Thr	Gly	Arg	Phe	Val	Phe	Ser	Leu	Asp	Thr	Ser	Val	Ser	Thr	Ala	Tyr	
65					70					75					80	

ctg	cag	atc	agc	agt	tta	aag	gct	gag	gac	tct	gcc	gtg	tat	tac	tgt	288
Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	
			85						90					95		

acg	aga	gag	cga	ttt	ttg	gag	tgg	tta	cac	ttt	gac	tac	tgg	ggc	cag	336
Thr	Arg	Glu	Arg	Phe	Leu	Glu	Trp	Leu	His	Phe	Asp	Tyr	Trp	Gly	Gln	
			100					105						110		

gga	acc	ctg	gtc	acc	gtc	tcc	agt									360
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser									
		115					120									

<210> 20
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 20

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

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

Ala Met Asn Trp Val Arg Gln Ala Pro Gly His Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Ala Asn Thr Gly Asp Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Glu Arg Phe Leu Glu Trp Leu His Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 21
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> MF3178

<220>
<221> CDS
<222> (1)..(372)

<400> 21
cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg gcc 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

tca gtg aag gtc tcc tgc aag gct tct gga tac acc ttc acc ggc tac 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

gga tgg atc aac cct aac agt ggt ggc aca aac tat gca cag aag ttt	192
Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe	
50 55 60	

cag ggc agg gtc acg atg acc agg gac acg tcc atc agc aca gcc tac	240
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr	
65 70 75 80	

atg gag ctg agc agg ctg aga tct gac gac acg gct gtg tat tac tgt	288
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	

gca aga gat cat ggt tct cgt cat ttc tgg tct tac tgg ggc ttt gat	336
Ala Arg Asp His Gly Ser Arg His Phe Trp Ser Tyr Trp Gly Phe Asp	
100 105 110	

tat tgg ggc caa ggt acc ctg gtc acc gtc tcc agt	372
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser	
115 120	

<210> 22
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 22

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

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

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Asp His Gly Ser Arg His Phe Trp Ser Tyr Trp Gly Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 23
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> MF5790

<220>
<221> CDS
<222> (1)..(378)

<400> 23
cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gag 48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc ttc agc agt agt 96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Ser Ser
20 25 30

agt tcc tac tgg ggc tgg atc cgc cag ccc cca ggg aag ggg ctg gag 144
Ser Ser Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

tgg att ggg agt ttc tat tat agt ggg aac acc tac tac aac ccg tcc 192
Trp Ile Gly Ser Phe Tyr Tyr Ser Gly Asn Thr Tyr Tyr Asn Pro Ser
50 55 60

ctc aag agt cga gtc acc ata tcc gaa gac acg tcc aag aac cag ttc 240
Leu Lys Ser Arg Val Thr Ile Ser Glu Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

tcc ctg aag ctg agc tct gtg acc gcc gca gac acg gct gtg tat tac 288
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

85	90	95	
tgt gcg aga cag acg tat agc agc agc tgg gac ggg gtc ctg tac tac			336
Cys Ala Arg Gln Thr Tyr Ser Ser Ser Trp Asp Gly Val Leu Tyr Tyr			
100	105	110	

ttt gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc agt		378
Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser		
115	120	125

<210> 24
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 24

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Ser Ser
20 25 30

Ser Ser Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Ser Phe Tyr Tyr Ser Gly Asn Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Glu Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Gln Thr Tyr Ser Ser Ser Trp Asp Gly Val Leu Tyr Tyr
100 105 110

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

125

<210> 25
 <211> 381
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF5816

<220>
 <221> CDS
 <222> (1)..(381)

<400> 25
 gag gtg cag ctg gtg cag tct ggg tct aaa ttg aag aag cct ggg gcc 48
 Glu Val Gln Leu Val Gln Ser Gly Ser Lys Leu Lys Lys Pro Gly Ala
 1 5 10 15

tca gtg aag gtt tcc tgc aag gct tct gga tac acc ttc act agc tat 96
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

act atg aat tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
 Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

gga tgg atc aac acc gac act ggg gac cca acg tat gcc cag ggc ttc 192
 Gly Trp Ile Asn Thr Asp Thr Gly Asp Pro Thr Tyr Ala Gln Gly Phe
 50 55 60

aca gga cgg ttt gtc ttc tcc ttg gac acc tct gtc agc acg gca ttt 240
 Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Phe
 65 70 75 80

cta cag atc aac agc cta aag gct gag gac act gcc gta tat tac tgt 288
 Leu Gln Ile Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gga gat tgt gat agt acc agc tgc tat aga tac agt tat ggt 336
 Ala Arg Gly Asp Cys Asp Ser Thr Ser Cys Tyr Arg Tyr Ser Tyr Gly
 100 105 110

tac gag gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc agt 381
 Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 26
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 26

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

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

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

Gly Trp Ile Asn Thr Asp Thr Gly Asp Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Phe
65 70 75 80

Leu Gln Ile Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 27
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> MF3125

<220>

<221> CDS

<222> (1)..(372)

<400> 27

cag	gtg	cag	ctg	gtg	gag	tct	ggg	gga	ggc	gtg	gtc	cag	cct	ggg	agg	48
Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	
1				5					10					15		

tcc	ctg	aga	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	acc	ttc	agt	agc	tat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	
			20					25					30			

ggc	atg	cac	tgg	gtc	cgc	cag	gct	cca	ggc	aag	ggg	ctg	gag	tgg	gtg	144
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				

gca	gtt	ata	tca	tat	gat	gga	agt	aat	aaa	tac	tat	gca	gac	tcc	gtg	192
Ala	Val	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	
	50					55					60					

aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	aat	tcc	aag	aac	acg	ctg	tat	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
65					70				75					80		

ctg	caa	atg	aac	agc	ctg	aga	gct	gag	gac	acg	gcc	gtg	tat	tac	tgt	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		

gca	aaa	ggc	tct	tct	ggc	tgg	ccg	tct	tac	tct	aac	tgg	ggc	ttt	gat	336
Ala	Lys	Gly	Ser	Ser	Gly	Trp	Pro	Ser	Tyr	Ser	Asn	Trp	Gly	Phe	Asp	
			100					105					110			

tat	tgg	ggc	caa	ggc	acc	ctg	gtc	acc	gtc	tcc	agt					372
Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser					
		115					120									

<210> 28

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 28

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	
			20					25					30			
gcc	atg	agc	tgg	gtc	cgc	cag	gct	cca	ggg	aag	ggg	ctg	gag	tgg	gtc	144
Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
tca	gct	att	agt	ggg	agt	ggg	ggg	agc	aca	tac	tac	gca	gac	tcc	gtg	192
Ser	Ala	Ile	Ser	Gly	Ser	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	
		50				55					60					
aag	ggc	cgg	ttc	acc	atc	tcc	aga	gac	aat	tcc	aag	aac	acg	ctg	tat	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
65					70				75					80		
ctg	caa	atg	aac	agc	ctg	aga	gcc	gag	gac	acg	gct	gtg	tat	tac	tgt	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85						90					95		
gca	aga	gat	tgg	tgg	tac	ccg	ccg	tac	tac	tgg	ggc	ttt	gat	tat	tgg	336
Ala	Arg	Asp	Trp	Trp	Tyr	Pro	Pro	Tyr	Tyr	Trp	Gly	Phe	Asp	Tyr	Trp	
			100					105					110			
ggc	caa	ggg	acc	ctg	gtc	acc	gtc	tcc	agt							366
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
		115					120									

<210> 30
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 30

Glu	Val	Gln	Leu	Leu	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	Ser	Tyr	
			20					25					30			
Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys 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 Trp Trp Tyr Pro Pro Tyr Tyr Trp Gly Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 31
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> MF4863

<220>
<221> CDS
<222> (1)..(366)

<400> 31
gag gtg cag ctg gtg cag tct ggg tct gag ttg aag aag cct ggg gcc 48
Glu Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

tca gtg aag gtt tcc tgc aag gct tct gga tac acc tcc att aga tat 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Ser Ile Arg Tyr
20 25 30

gct ttg aac tgg gtg cga cag gcc cct gga caa ggc ctt gag tgg ctg 144
Ala Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Leu
35 40 45

gga tgg atc aac acc aac act ggg aac cca acg tat gcc cgg ggc ttc 192
Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Arg Gly Phe
50 55 60

Ala Arg Asp Thr Tyr Asp Ser Thr Gly Tyr Leu Trp Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 33
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> MF3370

<220>
<221> CDS
<222> (1)..(366)

<400> 33
cag gtt cag ctg gtg cag tct gga gct gag gtg aag aag cct ggg gcc 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
tca gtg aag gtc tcc tgc aag gct tct ggt tac acc ttt acc agc tat 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
ggt atc agc tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
gga tgg atc agc gct tac aat ggt aac aca aac tat gca cag aag ctc 192
Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60
cag ggc aga gtc acc atg acc aca gac aca tcc acg agc aca gcc tac 240
Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80
atg gag ctg agg agc ctg aga tct gac gac acg gct gtg tat tac tgt 288
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
gca aaa gat cgt cat tgg cat tgg tgg ctg gac gcc ttt gat tat tgg 336
Ala Lys Asp Arg His Trp His Trp Trp Leu Asp Ala Phe Asp Tyr Trp
100 105 110

ggc caa ggt acc ctg gtc acc gtc tcc agt
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

366

<210> 34
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 34

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

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

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

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
 50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

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

Ala Lys Asp Arg His Trp His Trp Trp Leu Asp Ala Phe Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 35
 <211> 375

<212> DNA
<213> Artificial Sequence

<220>
<223> MF4280

<220>
<221> CDS
<222> (1)..(375)

<400> 35
cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg gcc 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

tca gtg aag gtc tcc tgc aag gtt tcc gga tac acc ctc act gaa tta 96
Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu
20 25 30

tcc atg cac tgg gtg cga cag gct cct ggt aaa ggg ctt gaa tgg atg 144
Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

gga ggc ttt gat cct gag tat ggt aaa aca ttc ttc gca cag aac ttc 192
Gly Gly Phe Asp Pro Glu Tyr Gly Lys Thr Phe Phe Ala Gln Asn Phe
50 55 60

cag ggc aga gtc acc atg acc gag gac aca tct gca gac aca gcc tac 240
Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Ala Asp Thr Ala Tyr
65 70 75 80

atg gag cta agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt 288
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gca aca gag ggg tat tat gag act act act tat tac tac aac ctt ttt 336
Ala Thr Glu Gly Tyr Tyr Glu Thr Thr Thr Tyr Tyr Tyr Asn Leu Phe
100 105 110

gac tcc tgg ggc cag gga acc ctg gtc acc gtc tcc agt 375
Asp Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 36
<211> 125
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 36

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

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

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

Gly Gly Phe Asp Pro Glu Tyr Gly Lys Thr Phe Phe Ala Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Ala Asp Thr Ala Tyr
65 70 75 80

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

Ala Thr Glu Gly Tyr Tyr Glu Thr Thr Thr Tyr Tyr Tyr Asn Leu Phe
100 105 110

Asp Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 37

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> MF4289

<220>

<221> CDS

<222> (1)..(357)

<400> 37
cag gtg cag ctg gtg caa tct ggg tct gaa ttg aag aag cct ggg gcc 48
Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

tca gtg aag gtt tcc tgc aag act tct gga tac acc ttc act gac tat 96
Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

gct atg act tgg gtg cga cag gcc cct gga caa ggg ctt gaa tgg atg 144
Ala Met Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

gga tgg atc acc acc aac act ggg gac cca acg tat gcc ccg ggc ttc 192
Gly Trp Ile Thr Thr Asn Thr Gly Asp Pro Thr Tyr Ala Pro Gly Phe
50 55 60

aca gga cgg ttt gtc ttc tcc ttg gac acc tct gtc agc acg gca tat 240
Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

ctg cag atc agc agc cta aag gcc gag gac act gcc gta tat tac tgt 288
Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg aga gtg tat cat tgg ata cgg gga ttt gag ttt tgg ggc cag gga 336
Ala Arg Val Tyr His Trp Ile Arg Gly Phe Glu Phe Trp Gly Gln Gly
100 105 110

acc ctg gtc acc gtc tcc agt 357
Thr Leu Val Thr Val Ser Ser
115

<210> 38
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 38
Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

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

Ala Met Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Thr Thr Asn Thr Gly Asp Pro Thr Tyr Ala Pro Gly Phe
 50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
 65 70 75 80

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Val Tyr His Trp Ile Arg Gly Phe Glu Phe Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 39
 <211> 345
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF5777

<220>
 <221> CDS
 <222> (1)..(345)

<400> 39
 cag gtg cag ctg gtg caa tct ggg tct gag ttg aag aag cct ggg gcc 48
 Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
 1 5 10 15

tca gtg aag gtt tcc tgc aag gct tct gga tac acc ttc act aac tat 96
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

gtt atg aat tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
 Val Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35	40	45	
gga tgg atc aac acc aac act	ggg aac cca acg tat gcc cag ggc ttc	192	
Gly Trp Ile Asn Thr Asn Thr	Gly Asn Pro Thr Tyr Ala Gln Gly Phe		
50	55 60		
aca gga cgg ttt gtc ttc tcc ttg gac acc tct gtc agc acg gca tat	240		
Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr			
65	70 75 80		
ctg cag atc agc agc cta aag gct gag gac act gcc gtg tat tac tgt	288		
Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90 95		
gcg agg tgg gag cta cta gac tac tgg ggc cag gga acc ctg gtc acc	336		
Ala Arg Trp Glu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr			
100	105 110		
gtc tcc agt	345		
Val Ser Ser			
115			

<210> 40
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 40

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

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr

65		70		75		80									
Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Arg	Trp	Glu	Leu	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr
			100					105					110		
Val	Ser	Ser													
			115												

<210> 41
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF5781

<220>
 <221> CDS
 <222> (1)..(348)

<400> 41	
gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg	48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	
tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc agc tat	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	
20 25 30	
gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc	144
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
tca gtt att agt ggt agt ggt ggg acc aca tac tac gca gac tcc gtg	192
Ser Val Ile Ser Gly Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val	
50 55 60	
aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tac tgt	288

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

gcg aaa ggg gct ggg gag ctt gac tac tgg ggc cag gga acc ctg gtc 336
Ala Lys Gly Ala Gly Glu Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

acc gtc tcc agt 348
Thr Val Ser Ser
115

<210> 42
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 42

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 Ser Tyr
20 25 30

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

Ser Val Ile Ser Gly Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys 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 Lys Gly Ala Gly Glu Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 43
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> MF5803

<220>
<221> CDS
<222> (1)..(378)

<400> 43
cag gtg cag ctg cag gag tcg ggg cca gga ctg gtg aag cct tcg gag 48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15
acc ctg tcc ctc acc tgc act gtc tct aat ggc tcc atc agt act tac 96
Thr Leu Ser Leu Thr Cys Thr Val Ser Asn Gly Ser Ile Ser Thr Tyr
20 25 30
tac tgg agc tgg atc cgg cag ccc cca ggg aag ggg ctg gag tgg att 144
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45
gga tat gtc tat tac act ggg cgc acc aag tac aac ccc tcc ctc aag 192
Gly Tyr Val Tyr Tyr Thr Gly Arg Thr Lys Tyr Asn Pro Ser Leu Lys
50 55 60
agt cga gtc acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg 240
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80
aac ctg agt tct gtg acc gct gcg gac acg gcc gtg tat tac tgt gcg 288
Asn Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
aga ggg ggt att gta gta gtc cca gct gcg cgg gac tat tac tac tac 336
Arg Gly Gly Ile Val Val Val Pro Ala Ala Arg Asp Tyr Tyr Tyr Tyr
100 105 110
atg gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc agt 378
Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 44
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 44

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

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

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Val Tyr Tyr Thr Gly Arg Thr Lys Tyr Asn Pro Ser Leu Lys
50 55 60

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

Asn Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

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

Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 45
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> MF5805

<220>

<221> CDS

<222> (1)..(360)

<400> 45

gag	gtg	caa	ctg	gtg	cag	tct	gga	gca	gag	gtg	aaa	aag	ccc	ggg	gag	48
Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu	
1				5					10					15		

tct	ctg	aag	atc	gcc	tgt	aag	ggt	tct	gga	ttc	agt	ttt	acc	agc	cac	96
Ser	Leu	Lys	Ile	Ala	Cys	Lys	Gly	Ser	Gly	Phe	Ser	Phe	Thr	Ser	His	
			20					25					30			

tgg	atc	ggc	tgg	gtg	cgc	cag	aag	ccc	ggg	aga	ggc	ctg	gag	tgg	atg	144
Trp	Ile	Gly	Trp	Val	Arg	Gln	Lys	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Met	
		35					40					45				

ggg	gtc	atc	tat	cct	ggt	gac	tct	gat	acc	aga	tac	agc	ccg	tcc	ttc	192
Gly	Val	Ile	Tyr	Pro	Gly	Asp	Ser	Asp	Thr	Arg	Tyr	Ser	Pro	Ser	Phe	
	50					55					60					

caa	ggc	cag	gtc	acc	gtc	tca	gcc	gac	aag	tcc	atc	aat	acc	gcc	tac	240
Gln	Gly	Gln	Val	Thr	Val	Ser	Ala	Asp	Lys	Ser	Ile	Asn	Thr	Ala	Tyr	
65					70					75					80	

ctg	cag	tgg	aac	agc	ctg	aag	gcc	tcg	gac	acc	gcc	ata	tat	tac	tgt	288
Leu	Gln	Trp	Asn	Ser	Leu	Lys	Ala	Ser	Asp	Thr	Ala	Ile	Tyr	Tyr	Cys	
			85						90					95		

gcg	aga	ccg	aac	agt	ggg	agt	ccc	cgg	tac	ttc	gag	ttc	tgg	ggc	cgt	336
Ala	Arg	Pro	Asn	Ser	Gly	Ser	Pro	Arg	Tyr	Phe	Glu	Phe	Trp	Gly	Arg	
			100					105					110			

ggc	acc	ctg	gtc	acc	gtc	tcc	agt									360
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser									
		115				120										

<210> 46

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 46

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

Ser Leu Lys Ile Ala Cys Lys Gly Ser Gly Phe Ser Phe Thr Ser His
20 25 30

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

Gly Val Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Val Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr
65 70 75 80

Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Pro Asn Ser Gly Ser Pro Arg Tyr Phe Glu Phe Trp Gly Arg
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 47
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> MF5808

<220>
<221> CDS
<222> (1)..(378)

<400> 47
cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gag
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc agc agt agt	96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser	
20 25 30	
agt tac tac tgg ggc tgg atc cgc cag ccc cca ggg aag ggg ctg gag	144
Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu	
35 40 45	
tgg att ggg agt ttc tat tat agt ggg aac acc tac tac aac ccg tcc	192
Trp Ile Gly Ser Phe Tyr Tyr Ser Gly Asn Thr Tyr Tyr Asn Pro Ser	
50 55 60	
ctc aag agt cga gtc acc ata tcc gta gac acg tcc aag aac cag ttc	240
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe	
65 70 75 80	
tcc ctg aag ctg agc tct gtg acc gcc gca gac acg gct gtg tat tac	288
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr	
85 90 95	
tgt gcg aga cag gag tat tac tat ggt tcg ggg agt cct tcg tac tac	336
Cys Ala Arg Gln Glu Tyr Tyr Tyr Gly Ser Gly Ser Pro Ser Tyr Tyr	
100 105 110	
ttt gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc agt	378
Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser	
115 120 125	

<210> 48
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 48

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

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

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Ser Phe Tyr Tyr Ser Gly Asn Thr Tyr Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Gln Glu Tyr Tyr Tyr Gly Ser Gly Ser Pro Ser Tyr Tyr
100 105 110

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 49
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> MF5809

<220>
<221> CDS
<222> (1)..(360)

<400> 49
gag gtg cag ctg gtg cag tct gga gca gag gtg aaa aag ccc ggg gag 48
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

tct ctg aag atc tcc tgt aag ggt tct gga gac agt ttt atc agc cac 96
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Asp Ser Phe Ile Ser His
20 25 30

tgg atc gcc tgg gtg cgc cag atg ccc ggg aaa ggc ctg gag tgg atg 144
Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

ggg atc gtc tat cct ggt gac tct gat acc aga tac agc ccg tcc ttc 192
Gly Ile Val Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

caa ggc cag gtc acc atc tca gcc gac aag tcc atc acc acc gcc tac 240
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Thr Thr Ala Tyr
65 70 75 80

ttg	cag	tgg	agc	agc	ctg	aag	gcc	tcg	gac	acc	gcc	atg	tat	tac	tgt	288
Leu	Gln	Trp	Ser	Ser	Leu	Lys	Ala	Ser	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	
			85					90					95			

gcg aga cac gag tgg gaa cta ctt ggc ccc ttt gac tac tgg ggc cag 336
Ala Arg His Glu Trp Glu Leu Leu Gly Pro Phe Asp Tyr Trp Gly Gln
100 105 110

gga acc ctg gtc acc gtc tcc agt	360
Gly Thr Leu Val Thr Val Ser Ser	
115	120

$\langle 210 \rangle$	50
$\langle 211 \rangle$	120
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial Sequence

<220>
<223> Synthetic Construct

<400> 50

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Asp Ser Phe Ile Ser His
20 25 30

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

Gly Ile Val Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Thr Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala	Arg	His	Glu	Trp	Glu	Leu	Leu	Gly	Pro	Phe	Asp	Tyr	Trp	Gly	Gln
			100					105					110		

Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
		115				120	

<210> 51
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF5814

<220>
 <221> CDS
 <222> (1)..(363)

<400> 51	
gag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg tcc	48
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser	
1 5 10 15	
tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc tcc act aac gat	96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Ser Thr Asn Asp	
20 25 30	
gct atc agt tgg gtg cga cag acc cct gga caa ggg ctt gag tgg atg	144
Ala Ile Ser Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Met	
35 40 45	
gga agt atc atc cct atc ctt gat aca aca gac cac gca cag aag ttc	192
Gly Ser Ile Ile Pro Ile Leu Asp Thr Thr Asp His Ala Gln Lys Phe	
50 55 60	
cag ggc aga gtc acg att acc gcg gac aaa tcc acg aac aca gcc tac	240
Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn Thr Ala Tyr	
65 70 75 80	
atg gag ctg aac agc ctg aga tct gat gac acg gcc gtg tat tac tgt	288
Met Glu Leu Asn Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gcg aga gag cat ata gca gct cgt cag gac tac ttt gac tat tgg ggc	336
Ala Arg Glu His Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly	

<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> MF5817

<220>
<221> CDS
<222> (1)..(357)

<400> 53
cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg tcc 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

tcg gtg aag gtc tcc tgc aag gtt tct gga ggc acc ttc agg agc tat 96
Ser Val Lys Val Ser Cys Lys Val Ser Gly Gly Thr Phe Arg Ser Tyr
20 25 30

gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

gga ggg atc atc cct atc ttt gat aca aga aac tac gca cag att ctt 192
Gly Gly Ile Ile Pro Ile Phe Asp Thr Arg Asn Tyr Ala Gln Ile Leu
50 55 60

cag ggc aga gtc acg att acc gcg gac tta tcc acg agc aca gcc tac 240
Gln Gly Arg Val Thr Ile Thr Ala Asp Leu Ser Thr Ser Thr Ala Tyr
65 70 75 80

atg gag ctg aac agt ctg aga tct gag gac acg gcc att tat tac tgt 288
Met Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

gcg aga ggg agc gac gag ggg gac tgg ttc gac ccc tgg ggc caa gga 336
Ala Arg Gly Ser Asp Glu Gly Asp Trp Phe Asp Pro Trp Gly Gln Gly
100 105 110

acc ctg gtc acc gtc tcc agt 357
Thr Leu Val Thr Val Ser Ser
115

<210> 54
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 54

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

Ser Val Lys Val Ser Cys Lys Val Ser Gly Gly Thr Phe Arg Ser Tyr
20 25 30

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

Gly Gly Ile Ile Pro Ile Phe Asp Thr Arg Asn Tyr Ala Gln Ile Leu
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Leu Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Ser Asp Glu Gly Asp Trp Phe Asp Pro Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 55

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> MF5818

<220>

<221> CDS

<222> (1)..(363)

<400> 55
gag gtg cag ctg gtg cag tct ggg act gag gtg agg aag cct ggg tcc 48
Glu Val Gln Leu Val Gln Ser Gly Thr Glu Val Arg Lys Pro Gly Ser
1 5 10 15

tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc agc aac tat 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asn Tyr
20 25 30

gct atc agc tgg gtg cga cag gcc cct gga cag ggg ctt gag tgg atg 144
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

gga agt atc atc cct atc ctt gga aca aca gac cac gca cag aag ttc 192
Gly Ser Ile Ile Pro Ile Leu Gly Thr Thr Asp His Ala Gln Lys Phe
50 55 60

cag gac aga gtc acg att acc gcg gac aaa tcc tcg aac aca acc tac 240
Gln Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Ser Asn Thr Thr Tyr
65 70 75 80

atg gag ctg agc agc ctg aga tct gat gac acg gcc gta tat tac tgt 288
Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcg aga gag tat ata gca gct cgt ctg gac tac ttt gac tct tgg ggc 336
Ala Arg Glu Tyr Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
100 105 110

cag gga acc ctg gtc acc gtc tcc agt 363
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 56
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 56
Glu Val Gln Leu Val Gln Ser Gly Thr Glu Val Arg Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asn Tyr

20

25

30

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

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

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

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

Ala Arg Glu Tyr Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 57
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF5832

<220>
 <221> CDS
 <222> (1)..(366)

<400> 57
 gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gta gtc tct gga ttc acc ttc agt tac tac 96
 Ser Leu Arg Leu Ser Cys Val Val Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30

gac atg cac tgg gtc cgc caa gtc aca gga aaa ggt ctg gag tgg gtc 144

Asp Met His Trp Val Arg Gln Val Thr Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca gct att ggc act gct ggt gcc aca tac tat cca ggc tcc gtg aag 192
 Ser Ala Ile Gly Thr Ala Gly Ala Thr Tyr Tyr Pro Gly Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gaa aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aat agc ctg aga gcc ggg gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

aga gat cgt gga tat agt ggc tac gat gcg tac tac ttt gac ttc tgg 336
 Arg Asp Arg Gly Tyr Ser Gly Tyr Asp Ala Tyr Tyr Phe Asp Phe Trp
 100 105 110

ggc cag gga acc ctg gtc acc gtc tcc agt 366
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 58
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 58

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 Val Val Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30

Asp Met His Trp Val Arg Gln Val Thr Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Gly Thr Ala Gly Ala Thr Tyr Tyr Pro Gly Ser Val Lys
 50 55 60

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

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

Arg Asp Arg Gly Tyr Ser Gly Tyr Asp Ala Tyr Tyr Phe Asp Phe Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 59
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> MF5836

<220>
<221> CDS
<222> (1)..(372)

<400> 59
cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gag 48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc agc agt agt 96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

aat tac tac tgg ggc tgg atc cgc cag ccc cca ggg aag ggg ctg gag 144
Asn Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

tgg att ggg aat atc tat tat aga ggg tac acc tat tat aac ccg tcc 192
Trp Ile Gly Asn Ile Tyr Tyr Arg Gly Tyr Thr Tyr Tyr Asn Pro Ser
50 55 60

ctc aag agt cga gtc acc ata tcc gta gac acg tcc aag aag cag ttc 240
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Lys Gln Phe
65 70 75 80

tcc	ctg	acg	ctg	agc	tct	gtg	acc	gcc	gca	gac	acg	gct	atg	tat	tac	288
Ser	Leu	Thr	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Met	Tyr	Tyr	
				85				90						95		

tgt	gcg	aga	gag	ggg	agt	gac	tac	ggt	gac	tac	gta	gga	gct	ttt	gat	336
Cys	Ala	Arg	Glu	Gly	Ser	Asp	Tyr	Gly	Asp	Tyr	Val	Gly	Ala	Phe	Asp	
			100					105					110			

atc	tgg	gac	caa	ggg	aca	atg	gtc	acc	gtc	tcc	agt	372
Ile	Trp	Asp	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser	
		115					120					

<210> 60
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 60

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

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

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

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

Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Val	Asp	Thr	Ser	Lys	Lys	Gln	Phe
65				70					75					80	

Ser	Leu	Thr	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Met	Tyr	Tyr
			85					90					95		

Cys	Ala	Arg	Glu	Gly	Ser	Asp	Tyr	Gly	Asp	Tyr	Val	Gly	Ala	Phe	Asp
			100					105					110		

Ile Trp Asp Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 61
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF5839

<220>
 <221> CDS
 <222> (1)..(366)

<400> 61
 gag gtg cag ctg gtg cag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt tac tac 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30
 gac atg cac tgg gtc cgc caa gtt aca gga aaa ggt ctg gag tgg gtc 144
 Asp Met His Trp Val Arg Gln Val Thr Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca act att ggt gct act ggt gac aca tac tat tca gac tcc gtg aag 192
 Ser Thr Ile Gly Ala Thr Gly Asp Thr Tyr Tyr Ser Asp Ser Val Lys
 50 55 60
 ggc cga ttt acc atc tcc aga caa aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Gln Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa ata aac agc ctg aga gcc ggg gac acg gct gta tat tac tgt gta 288
 Gln Ile Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Val
 85 90 95
 aga gat cgt gga tat att ggc tac gat tcg tac tac ttt gac aac tgg 336
 Arg Asp Arg Gly Tyr Ile Gly Tyr Asp Ser Tyr Tyr Phe Asp Asn Trp
 100 105 110
 ggc cag gga acc ctg gtc acc gtc tcc agt 366
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 62
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 62

Glu Val Gln Leu Val Gln 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 Tyr Tyr
20 25 30

Asp Met His Trp Val Arg Gln Val Thr Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Gly Ala Thr Gly Asp Thr Tyr Tyr Ser Asp Ser Val Lys
50 55 60

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

Gln Ile Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Val
85 90 95

Arg Asp Arg Gly Tyr Ile Gly Tyr Asp Ser Tyr Tyr Phe Asp Asn Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 63
<211> 360
<212> DNA
<213> Artificial Sequence

<220>

<223> M5850

<220>

<221> CDS

<222> (1)..(360)

<400> 63

cag	gtg	cag	ctg	gtg	cag	tct	ggg	tct	gag	ttg	aag	aag	cct	ggg	gcc	48
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ser	Glu	Leu	Lys	Lys	Pro	Gly	Ala	
1				5					10					15		

tca	gtg	aag	gtt	tcc	tgc	aag	gct	tct	gga	tac	acc	ttc	act	agg	tat	96
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	
			20					25					30			

cct	atg	aat	tgg	gtg	cga	cag	gcc	cct	gga	caa	ggg	ctt	gag	tgg	atg	144
Pro	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
		35					40					45				

gga	tgg	atc	aac	acc	aac	act	ggg	aac	cca	aca	tat	gcc	cag	ggc	ttc	192
Gly	Trp	Ile	Asn	Thr	Asn	Thr	Gly	Asn	Pro	Thr	Tyr	Ala	Gln	Gly	Phe	
	50					55					60					

aca	gga	cgg	ttt	gtc	ttc	tcc	ttg	gac	acc	tct	gtc	agc	acg	gca	ttt	240
Thr	Gly	Arg	Phe	Val	Phe	Ser	Leu	Asp	Thr	Ser	Val	Ser	Thr	Ala	Phe	
65				70					75					80		

ctg	cag	atc	agc	agc	cta	aag	gct	gag	gac	act	gcc	gtg	tat	tac	tgt	288
Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90					95			

gcg	aga	gag	agg	act	aac	ttt	tat	gat	gct	ttt	gat	atc	tgg	ggc	caa	336
Ala	Arg	Glu	Arg	Thr	Asn	Phe	Tyr	Asp	Ala	Phe	Asp	Ile	Trp	Gly	Gln	
			100					105					110			

ggg	aca	atg	gtc	acc	gtc	tcc	agt									360
Gly	Thr	Met	Val	Thr	Val	Ser	Ser									
		115				120										

<210> 64

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 64

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

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Phe
65 70 75 80

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Arg Thr Asn Phe Tyr Asp Ala Phe Asp Ile Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 65
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> MF5853

<220>
<221> CDS
<222> (1)..(360)

<400> 65
cag gtg cag ctg gtg caa tct ggg tct gag ttg aag aag cct ggg gcc
Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

tca gtg aag gtt tcc tgc aag gct tct gga tat acc ttc aat agc tat	96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Ser Tyr	
20 25 30	
gct atg gat tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg	144
Ala Met Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	
35 40 45	
gga tgg atc aac acc aat act ggg aac cca acg tat gcc cag gcc ttc	192
Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Ala Phe	
50 55 60	
aca gga cgg ttt gtc ttc tcc ttg gac acc tct gtc agc acg gca tat	240
Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr	
65 70 75 80	
ctg gag atc agc agc cta aag gct gag gac act gcc gtg tat tac tgt	288
Leu Glu Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gcg aga gag agg cat gga tat ttt gaa gct ttt gat atc tgg ggc caa	336
Ala Arg Glu Arg His Gly Tyr Phe Glu Ala Phe Asp Ile Trp Gly Gln	
100 105 110	
ggg acc acg gtc acc gtc tcc agt	360
Gly Thr Thr Val Thr Val Ser Ser	
115 120	

<210> 66
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 66

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala	
1 5 10 15	
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Ser Tyr	
20 25 30	
Ala Met Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	
35 40 45	

Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Ala Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Glu Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Arg His Gly Tyr Phe Glu Ala Phe Asp Ile Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 67
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> MF5855

<220>
<221> CDS
<222> (1)..(360)

<400> 67
cag gtg cag ctg gtg caa tct ggg tct gag ttg aag aag cct ggg gcc 48
Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

tca gtg aag gtt tcc tgc aag gct tct gga tac acc ttc act aag tat 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Tyr
20 25 30

gtt atg aat tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
Val Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

gga tgg atc aac acc aac act ggg aac cca acg tat gcc cag ggc ttc 192
Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe

50	55	60	
aca gga cgg ttt gtc ttc tcc ttg gac acc tct gtc agc acg gca tat			240
Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr			
65	70	75	80
ctg cag gtc agc agt cta agg gct gag gac act gcc ctg tat tac tgt			288
Leu Gln Val Ser Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys			
	85	90	95
gcg aga gag tct aac tgg aac tac gac tac ttt gac tac tgg ggc cag			336
Ala Arg Glu Ser Asn Trp Asn Tyr Asp Tyr Phe Asp Tyr Trp Gly Gln			
	100	105	110
ggc acc ctg gtc acc gtc tcc agt			360
Gly Thr Leu Val Thr Val Ser Ser			
	115	120	

<210> 68
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 68

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

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Val Ser Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys

85

90

95

Ala Arg Glu Ser Asn Trp Asn Tyr Asp Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 69
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF5862

<220>
 <221> CDS
 <222> (1)..(366)

<400> 69
 cag gtg cag ctg gtg cag tct gga aca gag gtg aaa aag ccc ggg gag 48
 Gln Val Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro Gly Glu
 1 5 10 15

tct ctg aag atc tcc tgt aag ggt tct gga tac agc ttt acc acc tac 96
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Thr Tyr
 20 25 30

tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg gag tgg atg 144
 Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

gga atc atc tat cct ggt gac tct gat acc aga tac agc ccg tcc ttc 192
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60

caa ggc cag gtc acc atc tca gcc gac aag tcc atc agc acc gcc tac 240
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80

ctg cag ttg agc agc ctg aag gcc tcg gac acc gcc atg tat tac tgt 288
 Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

gcg aga cgg ggt ctt agt atg gtt cgg ttg agc gct ttt gat gtc tgg 336

Ala Arg Arg Gly Leu Ser Met Val Arg Leu Ser Ala Phe Asp Val Trp
100 105 110

ggc caa gga acc ctg gtc acc gtc tcc agt
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

366

<210> 70
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 70

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Thr Tyr
20 25 30

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

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Arg Gly Leu Ser Met Val Arg Leu Ser Ala Phe Asp Val Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 71
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF5882

<220>
 <221> CDS
 <222> (1)..(360)

<400> 71
 cag gtg cag ctg gtg caa tct ggg tct gag ttg aag aag cct ggg gcc 48
 Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
 1 5 10 15
 tca gtg aag gtt tcc tgc aag gct tct gga tac acc ttc act aga tat 96
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30
 gct atg aat tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
 Ala Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 gga tgg atc aac acc aaa act ggg aac cca acg tat gcc cag ggc ttc 192
 Gly Trp Ile Asn Thr Lys Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
 50 55 60
 aca gga cgg ttt gtc ttc tcc ttg gac acc tct gtc agc acg gca tat 240
 Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
 65 70 75 80
 ctg cag atc agc agc cta aag gct gag gac act gcc gtg tat tac tgt 288
 Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcg aga gat cgt ggg agc tac tat gat gct ttt gat atc tgg ggc caa 336
 Ala Arg Asp Arg Gly Ser Tyr Tyr Asp Ala Phe Asp Ile Trp Gly Gln
 100 105 110
 ggg aca atg gtc acc gtc tcc agt 360
 Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 72
 <211> 120
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 72

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

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

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

Gly Trp Ile Asn Thr Lys Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Gly Ser Tyr Tyr Asp Ala Phe Asp Ile Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 73

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> MF5884

<220>

<221> CDS

<222> (1)..(360)

<400> 73

gag	gtg	cag	ctg	gtg	cag	tct	ggg	tct	gaa	ttg	aag	aag	cct	ggg	gcc	48
Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ser	Glu	Leu	Lys	Lys	Pro	Gly	Ala	
1				5					10					15		

tca	gtg	aag	gtt	tcc	tgc	aag	gct	tct	gga	tac	acc	ttc	act	aag	tat	96
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Lys	Tyr	
			20					25					30			

gct	atg	aat	tgg	gtg	cga	cag	gtc	cct	gga	caa	ggg	ctt	gag	tgg	atg	144
Ala	Met	Asn	Trp	Val	Arg	Gln	Val	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
		35					40					45				

gga	tgg	atc	aac	acc	aac	act	ggg	aac	cca	acg	tat	gcc	cag	ggc	ttc	192
Gly	Trp	Ile	Asn	Thr	Asn	Thr	Gly	Asn	Pro	Thr	Tyr	Ala	Gln	Gly	Phe	
	50					55					60					

aca	gga	cgg	ttt	gtc	ttc	tcc	ttg	gac	acc	tct	gtc	cgc	acg	gca	tat	240
Thr	Gly	Arg	Phe	Val	Phe	Ser	Leu	Asp	Thr	Ser	Val	Arg	Thr	Ala	Tyr	
65					70					75				80		

ctg	cag	atc	agc	agc	cta	aag	gct	gag	gac	act	gcc	gtg	tat	tac	tgt	288
Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85						90					95		

gcg	aga	aaa	ggg	ggg	agc	tac	tac	gac	tgg	ttc	gac	ccc	tgg	ggc	cag	336
Ala	Arg	Lys	Gly	Gly	Ser	Tyr	Tyr	Asp	Trp	Phe	Asp	Pro	Trp	Gly	Gln	
			100					105					110			

gga	acc	ctg	gtc	acc	gtc	tcc	agt									360
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser									
		115					120									

<210> 74

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 74

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

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Arg Thr Ala Tyr
65 70 75 80

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Lys Gly Gly Ser Tyr Tyr Asp Trp Phe Asp Pro Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 75
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> MF5887

<220>
<221> CDS
<222> (1)..(369)

<400> 75
cag gtg cag ctg gtg cag tct ggg tct gag ttg aag aag cct ggg gcc 48
Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

tca gtg aag gtt tcc tgc aag gct tct gga tac acc ttc act cgc tat 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

gct atg aat tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg	144
Ala Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	
35 40 45	

gga tgg atc aac acc aac act ggg aaa cca acg tat gcc cag ggc ttc	192
Gly Trp Ile Asn Thr Asn Thr Gly Lys Pro Thr Tyr Ala Gln Gly Phe	
50 55 60	

aca gga cgg ttt gtc ttc tcc ttg gac acc tct gtc agc acg gca tat	240
Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr	
65 70 75 80	

ctg cag atc agc agc ctg aag gct gag gac act gcc gtg tat tac tgt	288
Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	

gcg aga gat aag ggc tat aac tgg aac tac atg ggt gct ttt gat atc	336
Ala Arg Asp Lys Gly Tyr Asn Trp Asn Tyr Met Gly Ala Phe Asp Ile	
100 105 110	

tgg ggc caa ggg acc acg gtc acc gtc tcc agt	369
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
115 120	

<210> 76
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 76

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

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Lys Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Lys Gly Tyr Asn Trp Asn Tyr Met Gly Ala Phe Asp Ile
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 77
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> MF5888

<220>
<221> CDS
<222> (1)..(360)

<400> 77
cag gtg cag ctg gtg cag tct ggg tct gag ttg aag aag ccc ggg ggc 48
Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Gly
1 5 10 15

tca atg aag gtt tcc tgc aag gct tct gga tac acc ttc act aga tat 96
Ser Met Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

gct atg aat tgg ttg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
Ala Met Asn Trp Leu Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

gga tgg atc aac acc aac act ggg aac cca acg tat gcc cag ggc ttc 192
Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
50 55 60

aca gga cgg ttt gtc ttc tcc ttg gac acc tct gtc agc acg gca tat 240
Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

ctg	cag	atc	agc	agc	cta	aag	gct	gag	gac	act	gcc	gtc	tat	tat	tgt	288
Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90					95			

gcg	aga	cgg	agt	ggg	agc	tac	tac	gac	tac	ttt	gac	tac	tgg	ggc	cag	336
Ala	Arg	Arg	Ser	Gly	Ser	Tyr	Tyr	Asp	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	
			100					105					110			

gga	acc	ctg	gtc	acc	gtc	tcc	agt									360
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser									
		115				120										

<210> 78
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 78

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

Ser	Met	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr
		20					25					30			

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

Gly	Trp	Ile	Asn	Thr	Asn	Thr	Gly	Asn	Pro	Thr	Tyr	Ala	Gln	Gly	Phe
	50				55					60					

Thr	Gly	Arg	Phe	Val	Phe	Ser	Leu	Asp	Thr	Ser	Val	Ser	Thr	Ala	Tyr
65			70						75					80	

Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		

Ala	Arg	Arg	Ser	Gly	Ser	Tyr	Tyr	Asp	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln
			100					105					110		

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 79
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> common light chain - 1

<220>
<221> CDS
<222> (1)..(321)

<400> 79
gac atc cag atg acc cag tct cca tcc tcc ctg tct gca tct gta gga 48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

gac aga gtc acc atc act tgc cgg gca agt cag agc att agc agc tac 96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

tta aat tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc 144
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

tat gct gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt ggc 192
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

agt gga tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct 240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

gaa gat ttt gca act tac tac tgt caa cag agt tac agt acc cct cca 288
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95

acg ttc ggc caa ggg acc aag gtg gag atc aaa 321
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 80

<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 80

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 Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

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

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

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

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

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

<210> 81
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> common light chain - 2

<220>
<221> CDS
<222> (1)..(324)

<400> 81
cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag 48
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15
cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc 96
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30
tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa 144
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45
tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc 192
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60
acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag 240
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80
aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg 288
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95
ccc gtc aca aag agc ttc aac agg gga gag tgt tag 324
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 82
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 82
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

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

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

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

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

<210> 83
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> VH-CH1

<220>
<221> CDS
<222> (1)..(294)

<400> 83
gct agc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag 48
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac 96
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc 144
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc 192
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

ctc agc agc gtc gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc 240
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr

65	70	75	80	
tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag	288			
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys				
85 90 95				
aga gtt	294			
Arg Val				

<210> 84
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 84

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

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

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

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

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

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

Arg Val

<210> 85

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> VH-hinge

<220>
<221> CDS
<222> (1)..(45)

<400> 85
gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca 45
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 86
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 86
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 87
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> VH-CH2

<220>
<221> CDS
<222> (1)..(330)

<400> 87
gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa 48
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15

ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg	96
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val	
20 25 30	

gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac	144
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr	
35 40 45	

gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag	192
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu	
50 55 60	

cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac	240
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His	
65 70 75 80	

cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa	288
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys	
85 90 95	

gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa	330
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys	
100 105 110	

<210> 88
 <211> 110
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 88

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

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

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

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

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

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

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

<210> 89
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> VH-CH3

<220>
<221> CDS
<222> (1)..(321)

<400> 89
ggg cag ccc cga gaa cca cag gtg tac acc aag ccc cca tcc cgg gag 48
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Lys Pro Pro Ser Arg Glu
1 5 10 15

gag atg acc aag aac cag gtc agc ctg aag tgc ctg gtc aaa ggc ttc 96
Glu Met Thr Lys Asn Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe
20 25 30

tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag 144
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc 192
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

ttc ctc tat agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg 240
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac 288
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

acg cag aag agc ctc tcc ctg tct ccg ggt tga
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
100 105

321

<210> 90
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 90

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

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

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
100 105

<210> 91
<211> 321
<212> DNA
<213> Artificial Sequence

<220>

<223> VH-CH3

<220>

<221> CDS

<222> (1)..(321)

<400> 91

ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	gac	ccc	cca	tcc	cgg	gag	48
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Asp	Pro	Pro	Ser	Arg	Glu	
1				5					10					15		

gag	atg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	gag	gtc	aaa	ggc	ttc	96
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Glu	Val	Lys	Gly	Phe	
			20					25					30			

tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	144
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	
			35				40					45				

aac	aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	192
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	
		50				55				60						

ttc	ctc	tat	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	240
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	
65					70				75						80	

aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	288
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	
				85					90				95			

acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggt	tga						321
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly							
			100					105								

<210> 92

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 92

Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Asp	Pro	Pro	Ser	Arg	Glu
1				5					10					15	

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

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
100 105

<210> 93
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> VH1-69 J00256-AEHJ2

<400> 93

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Lys
50 55 60

Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala
65 70 75 80

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

Cys Ala Arg Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
100 105 110

<210> 94
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> member of supercluster 1

<400> 94

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

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

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

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

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

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

Ala Arg Glu His Ile Ala Ala Arg Leu Asp Tyr Phe Asp Tyr Trp Asp
100 105 110

Leu Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 95
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> member of supercluster 1

<400> 95

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Ser Thr Asn Asp
20 25 30

Ala Ile Ser Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

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

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

Ala Arg Glu His Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 96
<211> 121
<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 96

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

Ser Val Lys Val Ser Cys Arg Ala Ser Gly Asp Ser Val Ser Asn Tyr
20 25 30

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

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

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

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

Ala Arg Glu Arg Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 97

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 97

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asn Tyr	20	25	30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	35	40	45
Gly Ser Ile Ile Pro Ile Leu Gly Thr Thr Asp His Ala Gln Lys Phe	50	55	60
Gln Asp Arg Val Thr Ile Thr Ala Asp Arg Ser Ser Asn Thr Thr Tyr	65	70	75
Met Asp Leu Asn Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys	85	90	95
Ala Arg Glu Leu Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly	100	105	110
Gln Gly Thr Leu Val Thr Val Ser Ser	115	120	

<210> 98
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> member of supercluster 1

<400> 98

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

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

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

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

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

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

Ala Arg Glu Arg Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 99

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 99

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

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

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

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

Gln Asp Arg Val Thr Ile Thr Ala Asp Lys Leu Ser Asn Thr Thr Tyr

65		70		75		80									
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		

Ala	Ile	Glu	Leu	Ile	Ala	Ala	Arg	Leu	Asp	Tyr	Phe	His	Ser	Trp	Gly
		100						105					110		

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
	115						120	

<210> 100
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> member of supercluster 1

<400> 100

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

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

Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Asp	Trp	Met
		35					40					45			

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

Gln	Gly	Arg	Val	Thr	Phe	Thr	Ala	Asp	Lys	Ser	Thr	Asn	Thr	Ser	Tyr
65					70					75					80

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

Ala	Arg	Glu	Leu	Ile	Ala	Ala	Arg	Gln	Asp	Tyr	Phe	Asp	Tyr	Trp	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

100

105

110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 101

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 101

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

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

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

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

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

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

Ala Arg Glu Leu Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 102

<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> member of supercluster 1

<400> 102

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Ser Thr Asn Asp
20 25 30

Ala Ile Ser Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

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

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

Ala Arg Glu His Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 103
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> member of supercluster 1

<400> 103

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

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

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

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

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

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

Ala Ile Glu Leu Ile Ala Ala Arg Leu Asp Tyr Phe His Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 104

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 104

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

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

Ala Ile Ser Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

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

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

Ala Arg Glu His Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 105

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 105

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Ser Thr Asn Asp
20 25 30

Ala Ile Ser Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Arg Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Glu His Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 106

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 106

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

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

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

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

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

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

Ala Arg Glu Arg Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 107

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 107

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

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

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

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

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

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

Ala Arg Glu Arg Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 108
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> member of supercluster 1

<400> 108

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

Ser Val Lys Val Ser Cys Arg Ala Ser Gly Asp Ser Val Ser Asn Tyr
20 25 30

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

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

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

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

Ala Arg Glu Arg Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 109
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> member of supercluster 1

<400> 109

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

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

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

Gly Ser Ile Ile Pro Ile Leu Gly Thr Thr Asp His Ala Glu Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Asp Leu Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp
85 90 95

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Phe Ile Ala Ala Arg Gln
100 105 110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 110

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 110

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asn Tyr

20

25

30

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

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

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

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

Ala Arg Glu Arg Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 111

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 111

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

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

Ala Ile Ser Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Ser Ile Ile Pro Ile Leu Asp Thr Thr Asp His Ala Gln Lys Phe

50

55

60

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

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

Ala Arg Glu His Ile Ala Ala Arg Leu Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 112

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 112

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

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

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

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

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

Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Glu His Ile Ala Ala Arg Leu Asp Tyr Phe Asp Tyr Trp Asp
 100 105 110

Leu Gly Ile Leu Val Thr Val Ser Ser
 115 120

<210> 113

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 113

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

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

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

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

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

Met Glu Leu Ile Gly Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Arg Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 114

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 114

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

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

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

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

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

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

Ala Arg Glu His Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
 100 105 110

Leu Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 115

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 115

Arg Cys Ser Met Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Arg Ala Ser Gly Asp Ser Val Ser Asn Tyr
20 25 30

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

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

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

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

Ala Arg Glu Arg Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 116

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 116

Arg Cys Ser Met Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

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

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

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

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

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

Ala Arg Glu Leu Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 117

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 117

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

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

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

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

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

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

Ala Arg Glu Arg Ile Ala Ala Arg Gln Asp Tyr Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 118
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> member of supercluster 1

<400> 118

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Ser Thr Asn Asp
20 25 30

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

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

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

Met Glu Leu Ile Gly Leu Lys Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Arg Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 119

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 119

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Ser Thr Asn Asp
20 25 30

Ala Ile Ser Trp Val Arg Gln Thr Pro Glu Gln Gly Leu Glu Trp Met
35 40 45

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Arg Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Glu Leu Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 120

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 120

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

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

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

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Arg Ser Ala Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Glu His Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Glu Thr Leu Val Thr Val Ser Ser
115 120

<210> 121

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 121

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

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

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

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Ile Ser Thr Ile Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Glu Arg Ile Ala Ala Arg Gln Asp Tyr Phe Asp Phe Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 122

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 122

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asn Tyr	20	25	30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	35	40	45
Gly Ser Ile Ile Pro Ile Leu Gly Thr Thr Asp His Ala Gln Lys Phe	50	55	60
Gln Asp Arg Val Thr Ile Thr Ala Gly Lys Ser Ser Asn Thr Thr Tyr	65	70	75
Met Asp Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys	85	90	95
Ala Arg Glu Arg Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly	100	105	110
Gln Gly Thr Leu Val Thr Val Ser Ser	115	120	

<210> 123
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> member of supercluster 1

<400> 123

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Ser Thr Asn Asp	20	25	30
---	----	----	----

Ala Ile Ser Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

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

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

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

Ala Arg Glu His Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 124

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 124

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Ser Thr Asn Asp
 20 25 30

Ala Ile Ser Trp Val Arg Gln Thr Pro Glu Gln Gly Leu Glu Trp Met
 35 40 45

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn Thr Val Tyr

65		70		75		80									
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Arg	Glu	His	Ile	Ala	Ala	Arg	Leu	Asp	Tyr	Phe	Asp	Tyr	Trp	Asp
			100					105					110		
Leu	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
		115					120								
<210>	125														
<211>	121														
<212>	PRT														
<213>	Artificial Sequence														
<220>															
<223>	member of supercluster 1														
<400>	125														
Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1			5					10						15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Asp	Thr	Ser	Thr	Asn	Tyr
			20					25						30	
Ala	Ile	Ser	Trp	Val	Arg	Gln	Thr	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
			35				40					45			
Gly	Ser	Ile	Ile	Pro	Ile	Leu	Gly	Thr	Thr	Asp	His	Thr	Gln	Lys	Phe
	50					55					60				
Gln	Asp	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Asn	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Asn	Ser	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Arg	Glu	His	Ile	Ala	Ser	Arg	Gln	Asp	Phe	Phe	Asp	Tyr	Trp	Gly

100

105

110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 126

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 126

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

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

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

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

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

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

Ala Arg Glu Arg Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 127

<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> member of supercluster 1

<400> 127

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

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

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

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

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

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

Ala Arg Glu Arg Ile Ala Ala Arg Leu Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 128
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> member of supercluster 1

<400> 128

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

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

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

Gly Ser Ile Ile Pro Ile Leu Gly Thr Thr Asp His Ala Glu Lys Phe
50 55 60

Gln Gly Lys Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Asp Leu Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp
85 90 95

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Phe Ile Ala Ala Arg Gln
100 105 110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 129

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 129

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

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

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

Gly Ser Ile Ile Pro Ile Phe Gly Thr Ala Asp Asn Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Glu Arg Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 130

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 130

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Ser Thr Asn Asp
20 25 30

Ala Ile Ser Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Arg Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Glu His Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 131

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 131

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Ser Thr Asn Asp
20 25 30

Ala Ile Ser Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Arg Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Glu His Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 132

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 132

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

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

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

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

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

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

Ala Arg Glu Arg Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 133
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> member of supercluster 1

<400> 133

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Ser Thr Asn Asp
20 25 30

Ala Ile Ser Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Arg Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Glu His Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 134
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> member of supercluster 1

<400> 134

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

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

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

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

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

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

Ala Arg Glu His Ile Ala Ala Arg Leu Asp Tyr Phe Asp Tyr Trp Asp
100 105 110

Leu Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 135

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 135

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr

20

25

30

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

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

Gln Gly Arg Val Thr Phe Thr Ala Asp Lys Ser Thr Asn Thr Ser Tyr
 65 70 75 80

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

Ala Arg Glu Arg Ile Ala Ala Arg Gln Asp Tyr Phe Asp Ser Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 136

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 136

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

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

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

Gly Ser Ile Ile Pro Ile Leu Gly Thr Thr Asp His Ala Gln Lys Phe

50

55

60

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

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

Ala Arg Glu Arg Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 137

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 137

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

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

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

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

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

Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Arg Glu His Ile Ala Ala Arg Leu Asp Tyr Phe Asp Tyr Trp Asp
 100 105 110

Leu Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 138

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 138

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

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

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

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Glu Arg Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 139
 <211> 128
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> member of supercluster 1

<400> 139

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

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

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

Gly Ser Ile Ile Pro Ile Leu Gly Thr Thr Asp His Ala Glu Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Asp Leu Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp
 85 90 95

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Phe Ile Ala Ala Arg Gln
 100 105 110

Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 140
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 140

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

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

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

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

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

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

Ala Arg Glu His Ile Ala Ala Arg Leu Asp Tyr Phe Asp Tyr Trp Asp
100 105 110

Leu Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 141

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 141

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

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

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

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

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

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

Ala Arg Glu His Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 142

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 142

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

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

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

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

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

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

Ala Arg Glu Tyr Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 143
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> member of supercluster 1

<400> 143

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

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

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

Gly Ser Ile Ile Pro Ile Leu Gly Thr Thr Asp His Ala Glu Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Glu Phe Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 144
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> member of supercluster 1

<400> 144

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

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

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

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

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

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

Ala Arg Glu Arg Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 145

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 145

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

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

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

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

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

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

Ala Arg Glu Arg Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 146

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 146

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

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

Ala Ile Ser Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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

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

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

Ala Arg Glu His Ile Ala Ala Arg Leu Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 147

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 147

Glu Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ser

1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asn Tyr	20	25	30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	35	40	45
Gly Ser Ile Ile Pro Ile Leu Gly Thr Thr Asp His Ala Gln Lys Phe	50	55	60
Gln Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Ser Asn Thr Thr Tyr	65	70	75
Met Asp Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys	85	90	95
Ala Arg Glu Arg Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly	100	105	110
Gln Gly Thr Leu Val Thr Val Ser Ser	115	120	

<210> 148
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> member of supercluster 1

<400> 148

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

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

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

Gly Ser Ile Ile Pro Ile Leu Gly Thr Thr Asp His Val Glu Lys Phe
 50 55 60

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

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

Ala Arg Glu Leu Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 149

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 149

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

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

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

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

Gln Gly Arg Val Thr Phe Thr Ala Asp Lys Ser Thr Asn Thr Ser Tyr

65		70		75		80									
Met	Glu	Leu	Asn	Ser	Leu	Arg	Ser	Asp	Asp	Ser	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Arg	Glu	Arg	Ile	Ala	Ala	Arg	Gln	Asp	Tyr	Phe	Asp	Ser	Trp	Gly
			100					105					110		
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
		115					120								
<210>	150														
<211>	121														
<212>	PRT														
<213>	Artificial Sequence														
<220>															
<223>	member of supercluster 1														
<400>	150														
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1			5					10						15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Ser	Thr	Asn	Asp
			20					25						30	
Ala	Ile	Ser	Trp	Val	Arg	Gln	Thr	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Met
			35				40					45			
Gly	Ser	Ile	Ile	Pro	Ile	Leu	Asp	Thr	Thr	Asp	His	Ala	Gln	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Arg	Ser	Thr	Asn	Thr	Ala	Tyr
65				70						75				80	
Met	Glu	Leu	Asn	Ser	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Arg	Glu	His	Ile	Ala	Ala	Arg	Gln	Asp	Tyr	Phe	Asp	Tyr	Trp	Gly

100

105

110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 151

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 151

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

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

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

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

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

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

Ala Arg Glu His Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 152

<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> member of supercluster 1

<400> 152

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

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

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

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

Gln Gly Arg Val Thr Phe Thr Ala Asp Lys Ser Thr Asn Thr Ser Tyr
65 70 75 80

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

Ala Arg Glu Arg Ile Ala Ala Arg Gln Asp Tyr Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 153
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> member of supercluster 1

<400> 153

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

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

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

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

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

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

Ala Arg Glu Leu Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 154

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 154

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

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

Ala Ile Ser Trp Val Arg Gln Thr Pro Glu Gln Gly Leu Glu Trp Met
35 40 45

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Arg Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Glu His Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 155

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 155

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

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

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

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

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

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

Ala Arg Glu His Ile Ala Ala Arg Leu Asp Tyr Phe Asp Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 156

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 1

<400> 156

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

Ser Val Lys Val Ser Cys Arg Ala Ser Gly Asp Ser Val Ser Asn Tyr
20 25 30

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

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

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

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

Ala Arg Glu Arg Ile Ala Ala Arg Gln Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 157
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> VH4-39|J00256-AEHJ6

<400> 157

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

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

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg

<210> 158
<211> 126
<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 8

<400> 158

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Ser Ser
20 25 30

Ser Ser Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Ser Phe Tyr Tyr Ser Gly Asn Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Glu Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Gln Thr Tyr Ser Ser Ser Trp Asp Gly Val Leu Tyr Tyr
100 105 110

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 159

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster 8

<400> 159

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1	5	10	15
Thr	Leu	Ser	Leu
	20		
Thr	Cys	Thr	Val
		25	
Ser	Gly	Gly	Ser
			30
Phe	Ser	Ser	Ser
Ser	Ser	Tyr	Trp
	35		
Gly	Trp	Ile	Arg
		40	
Gln	Pro	Pro	Gly
			45
Lys	Gly	Leu	Glu
Trp	Ile	Gly	Ser
	50		
Phe	Tyr	Tyr	Ser
		55	
Gly	Asn	Thr	Tyr
			60
Tyr	Tyr	Asn	Pro
Ser	Ser	Ser	Ser
Leu	Lys	Ser	Arg
	65		
Val	Thr	Ile	Ser
	70		
Val	Asp	Thr	Ser
		75	
Lys	Asn	Gln	Phe
			80
Ser	Leu	Lys	Leu
Ser	Ser	Val	Thr
	85		
Ala	Ala	Asp	Thr
	90		
Ala	Val	Tyr	Tyr
		95	
Cys	Ala	Arg	Gln
Thr	Tyr	Ser	Ser
	100		
Ser	Ser	Ser	Trp
		105	
Asp	Gly	Val	Leu
			110
Tyr	Tyr		
Phe	Asp	Tyr	Trp
	115		
Gly	Gln	Gly	Thr
			120
Leu	Val	Thr	Val
			125
Ser	Ser		

<210> 160
 <211> 124
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> member of supercluster 8

 <400> 160

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
1			5					10						15	
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Ser	Ser	Ser
			20					25					30		
Tyr	Trp	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile

35

40

45

Gly Ser Phe Tyr Tyr Ser Gly Asn Thr Tyr Tyr Asn Pro Ser Leu Lys
 50 55 60

Ser Arg Val Thr Ile Ser Glu Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80

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

Arg Gln Thr Tyr Ser Ser Ser Trp Asp Gly Val Leu Tyr Tyr Phe Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 161

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster10

<400> 161

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

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
 50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr

65		70		75		80									
Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	

Ala	Arg	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
			100					105				

<210> 162
 <211> 127
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> member of supercluster10

<400> 162

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

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

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

Gly	Trp	Ile	Asn	Thr	Asp	Thr	Gly	Asp	Pro	Thr	Tyr	Ala	Gln	Gly	Phe
	50					55					60				

Thr	Gly	Arg	Phe	Val	Phe	Ser	Leu	Asp	Thr	Ser	Val	Ser	Thr	Ala	Phe
65					70					75					80

Leu	Gln	Ile	Asn	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	

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

Tyr	Glu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115

120

125

<210> 163
 <211> 127
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> member of supercluster10

<400> 163

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

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

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

Gly Trp Ile Asn Thr Asp Thr Gly Asp Pro Thr Tyr Ala Gln Gly Phe
 50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Phe
 65 70 75 80

Leu Gln Ile Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

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

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 164
 <211> 127
 <212> PRT
 <213> Artificial Sequence

<220>

<223> member of supercluster10

<400> 164

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

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

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

Gly Trp Ile Asn Thr Gln Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 165

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster10

<400> 165

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

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

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

Gly Trp Ile Asp Thr Asn Thr Gly Asp Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Thr Thr Ala Phe
65 70 75 80

Leu Gln Ile Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 166

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster10

<400> 166

Gly Cys Ser Met Val Gln Ser Gly Ser Glu Ser Lys Lys Pro Gly Ala
1 5 10 15

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Phe
65 70 75 80

Leu Gln Ile Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 167

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster10

<400> 167

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

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Thr Thr Ala Phe
65 70 75 80

Leu Gln Ile Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 168

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster10

<400> 168

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

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Phe
65 70 75 80

Leu Gln Ile Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 169

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster10

<400> 169

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

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

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

Gly Trp Ile Asn Thr Tyr Thr Gly Asp Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 170

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster10

<400> 170

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

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

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

Gly Trp Ile Asn Thr Asp Thr Gly Asp Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Phe
65 70 75 80

Leu Gln Ile Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 171

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster10

<400> 171

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala

1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr	20	25	30
Thr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	35	40	45
Gly Trp Ile Asp Thr Asn Thr Gly Asp Pro Thr Tyr Ala Gln Gly Phe	50	55	60
Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Thr Thr Ala Phe	65	70	75
Leu Gln Ile Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys	85	90	95
Ala Arg Gly Asp Cys Asp Ser Thr Ser Cys Tyr Arg Tyr Ser Tyr Gly	100	105	110
Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser	115	120	125

<210> 172
 <211> 127
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> member of supercluster10

<400> 172

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

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

Ala Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

35

40

45

Gly Trp Ile Asn Thr Asn Thr Gly Asp Pro Thr Tyr Ala Gln Gly Phe
 50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Ser Ala Phe
 65 70 75 80

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

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

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 173

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster10

<400> 173

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

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Asp Pro Thr Tyr Ala Gln Gly Phe
 50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Phe

65		70		75		80									
Leu	Gln	Ile	Asn	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Arg	Gly	Asp	Cys	Asp	Ser	Thr	Ser	Cys	Tyr	Arg	Tyr	Ser	Tyr	Gly
			100					105					110		
Tyr	Glu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	
		115					120					125			
<210> 174															
<211> 127															
<212> PRT															
<213> Artificial Sequence															
<220>															
<223> member of supercluster10															
<400> 174															
Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ser	Lys	Leu	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
			20					25					30		
Thr	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Trp	Ile	Asn	Thr	Asp	Thr	Gly	Asp	Pro	Thr	Tyr	Ala	Gln	Gly	Phe
	50					55					60				
Thr	Gly	Arg	Phe	Val	Phe	Ser	Leu	Asp	Thr	Ser	Val	Ser	Thr	Ala	Phe
65				70					75					80	
Leu	Gln	Ile	Asn	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Arg	Gly	Asp	Cys	Asp	Ser	Thr	Ser	Cys	Tyr	Arg	Tyr	Ser	Tyr	Gly

100

105

110

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 175

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster10

<400> 175

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

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

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

Gly Trp Ile Asn Thr Asp Thr Gly Asp Pro Thr Tyr Ala Gln Gly Phe
 50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Phe
 65 70 75 80

Leu Gln Ile Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

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

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 176

<211> 127
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<213> Artificial Sequence

<220>
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<400> 176

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

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

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

Gly Trp Ile Asn Thr Tyr Thr Gly Asp Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 177
<211> 127
<212> PRT
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<220>
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<400> 177

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

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

Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 178

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> member of supercluster10

<400> 178

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

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Asp Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Phe
65 70 75 80

Leu Gln Ile Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 179

<211> 127

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<220>

<223> member of supercluster10

<400> 179

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

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 180

<211> 127

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

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

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

Gly Trp Ile Asn Thr Asn Thr Gly Asp Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Phe
65 70 75 80

Leu Gln Ile Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Gly Asp Cys Asp Ser Thr Asn Cys Tyr Arg Tyr Ser Tyr Gly
100 105 110

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 181

<211> 127

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<223> member of supercluster10

<400> 181

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

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

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

Gly Trp Ile Asp Thr Asn Thr Gly Asp Pro Thr Tyr Ala Gln Gly Phe
50 55 60

Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Thr Thr Ala Phe
65 70 75 80

Leu Gln Ile Asn Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

Tyr Glu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125