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<110> STEM CENTRX, INC.

<120> NOVEL MODULATORS AND METHODS OF USE

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850 855 860

Leu Ser Asn Asn Arg Phe Val His Lys Asp Leu Ala Ala Arg Asn Cys
865 870 875 880

Leu Val Ser Ala Gln Arg Gln Val Lys Val Ser Ala Leu Gly Leu Ser
885 890 895

Lys Asp Val Tyr Asn Ser Glu Tyr Tyr His Phe Arg Gln Ala Trp Val
900 905 910

Pro Leu Arg Trp Met Ser Pro Glu Ala Ile Leu Glu Gly Asp Phe Ser
915 920 925

Thr Lys Ser Asp Val Trp Ala Phe Gly Val Leu Met Trp Glu Val Phe
930 935 940

Thr His Gly Glu Met Pro His Gly Gly Gln Ala Asp Asp Glu Val Leu
945 950 955 960

Ala Asp Leu Gln Ala Gly Lys Ala Arg Leu Pro Gln Pro Glu Gly Cys
965 970 975

Pro Ser Lys Leu Tyr Arg Leu Met Gln Arg Cys Trp Ala Leu Ser Pro
980 985 990

Lys Asp Arg Pro Ser Phe Ser Glu Ile Ala Ser Ala Leu Gly Asp Ser
995 1000 1005

Thr Val Asp Ser Lys Pro
1010

<210> 5
<211> 1030
<212> PRT
<213> Homo sapiens

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

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

Val Phe Ile Lys Gln Pro Ser Ser Gln Asp Ala Leu Gln Gly Arg Arg
35 40 45

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

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

Gln Gly Ser Ser Leu Ser Phe Ala Ala Val Asp Arg Leu Gln Asp Ser
85 90 95

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

Arg Ser Ala Asn Ala Ser Phe Asn Ile Lys Trp Ile Glu Ala Gly Pro
115 120 125

Val Val Leu Lys His Pro Ala Ser Glu Ala Glu Ile Gln Pro Gln Thr
130 135 140

Gln Val Thr Leu Arg Cys His Ile Asp Gly His Pro Arg Pro Thr Tyr
145 150 155 160

Gln Trp Phe Arg Asp Gly Thr Pro Leu Ser Asp Gly Gln Ser Asn His
165 170 175

Thr Val Ser Ser Lys Glu Arg Asn Leu Thr Leu Arg Pro Ala Gly Pro
180 185 190

Glu His Ser Gly Leu Tyr Ser Cys Cys Ala His Ser Ala Phe Gly Gln
195 200 205

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

Ala Arg Val Val Leu Ala Pro Gln Asp Val Val Val Ala Arg Tyr Glu
225 230 235 240

Glu Ala Met Phe His Cys Gln Phe Ser Ala Gln Pro Pro Pro Ser Leu
245 250 255

Gln Trp Leu Phe Glu Asp Glu Thr Pro Ile Thr Asn Arg Ser Arg Pro
260 265 270

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

Thr Gln Val Arg Pro Arg Asn Ala Gly Ile Tyr Arg Cys Ile Gly Gln
290 295 300

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

Glu Ile Glu Asp Met Pro Leu Phe Glu Pro Arg Val Phe Thr Ala Gly
325 330 335

Ser Glu Glu Arg Val Thr Cys Leu Pro Pro Lys Gly Leu Pro Glu Pro
340 345 350

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

Val Tyr Gln Lys Gly His Glu Leu Val Leu Ala Asn Ile Ala Glu Ser
370 375 380

Asp Ala Gly Val Tyr Thr Cys His Ala Ala Asn Leu Ala Gly Gln Arg
385 390 395 400

Arg Gln Asp Val Asn Ile Thr Val Ala Thr Val Pro Ser Trp Leu Lys
405 410 415

Lys Pro Gln Asp Ser Gln Leu Glu Glu Gly Lys Pro Gly Tyr Leu Asp
420 425 430

Cys Leu Thr Gln Ala Thr Pro Lys Pro Thr Val Val Trp Tyr Arg Asn
435 440 445

Gln Met Leu Ile Ser Glu Asp Ser Arg Phe Glu Val Phe Lys Asn Gly
450 455 460

Thr Leu Arg Ile Asn Ser Val Glu Val Tyr Asp Gly Thr Trp Tyr Arg
465 470 475 480

Cys Met Ser Ser Thr Pro Ala Gly Ser Ile Glu Ala Gln Ala Arg Val
485 490 495

Gln Val Leu Asp Gly Ser Ser Leu Pro Glu Trp Val Thr Asp Asn Ala
500 505 510

Gly Thr Leu His Phe Ala Arg Val Thr Arg Asp Asp Ala Gly Asn Tyr
515 520 525

Thr Cys Ile Ala Ser Asn Gly Pro Gln Gly Gln Ile Arg Ala His Val
530 535 540

Gln Leu Thr Val Ala Val Phe Ile Thr Phe Lys Val Glu Pro Glu Arg
545 550 555 560

Thr Thr Val Tyr Gln Gly His Thr Ala Leu Leu Gln Cys Glu Ala Gln
565 570 575

Gly Asp Pro Lys Pro Leu Ile Gln Trp Lys Gly Lys Asp Arg Ile Leu
580 585 590

Asp Pro Thr Lys Leu Gly Pro Arg Met His Ile Phe Gln Asn Gly Ser
595 600 605

Leu Val Ile His Asp Val Ala Pro Glu Asp Ser Gly Arg Tyr Thr Cys
610 615 620

Ile Ala Gly Asn Ser Cys Asn Ile Lys His Thr Glu Ala Pro Leu Tyr
625 630 635 640

Val Val Asp Lys Pro Val Pro Glu Glu Ser Glu Gly Pro Gly Ser Pro
645 650 655

Pro Pro Tyr Lys Met Ile Gln Thr Ile Gly Leu Ser Val Gly Ala Ala

660 665 670

Val Ala Tyr Ile Ile Ala Val Leu Gly Leu Met Phe Tyr Cys Lys Lys
675 680 685

Arg Cys Lys Ala Lys Arg Leu Gln Lys Gln Pro Glu Gly Glu Glu Pro
690 695 700

Glu Met Glu Cys Leu Asn Gly Gly Pro Leu Gln Asn Gly Gln Pro Ser
705 710 715 720

Ala Glu Ile Gln Glu Glu Val Ala Leu Thr Ser Leu Gly Ser Gly Pro
725 730 735

Ala Ala Thr Asn Lys Arg His Ser Thr Ser Asp Lys Met His Phe Pro
740 745 750

Arg Ser Ser Leu Gln Pro Ile Thr Thr Leu Gly Lys Ser Glu Phe Gly
755 760 765

Glu Val Phe Leu Ala Lys Ala Gln Gly Leu Glu Glu Gly Val Ala Glu
770 775 780

Thr Leu Val Leu Val Lys Ser Leu Gln Ser Lys Asp Glu Gln Gln Gln
785 790 795 800

Leu Asp Phe Arg Arg Glu Leu Glu Met Phe Gly Lys Leu Asn His Ala
805 810 815

Asn Val Val Arg Leu Leu Gly Leu Cys Arg Glu Ala Glu Pro His Tyr
820 825 830

Met Val Leu Glu Tyr Val Asp Leu Gly Asp Leu Lys Gln Phe Leu Arg
835 840 845

Ile Ser Lys Ser Lys Asp Glu Lys Leu Lys Ser Gln Pro Leu Ser Thr
850 855 860

Lys Gln Lys Val Ala Leu Cys Thr Gln Val Ala Leu Gly Met Glu His
865 870 875 880

Leu Ser Asn Asn Arg Phe Val His Lys Asp Leu Ala Ala Arg Asn Cys
885 890 895

Leu Val Ser Ala Gln Arg Gln Val Lys Val Ser Ala Leu Gly Leu Ser
900 905 910

Lys Asp Val Tyr Asn Ser Glu Tyr Tyr His Phe Arg Gln Ala Trp Val
915 920 925

Pro Leu Arg Trp Met Ser Pro Glu Ala Ile Leu Glu Gly Asp Phe Ser
930 935 940

Thr Lys Ser Asp Val Trp Ala Phe Gly Val Leu Met Trp Glu Val Phe
945 950 955 960

Thr His Gly Glu Met Pro His Gly Gly Gln Ala Asp Asp Glu Val Leu
965 970 975

Ala Asp Leu Gln Ala Gly Lys Ala Arg Leu Pro Gln Pro Glu Gly Cys
980 985 990

Pro Ser Lys Leu Tyr Arg Leu Met Gln Arg Cys Trp Ala Leu Ser Pro
995 1000 1005

Lys Asp Arg Pro Ser Phe Ser Glu Ile Ala Ser Ala Leu Gly Asp
1010 1015 1020

Ser Thr Val Asp Ser Lys Pro
1025 1030

<210> 6
<211> 940
<212> PRT
<213> Homo sapiens

<400> 6
Met Gly Ala Ala Arg Gly Ser Pro Ala Arg Pro Arg Arg Leu Pro Leu
1 5 10 15

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

Val Phe Ile Lys Gln Pro Ser Ser Gln Asp Ala Leu Gln Gly Arg Arg
35 40 45

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

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

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

85 90 95

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

Arg Ser Ala Asn Ala Ser Phe Asn Ile Lys Trp Ile Glu Ala Gly Pro
115 120 125

Val Val Leu Lys His Pro Ala Ser Glu Ala Glu Ile Gln Pro Gln Thr
130 135 140

Gln Val Thr Leu Arg Cys His Ile Asp Gly His Pro Arg Pro Thr Tyr
145 150 155 160

Gln Trp Phe Arg Asp Gly Thr Pro Leu Ser Asp Gly Gln Ser Asn His
165 170 175

Thr Val Ser Ser Lys Glu Arg Asn Leu Thr Leu Arg Pro Ala Gly Pro
180 185 190

Glu His Ser Gly Leu Tyr Ser Cys Cys Ala His Ser Ala Phe Gly Gln
195 200 205

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

Ala Arg Val Val Leu Ala Pro Gln Asp Val Val Val Ala Arg Tyr Glu
225 230 235 240

Glu Ala Met Phe His Cys Gln Phe Ser Ala Gln Pro Pro Pro Ser Leu
245 250 255

Gln Trp Leu Phe Glu Asp Glu Thr Pro Ile Thr Asn Arg Ser Arg Pro
260 265 270

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

Thr Gln Val Arg Pro Arg Asn Ala Gly Ile Tyr Arg Cys Ile Gly Gln
290 295 300

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

Glu Ile Glu Asp Met Pro Leu Phe Glu Pro Arg Val Phe Thr Ala Gly
325 330 335

Ser Glu Glu Arg Val Thr Cys Leu Pro Pro Lys Gly Leu Pro Glu Pro
340 345 350

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

Val Tyr Gln Lys Gly His Glu Leu Val Leu Ala Asn Ile Ala Glu Ser
370 375 380

Asp Ala Gly Val Tyr Thr Cys His Ala Ala Asn Leu Ala Gly Gln Arg
385 390 395 400

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

Trp Val Thr Asp Asn Ala Gly Thr Leu His Phe Ala Arg Val Thr Arg
420 425 430

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

Gln Ile Arg Ala His Val Gln Leu Thr Val Ala Val Phe Ile Thr Phe
450 455 460

Lys Val Glu Pro Glu Arg Thr Thr Val Tyr Gln Gly His Thr Ala Leu
465 470 475 480

Leu Gln Cys Glu Ala Gln Gly Asp Pro Lys Pro Leu Ile Gln Trp Lys
485 490 495

Gly Lys Asp Arg Ile Leu Asp Pro Thr Lys Leu Gly Pro Arg Met His
500 505 510

Ile Phe Gln Asn Gly Ser Leu Val Ile His Asp Val Ala Pro Glu Asp
515 520 525

Ser Gly Arg Tyr Thr Cys Ile Ala Gly Asn Ser Cys Asn Ile Lys His
530 535 540

Thr Glu Ala Pro Leu Tyr Val Val Asp Lys Pro Val Pro Glu Glu Ser
545 550 555 560

Glu Gly Pro Gly Ser Pro Pro Pro Tyr Lys Met Ile Gln Thr Ile Gly
565 570 575

Leu Ser Val Gly Ala Ala Val Ala Tyr Ile Ile Ala Val Leu Gly Leu
580 585 590

Met Phe Tyr Cys Lys Lys Arg Cys Lys Ala Lys Arg Leu Gln Lys Gln
595 600 605

Pro Glu Gly Glu Glu Pro Glu Met Glu Cys Leu Asn Gly Gly Pro Leu
610 615 620

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

Ser Leu Gly Ser Gly Pro Ala Ala Thr Asn Lys Arg His Ser Thr Ser
645 650 655

Asp Lys Met His Phe Pro Arg Ser Ser Leu Gln Pro Ile Thr Thr Leu
660 665 670

Gly Lys Ser Glu Phe Gly Glu Val Phe Leu Ala Lys Ala Gln Gly Leu
675 680 685

Glu Glu Gly Val Ala Glu Thr Leu Val Leu Val Lys Ser Leu Gln Ser
690 695 700

Lys Asp Glu Gln Gln Gln Leu Asp Phe Arg Arg Glu Leu Glu Met Phe
705 710 715 720

Gly Lys Leu Asn His Ala Asn Val Val Arg Leu Leu Gly Leu Cys Arg
725 730 735

Glu Ala Glu Pro His Tyr Met Val Leu Glu Tyr Val Asp Leu Gly Asp
740 745 750

Leu Lys Gln Phe Leu Arg Ile Ser Lys Ser Lys Asp Glu Lys Leu Lys
755 760 765

Ser Gln Pro Leu Ser Thr Lys Gln Lys Val Ala Leu Cys Thr Gln Val
770 775 780

Ala Leu Gly Met Glu His Leu Ser Asn Asn Arg Phe Val His Lys Asp
785 790 795 800

Leu Ala Ala Arg Asn Cys Leu Val Ser Ala Gln Arg Gln Val Lys Val
805 810 815

Ser Ala Leu Gly Leu Ser Lys Asp Val Tyr Asn Ser Glu Tyr Tyr His
820 825 830

Phe Arg Gln Ala Trp Val Pro Leu Arg Trp Met Ser Pro Glu Ala Ile
835 840 845

Leu Glu Gly Asp Phe Ser Thr Lys Ser Asp Val Trp Ala Phe Gly Val
850 855 860

Leu Met Trp Glu Val Phe Thr His Gly Glu Met Pro His Gly Gly Gln
865 870 875 880

Ala Asp Asp Glu Val Leu Ala Asp Leu Gln Ala Gly Lys Ala Arg Leu
885 890 895

Pro Gln Pro Glu Gly Cys Pro Ser Lys Leu Tyr Arg Leu Met Gln Arg
900 905 910

Cys Trp Ala Leu Ser Pro Lys Asp Arg Pro Ser Phe Ser Glu Ile Ala
915 920 925

Ser Ala Leu Gly Asp Ser Thr Val Asp Ser Lys Pro
930 935 940

<210> 7
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
6xHis tag"

<400> 7
His His His His His His
1 5

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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
8xHis tag"

<400> 8
His His His His His His His His
1 5

<210> 9
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 9
gccattgtct tcatcaagca gcc 23

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 10
ctggatcatc ttgtaggggg gag 23

<210> 11
<211> 8
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown: motif peptide"

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Any amino acid

<400> 11
Gly Xaa Gly Xaa Phe Gly Xaa Val
1 5

<210> 12
<211> 8

<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown: motif peptide"

<220>
<221> MOD_RES
<222> (5)..(7)
<223> Any amino acid

<400> 12
His Arg Asp Leu Xaa Xaa Xaa Asn
1 5

<210> 13
<211> 7
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown: motif peptide"

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Any amino acid

<400> 13
Ser Asp Val Trp Ser Xaa Gly
1 5

<210> 14

<400> 14
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<210> 15

<400> 15
000

<210> 16

<400> 16
000

<210> 17

<400> 17
000

<210> 18

<400> 18
000

<210> 19

<400> 19
000

<210> 20
<211> 112
<212> PRT
<213> Mus sp.

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

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

Gly Asn Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Gly Ser Gly Val Pro Ala
50 55 60

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

Pro Val Glu Glu Asp Asp Ser Ala Met Tyr Phe Cys Gln Gln Ser Lys
85 90 95

Glu Val Pro Arg Thr Phe Gly Gly Gly Ser Arg Leu Glu Ile Lys Arg
100 105 110

<210> 21
<211> 113
<212> PRT
<213> Mus sp.

<400> 21
Gln Val Gln Met Gln Gln Ser Gly Ala Glu Leu Met Lys Pro Gly Ala
1 5 10 15

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

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

Gly Glu Ile Leu Pro Gly Ser Gly Arg Ser Asn Ser Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Lys Leu Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ala

<210> 22
<211> 108
<212> PRT
<213> Mus sp.

<400> 22
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

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

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

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

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

Glu Asp Leu Ala Glu Tyr Phe Cys Gln His Tyr Asn Ser Phe Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 23
<211> 115
<212> PRT

<213> Mus sp.

<400> 23
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Val
1 5 10 15

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

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

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

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

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

Ala Arg Asn Asp Leu Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 24
<211> 94
<212> PRT
<213> Mus sp.

<400> 24
Leu Gly Gly Arg Val Thr Ile Thr Cys Lys Ala Ser Asp His Ile Asn
1 5 10 15

Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Arg Leu
20 25 30

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

Ser Gly Ser Gly Ser Gly Lys Asp Tyr Thr Leu Ser Ile Thr Ser Leu
50 55 60

Gln Thr Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ser Ile
65 70 75 80

Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
85 90

<210> 25
<211> 123
<212> PRT
<213> Mus sp.

<400> 25
Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser
1 5 10 15

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

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

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

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

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

Arg Gly Asp Ala Tyr Asp Val Arg Arg Ser Thr Tyr Tyr Phe Asp Tyr
100 105 110

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

<210> 26
<211> 108
<212> PRT
<213> Mus sp.

<400> 26
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1 5 10 15

Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Asn
20 25 30

Leu His Trp Tyr Gln Gln Lys Ser His Ala Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Thr
65 70 75 80

Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Tyr Ser Trp Pro Arg
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 27
<211> 114
<212> PRT
<213> Mus sp.

<400> 27
Gln Leu Glu Glu Ser Gly Ala Glu Leu Met Gln Pro Gly Ala Ser Val
1 5 10 15

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

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

Ile Gly Glu Ile Leu Pro Gly Ser Gly Ser Thr Asp Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Phe Thr Ala Asp Ser Ser Ser Asn Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Thr Glu Asp Ser Ala Ile Tyr Tyr
85 90 95

Cys Ala Arg Gly Lys Leu His Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ala

<210> 28
<211> 114
<212> PRT
<213> Mus sp.

<400> 28
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ala Gly
1 5 10 15

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

Gly Asn Gln Gln Asn Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

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

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

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

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

Lys Arg

<210> 29
<211> 118
<212> PRT
<213> Mus sp.

<400> 29
Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Lys Asp
20 25 30

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

Gly Glu Ile Asn Pro Asp Ser Arg Thr Ile Asn Tyr Ala Pro Ser Leu
50 55 60

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

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

Ala Arg Trp Asp Tyr Asp Gly Gly Met Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Ser Val Thr Val Ser Ser
115

<210> 30
<211> 116
<212> PRT
<213> Mus sp.

<400> 30
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Thr Ser Glu Asn Ile Tyr Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Gln Leu Ala Trp Tyr Gln Gln Lys Gln
35 40 45

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser
65 70 75 80

Leu Arg Ile Asn Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys
85 90 95

Gln His His Tyr Gly Ile Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu
100 105 110

Glu Val Glu Arg
115

<210> 31
<211> 118
<212> PRT
<213> Mus sp.

<400> 31
Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr
20 25 30

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

Gly Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ser Leu
50 55 60

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

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

Ala Arg Pro Gly Tyr Gly Asn Leu Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ala
115

<210> 32
<211> 111
<212> PRT
<213> Mus sp.

<400> 32
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

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

Gly Met Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Asp Ser Gly Ile Pro Ala
50 55 60

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

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Cys Ile
85 90 95

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

<210> 33
<211> 122
<212> PRT
<213> Mus sp.

<400> 33
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

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

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

Gly Tyr Ile Ile Asn Pro Phe Ser Asp Gly Thr Lys Phe Thr Glu Lys
50 55 60

Phe Lys Gly Lys Ala Ser Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

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

Cys Ala Arg Arg Gly Pro Tyr Tyr Tyr Gly Thr Ala Met Asp Tyr Trp
100 105 110

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

<210> 34
<211> 107
<212> PRT
<213> Mus sp.

<400> 34
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Val Ser Val Gly
1 5 10 15

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Asn
20 25 30

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

Asn Ala Ala Thr Asn Leu Ala Asp Gly Val Ser Ser Arg Phe Arg Gly
50 55 60

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

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ile Thr Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Arg Lys
100 105

<210> 35
<211> 122
<212> PRT
<213> Mus sp.

<400> 35
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Gly Arg Pro Gly Ala
1 5 10 15

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

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

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

Lys Gly Lys Ser Thr Leu Ser Ala Asp Lys Ser Ser Asn Thr Ala Ser
65 70 75 80

Met His Leu Ser Ser Leu Ala Ser Asp Asp Ser Ala Val Tyr Tyr Cys
85 90 95

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

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

<210> 36
<211> 111
<212> PRT
<213> Mus sp.

<400> 36
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

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

Gly Ile Ser Phe Met His Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Gly Ser Gly Val Pro Ala
50 55 60

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

Pro Leu Glu Glu Ala Asp Thr Ala Met Tyr Phe Cys Gln Gln Ser Lys
85 90 95

Glu Val Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 37
<211> 113
<212> PRT
<213> Mus sp.

<400> 37
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Met Lys Pro Gly Ala
1 5 10 15

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

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

Gly Glu Ile Leu Pro Gly Arg Gly Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

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

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

Ser

<210> 38
<211> 108
<212> PRT
<213> Mus sp.

<400> 38

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

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

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

Tyr Tyr Ala Ser Lys His Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

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

Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 39
<211> 120
<212> PRT
<213> Mus sp.

<400> 39
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

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

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

Gly Glu Ile Asn Pro Ser Asn Gly Arg Ser Asn Tyr Asn Glu Lys Phe
50 55 60

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

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

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

Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 40
<211> 111
<212> PRT
<213> Mus sp.

<400> 40
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

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

Thr Ser Ile Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Ile Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Glu Glu Asp Thr Ala Thr Tyr Tyr Cys Gln His Ser Trp
85 90 95

Glu Ile Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 41
<211> 118
<212> PRT
<213> Mus sp.

<400> 41
Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

Gly Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ser Leu
50 55 60

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

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

Ala Arg Pro Gly Tyr Gly Asn Leu Phe Val Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 42
<211> 114
<212> PRT
<213> Mus sp.

<400> 42
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

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

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

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

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

Asp His Thr Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

Lys Arg

<210> 43
<211> 116
<212> PRT
<213> Mus sp.

<400> 43
Glu Val Lys 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 Asp Phe Ser Lys Asp
20 25 30

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

Gly Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ala Leu
50 55 60

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

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

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

Thr Val Ser Ser
115

<210> 44
<211> 107
<212> PRT
<213> Mus sp.

<400> 44
Asp Ile Gln Met Thr Gln Thr Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Thr Leu Glu Gln
65 70 75 80

Glu Asp Ile Gly Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 45
<211> 116
<212> PRT
<213> Mus sp.

<400> 45
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

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

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

Gly Arg Ile Tyr Leu Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

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

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

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

Thr Val Ser Ser
115

<210> 46
<211> 113
<212> PRT
<213> Mus sp.

<400> 46
Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
1 5 10 15

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

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

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

50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

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

Tyr Tyr Ser Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 47
<211> 118
<212> PRT
<213> Mus sp.

<400> 47
Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser
1 5 10 15

Gln Thr Leu Ser Leu Thr Cys Ser Val Pro Asp Tyr Ser Ile Thr Ser
20 25 30

Asp Tyr His Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu
35 40 45

Trp Met Gly Tyr Ile Ser Ser Arg Gly Ser Thr Asn Tyr Asn Pro Ser
50 55 60

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

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

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

Thr Leu Thr Val Ser Ser
115

<210> 48
<211> 107
<212> PRT
<213> Mus sp.

<400> 48
Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15

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

Leu Asn Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
35 40 45

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

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

Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 49
<211> 120
<212> PRT
<213> Mus sp.

<400> 49
Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Lys Pro Ser Gln
1 5 10 15

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

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

Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60

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

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

Cys Val Arg Ser Asn Tyr Gly Tyr Ala Trp Phe Ala Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 50
<211> 111
<212> PRT
<213> *Mus sp.*

<400> 50
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

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

Gly Lys Ser Phe Met His Trp Tyr Gln Gln Arg Pro Gly Gln Pro Pro
35 40 45

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

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

Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 51
<211> 119
<212> PRT
<213> Mus sp.

<400> 51
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Val Val Arg Pro Gly Val
1 5 10 15

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

Ala Val His Trp Val Lys Leu Ser His Ala Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Ser Thr Tyr Asn Asp Tyr Thr Tyr Asn Asn Gln Asp Phe
50 55 60

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

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

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

Thr Ser Val Thr Val Ser Ser
115

<210> 52
<211> 111
<212> PRT
<213> Mus sp.

<400> 52
Asp Ile Ala Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

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

Gly Ile Cys Phe Val Asn Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Gln Gly Ser Gly Val Pro Ala
50 55 60

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

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

Glu Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 53
<211> 121
<212> PRT
<213> Mus sp.

<400> 53
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Ser Pro Gly Thr
1 5 10 15

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

Gly Ile Ser Trp Val Lys Gln Lys Thr Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Tyr Pro Gly Ser Tyr Asn Ala Tyr Tyr Asn Asp Lys Phe
50 55 60

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

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

Ala Arg Asp Tyr Gly Asp Pro Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 54
<211> 111
<212> PRT
<213> Mus sp.

<400> 54
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Thr Val Ser Leu Gly
1 5 10 15

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

Thr Phe Asn Tyr Met Asn Trp Tyr Gln Gln Lys Leu Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60

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

Pro Val Glu Glu Glu Asp Ile Ala Thr Tyr Tyr Cys Gln His Ser Trp
85 90 95

Glu Ile Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 55
<211> 118
<212> PRT
<213> Mus sp.

<400> 55
Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Gln Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr
20 25 30

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

Gly Glu Ile Asn Pro Asp Ser Ser Thr Val Asn Tyr Thr Pro Ser Leu
50 55 60

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

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

Ala Arg Pro Gly Tyr Gly Asn Leu Phe Val Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ala
115

<210> 56
<211> 113
<212> PRT
<213> Mus sp.

<400> 56
Asp Ile Val Leu Thr Gln Ala Thr Pro Ser Val Pro Val Thr Pro Gly
1 5 10 15

Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Thr
20 25 30

Lys Gly Asp Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His
85 90 95

Leu Glu Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg

<210> 57
<211> 118
<212> PRT
<213> Mus sp.

<400> 57
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Ser Val Arg Ser Gly Ala
1 5 10 15

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

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

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

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

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

Asn Ala Cys Asn Tyr Gly Ser Ala Tyr Gly Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 58
<211> 107
<212> PRT
<213> Mus sp.

<400> 58

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

Glu Lys Val Thr Ile Arg Cys Ile Thr Asn Thr Asp Ile Asp Asp Asp
20 25 30

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

Ser Glu Gly Asn Gly Leu Arg Pro Gly Val Pro Ser Arg Phe Ser Ser
50 55 60

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

Glu Asp Val Ala Asp Tyr Tyr Cys Leu Gln Ser Asp Asn Leu Pro Leu
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 59
<211> 120
<212> PRT
<213> Mus sp.

<400> 59
Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr
20 25 30

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

Gly Asp Leu Asn Pro Asp Ser Ser Ala Ile Asn Tyr Thr Pro Ser Leu
50 55 60

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

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

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

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 60
<211> 113
<212> PRT
<213> Mus sp.

<400> 60
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

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

Gly Asp Gln Lys Asn Cys Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

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

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

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

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
100 105 110

Lys

<210> 61
<211> 120
<212> PRT
<213> Mus sp.

<400> 61
Glu Ile His Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

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

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

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

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

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

Ala Arg Thr Ala Arg Ala Ser Asn Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 62
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 62
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Thr Leu Ile
35 40 45

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

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

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

Thr Lys Leu Glu Ile Lys Arg
100

<210> 63
<211> 120

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 63
Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

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

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

Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Ser Pro Ser
50 55 60

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Val Arg Ser Asn Tyr Gly Tyr Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 64
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 64
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr
20 25 30

Gly Lys Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro

35 40 45

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

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

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Asn
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

<210> 65
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 65
Gln Val Gln Leu Val Gln Ser Gly Pro 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 Asp Tyr
20 25 30

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

Gly Val Ile Ser Thr Tyr Asn Asp Tyr Thr Tyr Asn Asn Gln Asp Phe
50 55 60

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

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

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

Thr Ser Val Thr Val Ser Ser
115

<210> 66
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 66
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Thr
20 25 30

Lys Gly Asp Thr Tyr Leu Tyr Trp Phe Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His
85 90 95

Leu Glu Tyr Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg

<210> 67
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 67
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 Lys Asp 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 Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Glu Phe
50 55 60

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

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

Asn Ala Cys Asn Tyr Gly Ser Ala Tyr Gly Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 68
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 68
Glu Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly
1 5 10 15

Asp Lys Val Asn Ile Ser Cys Ile Thr Asn Thr Asp Ile Asp Asp Asp
20 25 30

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

Ser Glu Gly Asn Gly Leu Arg Pro Gly Ile Pro Pro Arg Phe Ser Gly
50 55 60

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

Glu Asp Ala Ala Tyr Tyr Phe Cys Leu Gln Ser Asp Asn Leu Pro Leu
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 69
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 69
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 Asp Phe Ser Arg Tyr
20 25 30

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

Gly Asp Leu Asn Pro Asp Ser Ser Ala Ile Asn Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser 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

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

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 70
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 70
Ala Ile Val Phe Ile Lys Gln Pro Ser Ser Gln Asp Ala Leu Gln Gly
1 5 10 15

Arg Arg Ala Leu Leu Arg Cys Glu Val Glu Ala Pro Gly Pro Val His
20 25 30

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

Phe Ala Gln Gly Ser Ser Leu Ser Phe Ala Ala Val Asp Arg Leu Gln
50 55 60

Asp Ser Gly Thr Phe Gln Cys Val Ala Arg Asp Asp Val Thr Gly Glu
65 70 75 80

Glu Ala Arg Ser Ala Asn Ala Ser Phe Asn Ile Lys Trp Ile Glu Ala
85 90 95

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

Gln Thr Gln Val Thr Leu Arg Cys His Ile Asp Gly His Pro Arg Pro
115 120 125

Thr Tyr Gln Trp Phe Arg Asp Gly Thr Pro Leu Ser Asp Gly Gln Ser
130 135 140

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

Gly Pro Glu His Ser Gly Leu Tyr Ser Cys Cys Ala His Ser Ala Phe
165 170 175

Gly Gln Ala Cys Ser Ser Gln Asn Phe Thr Leu Ser Ile Ala Asp Glu
180 185 190

Ser Phe Ala Arg Val Val Leu Ala Pro Gln Asp Val Val Val His Pro
195 200 205

Val Arg Ser Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
210 215 220

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
225 230 235 240

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
245 250 255

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
260 265 270

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
275 280 285

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

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

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

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

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
355 360 365

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met
370 375 380

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
385 390 395 400

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
405 410 415

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
420 425 430

Gly Lys

<210> 71
<211> 702
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 71
Ala Pro Gln Asp Val Val Val Ala Arg Tyr Glu Glu Ala Met Phe His
1 5 10 15

Cys Gln Phe Ser Ala Gln Pro Pro Pro Ser Leu Gln Trp Leu Phe Glu
20 25 30

Asp Glu Thr Pro Ile Thr Asn Arg Ser Arg Pro Pro His Leu Arg Arg
35 40 45

Ala Thr Val Phe Ala Asn Gly Ser Leu Leu Leu Thr Gln Val Arg Pro
50 55 60

Arg Asn Ala Gly Ile Tyr Arg Cys Ile Gly Gln Gly Gln Arg Gly Pro
65 70 75 80

Pro Ile Ile Leu Glu Ala Thr Leu His Leu Ala Glu Ile Glu Asp Met
85 90 95

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

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

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

His Glu Leu Val Leu Ala Asn Ile Ala Glu Ser Asp Ala Gly Val Tyr
145 150 155 160

Thr Cys His Ala Ala Asn Leu Ala Gly Gln Arg Arg Gln Asp Val Asn
165 170 175

Ile Thr Val Ala Thr Val Pro Ser Trp Leu Lys Lys Pro Gln Asp Ser
180 185 190

Gln Leu Glu Glu Gly Lys Pro Gly Tyr Leu Asp Cys Leu Thr Gln Ala
195 200 205

Thr Pro Lys Pro Thr Val Val Trp Tyr Arg Asn Gln Met Leu Ile Ser
210 215 220

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

Ser Val Glu Val Tyr Asp Gly Thr Trp Tyr Arg Cys Met Ser Ser Thr
245 250 255

Pro Ala Gly Ser Ile Glu Ala Gln Ala Arg Val Gln Val Leu Glu Lys
260 265 270

Leu Lys Phe Thr Pro Pro Pro Gln Pro Gln Gln Cys Met Glu Phe Asp
275 280 285

Lys Glu Ala Thr Val Pro Cys Ser Ala Thr Gly Arg Glu Lys Pro Thr
290 295 300

Ile Lys Trp Glu Arg Ala Asp Gly Ser Ser Leu Pro Glu Trp Val Thr
305 310 315 320

Asp Asn Ala Gly Thr Leu His Phe Ala Arg Val Thr Arg Asp Asp Ala
325 330 335

Gly Asn Tyr Thr Cys Ile Ala Ser Asn Gly Pro Gln Gly Gln Ile Arg
340 345 350

Ala His Val Gln Leu Thr Val Ala Val Phe Ile Thr Phe Lys Val Glu
355 360 365

Pro Glu Arg Thr Thr Val Tyr Gln Gly His Thr Ala Leu Leu Gln Cys
370 375 380

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

Arg Ile Leu Asp Pro Thr Lys Leu Gly Pro Arg Met His Ile Phe Gln
405 410 415

Asn Gly Ser Leu Val Ile His Asp Val Ala Pro Glu Asp Ser Gly Arg
420 425 430

Tyr Thr Cys Ile Ala Gly Asn Ser Cys Asn Ile Lys His Thr Glu Ala
435 440 445

Pro Leu Tyr Val Val Asp Lys Pro Val Pro Glu Glu Ser Glu Gly Pro
450 455 460

Gly Ser Pro Pro Pro Tyr Lys Met Ile Gln His Pro Val Arg Ser Val
465 470 475 480

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
485 490 495

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
500 505 510

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
515 520 525

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
530 535 540

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
545 550 555 560

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
565 570 575

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

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
595 600 605

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
610 615 620

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
625 630 635 640

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
645 650 655

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
660 665 670

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
675 680 685

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
690 695 700

<210> 72
<211> 708
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 72
Ala Ile Val Phe Ile Lys Gln Pro Ser Ser Gln Asp Ala Leu Gln Gly
1 5 10 15

Arg Arg Ala Leu Leu Arg Cys Glu Val Glu Ala Pro Gly Pro Val His
20 25 30

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

Phe Ala Gln Gly Ser Ser Leu Ser Phe Ala Ala Val Asp Arg Leu Gln
50 55 60

Asp Ser Gly Thr Phe Gln Cys Val Ala Arg Asp Asp Val Thr Gly Glu
65 70 75 80

Glu Ala Arg Ser Ala Asn Ala Ser Phe Asn Ile Lys Trp Ile Glu Ala
85 90 95

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

Gln Thr Gln Val Thr Leu Arg Cys His Ile Asp Gly His Pro Arg Pro
115 120 125

Thr Tyr Gln Trp Phe Arg Asp Gly Thr Pro Leu Ser Asp Gly Gln Ser
130 135 140

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

Gly Pro Glu His Ser Gly Leu Tyr Ser Cys Cys Ala His Ser Ala Phe
165 170 175

Gly Gln Ala Cys Ser Ser Gln Asn Phe Thr Leu Ser Ile Ala Asp Glu
180 185 190

Ser Phe Ala Arg Val Val Leu Ala Pro Gln Asp Val Val Val Ala Arg
195 200 205

Tyr Glu Glu Ala Met Phe His Cys Gln Phe Ser Ala Gln Pro Pro Pro
210 215 220

Ser Leu Gln Trp Leu Phe Glu Asp Glu Thr Pro Ile Thr Asn Arg Ser
225 230 235 240

Arg Pro Pro His Leu Arg Arg Ala Thr Val Phe Ala Asn Gly Ser Leu
245 250 255

Leu Leu Thr Gln Val Arg Pro Arg Asn Ala Gly Ile Tyr Arg Cys Ile
260 265 270

Gly Gln Gly Gln Arg Gly Pro Pro Ile Ile Leu Glu Ala Thr Leu His
275 280 285

Leu Ala Glu Ile Glu Asp Met Pro Leu Phe Glu Pro Arg Val Phe Thr
290 295 300

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

Glu Pro Ser Val Trp Trp Glu His Ala Gly Val Arg Leu Pro Thr His
325 330 335

Gly Arg Val Tyr Gln Lys Gly His Glu Leu Val Leu Ala Asn Ile Ala
340 345 350

Glu Ser Asp Ala Gly Val Tyr Thr Cys His Ala Ala Asn Leu Ala Gly
355 360 365

Gln Arg Arg Gln Asp Val Asn Ile Thr Val Ala Thr Val Pro Ser Trp
370 375 380

Leu Lys Lys Pro Gln Asp Ser Gln Leu Glu Glu Gly Lys Pro Gly Tyr
385 390 395 400

Leu Asp Cys Leu Thr Gln Ala Thr Pro Lys Pro Thr Val Val Trp Tyr
405 410 415

Arg Asn Gln Met Leu Ile Ser Glu Asp Ser Arg Phe Glu Val Phe Lys
420 425 430

Asn Gly Thr Leu Arg Ile Asn Ser Val Glu Val Tyr Asp Gly Thr Trp
435 440 445

Tyr Arg Cys Met Ser Ser Thr Pro Ala Gly Ser Ile Glu Ala Gln Ala
450 455 460

Arg Val Gln Val Leu Glu Lys Leu Lys Phe Thr Pro Pro Pro Gln Pro
465 470 475 480

His Pro Val Arg Ser Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
485 490 495

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
515 520 525

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
530 535 540

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
545 550 555 560

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

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
580 585 590

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
595 600 605

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
610 615 620

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
625 630 635 640

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
645 650 655

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
660 665 670

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
675 680 685

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
690 695 700

Ser Pro Gly Lys
705

<210> 73

<211> 429
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 73
Lys Phe Thr Pro Pro Pro Gln Pro Gln Gln Cys Met Glu Phe Asp Lys
1 5 10 15

Glu Ala Thr Val Pro Cys Ser Ala Thr Gly Arg Glu Lys Pro Thr Ile
20 25 30

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

Asn Ala Gly Thr Leu His Phe Ala Arg Val Thr Arg Asp Asp Ala Gly
50 55 60

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

His Val Gln Leu Thr Val Ala Val Phe Ile Thr Phe Lys Val Glu Pro
85 90 95

Glu Arg Thr Thr Val Tyr Gln Gly His Thr Ala Leu Leu Gln Cys Glu
100 105 110

Ala Gln Gly Asp Pro Lys Pro Leu Ile Gln Trp Lys Gly Lys Asp Arg
115 120 125

Ile Leu Asp Pro Thr Lys Leu Gly Pro Arg Met His Ile Phe Gln Asn
130 135 140

Gly Ser Leu Val Ile His Asp Val Ala Pro Glu Asp Ser Gly Arg Tyr
145 150 155 160

Thr Cys Ile Ala Gly Asn Ser Cys Asn Ile Lys His Thr Glu Ala Pro
165 170 175

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

Ser Pro Pro Pro Tyr Lys Met Ile Gln His Pro Val Arg Ser Val Glu
195 200 205

Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu
210 215 220

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
225 230 235 240

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln
245 250 255

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
260 265 270

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

Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
290 295 300

Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
305 310 315 320

Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
325 330 335

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

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
355 360 365

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

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
385 390 395 400

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
405 410 415

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

<210> 74
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 74
Glu Glu Ala Arg Ser Ala Asn Ala Ser Phe Asn Ile Lys Trp Ile Glu
1 5 10 15

Ala Gly Pro Val Val Leu Lys His Pro Ala Ser Glu Ala Glu Ile Gln
20 25 30

Pro Gln Thr Gln Val Thr Leu Arg Cys His Ile Asp Gly His Pro Arg
35 40 45

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

Ser Asn His Thr Val Ser Ser Lys Glu Arg Asn Leu Thr Leu Arg Pro
65 70 75 80

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

Phe Gly Gln Ala Cys Ser Ser Gln Asn Phe Thr Leu Ser Ile Ala Asp
100 105 110

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

Arg Tyr Glu Glu Ala Met Phe His Cys Gln Phe Ser Ala Gln Pro Pro
130 135 140

Pro Ser Leu Gln Trp Leu Phe Glu Asp Glu Thr Pro Ile Thr Asn Arg
145 150 155 160

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

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

Ile Gly Gln Gly Gln Arg Gly Pro Pro Ile Ile Leu Glu Ala Thr Leu
195 200 205

His Leu Ala Glu His Pro Val Arg Ser Val Glu Cys Pro Pro Cys Pro
210 215 220

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

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

Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
260 265 270

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
275 280 285

Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
290 295 300

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
305 310 315 320

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
325 330 335

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

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
370 375 380

Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
385 390 395 400

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
405 410 415

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
420 425 430

Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 75
<211> 607
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 75
Ala Ile Val Phe Ile Lys Gln Pro Ser Ser Gln Asp Ala Leu Gln Gly
1 5 10 15

Arg Arg Ala Leu Leu Arg Cys Glu Val Glu Ala Pro Gly Pro Val His
20 25 30

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

Phe Ala Gln Gly Ser Ser Leu Ser Phe Ala Ala Val Asp Arg Leu Gln
50 55 60

Asp Ser Gly Thr Phe Gln Cys Val Ala Arg Asp Asp Val Thr Gly Glu
65 70 75 80

Glu Ala Arg Ser Ala Asn Ala Ser Phe Asn Ile Lys Trp Ile Glu Ala
85 90 95

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

Gln Thr Gln Val Thr Leu Arg Cys His Ile Asp Gly His Pro Arg Pro
115 120 125

Thr Tyr Gln Trp Phe Arg Asp Gly Thr Pro Leu Ser Asp Gly Gln Ser
130 135 140

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

Gly Pro Glu His Ser Gly Leu Tyr Ser Cys Cys Ala His Ser Ala Phe
165 170 175

Gly Gln Ala Cys Ser Ser Gln Asn Phe Thr Leu Ser Ile Ala Asp Glu
180 185 190

Ser Phe Ala Arg Val Val Leu Ala Pro Gln Asp Val Val Val Ala Arg
195 200 205

Tyr Glu Glu Ala Met Phe His Cys Gln Phe Ser Ala Gln Pro Pro Pro

210 215 220

Ser Leu Gln Trp Leu Phe Glu Asp Glu Thr Pro Ile Thr Asn Arg Ser
225 230 235 240

Arg Pro Pro His Leu Arg Arg Ala Thr Val Phe Ala Asn Gly Ser Leu
245 250 255

Leu Leu Thr Gln Val Arg Pro Arg Asn Ala Gly Ile Tyr Arg Cys Ile
260 265 270

Gly Gln Gly Gln Arg Gly Pro Pro Ile Ile Leu Glu Ala Thr Leu His
275 280 285

Leu Ala Glu Ile Glu Asp Met Pro Leu Phe Glu Pro Arg Val Phe Thr
290 295 300

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

Glu Pro Ser Val Trp Trp Glu His Ala Gly Val Arg Leu Pro Thr His
325 330 335

Gly Arg Val Tyr Gln Lys Gly His Glu Leu Val Leu Ala Asn Ile Ala
340 345 350

Glu Ser Asp Ala Gly Val Tyr Thr Cys His Ala Ala Asn Leu Ala Gly
355 360 365

Gln Arg Arg Gln Asp Val Asn Ile Thr Val Ala His Pro Val Arg Ser
370 375 380

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
385 390 395 400

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

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
420 425 430

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
435 440 445

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
450 455 460

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
465 470 475 480

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
485 490 495

Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
500 505 510

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
515 520 525

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
530 535 540

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
545 550 555 560

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
565 570 575

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
580 585 590

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
595 600 605

<210> 76

<400> 76
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<210> 118

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<210> 119

<400> 119
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<210> 120
<211> 336
<212> DNA

<213> Mus sp.

<400> 120
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atatcctgca gagccagtga aagtgttgat agttttggca atagttttat gcactggtac 120

cagcagaaac caggacagcc acccaaactc ctcatctatg ctgcatccaa cctaggatcc 180

ggggtccctg ccaggtttag tggcagtggg tctgggacag acttcagcct caacatccat 240

cctgtggagg aggatgattc tgcaatgtat ttctgtcagc aaagtaagga ggttcctcgg 300

acgttcggtg gaggctccag gctggaaatc aaacgg 336

<210> 121
<211> 339
<212> DNA
<213> Mus sp.

<400> 121
caggtccaaa tgcagcagtc tggagctgag ctgatgaagc ctggggcctc agtgaagctt 60

tcctgcaagg ctactggcta cacattcact ggctactgga ttgagtgggt aaagcagagg 120

cctggacatg gccttgagtg gattggagag attttacctg gaagtggtcg ttctaactcc 180

aatgagaagt tcaagggcaa ggccacattc actgctgata catcctccaa cacagcctac 240

atgcaactca gcagcctgac aactgaggac tctgccatct attactgtgc aagagggaag 300

ctttcctggg gccaagggac tctggtcact gtctctgca 339

<210> 122
<211> 324
<212> DNA
<213> Mus sp.

<400> 122
gacattgtga tgacccagtc tcaaaaattc atgtccacat cagtaggaga cagggtcaac 60

gtcacctgca aggccagtca gaatgtgggt actaatgtag tctggtatca acagaaaaca 120

gggcaatctc ctaaagcact gattcactcg gcatcctacc ggtacagtgg agtccctgat 180

cgcttcacag gcagtggatc tgggacagat ttcactctca ccctcagcaa tgtacagtct 240

gaagacttgg cagagtattt ctgtcagcac tataacagct ttccgtacac gttcggaggg 300

gggaccaagc tggaaataaa acgg 324

<210> 123
<211> 345
<212> DNA
<213> Mus sp.

<400> 123
caggtccagc tgcagcagtc tggggctgaa ctggtgaggc ctggggtctc agtgaagatt 60

tcctgcaagg gttctggcta cagattcact gattatccta tacactgggt gaagcagagt 120

catgcaaaga gtctagagtg gattggaatt attagtactt actatggtga tgttaccaac 180

aacccgaagt tcaggggcaa ggccacaatg actgtagaca aatcctccac cacagcctat 240

atggaacttg ccagactgac atctgaggat tctgccatct attactgtgc aagaaatgat 300

ctttttgctt actggggcca agggactctg gtcactgtct ctgca 345

<210> 124
<211> 282
<212> DNA
<213> Mus sp.

<400> 124
ctaggaggca gagtcaccat tacttgcaag gcaagtgacc acattaataa ttggttagcc 60

tggtatcagc agaaaccagg aaatgctcct aggctcttaa tatctggtgc taccactttg 120

gaaactgggg ttccttcaag attcagtggc agtggatctg gaaaggatta cactctcagc 180

ataaccagtc ttcagactga agatgttgct acttattact gtcaacagta ttggagtatt 240

ccgtacacgt tcggaggggg gaccaagctg gaaataaaac gg 282

<210> 125
<211> 375
<212> DNA
<213> Mus sp.

<400> 125
tctgatgtgc agcttcagga gtcgggacct ggcctggtga aaccttctca gtctctgtcc 60

ctcacctgca ctgtcactgg ctactcaatc accagtgatt atgcctggaa ctggatccgg 120

cagtttccag gaaacaaact ggagtggatg ggctacataa gctacagtgg ttacactaac 180

tacaacccat ctctcaaaag tcgaatctct atcactcgag acacatccaa gaaccagttc 240

ttcctgcagt tgatttctgt gactactgag gacacagcca catattactg tgcaagaggg 300

gatgcttacg acgtccggag aagtacgtac tactttgact actggggcca aggcaccact 360

ctcacagtct cctcg 375

<210> 126
<211> 324
<212> DNA
<213> Mus sp.

<400> 126
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ctttcctgca gggccagcca aagtgttagc aacaacctac actggtatca acaaaaatca 120

catgcgtctc caaggcttct catcaagtat gcttcccagt ccatctctgg gatcccctcc 180

aggttcagtg gcagtggatc agggacagat ttcactctca gtatcaacag tgtggagact 240

gaagattttg gaatgtattt ctgtcaacag agttacagct ggcctcggac gttcggtgga 300

ggcaccaagc tggaaatcaa acgg 324

<210> 127
<211> 333
<212> DNA
<213> Mus sp.

<400> 127
cagctggagg agtcaggtgc tgagctgatg cagcctgggg cctcagtgaa ggtttcctgc 60

aaggccactg gctacacatt cactgtctac tggatagagt gggtaaaaca gaggcctgga 120

catggccttg aatggattgg agagatttta cctggaagtg gtagtactga ttacaatgag 180

aagttcaagg gcaaggccac attcactgca gattcatcct ccaacacagc ctacatgcaa 240

ctcagcagcc tgacaactga ggactctgcc atctattact gtgcaagagg gaagcttcac 300

tggggccaag ggactctggt cacagtctct gca 333

<210> 128
<211> 341
<212> DNA
<213> Mus sp.

<400> 128
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atgagctgca agtccagtca gagtctgtta aacggtggaa atcaacagaa ctccttggcc 120

tggtaccagc agaaaccagg gcagcctcct aaactgttga tctacggggc ttccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg gaaccgattt cgctcttacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga tcatacttat 300

ccgtacacgt tcggaggggg gaccgagctg gaaataaaac g 341

<210> 129
<211> 354
<212> DNA
<213> Mus sp.

<400> 129
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tcctgtgcag cctcaggatt cgattttagt aaagactgga tgagttgggt ccggcaggct 120

ccagggaaag ggctagaatg gattggagaa attaatccag atagccgtac gataaattat 180

gcaccatctc taaaggataa attcatcatc tccagagaga acgccaaaaa tacgctgtac 240

ctgcaaatga gtaaagtgag atctgaggac acagcccttt attactgtgc aagatgggat 300

tacgacggtg gtatggacta ctggggtcaa ggaacctcag tcaccgtctc ctca 354

<210> 130
<211> 323
<212> DNA
<213> Mus sp.

<400> 130
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atcacatgtc gaacaagtga gaatatttac agttatttag catggtatca gcagaaacag 120

ggaaaatctc ctcagctcct ggtccacaat gcaaacacct tagcagaagg tgtgccatca 180

aggttcagtg gcagtggatc aggcacacag ttttctctga ggatcaacag cctgcagcct 240

gaagattttg ggagttatta ttgtcagcat cattatggta ttccgttcac gttcggaggg 300

gggaccaagc tggaagtaga acg 323

<210> 131
<211> 354
<212> DNA
<213> Mus sp.

<400> 131
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tcctgtgcag cctcaggatt cgattttagt agatactgga tgagttgggt ccggcaggct 120

ccagggaaag ggctagaatg gattggagaa attaatccag atagcagtac gataaactat 180

acgccatctc taaaggataa attcatcatc tccagagaca acgccaaaaa tacgctgtac 240

ctgcaaatga gcaaagtgag atctgaggac acagcccttt attactgtgc aagaccggga 300

tatggtaact tgtttgctta ctggggccaa gggactctgg tcactgtctc tgca 354

<210> 132
<211> 334
<212> DNA
<213> Mus sp.

<400> 132
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gtcttctgca gagccagcca gactgtcgat tataatggaa tgagttatat gcactggttc 120

caacagaaac caggacagcc acccaaactc ctcatctatg ctgcatccaa cctagattct 180

gggatccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat 240

cctgtggagg aggaagatgc tgcaacctat tactgtcagc aatgtattga ggatccgctc 300

acgttcggtg ctgggaccat gctggaggtg aaac 334

<210> 133
<211> 363
<212> DNA
<213> Mus sp.

<400> 133
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cctgggcagg gccttgagtg gattggatat attaatcctt tcagtgatgg tactaagttt 180

actgagaagt tcaaaggcaa ggcctcactg acttcagaca aatcgtccag cacagcctac 240

atggagctca acagcctgac ctctgaggac tctgcggtct attactgtgc aagaagaggt 300

ccttattatt acggtaccgc tatggactac tggggtcaag gaacctcagt caccgtctcc 360

tca 363

<210> 134
<211> 322
<212> DNA
<213> Mus sp.

<400> 134
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atcacatgtc gagcaagtga gaatatttac agtaatttag catggtatca acagaaacag 120

ggaaaatctc ctcagctcct ggtcaatgct gcaacaaact tagcagatgg tgtgtcatcg 180

aggttccgtg gcagtggatc aggcacacag tattccctca agatcaacag cctgcagtct 240

gaagattttg ggagttatta ttgtcaacat ttttggatta ctccattcac gttcggctcg 300

gggacaaagt tggaaagaaa ac 322

<210> 135
<211> 366
<212> DNA
<213> Mus sp.

<400> 135
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tcctgcaagg attctggcta caccattact atctactgga tgcagtgggt aaaacagagg 120

cctggacagg gtctggaatg gattggggct atttatcctg gagatggtga tactaggtac 180

cctcagaagt tcaagggcaa gtccacattg tctgcagata aatcctccaa cacagcctcc 240

atgcacctca gcagcttggc atctgatgac tctgcggtct attactgttc aagaggaggg 300

tcaaccaact atgattacga cggatttgct tactggggcc aagggactct ggtcactgtc 360

tctgca 366

<210> 136
<211> 334
<212> DNA
<213> Mus sp.

<400> 136
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atctcctgca gagccagcga aagtgttgat aattatggca ttagttttat gcactggttc 120

caacagaaac caggacagcc acccaaactc ctcatctatg ctgcatccaa cctaggatcc 180

ggggtccctg ccaggtttag tggcagtggg tctgggacag acttcagcct caacatccat 240

cctctggagg aggctgatac tgcaatgtat ttctgtcagc agagtaagga ggttcctcgg 300

acgttcggtg gaggcaccaa gctggaaatc aaac 334

<210> 137
<211> 339
<212> DNA
<213> Mus sp.

<400> 137
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tcctgcaagg ctactggcta cacattcagt aactactgga tagagtgggt aaagcagagg 120

cctggacatg gccttgagtg gattggagag attttacctg gaaggggtag tactaactac 180

aatgagaagt tcaagggcaa ggccacattc actgcagata cttcctccaa cacagcctac 240

atgcaactca gcagcctgac ctctgaggac tctgccgtct attactgtgc aagagggaaa 300

caatactggg gccaaggcac cactctcaca gtctcctca 339

<210> 138
<211> 323
<212> DNA
<213> Mus sp.

<400> 138
agtattgtgc tgacccagtc tctcaaattc ctgcttgtgt cagcaggaga cagggttacc 60

atgacctgca aggccagtca gagtgtgact aatgatgtag cttggtacca acagaagcca 120

gggcagtctc ctaaactgct gatatactat gcatccaaac actacactgg agtccctgat 180

cgcttcactg gcagtggata tgggacggat ttcactttca ccatcagcac tgtgcaggct 240

gaagacctgg cagtttattt ctgtcagcag gattatagct ctccgtacac gttcggaggg 300

gggaccaagc tggaaataaa acg 323

<210> 139
<211> 360
<212> DNA
<213> Mus sp.

<400> 139
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tcctgcaagg cttctggcta caccttcacc agctactgga tgcactgggt gaagcagagg 120

cctggacaag gccttgagtg gattggagag attaatccta gcaacggtcg ttctaactac 180

aatgagaagt tcaagagcaa ggccacactg actgtagaca aatcctccag cacagcctac 240

atgcaactca gcagcctgac atctgaggac tctgcggtct atttctgtgc acattactac 300

gatggtagtt acgggttctt tgactattgg ggccaaggca ccactctcac agtctcctca 360

<210> 140
<211> 334
<212> DNA
<213> Mus sp.

<400> 140
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atctcatgca gggccagcca aagtgtcagt acatctacct ctatttatat gcactggtac 120

caacagaaac caggacagcc acccaaactc ctcatcaagt atgcatccaa cctagaatct 180

ggggtccctg ccaggttcag tggcagtggg tctgggacag aaatcaccct caacatccat 240

cctgtggagg aggaggatac tgcaacatat tactgtcagc acagttggga gattccgtgg 300

acgttcggtg gaggcaccaa gctggaaatc aaac 334

<210> 141
<211> 354
<212> DNA
<213> Mus sp.

<400> 141
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tcctgtacag cctcaggatt cgattttagt agatattgga tgagttgggt ccggcaggct 120

ccagggaaag ggctagaatg gattggagaa attaatccag atagcagtac gataaactat 180

acgccatctc tgaaggataa attcatcatc tccagagaca acgccaaaaa tacgctgtac 240

ctgcaaatga gcaaagtgag atctgaggac acagcccttt attactgtgc aagaccggga 300

tatggtaacc tctttgttta ctggggccaa gggactctgg tcactgtctc ctca 354

<210> 142
<211> 341
<212> DNA
<213> Mus sp.

<400> 142
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atgagctgca agtccagtca gagtctgtta aacagtggaa atccaaagaa ctacttggcc 120

tggtaccagc agaagccagg gcagcctcct aaactgttga tctacggggc atccactagg 180

ggatctgggg tccctgatcg cttcacaggc agtggatctg ggaccgattt cactcttacc 240

atcagcagtg tgcaggctga agacctggca gtttactact gtcagaatga tcatactttt 300

ccgtacacgt tcggaggggg gaccaagctg gaaataaaac g 341

<210> 143
<211> 348
<212> DNA
<213> Mus sp.

<400> 143
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tcctgtgcag cctcaggatt cgattttagt aaagactgga tgagttgggt ccggcaggct 120

ccagggaaag ggctagaatg gattggagaa attaatccag acagtagtac gataaactat 180

gcaccagctc taaaggataa attcatcatc tccagagaga acgccaaaaa tacgctgtac 240

ctgcaaatga acaaagtgag atctgaggac acagcccttt attactgtgc aagatggtca 300

actgggcttg actactgggg ccaaggcacc actctcacag tctcctca 348

<210> 144
<211> 321
<212> DNA
<213> Mus sp.

<400> 144
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atcaattgca gggcaagtca gggcctcagc aattatttaa actggtatca gcagaaacca 120

gatggaactg ttaaactcct gatctactac gcatcaatat tacactcagg agtcccatca 180

aggttcactg gcagtgggtc tggaacagat tattctctca ccattagcac cctggagcaa 240

gaggatattg gcacttactt ttgccaacag ggtaatacgc ttccgtggac gttcggtgga 300

ggcaccaaac tggaaatcaa c 321

<210> 145
<211> 348
<212> DNA
<213> Mus sp.

<400> 145
caggttcaac tgcagcagtc tggacctgag ctggtgaagc ctggggcctc agtgaagatt 60

tcctgcaagg cttctggcta tccattcagt acctcctgga tgaactgggt gaagcagagg 120

cctggaaagg gtcttgagtg gattggacgg atttatcttg gagatggaga tactaactac 180

aatgggaagt tcacgggcaa ggccacactg actgcagaca aatcctccag cacagtttac 240

atgcaactca gcagcctgac atctgaggac tctgcggtct acttctgtgc aagatggagg 300

ggtgactacg actactgggg ccaaggcacc actctcacag tctcctca 348

<210> 146
<211> 340
<212> DNA
<213> Mus sp.

<400> 146
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ctgagctgca agtccagtca gagcctttta tatagtagca ctcaaaacaa ctacttggcc 120

tggtaccagc agacaccagg gcagtctcct aaactgctga tttactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgaaggctga agacctggca gtttattact gtcagcaata ttatagctat 300

ccgtggacgt tcggtggagg caccaagctg gaaatcaaac 340

<210> 147
<211> 354
<212> DNA
<213> Mus sp.

<400> 147
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ctcacctgct ctgtccctga ctactccatc accagtgatt atcactggca ctggatcagg 120

cagtttccag gaaacaaact ggagtggatg ggatacataa gctcaagggg tagtactaac 180

tacaacccat ctctcaaaaa tcgaatctcc atcactcatg acacatctga gaatcagttc 240

ttcctgaaat tgacttctgt gactactgag gactcagcca catattattg tgcaggcttg 300

tcccagttag ctcttgacta ctggggccaa ggcaccactc tcacagtctc ctca 354

<210> 148
<211> 322
<212> DNA
<213> Mus sp.

<400> 148
gacatcaaga tgacccagtc tccatcttcc atgtatgcat ctctaggaga gagagtcact 60

atcacttgca aggcgagtca ggacatttat ccctatttaa actggttcca acaaaaacca 120

gggaaatctc ctaagaccct gatctatcgt acaaatagat tgctagatgg ggtcccatca 180

aggttcagtg gcagtggatc tggacaagat tattctctca ccatcagcag cctggactat 240

gaagatatgg gaatttatta ttgtctacag tatgatgagt ttccgctcac gttcggtgct 300

gggaccaagc tggagctgaa ac 322

<210> 149
<211> 360
<212> DNA
<213> Mus sp.

<400> 149
caagttactc taaaagagtc tggccctggg atattgaagc cctcacagac cctcagtctg 60

acttgttctt tctctgggtt ttcactgagc acttctaata tgggtgtagg ctggattcgt 120

cagccttcag ggaagggtct ggagtggctg gcacacattt ggtgggatga tgataagtat 180

tataacccat ccctgaagag ccagctcaca atctccaagg atacctccag aaaccaggtc 240

ttcctcaaga tcaccagtgt ggacactgaa gatactgcca cttactactg tgttcgaagt 300

aactatggtt acgcctggtt tgcttactgg ggccaaggga ctctggtcac tgtctctgca 360

<210> 150
<211> 334
<212> DNA
<213> Mus sp.

<400> 150
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atatcctgca gagccagtga aagtgttgat agctatggca aaagttttat gcactggtac 120

cagcagagac caggacagcc acccaaactc ctcatctatc gtgcatccaa cctagaatct 180

gggatccctg ccaggttcag tggcagtggg tctaggacag acttcaccct caccattaat 240

cctgtggagg ctgatgatgt tgcaacctat tactgtcaac aaagtaatga ggatccgtgg 300

acgttcggtg gaggcaccaa gctggaaatc aaac 334

<210> 151
<211> 357
<212> DNA
<213> Mus sp.

<400> 151
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tcctgcaagg gttccggcta cacattcact gattatgctg tgcactgggt gaagctgagt 120

catgcaaaga gtctggagtg gattggagtt attagtactt acaatgatta tacatacaac 180

aaccaggatt ttaagggcaa ggccacaatg actgtagaca aatcctccag cacagcctat 240

atggaacttg ccagattgac atctgaggat tctgccatct attactgtgc aagaggtaac 300

tcctacttct atgctttgga ctactggggt caaggaacct cagtcaccgt ctcctca 357

<210> 152

<211> 334
<212> DNA
<213> Mus sp.

<400> 152
gacattgcgc tgacccaatc tccagcttct ttggctgtgt ctctggggca gagggccacc 60

atttcctgca gagccagcga aagtgttgat aattctggca tttgttttgt gaactggttc 120

caacagaaac caggacagcc acccaaactc ctcatctatg ctgcatccaa ccaaggatcc 180

ggggtccctg ccaggtttag tggcagtggg tctgggacag acttcagcct caacatccat 240

cctatggaga aggatgatac tgcaatgtat ttctgtcagc aaagtaagga ggttccgtgg 300

acgttcggtg gaggcaccaa gctggaaatc aaac 334

<210> 153
<211> 363
<212> DNA
<213> Mus sp.

<400> 153
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tcctgcaagg cttctggata caccttcaca ttctatggta taagctgggt gaagcagaaa 120

actggacagg gccttgagtg gattggagag atttatcctg gaagttataa tgcttactac 180

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atgcagctca gcagcctgac atctgaggac tctgccgtct atttctgtgc cagagactat 300

ggtgacccgt attactatgc tatggactac tggggtcaag gaacctcagt caccgtctcc 360

tca 363

<210> 154
<211> 334
<212> DNA
<213> Mus sp.

<400> 154
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atctcatgca gggccagcca aagtgtcagt acatctacct ttaattatat gaactggtac 120

caacagaaac taggacagcc acccaaactc ctcatcaagt atgcatccaa cctagaatct 180

ggggtccctg ccaggttcag tggcagtggg tctgggacag acttcaccct caacatccat 240

cctgtggagg aggaggatat tgcaacatat tactgtcagc acagttggga gattccgtgg 300

acgttcggtg gaggcaccaa gctggaaatc aaac 334

<210> 155
<211> 354
<212> DNA

<213> Mus sp.

<400> 155
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tcctgtgcag cctcaggatt cgatttcagt agatactgga tgagttgggt ccggcaggct 120

ccagggaaag ggctagaatg gattggagaa attaatccag atagcagtac ggtaaactat 180

acgccatctc taaaggataa attcatcatc tccagagaca acgccaaaaa tacgctgtac 240

ctgcaaatga gtaaagtgag atctgaggac acagcccttt attactgtgc aagaccggga 300

tatggtaacc tctttgttta ctggggccaa gggactctgg tcactgtctc ctca 354

<210> 156
<211> 337
<212> DNA
<213> Mus sp.

<400> 156
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atctcctgca ggtctagtaa gagtctcctg catactaagg gcgacactta cttgtattgg 120

ttcctgcaga ggccaggcca gtctcctcag ctcctgatat atcggatgtc caaccttgcc 180

tcaggagtcc cagacaggtt cagtggcagt gggtcaggaa ctgttttcac actgagaatc 240

agtagagtgg aggctgagga tgtgggtgtt tattactgta tgcaacatct agaatatcca 300

ttcacgttcg gctcggggac aaagttggaa ataaaac 337

<210> 157
<211> 354
<212> DNA
<213> Mus sp.

<400> 157
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tcctgcaccg cttctggcct caatattaaa gactactata tgcactgggt gaacctgagg 120

cctgaacagg gcctggagtg gattggatgg attgatcctg agaatggtga tactgaatat 180

gccccggagt tccagggcaa ggccactatg actgcagaca catcttccaa cacagcctac 240

ctgcagctca gcagcctgac atctgaggac actgccgtct attactgtaa tgcttgcaac 300

tacggtagtg cctacggcta ctggggccaa ggcaccactc tcacagtctc ctca 354

<210> 158
<211> 322
<212> DNA
<213> Mus sp.

<400> 158
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atcagatgca taaccaacac tgatattgat gatgatatga actggtacca gcagaagcca 120

ggggaacctc ctaagctcct tatttcagaa ggcaatggtc ttcgtcctgg agtcccatcc 180

cgattctcca gcagtggcta tggcacagat tttgttttta caattgaaaa catgctctca 240

gaagatgttg cagattacta ctgtttgcaa agtgataact tgcctctcac gttcggctcg 300

gggacaaagt tggaaataaa ac 322

<210> 159
<211> 360
<212> DNA
<213> Mus sp.

<400> 159
gaggtgaagc ttctcgagtc tggaggtggc ctggtgcagc ctggaggatc cctgaaactc 60

tcctgtgcag cctcaggatt cgattttagt agatactgga tgagttgggt ccggcaggct 120

ccagggaaag gactagaatg gattggagat cttaatccag atagcagtgc gataaactat 180

acgccatctc taaaggataa attcatcatc tccagagaca acgccaaaaa tacgctgtac 240

ctgcaaatga gcaaagtgag atctgaggac acagcccttt attactgtac actcattact 300

acgttagtac cctatactat ggacttctgg ggtcaaggaa cctcagtcac cgtctcctca 360

<210> 160
<211> 340
<212> DNA
<213> Mus sp.

<400> 160
gacattgtga tgactcagtc tccatcctcc ctgactgtga cagcaggagt gaaggtcact 60

atgagctgca agtccagtca gagtctgtta aacagtggag atcaaaagaa ctgcttgact 120

tggtaccagc agaaaccagg gcagccacct aaactgttga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300

ccgctcacgt tcggtgctgg gaccaagctg gagctgaaac 340

<210> 161
<211> 360
<212> DNA
<213> Mus sp.

<400> 161
gaaatacatc tggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaagtc 60

tcctgtgcag cctctggatt cactttcagt aggtatgcca tgtcttgggt tcgccagact 120

ccggagaaga ggctggagtg ggtcgcaacc attagtggtg gtggtcgtta cacctactat 180

ccagaccttg tgaagggtcg attcaccatc tccagagaca ttgccaggac caccctgtac 240

ctgcaaatga gcagtctgag gtctgaggac acggccatgt attactgtgc aagaacagct 300

cgggcttcga attatgctat ggactactgg ggtcaaggaa cctcagtcac cgtctcctca 360

<210> 162
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 162
gacatccaga tgacccagtc tccatcttcc ctgtctgcat ctgtaggaga tagagtcact 60

atcacttgca aggcgagtca ggacatttat ccctatttaa actggttcca acaaaaacca 120

gggaaagctc ctaagaccct gatctatcgt acaaatagat tgctagatgg ggtcccatca 180

aggttcagtg gcagtggatc tggaacagat tttactttca ccatcagcag cctgcaacct 240

gaagatattg caacttatta ttgtctacag tatgatgagt ttccgctcac gttcggtgct 300

gggaccaagc tggaaatcaa ac 322

<210> 163
<211> 361
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 163
cagatcacct tgaaggagtc tggtcctacg ctggtgaaac ccacacagac cctcacgctg 60

acctgcacct tctctgggtt ctcactcagc actagtaaca tgggtgtggg ctggatccgt 120

cagcccccag gaaaggccct ggagtggctt gcacacattt ggtgggatga tgataagtac 180

tacagcccat ctctgaagag caggctcacc atcaccaagg acacctccaa aaaccaggtg 240

gtccttacaa tgaccaacat ggaccctgtg gacacagcca catattactg tgttcgaagt 300

aactatggtt acgcctggtt tgcttactgg ggccaaggga ctctggtcac tgtctcttca 360

g 361

<210> 164
<211> 334
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 164
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtga gagtgttgac agctatggca aaagttttat gcactggtac 120

caacagaaac ctggccaggc tcccaggctc ctcatctata gggcatccaa cctggaatct 180

ggcatcccag ccaggttcag tggcagtggg tctgggacag acttcactct caccatcagc 240

agcctagagc ctgaagattt tgcagtttat tactgtcagc agagtaatga ggatccgtgg 300

acgttcggtg gaggcaccaa gctggaaatc aaac 334

<210> 165
<211> 358
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 165
caggtccagc ttgtgcagtc tgggcctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggata caccttcact gactatgctg tgcattgggt gcgccaggcc 120

cccggaaaaa ggcttgagtg gattggagtg atcagcactt acaatgatta cacatacaat 180

aaccaggact tcaagggcag agtcaccatg accagggaca tccgcgcgag cacagcctac 240

atggagctga gcagactgag atctgaagac acggctgtgt attactgtgc gagaggtaac 300

tcctacttct atgctttgga ctactggggt caaggaacct cagtcaccgt ctcctcag 358

<210> 166
<211> 337
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 166
gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 60

atctcctgca ggtctagtaa gagcctcctg catactaaag gagacaccta tttgtattgg 120

ttcctgcaga agccagggca gtctccacag ctcctgatct atcggatgtc taatcgggcc 180

tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240

agcagagtgg aggctgagga tgttggggtt tattactgta tgcaacatct agaatatcca 300

ttcacgttcg gccaggggac aaagttggaa atcaaac 337

<210> 167
<211> 355
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 167
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcaaa gactactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcgaccctg aaaatggtga cacagaatac 180

gcaccggagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtaa tgcttgcaac 300

tacggtagtg cctacggcta ctggggccaa ggcaccactc tcaccgtctc ctcag 355

<210> 168
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 168
gaaacgacac tcacgcagtc tccagcattc atgtcagcga ctccaggaga caaagtcaac 60

atctcctgca taaccaacac agacattgat gatgatatga actggtacca acagaaacca 120

ggagaagctg ctattctcct tatttcagaa ggtaatggtc tccgtcctgg aatcccacct 180

cgattcagtg gcagcgggta tggaacagat tttaccctca caattaataa catagaatct 240

gaggatgctg catattactt ctgtctacaa agtgataact tgcctctcac gttcggctcg 300

gggacaaagt tggaaataaa ac 322

<210> 169
<211> 361
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 169
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cgactttagt agatattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg gatcggcgac ctaaacccag attcaagtgc gataaactat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtac actcattact 300

acgttagtac cctatactat ggacttctgg ggtcaaggaa cctcagtcac cgtctcctca 360

g 361