SEQUENCE LISTING

<110> PALLEON PHARMACEUTICALS INC.

<120> ANTI-PD-L1 ANTIBODIES AND FUSION PROTEINS THEREOF

<130> PAL-024WO

<140> PCT/US2022/011504
<141> 2022-01-06

<150> 63/134,412
<151> 2021-01-06

<160> 259

<170> PatentIn version 3.5

<210> 1
<211> 380
<212> PRT
<213> Homo sapiens

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

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Cys Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

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<211> 385
<212> PRT
<213> Mus musculus

<400> 2
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1 5 10 15

Thr Leu Phe Arg Thr Gly Val His Ala Tyr Arg Ile Pro Ala Leu Leu
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Tyr Leu Lys Lys Gln Lys Thr Leu Leu Ala Phe Ala Glu Lys Arg Ala
35 40 45

Ser Lys Thr Asp Glu His Ala Glu Leu Ile Val Leu Arg Arg Gly Ser
50 55 60

Tyr Asn Glu Ala Thr Asn Arg Val Lys Trp Gln Pro Glu Glu Val Val
65 70 75 80

Thr Gln Ala Gln Leu Glu Gly His Arg Ser Met Asn Pro Cys Pro Leu
85 90 95

Tyr Asp Lys Gln Thr Lys Thr Leu Phe Leu Phe Phe Ile Ala Val Pro
100 105 110

Gly Arg Val Ser Glu His His Gln Leu His Thr Lys Val Asn Val Thr
115 120 125

Arg Leu Cys Cys Val Ser Ser Thr Asp His Gly Arg Thr Trp Ser Pro
130 135 140

Ile Gln Asp Leu Thr Glu Thr Thr Ile Gly Ser Thr His Gln Glu Trp
145 150 155 160

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

Ala Gly Ser Leu Leu Val Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro
180 185 190

Ala Gln Lys Pro Thr Pro Phe Ala Phe Cys Phe Ile Ser Leu Asp His
195 200 205

Gly His Thr Trp Lys Leu Gly Asn Phe Val Ala Glu Asn Ser Leu Glu
210 215 220

Cys Gln Val Ala Glu Val Gly Thr Gly Ala Gln Arg Met Val Tyr Leu
225 230 235 240

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

Asp Gly Leu Asp Phe Gln Asp Asn Arg Val Val Ser Lys Leu Val Glu
260 265 270

Pro Pro His Gly Cys His Gly Ser Val Val Ala Phe His Asn Pro Ile
275 280 285

Ser Lys Pro His Ala Leu Asp Thr Trp Leu Leu Tyr Thr His Pro Thr
290 295 300

Asp Ser Arg Asn Arg Thr Asn Leu Gly Val Tyr Leu Asn Gln Met Pro
305 310 315 320

Leu Asp Pro Thr Ala Trp Ser Glu Pro Thr Leu Leu Ala Met Gly Ile
325 330 335

Cys Ala Tyr Ser Asp Leu Gln Asn Met Gly Gln Gly Pro Asp Gly Ser
340 345 350

Pro Gln Phe Gly Cys Leu Tyr Glu Ser Gly Asn Tyr Glu Glu Ile Ile
355 360 365

Phe Leu Ile Phe Thr Leu Lys Gln Ala Phe Pro Thr Val Phe Asp Ala
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Gln
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<210> 3
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<212> PRT
<213> Mus musculus

<400> 4
Met Glu Asp Leu Arg Pro
1 5

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<211> 227
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
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Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20 25 30

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

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

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

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
130 135 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys
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<210> 6
<211> 1143
<212> DNA
<213> Salmonella typhimurium

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tgcaccacca gcaagggcac cattgtggtg ttcgccgacg ccagacacaa caccgccagc 180

gatcagagct tcatcgatac cgctgccgcc agatctaccg atggcggcaa gacctggaac 240

aagaagatcg ccatctacaa cgaccgcgtg aacagcaagc tgagcagagt gatggaccct 300

acctgcatcg tggccaacat ccagggcaga gaaaccatcc tggtcatggt cggaaagtgg 360

aacaacaacg ataagacctg gggcgcctac agagacaagg cccctgatac cgattgggac 420

ctcgtgctgt acaagagcac cgatgacggc gtgaccttca gcaaggtgga aacaaacatc 480

cacgacatcg tgaccaagaa cggcaccatc tctgccatgc tcggcggcgt tggatctggc 540

ctgcaactga atgatggcaa gctggtgttc cccgtgcaga tggtccgaac aaagaatatc 600

accaccgtgc tgaataccag cttcatctac agcaccgacg gcatcacatg gtccctgcct 660

agcggctact gtgaaggctt tggcagcgag aacaacatca tcgagttcaa cgccagcctg 720

gtcaacaaca tccggaacag cggcctgcgg agaagcttcg agacaaagga cttcggaaag 780

acgtggaccg agtttcctcc aatggacaag aaggtggaca accggaacca cggcgtgcag 840

ggcagcacaa tcacaatccc tagcggcaac aaactggtgg ccgctcactc tagcgcccag 900

aacaagaaca acgactacac cagaagcgac atcagcctgt acgcccacaa cctgtacagc 960

ggcgaagtga agctgatcga cgacttctac cccaaagtgg gcaatgccag cggagccggc 1020

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aac 1143

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<211> 364
<212> PRT
<213> Homo sapiens

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Pro Leu Ile Thr Ala Thr Pro Arg Gly Thr Leu Leu Ala Phe Ala Glu

35 40 45

Ala Arg Lys Met Ser Ser Ser Asp Glu Gly Ala Lys Phe Ile Ala Leu
50 55 60

Arg Arg Ser Met Asp Gln Gly Ser Thr Trp Ser Pro Thr Ala Phe Ile
65 70 75 80

Val Asn Asp Gly Asp Val Pro Asp Gly Leu Asn Leu Gly Ala Val Val
85 90 95

Ser Asp Val Glu Thr Gly Val Val Phe Leu Phe Tyr Ser Leu Cys Ala
100 105 110

His Lys Ala Gly Cys Gln Val Ala Ser Thr Met Leu Val Trp Ser Lys
115 120 125

Asp Asp Gly Val Ser Trp Ser Thr Pro Arg Asn Leu Ser Leu Asp Ile
130 135 140

Gly Thr Glu Val Phe Ala Pro Gly Pro Gly Ser Gly Ile Gln Lys Gln
145 150 155 160

Arg Glu Pro Arg Lys Gly Arg Leu Ile Val Cys Gly His Gly Thr Leu
165 170 175

Glu Arg Asp Gly Val Phe Cys Leu Leu Ser Asp Asp His Gly Ala Ser
180 185 190

Trp Arg Tyr Gly Ser Gly Val Ser Gly Ile Pro Tyr Gly Gln Pro Lys
195 200 205

Gln Glu Asn Asp Phe Asn Pro Asp Glu Cys Gln Pro Tyr Glu Leu Pro
210 215 220

Asp Gly Ser Val Val Ile Asn Ala Arg Asn Gln Asn Asn Tyr His Cys
225 230 235 240

His Cys Arg Ile Val Leu Arg Ser Tyr Asp Ala Cys Asp Thr Leu Arg
245 250 255

Pro Arg Asp Val Thr Phe Asp Pro Glu Leu Val Asp Pro Val Val Ala
260 265 270

Ala Gly Ala Val Val Thr Ser Ser Gly Ile Val Phe Phe Ser Asn Pro
275 280 285

Ala His Pro Glu Phe Arg Val Asn Leu Thr Leu Arg Trp Ser Phe Ser
290 295 300

Asn Gly Thr Ser Trp Arg Lys Glu Thr Val Gln Leu Trp Pro Gly Pro
305 310 315 320

Ser Gly Tyr Ser Ser Leu Ala Thr Leu Glu Gly Ser Met Asp Gly Glu
325 330 335

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

Tyr Thr Glu Ser Ile Ser Val Ala Lys Ile Ser Val
355 360

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<212> PRT
<213> Homo sapiens

<400> 8
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Pro Pro Thr His Thr Phe Leu Ala Phe Ala Glu Lys Arg Ser Thr Arg
35 40 45

Arg Asp Glu Asp Ala Leu His Leu Val Leu Arg Arg Gly Leu Arg Ile
50 55 60

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

Leu Pro Gly His Arg Thr Met Asn Pro Cys Pro Val Trp Glu Gln Lys
85 90 95

Ser Gly Cys Val Phe Leu Phe Phe Ile Cys Val Arg Gly His Val Thr
100 105 110

Glu Arg Gln Gln Ile Val Ser Gly Arg Asn Ala Ala Arg Leu Cys Phe
115 120 125

Ile Tyr Ser Gln Asp Ala Gly Cys Ser Trp Ser Glu Val Arg Asp Leu
130 135 140

Thr Glu Glu Val Ile Gly Ser Glu Leu Lys His Trp Ala Thr Phe Ala
145 150 155 160

Val Gly Pro Gly His Gly Ile Gln Leu Gln Ser Gly Arg Leu Val Ile
165 170 175

Pro Ala Tyr Thr Tyr Tyr Ile Pro Ser Trp Phe Phe Cys Phe Gln Leu
180 185 190

Pro Cys Lys Thr Arg Pro His Ser Leu Met Ile Tyr Ser Asp Asp Leu
195 200 205

Gly Val Thr Trp His His Gly Arg Leu Ile Arg Pro Met Val Thr Val
210 215 220

Glu Cys Glu Val Ala Glu Val Thr Gly Arg Ala Gly His Pro Val Leu
225 230 235 240

Tyr Cys Ser Ala Arg Thr Pro Asn Arg Cys Arg Ala Glu Ala Leu Ser
245 250 255

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

Cys Glu Pro Pro His Gly Cys Gln Gly Ser Val Val Ser Phe Arg Pro
275 280 285

Leu Glu Ile Pro His Arg Cys Gln Asp Ser Ser Ser Lys Asp Ala Pro

290 295 300

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

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

Arg Lys Gln Arg Val Asp Leu Gly Ile Tyr Leu Asn Gln Thr Pro Leu
340 345 350

Glu Ala Ala Cys Trp Ser Arg Pro Trp Ile Leu His Cys Gly Pro Cys
355 360 365

Gly Tyr Ser Asp Leu Ala Ala Leu Glu Glu Glu Gly Leu Phe Gly Cys
370 375 380

Leu Phe Glu Cys Gly Thr Lys Gln Glu Cys Glu Gln Ile Ala Phe Arg
385 390 395 400

Leu Phe Thr His Arg Glu Ile Leu Ser His Leu Gln Gly Asp Cys Thr
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Ser Pro Gly Arg Asn Pro Ser Gln Phe Lys Ser Asn
420 425

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<211> 461
<212> PRT
<213> Homo sapiens

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Val Met Glu Glu Val Thr Thr Cys Ser Phe Asn Ser Pro Leu Phe Arg
35 40 45

Gln Glu Asp Asp Arg Gly Ile Thr Tyr Arg Ile Pro Ala Leu Leu Tyr

50 55 60

Ile Pro Pro Thr His Thr Phe Leu Ala Phe Ala Glu Lys Arg Ser Thr
65 70 75 80

Arg Arg Asp Glu Asp Ala Leu His Leu Val Leu Arg Arg Gly Leu Arg
85 90 95

Ile Gly Gln Leu Val Gln Trp Gly Pro Leu Lys Pro Leu Met Glu Ala
100 105 110

Thr Leu Pro Gly His Arg Thr Met Asn Pro Cys Pro Val Trp Glu Gln
115 120 125

Lys Ser Gly Cys Val Phe Leu Phe Phe Ile Cys Val Arg Gly His Val
130 135 140

Thr Glu Arg Gln Gln Ile Val Ser Gly Arg Asn Ala Ala Arg Leu Cys
145 150 155 160

Phe Ile Tyr Ser Gln Asp Ala Gly Cys Ser Trp Ser Glu Val Arg Asp
165 170 175

Leu Thr Glu Glu Val Ile Gly Ser Glu Leu Lys His Trp Ala Thr Phe
180 185 190

Ala Val Gly Pro Gly His Gly Ile Gln Leu Gln Ser Gly Arg Leu Val
195 200 205

Ile Pro Ala Tyr Thr Tyr Tyr Ile Pro Ser Trp Phe Phe Cys Phe Gln
210 215 220

Leu Pro Cys Lys Thr Arg Pro His Ser Leu Met Ile Tyr Ser Asp Asp
225 230 235 240

Leu Gly Val Thr Trp His His Gly Arg Leu Ile Arg Pro Met Val Thr
245 250 255

Val Glu Cys Glu Val Ala Glu Val Thr Gly Arg Ala Gly His Pro Val
260 265 270

Leu Tyr Cys Ser Ala Arg Thr Pro Asn Arg Cys Arg Ala Glu Ala Leu
275 280 285

Ser Thr Asp His Gly Glu Gly Phe Gln Arg Leu Ala Leu Ser Arg Gln
290 295 300

Leu Cys Glu Pro Pro His Gly Cys Gln Gly Ser Val Val Ser Phe Arg
305 310 315 320

Pro Leu Glu Ile Pro His Arg Cys Gln Asp Ser Ser Ser Lys Asp Ala
325 330 335

Pro Thr Ile Gln Gln Ser Ser Pro Gly Ser Ser Leu Arg Leu Glu Glu
340 345 350

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

Ser Arg Lys Gln Arg Val Asp Leu Gly Ile Tyr Leu Asn Gln Thr Pro
370 375 380

Leu Glu Ala Ala Cys Trp Ser Arg Pro Trp Ile Leu His Cys Gly Pro
385 390 395 400

Cys Gly Tyr Ser Asp Leu Ala Ala Leu Glu Glu Glu Gly Leu Phe Gly
405 410 415

Cys Leu Phe Glu Cys Gly Thr Lys Gln Glu Cys Glu Gln Ile Ala Phe
420 425 430

Arg Leu Phe Thr His Arg Glu Ile Leu Ser His Leu Gln Gly Asp Cys
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Thr Ser Pro Gly Arg Asn Pro Ser Gln Phe Lys Ser Asn
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<211> 484
<212> PRT
<213> Homo sapiens

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Arg Thr Gly Leu Thr Tyr Arg Val Pro Ser Leu Leu Pro Val Pro Pro
20 25 30

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

Ser His Ala His Arg Leu Val Leu Arg Arg Gly Thr Leu Ala Gly Gly
50 55 60

Ser Val Arg Trp Gly Ala Leu His Val Leu Gly Thr Ala Ala Leu Ala
65 70 75 80

Glu His Arg Ser Met Asn Pro Cys Pro Val His Asp Ala Gly Thr Gly
85 90 95

Thr Val Phe Leu Phe Phe Ile Ala Val Leu Gly His Thr Pro Glu Ala
100 105 110

Val Gln Ile Ala Thr Gly Arg Asn Ala Ala Arg Leu Cys Cys Val Ala
115 120 125

Ser Arg Asp Ala Gly Leu Ser Trp Gly Ser Ala Arg Asp Leu Thr Glu
130 135 140

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

Pro Gly His Gly Val Gln Leu Pro Ser Gly Arg Leu Leu Val Pro Ala
165 170 175

Tyr Thr Tyr Arg Val Asp Arg Arg Glu Cys Phe Gly Lys Ile Cys Arg
180 185 190

Thr Ser Pro His Ser Phe Ala Phe Tyr Ser Asp Asp His Gly Arg Thr
195 200 205

Trp Arg Cys Gly Gly Leu Val Pro Asn Leu Arg Ser Gly Glu Cys Gln

210 215 220

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

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

Gly Thr Ser Phe Leu Pro Ala Glu Arg Val Ala Ser Leu Pro Glu Thr
260 265 270

Ala Trp Gly Cys Gln Gly Ser Ile Val Gly Phe Pro Ala Pro Ala Pro
275 280 285

Asn Arg Pro Arg Asp Asp Ser Trp Ser Val Gly Pro Gly Ser Pro Leu
290 295 300

Gln Pro Pro Leu Leu Gly Pro Gly Val His Glu Pro Pro Glu Glu Ala
305 310 315 320

Ala Val Asp Pro Arg Gly Gly Gln Val Pro Gly Gly Pro Phe Ser Arg
325 330 335

Leu Gln Pro Arg Gly Asp Gly Pro Arg Gln Pro Gly Pro Arg Pro Gly
340 345 350

Val Ser Gly Asp Val Gly Ser Trp Thr Leu Ala Leu Pro Met Pro Phe
355 360 365

Ala Ala Pro Pro Gln Ser Pro Thr Trp Leu Leu Tyr Ser His Pro Val
370 375 380

Gly Arg Arg Ala Arg Leu His Met Gly Ile Arg Leu Ser Gln Ser Pro
385 390 395 400

Leu Asp Pro Arg Ser Trp Thr Glu Pro Trp Val Ile Tyr Glu Gly Pro
405 410 415

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

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

Glu Ile Ser Phe Cys Thr Phe Ser Leu Arg Glu Val Leu Glu Asn Val
450 455 460

Pro Ala Ser Pro Lys Pro Pro Asn Leu Gly Asp Lys Pro Arg Gly Cys
465 470 475 480

Cys Trp Pro Ser

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<211> 496
<212> PRT
<213> Homo sapiens

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1 5 10 15

Arg Thr Pro Ser Arg Thr Val Leu Phe Glu Arg Glu Arg Thr Gly Leu
20 25 30

Thr Tyr Arg Val Pro Ser Leu Leu Pro Val Pro Pro Gly Pro Thr Leu
35 40 45

Leu Ala Phe Val Glu Gln Arg Leu Ser Pro Asp Asp Ser His Ala His
50 55 60

Arg Leu Val Leu Arg Arg Gly Thr Leu Ala Gly Gly Ser Val Arg Trp
65 70 75 80

Gly Ala Leu His Val Leu Gly Thr Ala Ala Leu Ala Glu His Arg Ser
85 90 95

Met Asn Pro Cys Pro Val His Asp Ala Gly Thr Gly Thr Val Phe Leu
100 105 110

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

Thr Gly Arg Asn Ala Ala Arg Leu Cys Cys Val Ala Ser Arg Asp Ala
130 135 140

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

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

Val Gln Leu Pro Ser Gly Arg Leu Leu Val Pro Ala Tyr Thr Tyr Arg
180 185 190

Val Asp Arg Arg Glu Cys Phe Gly Lys Ile Cys Arg Thr Ser Pro His
195 200 205

Ser Phe Ala Phe Tyr Ser Asp Asp His Gly Arg Thr Trp Arg Cys Gly
210 215 220

Gly Leu Val Pro Asn Leu Arg Ser Gly Glu Cys Gln Leu Ala Ala Val
225 230 235 240

Asp Gly Gly Gln Ala Gly Ser Phe Leu Tyr Cys Asn Ala Arg Ser Pro
245 250 255

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

Leu Pro Ala Glu Arg Val Ala Ser Leu Pro Glu Thr Ala Trp Gly Cys
275 280 285

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

Asp Asp Ser Trp Ser Val Gly Pro Gly Ser Pro Leu Gln Pro Pro Leu
305 310 315 320

Leu Gly Pro Gly Val His Glu Pro Pro Glu Glu Ala Ala Val Asp Pro
325 330 335

Arg Gly Gly Gln Val Pro Gly Gly Pro Phe Ser Arg Leu Gln Pro Arg

340 345 350

Gly Asp Gly Pro Arg Gln Pro Gly Pro Arg Pro Gly Val Ser Gly Asp
355 360 365

Val Gly Ser Trp Thr Leu Ala Leu Pro Met Pro Phe Ala Ala Pro Pro
370 375 380

Gln Ser Pro Thr Trp Leu Leu Tyr Ser His Pro Val Gly Arg Arg Ala
385 390 395 400

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

Ser Trp Thr Glu Pro Trp Val Ile Tyr Glu Gly Pro Ser Gly Tyr Ser
420 425 430

Asp Leu Ala Ser Ile Gly Pro Ala Pro Glu Gly Gly Leu Val Phe Ala
435 440 445

Cys Leu Tyr Glu Ser Gly Ala Arg Thr Ser Tyr Asp Glu Ile Ser Phe
450 455 460

Cys Thr Phe Ser Leu Arg Glu Val Leu Glu Asn Val Pro Ala Ser Pro
465 470 475 480

Lys Pro Pro Asn Leu Gly Asp Lys Pro Arg Gly Cys Cys Trp Pro Ser
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<213> Homo sapiens

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

<400> 13
Ala Ser Leu Pro
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<210> 14
<211> 8
<212> PRT
<213> Salmonella typhimurium

<400> 14
Thr Val Glu Lys Ser Val Val Phe
1 5

<210> 15
<211> 12
<212> PRT
<213> Homo sapiens

<400> 15
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1 5 10

<210> 16
<211> 8
<212> PRT
<213> Homo sapiens

<400> 16
Ser Met Asp Gln Gly Ser Thr Trp
1 5

<210> 17
<211> 8
<212> PRT
<213> Salmonella typhimurium

<400> 17
Ser Thr Asp Gly Gly Lys Thr Trp
1 5

<210> 18
<211> 8
<212> PRT
<213> Homo sapiens

<400> 18
Pro Arg Pro Pro Ala Pro Glu Ala
1 5

<210> 19
<211> 8
<212> PRT
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<400> 19
Gln Thr Pro Leu Glu Ala Ala Cys
1 5

<210> 20
<211> 9
<212> PRT
<213> Homo sapiens

<400> 20
Asn Pro Arg Pro Pro Ala Pro Glu Ala
1 5

<210> 21
<211> 7
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Recombinant mutant human sialidase substitution sequence

<400> 21
Ser Gln Asn Asp Gly Glu Ser
1 5

<210> 22
<211> 7
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Recombinant mutant human sialidase substitution sequence

<400> 22
Leu Ser His Ser Leu Ser Thr
1 5

<210> 23
<211> 1092
<212> DNA
<213> Homo sapiens

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ggcaccctgc tggcctttgc cgaggccaga aagatgagca gctctgacga gggcgccaag 180

tttattgccc tgaggcggtc tatggaccag ggctctacat ggtcccctac cgccttcatc 240

gtgaacgatg gcgacgtgcc cgatggcctg aatctgggag ctgtggtgtc cgatgtggaa 300

accggcgtgg tgttcctgtt ctacagcctg tgtgcccaca aggccggttg tcaggtggcc 360

agcacaatgc tcgtgtggtc caaggacgac ggcgtgtcct ggtctacccc tagaaacctg 420

agcctggaca tcggcaccga agtgtttgct ccaggacctg gctctggcat ccagaagcag 480

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ggaatccctt acggccagcc taagcaagag aacgatttca accccgacga gtgccagcct 660

tacgagctgc ctgatggcag cgtcgtgatc aacgcccgga accagaacaa ctaccactgc 720

cactgccgga tcgtgctgag aagctacgac gcctgcgata ccctgcggcc tagagatgtg 780

accttcgatc ctgagctggt ggaccctgtt gttgccgctg gtgccgtcgt gacatctagc 840

ggcatcgtgt tcttcagcaa ccctgctcac cccgagttca gagtgaatct gaccctgcgg 900

tggtccttca gcaatggcac aagctggcgg aaagaaaccg tgcagctttg gcctggacct 960

agcggctact cttctctggc tacactggaa ggcagcatgg acggcgaaga acaggcccct 1020

cagctgtacg tgctgtacga gaagggcaga aaccactaca ccgagagcat cagcgtggcc 1080

aagatcagcg tt 1092

<210> 24
<211> 1140
<212> DNA
<213> Homo sapiens

<400> 24
atggccagcc tgcctgtgct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gcccctacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgccc agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgtcaagt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccat ccagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agagccagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccacag ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agctgtgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

<210> 25
<211> 1284
<212> DNA
<213> Homo sapiens

<400> 25
atggaggaag tgaccacctg tagcttcaac agccctctgt tccggcaaga ggacgaccgg 60

ggcatcacct acagaatccc tgctctgctg tacatccctc ctacacacac ctttctggcc 120

ttcgccgaga agcggagcac cagacgagat gaagatgccc tgcacctggt gctgagaaga 180

ggcctgagaa tcggacagct ggtgcagtgg ggacctctga agcctctgat ggaagccaca 240

ctgcccggcc acagaaccat gaatccttgt cctgtgtggg agcagaaaag cggctgcgtg 300

ttcctgttct tcatctgcgt gcggggccac gtgaccgaga gacagcaaat cgtgtccggc 360

agaaacgccg ccagactgtg cttcatctac agccaggatg ccggctgctc ttggagcgaa 420

gttcgggatc tgaccgaaga agtgatcggc agcgagctga agcactgggc cacatttgct 480

gttggccctg gccacggaat ccagctgcaa tctggcagac tggtcatccc cgcctacacc 540

tactatatcc ccagctggtt cttctgcttc caactgcctt gcaagacccg gcctcacagc 600

ctgatgatct acagcgacga tctgggcgtg acatggcacc acggcagact gatcagaccc 660

atggtcaccg tggaatgcga ggtggccgaa gtgacaggca gagctggaca ccctgtgctg 720

tactgctctg ccagaacacc caaccggtgt agagccgagg ctctgtctac agatcacggc 780

gagggctttc agagactggc cctctctaga cagctgtgcg aacctcctca tggctgtcag 840

ggcagcgtgg tgtccttcag acctctggaa atccctcacc ggtgccagga cagcagctct 900

aaggatgccc ctaccatcca gcagtctagc cctggcagca gcctgagact ggaagaggaa 960

gccggaacac ctagcgagag ctggctgctg tactctcacc ccaccagcag aaagcagaga 1020

gtggacctgg gcatctacct gaatcagacc cctctggaag ccgcctgttg gagcagacct 1080

tggattctgc actgtggccc ttgcggctac tctgatctgg ccgctctgga agaagagggc 1140

ctgttcggct gcctgtttga gtgcggcaca aagcaagagt gcgagcagat cgccttccgg 1200

ctgttcaccc acagagagat cctgagccat ctgcagggcg actgcacaag cccaggcaga 1260

aatcccagcc agttcaagag caac 1284

<210> 26
<211> 1452
<212> DNA
<213> Homo sapiens

<400> 26
atgggcgtgc ccagaacacc cagcagaacc gtgctgttcg agagagagag gaccggcctg 60

acctacagag tgccttctct gctgcctgtg cctcctggac ctacactgct ggccttcgtg 120

gaacagagac tgagccccga tgattctcac gcccacagac tggtgctgag aagaggaaca 180

ctggctggcg gctctgttag atggggagca ctgcatgtgc tgggcacagc tgctcttgcc 240

gagcacagat ccatgaatcc ctgtcctgtg cacgacgccg gaaccggcac agtgtttctg 300

ttctttatcg ccgtgctggg ccacacacct gaggccgttc aaattgccac cggcagaaat 360

gccgccagac tgtgttgtgt ggcctccaga gatgccggcc tgtcttgggg atctgccaga 420

gatctgaccg aggaagccat tggcggagcc gttcaggatt gggccacatt tgctgttgga 480

cctggacacg gcgtgcagct gccaagtggt agactgctgg tgcctgccta cacatacaga 540

gtggatcgga gagagtgctt cggaaagatc tgccggacaa gccctcacag cttcgccttc 600

tactccgacg atcacggccg gacttggaga tgtggtggcc tggtgcctaa tctgagaagc 660

ggcgaatgtc aactggccgc cgttgatggt ggacaggctg gcagcttcct gtactgcaac 720

gccagatctc ctctgggctc tagagtgcag gccctgtcta ccgatgaggg caccagtttt 780

ctgcccgccg aaagagttgc ctctctgcct gaaacagcct ggggctgtca gggctctatc 840

gtgggatttc ctgctcctgc tccaaacaga ccccgggacg attcttggag tgtcggccct 900

ggatctccac tgcagcctcc attgcttgga ccaggcgttc acgagccacc tgaagaggct 960

gccgttgatc ctagaggcgg acaagttcct ggcggccctt ttagcagact gcagccaaga 1020

ggcgacggcc ctagacaacc tggaccaaga cctggcgtca gcggagatgt tggctcttgg 1080

acactggccc tgcctatgcc ttttgccgct cctcctcagt ctcctacctg gctgctgtac 1140

tctcaccctg ttggcagacg ggccagactg cacatgggca tcagactgtc tcagagccct 1200

ctggacccca gaagctggac agagccttgg gtcatctatg agggccctag cggctacagc 1260

gatctggcct ctattggccc agctcctgaa ggcggactgg tgttcgcttg tctgtatgag 1320

agcggcgcca gaaccagcta cgacgagatc agcttctgca ccttcagcct gcgcgaggtg 1380

ctggaaaatg tgcccgcctc tcctaagcct cctaacctgg gcgataagcc tagaggctgt 1440

tgctggccat ct 1452

<210> 27
<211> 47
<212> PRT
<213> Homo sapiens

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

Pro Arg Ile Leu Gly Phe Trp Gly Gly Cys Arg Val Trp Val Phe Ala
20 25 30

Ala Ile Phe Leu Leu Leu Ser Leu Ala Ala Ser Trp Ser Lys Ala
35 40 45

<210> 28
<211> 22
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
N-terminal signal peptide sequence

<400> 28
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Pro Gly Ala Arg Cys
20

<210> 29
<211> 4
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
C-terminal lysosomal signal motif sequence

<400> 29
Tyr Gly Thr Leu
1

<210> 30
<211> 382
<212> PRT
<213> Salmonella typhimurium

<400> 30
Met Thr Val Glu Lys Ser Val Val Phe Lys Ala Glu Gly Glu His Phe
1 5 10 15

Thr Asp Gln Lys Gly Asn Thr Ile Val Gly Ser Gly Ser Gly Gly Thr
20 25 30

Thr Lys Tyr Phe Arg Ile Pro Ala Met Cys Thr Thr Ser Lys Gly Thr
35 40 45

Ile Val Val Phe Ala Asp Ala Arg His Asn Thr Ala Ser Asp Gln Ser
50 55 60

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

Asn Lys Lys Ile Ala Ile Tyr Asn Asp Arg Val Asn Ser Lys Leu Ser

85 90 95

Arg Val Met Asp Pro Thr Cys Ile Val Ala Asn Ile Gln Gly Arg Glu
100 105 110

Thr Ile Leu Val Met Val Gly Lys Trp Asn Asn Asn Asp Lys Thr Trp
115 120 125

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

Tyr Lys Ser Thr Asp Asp Gly Val Thr Phe Ser Lys Val Glu Thr Asn
145 150 155 160

Ile His Asp Ile Val Thr Lys Asn Gly Thr Ile Ser Ala Met Leu Gly
165 170 175

Gly Val Gly Ser Gly Leu Gln Leu Asn Asp Gly Lys Leu Val Phe Pro
180 185 190

Val Gln Met Val Arg Thr Lys Asn Ile Thr Thr Val Leu Asn Thr Ser
195 200 205

Phe Ile Tyr Ser Thr Asp Gly Ile Thr Trp Ser Leu Pro Ser Gly Tyr
210 215 220

Cys Glu Gly Phe Gly Ser Glu Asn Asn Ile Ile Glu Phe Asn Ala Ser
225 230 235 240

Leu Val Asn Asn Ile Arg Asn Ser Gly Leu Arg Arg Ser Phe Glu Thr
245 250 255

Lys Asp Phe Gly Lys Thr Trp Thr Glu Phe Pro Pro Met Asp Lys Lys
260 265 270

Val Asp Asn Arg Asn His Gly Val Gln Gly Ser Thr Ile Thr Ile Pro
275 280 285

Ser Gly Asn Lys Leu Val Ala Ala His Ser Ser Ala Gln Asn Lys Asn
290 295 300

Asn Asp Tyr Thr Arg Ser Asp Ile Ser Leu Tyr Ala His Asn Leu Tyr
305 310 315 320

Ser Gly Glu Val Lys Leu Ile Asp Asp Phe Tyr Pro Lys Val Gly Asn
325 330 335

Ala Ser Gly Ala Gly Tyr Ser Cys Leu Ser Tyr Arg Lys Asn Val Asp
340 345 350

Lys Glu Thr Leu Tyr Val Val Tyr Glu Ala Asn Gly Ser Ile Glu Phe
355 360 365

Gln Asp Leu Ser Arg His Leu Pro Val Ile Lys Ser Tyr Asn
370 375 380

<210> 31
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 31
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 32
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 32
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

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

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

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

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
130 135 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys
225

<210> 33

<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 33
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
130 135 140

Lys Asn Gln Val Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 34
<211> 1383
<212> DNA
<213> Homo sapiens

<400> 34
atgagacctg cggacctgcc cccgcgcccc atggaagaat ccccggcgtc cagctctgcc 60

ccgacagaga cggaggagcc ggggtccagt gcagaggtca tggaagaagt gacaacatgc 120

tccttcaaca gccctctgtt ccggcaggaa gatgacagag ggattaccta ccggatccca 180

gccctgctct acataccccc cacccacacc ttcctggcct ttgcagagaa gcgttctacg 240

aggagagatg aggatgctct ccacctggtg ctgaggcgag ggttgaggat tgggcagttg 300

gtacagtggg ggcccctgaa gccactgatg gaagccacac taccggggca tcggaccatg 360

aacccctgtc ctgtatggga gcagaagagt ggttgtgtgt tcctgttctt catctgtgtg 420

cggggccatg tcacagagcg tcaacagatt gtgtcaggca ggaatgctgc ccgcctttgc 480

ttcatctaca gtcaggatgc tggatgttca tggagtgagg tgagggactt gactgaggag 540

gtcattggct cagagctgaa gcactgggcc acatttgctg tgggcccagg tcatggcatc 600

cagctgcagt cagggagact ggtcatccct gcgtatacct actacatccc ttcctggttc 660

ttttgcttcc agctaccatg taaaaccagg cctcattctc tgatgatcta cagtgatgac 720

ctaggggtca catggcacca tggtagactc attaggccca tggttacagt agaatgtgaa 780

gtggcagagg tgactgggag ggctggccac cctgtgctat attgcagtgc ccggacacca 840

aacaggtgcc gggcagaggc gctcagcact gaccatggtg aaggctttca gagactggcc 900

ctgagtcgac agctctgtga gcccccacat ggttgccaag ggagtgtggt aagtttccgg 960

cccctggaga tcccacatag gtgccaggac tctagcagca aagatgcacc caccattcag 1020

cagagctctc caggcagttc actgaggctg gaggaggaag ctggaacacc gtcagaatca 1080

tggctcttgt actcacaccc aaccagtagg aaacagaggg ttgacctagg tatctatctc 1140

aaccagaccc ccttggaggc tgcctgctgg tcccgcccct ggatcttgca ctgtgggccc 1200

tgtggctact ctgatctggc tgctctggag gaggagggct tgtttgggtg tttgtttgaa 1260

tgtgggacca agcaagagtg tgagcagatt gccttccgcc tgtttacaca ccgggagatc 1320

ctgagtcacc tgcaggggga ctgcaccagc cctggtagga acccaagcca attcaaaagc 1380

aat 1383

<210> 35
<211> 1488
<212> DNA
<213> Homo sapiens

<400> 35
atgatgagct ctgcagcctt cccaaggtgg ctgagcatgg gggtccctcg taccccttca 60

cggacagtgc tcttcgagcg ggagaggacg ggcctgacct accgcgtgcc ctcgctgctc 120

cccgtgcccc ccgggcccac cctgctggcc tttgtggagc agcggctcag ccctgacgac 180

tcccacgccc accgcctggt gctgaggagg ggcacgctgg ccgggggctc cgtgcggtgg 240

ggtgccctgc acgtgctggg gacagcagcc ctggcggagc accggtccat gaacccctgc 300

cctgtgcacg atgctggcac gggcaccgtc ttcctcttct tcatcgcggt gctgggccac 360

acgcctgagg ccgtgcagat cgccacggga aggaacgccg cgcgcctctg ctgtgtggcc 420

agccgtgacg ccggcctctc gtggggcagc gcccgggacc tcaccgagga ggccatcggt 480

ggtgccgtgc aggactgggc cacattcgct gtgggtcccg gccacggtgt gcagctgccc 540

tcaggccgcc tgctggtacc cgcctacacc taccgcgtgg accgccgaga gtgttttggc 600

aagatctgcc ggaccagccc tcactccttc gccttctaca gcgatgacca cggccgcacc 660

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gacggtgggc aggccggcag cttcctctac tgcaatgccc ggagcccact gggcagccgt 780

gtgcaggcgc tcagcactga cgagggcacc tccttcctgc ccgcagagcg cgtggcttcc 840

ctgcccgaga ctgcctgggg ctgccagggc agcatcgtgg gcttcccagc ccccgccccc 900

aacaggccac gggatgacag ttggtcagtg ggccccggga gtcccctcca gcctccactc 960

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cctgaggggg gcctggtttt tgcctgcctg tacgagagcg gggccaggac ctcctatgat 1380

gagatttcct tttgtacatt ctccctgcgt gaggtcctgg agaacgtgcc cgccagcccc 1440

aaaccgccca accttgggga caagcctcgg gggtgctgct ggccctcc 1488

<210> 36
<211> 781
<212> PRT
<213> Vibrio cholerae

<400> 36
Met Arg Phe Lys Asn Val Lys Lys Thr Ala Leu Met Leu Ala Met Phe
1 5 10 15

Gly Met Ala Thr Ser Ser Asn Ala Ala Leu Phe Asp Tyr Asn Ala Thr
20 25 30

Gly Asp Thr Glu Phe Asp Ser Pro Ala Lys Gln Gly Trp Met Gln Asp
35 40 45

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

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

Leu Ser Thr Asn Gln His Ala Gln Ala Ser Ser Phe Gly Trp Arg Met
85 90 95

Thr Thr Glu Met Lys Val Leu Ser Gly Gly Met Ile Thr Asn Tyr Tyr
100 105 110

Ala Asn Gly Thr Gln Arg Val Leu Pro Ile Ile Ser Leu Asp Ser Ser

115 120 125

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

Ala Thr Gly Thr Ala Ala Thr Glu Tyr His Lys Phe Glu Leu Val Phe
145 150 155 160

Leu Pro Gly Ser Asn Pro Ser Ala Ser Phe Tyr Phe Asp Gly Lys Leu
165 170 175

Ile Arg Asp Asn Ile Gln Pro Thr Ala Ser Lys Gln Asn Met Ile Val
180 185 190

Trp Gly Asn Gly Ser Ser Asn Thr Asp Gly Val Ala Ala Tyr Arg Asp
195 200 205

Ile Lys Phe Glu Ile Gln Gly Asp Val Ile Phe Arg Gly Pro Asp Arg
210 215 220

Ile Pro Ser Ile Val Ala Ser Ser Val Thr Pro Gly Val Val Thr Ala
225 230 235 240

Phe Ala Glu Lys Arg Val Gly Gly Gly Asp Pro Gly Ala Leu Ser Asn
245 250 255

Thr Asn Asp Ile Ile Thr Arg Thr Ser Arg Asp Gly Gly Ile Thr Trp
260 265 270

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

Asp Phe Ser Asp Pro Arg Pro Ile Tyr Asp Pro Ser Ser Asn Thr Val
290 295 300

Leu Val Ser Tyr Ala Arg Trp Pro Thr Asp Ala Ala Gln Asn Gly Asp
305 310 315 320

Arg Ile Lys Pro Trp Met Pro Asn Gly Ile Phe Tyr Ser Val Tyr Asp
325 330 335

Val Ala Ser Gly Asn Trp Gln Ala Pro Ile Asp Val Thr Asp Gln Val
340 345 350

Lys Glu Arg Ser Phe Gln Ile Ala Gly Trp Gly Gly Ser Glu Leu Tyr
355 360 365

Arg Arg Asn Thr Ser Leu Asn Ser Gln Gln Asp Trp Gln Ser Asn Ala
370 375 380

Lys Ile Arg Ile Val Asp Gly Ala Ala Asn Gln Ile Gln Val Ala Asp
385 390 395 400

Gly Ser Arg Lys Tyr Val Val Thr Leu Ser Ile Asp Glu Ser Gly Gly
405 410 415

Leu Val Ala Asn Leu Asn Gly Val Ser Ala Pro Ile Ile Leu Gln Ser
420 425 430

Glu His Ala Lys Val His Ser Phe His Asp Tyr Glu Leu Gln Tyr Ser
435 440 445

Ala Leu Asn His Thr Thr Thr Leu Phe Val Asp Gly Gln Gln Ile Thr
450 455 460

Thr Trp Ala Gly Glu Val Ser Gln Glu Asn Asn Ile Gln Phe Gly Asn
465 470 475 480

Ala Asp Ala Gln Ile Asp Gly Arg Leu His Val Gln Lys Ile Val Leu
485 490 495

Thr Gln Gln Gly His Asn Leu Val Glu Phe Asp Ala Phe Tyr Leu Ala
500 505 510

Gln Gln Thr Pro Glu Val Glu Lys Asp Leu Glu Lys Leu Gly Trp Thr
515 520 525

Lys Ile Lys Thr Gly Asn Thr Met Ser Leu Tyr Gly Asn Ala Ser Val
530 535 540

Asn Pro Gly Pro Gly His Gly Ile Thr Leu Thr Arg Gln Gln Asn Ile

545 550 555 560

Ser Gly Ser Gln Asn Gly Arg Leu Ile Tyr Pro Ala Ile Val Leu Asp
565 570 575

Arg Phe Phe Leu Asn Val Met Ser Ile Tyr Ser Asp Asp Gly Gly Ser
580 585 590

Asn Trp Gln Thr Gly Ser Thr Leu Pro Ile Pro Phe Arg Trp Lys Ser
595 600 605

Ser Ser Ile Leu Glu Thr Leu Glu Pro Ser Glu Ala Asp Met Val Glu
610 615 620

Leu Gln Asn Gly Asp Leu Leu Leu Thr Ala Arg Leu Asp Phe Asn Gln
625 630 635 640

Ile Val Asn Gly Val Asn Tyr Ser Pro Arg Gln Gln Phe Leu Ser Lys
645 650 655

Asp Gly Gly Ile Thr Trp Ser Leu Leu Glu Ala Asn Asn Ala Asn Val
660 665 670

Phe Ser Asn Ile Ser Thr Gly Thr Val Asp Ala Ser Ile Thr Arg Phe
675 680 685

Glu Gln Ser Asp Gly Ser His Phe Leu Leu Phe Thr Asn Pro Gln Gly
690 695 700

Asn Pro Ala Gly Thr Asn Gly Arg Gln Asn Leu Gly Leu Trp Phe Ser
705 710 715 720

Phe Asp Glu Gly Val Thr Trp Lys Gly Pro Ile Gln Leu Val Asn Gly
725 730 735

Ala Ser Ala Tyr Ser Asp Ile Tyr Gln Leu Asp Ser Glu Asn Ala Ile
740 745 750

Val Ile Val Glu Thr Asp Asn Ser Asn Met Arg Ile Leu Arg Met Pro
755 760 765

Ile Thr Leu Leu Lys Gln Lys Leu Thr Leu Ser Gln Asn
770 775 780

<210> 37
<211> 2424
<212> DNA
<213> Vibrio cholerae

<400> 37
ttgtcaatca agatgacttc acaacgaaga agagcatcga ttcacaagga aacagattct 60

aatataaagg gagtagatat gcgtttcaaa aacgtaaaga aaaccgcttt aatgcttgca 120

atgttcggta tggcgacaag ctcaaacgcc gcactttttg actataacgc aacgggtgac 180

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ggcgttttaa ccaatgcaga tggaatgccc gcttggttgg tgcaaggtat tggagggaga 300

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35 40 45

Gln Pro Leu Val Thr Met Glu Gln Leu Leu Trp Val Ser Gly Lys Gln
50 55 60

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

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

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

Ser Thr Trp Ser Ser Thr Ala Phe Ile Val Asp Asp Gly Glu Ala Ser
115 120 125

Asp Gly Leu Asn Leu Gly Ala Val Val Asn Asp Val Asp Thr Gly Ile
130 135 140

Val Phe Leu Ile Tyr Thr Leu Cys Ala His Lys Val Asn Cys Gln Val
145 150 155 160

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

Pro Pro Arg Asn Leu Ser Val Asp Ile Gly Thr Glu Met Phe Ala Pro
180 185 190

Gly Pro Gly Ser Gly Ile Gln Lys Gln Arg Glu Pro Gly Lys Gly Arg
195 200 205

Leu Ile Val Cys Gly His Gly Thr Leu Glu Arg Asp Gly Val Phe Cys
210 215 220

Leu Leu Ser Asp Asp His Gly Ala Ser Trp His Tyr Gly Thr Gly Val
225 230 235 240

Ser Gly Ile Pro Phe Gly Gln Pro Lys His Asp His Asp Phe Asn Pro
245 250 255

Asp Glu Cys Gln Pro Tyr Glu Leu Pro Asp Gly Ser Val Ile Ile Asn
260 265 270

Ala Arg Asn Gln Asn Asn Tyr His Cys Arg Cys Arg Ile Val Leu Arg
275 280 285

Ser Tyr Asp Ala Cys Asp Thr Leu Arg Pro Arg Asp Val Thr Phe Asp
290 295 300

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

Ser Gly Ile Val Phe Phe Ser Asn Pro Ala His Pro Glu Phe Arg Val
325 330 335

Asn Leu Thr Leu Arg Trp Ser Phe Ser Asn Gly Thr Ser Trp Leu Lys
340 345 350

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

Ala Leu Glu Asn Ser Thr Asp Gly Lys Lys Gln Pro Pro Gln Leu Phe
370 375 380

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Val Lys Ile Ser Val Tyr Gly Thr Leu
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<213> Mus musculus

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35 40 45

Leu Ala Phe Ala Glu Lys Arg Ala Ser Lys Thr Asp Glu His Ala Glu
50 55 60

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

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

Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Lys Gln Thr Lys Thr Leu
100 105 110

Phe Leu Phe Phe Ile Ala Val Pro Gly Arg Val Ser Glu His His Gln
115 120 125

Leu His Thr Lys Val Asn Val Thr Arg Leu Cys Cys Val Ser Ser Thr
130 135 140

Asp His Gly Arg Thr Trp Ser Pro Ile Gln Asp Leu Thr Glu Thr Thr
145 150 155 160

Ile Gly Ser Thr His Gln Glu Trp Ala Thr Phe Ala Val Gly Pro Gly
165 170 175

His Cys Leu Gln Leu Arg Asn Pro Ala Gly Ser Leu Leu Val Pro Ala
180 185 190

Tyr Ala Tyr Arg Lys Leu His Pro Ala Gln Lys Pro Thr Pro Phe Ala
195 200 205

Phe Cys Phe Ile Ser Leu Asp His Gly His Thr Trp Lys Leu Gly Asn
210 215 220

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

Gly Ala Gln Arg Met Val Tyr Leu Asn Ala Arg Ser Phe Leu Gly Ala
245 250 255

Arg Val Gln Ala Gln Ser Pro Asn Asp Gly Leu Asp Phe Gln Asp Asn
260 265 270

Arg Val Val Ser Lys Leu Val Glu Pro Pro His Gly Cys His Gly Ser
275 280 285

Val Val Ala Phe His Asn Pro Ile Ser Lys Pro His Ala Leu Asp Thr
290 295 300

Trp Leu Leu Tyr Thr His Pro Thr Asp Ser Arg Asn Arg Thr Asn Leu
305 310 315 320

Gly Val Tyr Leu Asn Gln Met Pro Leu Asp Pro Thr Ala Trp Ser Glu
325 330 335

Pro Thr Leu Leu Ala Met Gly Ile Cys Ala Tyr Ser Asp Leu Gln Asn
340 345 350

Met Gly Gln Gly Pro Asp Gly Ser Pro Gln Phe Gly Cys Leu Tyr Glu
355 360 365

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

Ala Phe Pro Thr Val Phe Asp Ala Gln
385 390

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<213> Mus musculus

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Pro Pro Thr His Thr Phe Leu Ala Phe Ala Glu Lys Arg Thr Ser Val
35 40 45

Arg Asp Glu Asp Ala Ala Cys Leu Val Leu Arg Arg Gly Leu Met Lys
50 55 60

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

Leu Pro Gly His Arg Thr Met Asn Pro Cys Pro Val Trp Glu Lys Asn
85 90 95

Thr Gly Arg Val Tyr Leu Phe Phe Ile Cys Val Arg Gly His Val Thr
100 105 110

Glu Arg Cys Gln Ile Val Trp Gly Lys Asn Ala Ala Arg Leu Cys Phe
115 120 125

Leu Cys Ser Glu Asp Ala Gly Cys Ser Trp Gly Glu Val Lys Asp Leu
130 135 140

Thr Glu Glu Val Ile Gly Ser Glu Val Lys Arg Trp Ala Thr Phe Ala
145 150 155 160

Val Gly Pro Gly His Gly Ile Gln Leu His Ser Gly Arg Leu Ile Ile
165 170 175

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

Ser Val Lys Pro His Ser Leu Met Ile Tyr Ser Asp Asp Phe Gly Val
195 200 205

Thr Trp His His Gly Lys Phe Ile Glu Pro Gln Val Thr Gly Glu Cys
210 215 220

Gln Val Ala Glu Val Ala Gly Thr Ala Gly Asn Pro Val Leu Tyr Cys
225 230 235 240

Ser Ala Arg Thr Pro Ser Arg Phe Arg Ala Glu Ala Phe Ser Thr Asp
245 250 255

Ser Gly Gly Cys Phe Gln Lys Pro Thr Leu Asn Pro Gln Leu His Glu
260 265 270

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

Met Pro Asn Thr Tyr Gln Asp Ser Ile Gly Lys Gly Ala Pro Ala Thr
290 295 300

Gln Lys Cys Pro Leu Leu Asp Ser Pro Leu Glu Val Glu Lys Gly Ala
305 310 315 320

Glu Thr Pro Ser Ala Thr Trp Leu Leu Tyr Ser His Pro Thr Ser Lys
325 330 335

Arg Lys Arg Ile Asn Leu Gly Ile Tyr Tyr Asn Arg Asn Pro Leu Glu
340 345 350

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

Tyr Ser Asp Leu Ala Val Val Glu Glu Gln Asp Leu Val Ala Cys Leu
370 375 380

Phe Glu Cys Gly Glu Lys Asn Glu Tyr Glu Arg Ile Asp Phe Cys Leu
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Phe Ser Asp His Glu Val Leu Ser Cys Glu Asp Cys Thr Ser Pro Ser
405 410 415

Ser Asp

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<213> Mus musculus

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Thr Val Leu Phe Gln Arg Glu Arg Thr Gly Leu Thr Tyr Arg Val Pro
35 40 45

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

Gln Arg Leu Ser Pro Asp Asp Ser His Ala His Arg Leu Val Leu Arg
65 70 75 80

Arg Gly Thr Leu Thr Arg Gly Ser Val Arg Trp Gly Thr Leu Ser Val
85 90 95

Leu Glu Thr Ala Val Leu Glu Glu His Arg Ser Met Asn Pro Cys Pro
100 105 110

Val Leu Asp Glu His Ser Gly Thr Ile Phe Leu Phe Phe Ile Ala Val
115 120 125

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

Ala Arg Leu Cys Cys Val Thr Ser Cys Asp Ala Gly Leu Thr Trp Gly
145 150 155 160

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

Trp Ala Thr Phe Ala Val Gly Pro Gly His Gly Val Gln Leu Arg Ser
180 185 190

Gly Arg Leu Leu Val Pro Ala Tyr Thr Tyr His Val Asp Arg Arg Glu
195 200 205

Cys Phe Gly Lys Ile Cys Trp Thr Ser Pro His Ser Leu Ala Phe Tyr
210 215 220

Ser Asp Asp His Gly Ile Ser Trp His Cys Gly Gly Leu Val Pro Asn
225 230 235 240

Leu Arg Ser Gly Glu Cys Gln Leu Ala Ala Val Asp Gly Asp Phe Leu
245 250 255

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

Ala Asp Glu Gly Thr Ser Phe Leu Pro Gly Glu Leu Val Pro Thr Leu
275 280 285

Ala Glu Thr Ala Arg Gly Cys Gln Gly Ser Ile Val Gly Phe Leu Ala
290 295 300

Pro Pro Ser Ile Glu Pro Gln Asp Asp Arg Trp Thr Gly Ser Pro Arg
305 310 315 320

Asn Thr Pro His Ser Pro Cys Phe Asn Leu Arg Val Gln Glu Ser Ser
325 330 335

Gly Glu Gly Ala Arg Gly Leu Leu Glu Arg Trp Met Pro Arg Leu Pro
340 345 350

Leu Cys Tyr Pro Gln Ser Arg Ser Pro Glu Asn His Gly Leu Glu Pro
355 360 365

Gly Ser Asp Gly Asp Lys Thr Ser Trp Thr Pro Glu Cys Pro Met Ser
370 375 380

Ser Asp Ser Met Leu Gln Ser Pro Thr Trp Leu Leu Tyr Ser His Pro
385 390 395 400

Ala Gly Arg Arg Ala Arg Leu His Met Gly Ile Tyr Leu Ser Arg Ser
405 410 415

Pro Leu Asp Pro His Ser Trp Thr Glu Pro Trp Val Ile Tyr Glu Gly
420 425 430

Pro Ser Gly Tyr Ser Asp Leu Ala Phe Leu Gly Pro Met Pro Gly Ala
435 440 445

Ser Leu Val Phe Ala Cys Leu Phe Glu Ser Gly Thr Arg Thr Ser Tyr
450 455 460

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
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Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
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Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
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polypeptide

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Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Xaa Xaa Asp Glu His
35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Xaa Leu Gln Leu His Asp Arg Xaa Arg Ser Leu Val Val

165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
245 250 255

Xaa Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Xaa
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
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Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
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Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
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polypeptide

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35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
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Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

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

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
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Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
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polypeptide

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Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro

180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Arg Phe Ile Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 50
<211> 380
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 50
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 51
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 51
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg

195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

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

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 52
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 52
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245 250 255

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

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
        275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
    290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
                325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
        355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370 375 380

<210> 53
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 53
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Thr Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val

210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

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

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 54
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 54
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly

1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

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

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 55
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

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

His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln Ser
20 25 30

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

Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His Gln
50 55 60

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

His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly Thr
85 90 95

Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln Gln
100 105 110

Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr Ser
115 120 125

Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp Ala
130 135 140

Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly Pro
145 150 155 160

Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val Pro
165 170 175

Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro Ser
180 185 190

Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg Gly
195 200 205

His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val Glu
210 215 220

Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu Arg

225 230 235 240

Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln Glu
245 250 255

Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys Gln
260 265 270

Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser Pro
275 280 285

Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg Ala
290 295 300

Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala Trp
305 310 315 320

Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Cys Ala Tyr Ser Asp Leu
325 330 335

Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys Leu
340 345 350

Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr Leu
355 360 365

Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375

<210> 56
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 56
Met Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln

20 25 30

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

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Cys Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 57
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 57
Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly Ala
1 5 10 15

His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln Ser
20 25 30

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

Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His Gln
50 55 60

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

His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly Thr
85 90 95

Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln Gln
100 105 110

Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr Ser
115 120 125

Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp Ala
130 135 140

Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly Pro
145 150 155 160

Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val Pro
165 170 175

Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro Ser
180 185 190

Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg Gly
195 200 205

His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val Glu
210 215 220

Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu Arg
225 230 235 240

Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln Glu

245 250 255

Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys Gln
260 265 270

Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser Pro
275 280 285

Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg Ala
290 295 300

Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala Trp
305 310 315 320

Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp Leu
325 330 335

Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys Leu
340 345 350

Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr Leu
355 360 365

Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375

<210> 58
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 58
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His

35 40 45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 59
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
                85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
            100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
        115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
                165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
    210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
                245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys

260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Cys Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 60
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 60
Ala Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His

50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 61
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 61
Met Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser

275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 62
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 62
Ala Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp

65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Cys Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 63
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 63
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

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

Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala Asp Thr 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 Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

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

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg

290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 64
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 64
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln

1 5 10 15

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

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

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

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

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

Ser Thr Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 65
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 65
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

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

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

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

Ser Thr Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 66
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 66
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

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

Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala Asp Thr 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 Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

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

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr

340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365

Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 67
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 67
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His

50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

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

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 68
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 68
Asp Ala Ser Leu Pro Tyr Leu Gln Asp Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His

35 40 45

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Arg Phe Ile Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His

465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

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

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 69
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 69
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln

20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu

450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

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

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 70
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 70
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly

1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

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

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

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

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 71
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 71
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

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

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

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

420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

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

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 72
<211> 617
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Thr Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

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

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

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

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 73
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 73
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

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

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

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

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    610   615

<210> 74
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

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

<220>
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<222> (9)..(9)
<223> Any amino acid

<220>
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<222> (62)..(62)
<223> Any amino acid

<220>
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<222> (93)..(93)
<223> Any amino acid

<220>
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<222> (187)..(187)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (270)..(270)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (301)..(302)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (332)..(332)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Any amino acid

<400> 74
Xaa Ala Ser Leu Pro Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly

145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

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

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 75
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MOD_RES
<222> (1)..(2)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (4)..(6)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Any amino acid

<220>
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<222> (44)..(45)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (54)..(54)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (69)..(69)

<223> Any amino acid

<220>
<221> MOD_RES
<222> (78)..(78)
<223> Any amino acid

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<222> (93)..(93)
<223> Any amino acid

<220>
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<222> (107)..(108)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (112)..(112)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (125)..(126)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (150)..(150)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (164)..(164)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (171)..(171)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (196)..(196)
<223> Any amino acid

<220>
<221> MOD_RES

<222> (217)..(217)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (249)..(249)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (251)..(251)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (257)..(257)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (270)..(270)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (272)..(272)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (292)..(292)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (301)..(302)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (325)..(325)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (332)..(332)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (352)..(352)
<223> Any amino acid

<220>

<221> MOD_RES
<222> (363)..(363)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Any amino acid

<400> 75
Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Xaa Xaa Asp Glu His
35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Xaa Leu Gln Leu His Asp Arg Xaa Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
245 250 255

Xaa Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Xaa
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

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

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 76
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 76
caatctgctc ttacacagcc tgccagcgtg tccggatctc ctggccagag catcaccatc 60

agctgtaccg gcaccagctc tgatgtcggc ggctacaatt acgtgtcctg gtatcagcag 120

caccccggca aggcccctaa gctgatgatc tacgacgtgt ccaacagacc cagcggcgtg 180

tccaatagat tctccggcag caagagcggc aacaccgcca gcctgacaat tagcggactg 240

caggccgagg acgaggccga ttactactgt agcagctaca ccagctccag caccagagtg 300

tttggcaccg gcacaaaagt gaccgtgctg ggccagccta aggccaatcc taccgtgaca 360

ctgttccctc caagcagcga ggaactgcag gctaacaagg ccacactcgt gtgcctgatc 420

agcgactttt atcctggcgc cgtgaccgtg gcctggaagg ctgatggatc tccagtgaaa 480

gccggcgtgg aaaccaccaa gcctagcaag cagagcaaca acaaatacgc cgccagcagc 540

tacctgagcc tgacacctga gcagtggaag tcccacagat cctacagctg ccaagtgacc 600

cacgagggca gcaccgtgga aaaaacagtg gcccctaccg agtgctct 648

<210> 77
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 77
gaggtgcagc tgctggaatc tggcggagga cttgttcagc ctggcggctc tctgagactg 60

tcttgtgccg ccagcggctt caccttcagc agctatatca tgatgtgggt ccgacaggcc 120

cctggcaaag gccttgaatg ggtgtccagc atctatccca gcggcggcat cacctttac 180

gccgacacag tgaagggcag attcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgag agccgaggac accgccgtgt actactgcgc cagaatcaag 300

ctgggcaccg tgaccaccgt ggattattgg ggacagggca ccctggtcac cgtgtcatct 360

gctagcacca agggcccatc cgtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcc 480

tggaactcag gcgctctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtctacaccc tgcccccatc ccgggaggag 1080

atgaccaaga accaggtcag cctgtactgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 78
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 78
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    450   455   460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465   470   475   480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500   505   510

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530   535   540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545   550   555   560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
                565   570   575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            580   585   590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        595   600   605

Ser Pro Gly Lys
    610

<210> 79
<211> 1836
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 79

gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgtcaagt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agagccagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccacag ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

ggcggaggcg gatccgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 1200

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 1260

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1500

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 1560

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1620

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680

cccgtgctgg actccgacgg ctccttcttc ctcactagca agctcaccgt ggacaagagc 1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctctc cctgtctccg ggtaaa 1836

<210> 80
<211> 1140
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 80
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgtcaagt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agagccagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccacag ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

<210> 81
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 81
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 82
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 82
Asp Ala Ser Leu Pro Tyr Leu Gln Asp Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Arg Phe Ile Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 83
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 83
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 84
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 84
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

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

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 85
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 85
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

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

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530   535   540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545   550   555   560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
                565   570   575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            580   585   590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        595   600   605

Ser Pro Gly Lys
    610

<210> 86
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 86
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1   5   10   15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
            20   25   30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Thr Thr His
    50   55   60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65   70   75   80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

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

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 87
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 87
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

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

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 88
<211> 608
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

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

<220>
<221> MOD_RES

<222> (9)..(9)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (270)..(270)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (301)..(302)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (332)..(332)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (381)..(381)
<223> Any amino acid

<400> 88
Xaa Ala Ser Leu Pro Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln

20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Asp Lys Thr
370 375 380

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
385 390 395 400

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

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

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

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val

450 455 460

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

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

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

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

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

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

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

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

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

<210> 89
<211> 608
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MOD_RES
<222> (1)..(2)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (4)..(6)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (44)..(45)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (54)..(54)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (69)..(69)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (78)..(78)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (107)..(108)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (112)..(112)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (125)..(126)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (150)..(150)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (164)..(164)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (171)..(171)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (196)..(196)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (217)..(217)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (249)..(249)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (251)..(251)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (257)..(257)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (270)..(270)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (272)..(272)

<223> Any amino acid

<220>
<221> MOD_RES
<222> (292)..(292)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (301)..(302)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (325)..(325)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (332)..(332)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (352)..(352)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (381)..(381)
<223> Any amino acid

<400> 89
Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Xaa Xaa Asp Glu His
35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
    50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
                85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
            100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
        115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
    130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Xaa Leu Gln Leu His Asp Arg Xaa Arg Ser Leu Val Val
                165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
            180 185 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
        195 200 205

Gly His Phe Val Ala Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
    210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
                245 250 255

Xaa Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Xaa

260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Asp Lys Thr
370 375 380

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
385 390 395 400

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 90
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 90
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 91
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

peptide

<400> 91
Glu Pro Lys Ser Ser
1 5

<210> 92
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 92
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

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

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

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

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
130 135 140

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

145 150 155 160

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 93
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 93
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

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

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

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

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
130 135 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys
225

<210> 94
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 94
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln

20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ala Arg Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 95
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 95
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

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

245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ala Arg Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

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

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 96
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 96
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu

225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ala Arg Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500 505 510

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
                565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        595 600 605

Ser Pro Gly Lys
    610

<210> 97
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 97
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val

210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 98
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 98
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly

1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

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

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 99
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 99
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser

420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 100
<211> 380
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 100
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 101
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 101
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg

195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

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

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 102

<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 102
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro

180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys

610

<210> 103
<211> 1836
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 103
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgtcaagt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agagccagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccacag ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

ggcggaggcg gatccgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 1200

gggggaccgt cagtcttcct cttccccccca aaacccaagg acaccctcat gatctcccgg 1260

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1500

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 1560

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1620

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680

cccgtgctgg actccgacgg ctccttcttc ctcactagca agctcaccgt ggacaagagc 1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctctc cctgtctccg ggtaaa 1836

<210> 104
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 104
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

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

Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala Asp Thr 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 Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

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

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Gly Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365

Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 105
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 105
gaggtgcagc tgctggaatc tggcggagga cttgttcagc ctggcggctc tctgagactg 60

tcttgtgccg ccagcggctt caccttcagc agctatatca tgatgtgggt ccgacaggcc 120

cctggcaaag gccttgaatg ggtgtccagc atctatccca gcggcggcat cacctttac 180

gccgacacag tgaagggcag attcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgag agccgaggac accgccgtgt actactgcgc cagaatcaag 300

ctgggcaccg tgaccaccgt ggattattgg ggacagggca ccctggtcac cgtgtcatct 360

gctagcacca agggcccatc cgtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcc 480

tggaactcag gcgctctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacggt 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtctacaccc tgcccccatc ccgggaggag 1080

atgaccaaga accaggtcag cctgtactgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 106
<211> 632
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 106
Thr Val Glu Lys Ser Val Val Phe Lys Ala Glu Gly Glu His Phe Thr

1 5 10 15

Asp Gln Lys Gly Asn Thr Ile Val Gly Ser Gly Ser Gly Gly Thr Thr
20 25 30

Lys Tyr Phe Arg Ile Pro Ala Met Cys Thr Thr Ser Lys Gly Thr Ile
35 40 45

Val Val Phe Ala Asp Ala Arg His Asn Thr Ala Ser Asp Gln Ser Phe
50 55 60

Ile Asp Thr Ala Ala Ala Arg Ser Thr Asp Gly Gly Lys Thr Trp Asn
65 70 75 80

Lys Lys Ile Ala Ile Tyr Asn Asp Arg Val Asn Ser Lys Leu Ser Arg
85 90 95

Val Met Asp Pro Thr Cys Ile Val Ala Asn Ile Gln Gly Arg Glu Thr
100 105 110

Ile Leu Val Met Val Gly Lys Trp Asn Asn Asn Asp Lys Thr Trp Gly
115 120 125

Ala Tyr Arg Asp Lys Ala Pro Asp Thr Asp Trp Asp Leu Val Leu Tyr
130 135 140

Lys Ser Thr Asp Asp Gly Val Thr Phe Ser Lys Val Glu Thr Asn Ile
145 150 155 160

His Asp Ile Val Thr Lys Asn Gly Thr Ile Ser Ala Met Leu Gly Gly
165 170 175

Val Gly Ser Gly Leu Gln Leu Asn Asp Gly Lys Leu Val Phe Pro Val
180 185 190

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

Ile Tyr Ser Thr Asp Gly Ile Thr Trp Ser Leu Pro Ser Gly Tyr Cys
210 215 220

Glu Gly Phe Gly Ser Glu Asn Asn Ile Ile Glu Phe Asn Ala Ser Leu
225 230 235 240

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

Asp Phe Gly Lys Thr Trp Thr Glu Phe Pro Pro Met Asp Lys Lys Val
260 265 270

Asp Asn Arg Asn His Gly Val Gln Gly Ser Thr Ile Thr Ile Pro Ser
275 280 285

Gly Asn Lys Leu Val Ala Ala His Ser Ser Ala Gln Asn Lys Asn Asn
290 295 300

Asp Tyr Thr Arg Ser Asp Ile Ser Leu Tyr Ala His Asn Leu Tyr Ser
305 310 315 320

Gly Glu Val Lys Leu Ile Asp Asp Phe Tyr Pro Lys Val Gly Asn Ala
325 330 335

Ser Gly Ala Gly Tyr Ser Cys Leu Ser Tyr Arg Lys Asn Val Asp Lys
340 345 350

Glu Thr Leu Tyr Val Val Tyr Glu Ala Asn Gly Ser Ile Glu Phe Gln
355 360 365

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

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
385 390 395 400

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
405 410 415

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
420 425 430

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

435 440 445

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
450 455 460

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
465 470 475 480

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
485 490 495

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
500 505 510

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
515 520 525

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
530 535 540

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
545 550 555 560

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

Leu Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
580 585 590

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
595 600 605

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Gly Gly Ser
610 615 620

His His His His His His His His
625 630

<210> 107
<211> 1896
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 107
acagtggaaa agtccgtggt gttcaaggcc gagggcgagc acttcaccga ccagaaaggc 60

aataccatcg tcggctctgg cagcggcggc accaccaagt actttagaat ccccgccatg 120

tgcaccacca gcaagggcac cattgtggtg ttcgccgacg ccagacacaa caccgccagc 180

gatcagagct tcatcgatac cgctgccgcc agaagtacag acggcggcaa gacctggaac 240

aagaagatcg ccatctacaa cgaccgcgtg aacagcaagc tgagcagagt gatggaccct 300

acctgcatcg tggccaacat ccagggcaga gaaaccatcc tggtcatggt cggaaagtgg 360

aacaacaacg ataagacctg gggcgcctac agagacaagg cccctgatac cgattgggac 420

ctcgtgctgt ataagagcac cgacgacggc gtgaccttca gcaaggtgga aacaaacatc 480

cacgacatcg tgaccaagaa cggcaccatc tctgccatgc tcggcggcgt tggatctggc 540

ctgcaactga atgatggcaa gctggtgttc cccgtgcaga tggtccgaac aaagaacatc 600

accaccgtgc tgaataccag cttcatctac tccaccgacg gcatcacatg gtccctgcct 660

agcggctact gtgaaggctt tggcagcgag aacaacatca tcgagttcaa cgccagcctg 720

gtcaacaaca tccggaacag cggcctgcgg agaagcttcg agacaaagga cttcggaaag 780

acgtggaccg agtttcctcc aatggacaag aaggtggaca accggaacca cggcgtgcag 840

ggcagcacaa tcacaatccc tagcggcaac aaactggtgg ccgctcactc tagcgcccag 900

aacaagaaca acgattacac cagaagcgac atcagcctgt acgcccacaa cctgtactcc 960

ggcgaagtga agctgatcga cgacttctac cccaaagtgg gcaatgccag cggagccggc 1020

tacagctgtc tgagctaccg gaaaaatgtg gacaaagaaa ccctgtacgt ggtgtacgag 1080

gccaacggca gcatcgagtt tcaggacctg agcagacatc tgcccgtgat caagagctac 1140

aatggcggag gtggaagtgg cggaggcgga tccgacaaaa ctcacacatg cccaccgtgc 1200

ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa acccaaggac 1260

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 1320

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1380

aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 1440

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 1500

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtctac 1560

accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1620

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1680

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct cactagcaag 1740

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1800

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaaagcggc 1860

ggaggcggat ctcatcatca ccatcatcac catcac 1896

<210> 108
<211> 632
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 108
Thr Val Glu Lys Ser Val Val Phe Lys Ala Glu Gly Glu His Phe Thr
1 5 10 15

Asp Gln Lys Gly Asn Thr Ile Val Gly Ser Gly Ser Gly Gly Thr Thr
20 25 30

Lys Tyr Phe Arg Ile Pro Ala Met Cys Thr Thr Ser Lys Gly Thr Ile
35 40 45

Val Val Phe Ala Asp Ala Arg His Asn Thr Ala Ser Asp Gln Ser Phe
50 55 60

Ile Asp Thr Ala Ala Ala Arg Ser Thr Asp Gly Gly Lys Thr Trp Asn
65 70 75 80

Lys Lys Ile Ala Ile Tyr Asn Asp Arg Val Asn Ser Lys Leu Ser Arg
85 90 95

Val Met Asp Pro Thr Cys Ile Val Ala Asn Ile Gln Gly Arg Glu Thr
100 105 110

Ile Leu Val Met Val Gly Lys Trp Asn Asn Asn Asp Lys Thr Trp Gly
115 120 125

Ala Tyr Arg Asp Lys Ala Pro Asp Thr Asp Trp Asp Leu Val Leu Tyr
130 135 140

Lys Ser Thr Asp Asp Gly Val Thr Phe Ser Lys Val Glu Thr Asn Ile
145 150 155 160

His Asp Ile Val Thr Lys Asn Gly Thr Ile Ser Ala Met Leu Gly Gly
165 170 175

Val Gly Ser Gly Leu Gln Leu Asn Asp Gly Lys Leu Val Phe Pro Val
180 185 190

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

Ile Tyr Ser Thr Asp Gly Ile Thr Trp Ser Leu Pro Ser Gly Tyr Cys
210 215 220

Glu Gly Phe Gly Ser Glu Asn Asn Ile Ile Glu Phe Asn Ala Ser Leu
225 230 235 240

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

Asp Phe Gly Lys Thr Trp Thr Glu Phe Pro Pro Met Asp Lys Lys Val
260 265 270

Asp Asn Arg Asn His Gly Val Gln Gly Ser Thr Ile Thr Ile Pro Ser
275 280 285

Gly Asn Lys Leu Val Ala Ala His Ser Ser Ala Gln Asn Lys Asn Asn
290 295 300

Asp Tyr Thr Arg Ser Asp Ile Ser Leu Tyr Ala His Asn Leu Tyr Ser
305 310 315 320

Gly Glu Val Lys Leu Ile Asp Asp Phe Tyr Pro Lys Val Gly Asn Ala
325 330 335

Ser Gly Ala Gly Tyr Ser Cys Leu Ser Tyr Arg Lys Asn Val Asp Lys
340 345 350

Glu Thr Leu Tyr Val Val Tyr Glu Ala Asn Gly Ser Ile Glu Phe Gln
355 360 365

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

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
385 390 395 400

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
405 410 415

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
420 425 430

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
435 440 445

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
450 455 460

Glu Gln Tyr Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
465 470 475 480

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
485 490 495

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
500 505 510

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
515 520 525

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
530 535 540

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
545 550 555 560

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

Leu Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
580 585 590

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
595 600 605

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ser Gly Gly Gly Gly Ser
610 615 620

His His His His His His His His
625 630

<210> 109
<211> 1896
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 109
acagtggaaa agtccgtggt gttcaaggcc gagggcgagc acttcaccga ccagaaaggc 60

aataccatcg tcggctctgg cagcggcggc accaccaagt actttagaat ccccgccatg 120

tgcaccacca gcaagggcac cattgtggtg ttcgccgacg ccagacacaa caccgccagc 180

gatcagagct tcatcgatac cgctgccgcc agaagtacag acggcggcaa gacctggaac 240

aagaagatcg ccatctacaa cgaccgcgtg aacagcaagc tgagcagagt gatggaccct 300

acctgcatcg tggccaacat ccagggcaga gaaaccatcc tggtcatggt cggaaagtgg 360

aacaacaacg ataagacctg gggcgcctac agagacaagg cccctgatac cgattgggac 420

ctcgtgctgt ataagagcac cgacgacggc gtgaccttca gcaaggtgga aacaaacatc 480

cacgacatcg tgaccaagaa cggcaccatc tctgccatgc tcggcggcgt tggatctggc 540

ctgcaactga atgatggcaa gctggtgttc cccgtgcaga tggtccgaac aaagaacatc 600

accaccgtgc tgaataccag cttcatctac tccaccgacg gcatcacatg gtccctgcct 660

agcggctact gtgaaggctt tggcagcgag aacaacatca tcgagttcaa cgccagcctg 720

gtcaacaaca tccggaacag cggcctgcgg agaagcttcg agacaaagga cttcggaaag 780

acgtggaccg agtttcctcc aatggacaag aaggtggaca accggaacca cggcgtgcag 840

ggcagcacaa tcacaatccc tagcggcaac aaactggtgg ccgctcactc tagcgcccag 900

aacaagaaca acgattacac cagaagcgac atcagcctgt acgcccacaa cctgtactcc 960

ggcgaagtga agctgatcga cgacttctac cccaaagtgg gcaatgccag cggagccggc 1020

tacagctgtc tgagctaccg gaaaaatgtg gacaaagaaa ccctgtacgt ggtgtacgag 1080

gccaacggca gcatcgagtt tcaggacctg agcagacatc tgcccgtgat caagagctac 1140

aatggcggag gtggaagtgg cggaggcgga tccgacaaaa ctcacacatg cccaccgtgc 1200

ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa acccaaggac 1260

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 1320

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 1380

aagccgcggg aggagcagta cggtagcacg taccgtgtgg tcagcgtcct caccgtcctg 1440

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 1500

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtctac 1560

accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc 1620

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1680

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct cactagcaag 1740

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1800

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaaagcggc 1860

ggaggcggat ctcatcatca ccatcatcac catcac 1896

<210> 110
<211> 715
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 110
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

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

Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala Asp Thr 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 Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

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

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365

Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

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

420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly
465 470 475 480

Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly
485 490 495

Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys
500 505 510

Leu Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg
515 520 525

Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly
530 535 540

Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser
545 550 555 560

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

Gln Pro Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
580 585 590

Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
595 600 605

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
610 615 620

Ser Ser Tyr Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
625 630 635 640

Glu Trp Val Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala
645 650 655

Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
660 665 670

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
675 680 685

Tyr Tyr Cys Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr
690 695 700

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
705 710 715

<210> 111
<211> 2145
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 111
gaggtgcagc tgctggaatc tggcggagga cttgttcagc ctggcggctc tctgagactg 60

tcttgtgccg ccagcggctt caccttcagc agctatatca tgatgtgggt ccgacaggcc 120

cctggcaaag gccttgaatg ggtgtccagc atctatccca gcggcggcat cacctttac 180

gccgacacag tgaagggcag attcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgag agccgaggac accgccgtgt actactgcgc cagaatcaag 300

ctgggcaccg tgaccaccgt ggattattgg ggacagggca ccctggtcac cgtgtcatct 360

gctagcacca agggcccatc cgtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcc 480

tggaactcag gcgctctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtctacaccc tgcccccatc ccgggaggag 1080

atgaccaaga accaggtcag cctgtactgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc taagcttgtc tccgggtaaa ggaggcggag gatctggcgg aggtggaagt 1380

ggcggaggcg gatctcaatc tgctcttaca cagcctgcca gcgtgtccgg atctcctggc 1440

cagagcatca ccatcagctg taccggcacc agctctgatg tcggcggcta caattacgtg 1500

tcctggtatc agcagcaccc cggcaaggcc cctaagctga tgatctacga cgtgtccaac 1560

agacccagcg gcgtgtccaa tagattctcc ggcagcaaga gcggcaacac cgccagcctg 1620

acaattagcg gactgcaggc cgaggacgag gccgattact actgtagcag ctacaccagc 1680

tccagcacca gagtgtttgg caccggcaca aaagtgaccg tgctgggcca gcctaaggcc 1740

ggtggaggtg ggtctggagg gggtggatct ggaggtggcg gatcggaggt gcagctgctg 1800

gaatctggcg gaggacttgt tcagcctggc ggctctctga gactgtcttg tgccgccagc 1860

ggcttcacct tcagcagcta tatcatgatg tgggtccgac aggcccctgg caaaggcctt 1920

gaatgggtgt ccagcatcta tcccagcggc ggcatcacct tttacgccga cacagtgaag 1980

ggcagattca ccatcagccg ggacaacagc aagaacaccc tgtacctgca gatgaacagc 2040

ctgagagccg aggacaccgc cgtgtactac tgcgccagaa tcaagctggg caccgtgacc 2100

accgtggatt attggggaca gggcaccctg gtcaccgtgt catct 2145

<210> 112
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 112
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

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

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 113
<211> 1851
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 113
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgtcaagt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agagccagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccacag ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

ggcggaggtg gaagtggcgg aggcggatcc gacaaaactc acacatgccc accgtgccca 1200

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 1260

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 1320

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 1380

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1440

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1500

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtctacacc 1560

ctgcccccat cccgggagga gatgaccaag aaccaggtca gcctgacctg cctggtcaaa 1620

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1680

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcac tagcaagctc 1740

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1800

gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa a 1851

<210> 114
<211> 877
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 114
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln

100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val

530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
610 615 620

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

Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val
645 650 655

Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala
660 665 670

Pro Lys Leu Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser
675 680 685

Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
690 695 700

Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr
705 710 715 720

Thr Ser Ser Ser Thr Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val
725 730 735

Leu Gly Gln Pro Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
755 760 765

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
770 775 780

Thr Phe Ser Ser Tyr Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys
785 790 795 800

Gly Leu Glu Trp Val Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe
805 810 815

Tyr Ala Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
820 825 830

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
835 840 845

Ala Val Tyr Tyr Cys Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val
850 855 860

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
865 870 875

<210> 115
<211> 2631
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 115
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgtcaagt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agagccagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccacag ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 1200

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 1260

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1500

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 1560

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1620

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680

cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc 1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctaag cttgtctccg ggtaaaggag gcggaggatc tggcggaggt 1860

ggaagtggcg gaggcggatc tcaatctgct cttacacagc ctgccagcgt gtccggatct 1920

cctggccaga gcatcaccat cagctgtacc ggcaccagct ctgatgtcgg cggctacaat 1980

tacgtgtcct ggtatcagca gcaccccggc aaggccccta agctgatgat ctacgacgtg 2040

tccaacagac ccagcggcgt gtccaataga ttctccggca gcaagagcgg caacaccgcc 2100

agcctgacaa ttagcggact gcaggccgag gacgaggccg attactactg tagcagctac 2160

accagctcca gcaccagagt gtttggcacc ggcacaaaag tgaccgtgct gggccagcct 2220

aaggccggtg gaggtgggtc tggagggggt ggatctggag gtggcggatc ggaggtgcag 2280

ctgctggaat ctggcggagg acttgttcag cctggcggct ctctgagact gtcttgtgcc 2340

gccagcggct tcaccttcag cagctatatc atgatgtggg tccgacaggc ccctggcaaa 2400

ggccttgaat gggtgtccag catctatccc agcggcggca tcacctttta cgccgacaca 2460

gtgaagggca gattcaccat cagccgggac aacagcaaga acaccctgta cctgcagatg 2520

aacagcctga gagccgagga caccgccgtg tactactgcg ccagaatcaa gctgggcacc 2580

gtgaccaccg tggattattg gggacagggc accctggtca ccgtgtcatc t 2631

<210> 116
<211> 608
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

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

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Any amino acid

<220>
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Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu

225 230 235 240

Arg Xaa Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Asp Lys Thr
370 375 380

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
385 390 395 400

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

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

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

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

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

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

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

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

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

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

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

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

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

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Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Xaa Xaa Asp Glu His
35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Xaa
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Xaa Leu Gln Leu His Asp Xaa Xaa Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Xaa Xaa Pro Ile Pro
180 185 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Xaa Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
210 215 220

Xaa Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser Xaa Xaa
225 230 235 240

Xaa Xaa Arg Xaa Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
245 250 255

Xaa Xaa Gln Xaa Val Lys Lys Leu Xaa Glu Pro Pro Pro Xaa Gly Xaa
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Asp Lys Thr
370 375 380

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
385 390 395 400

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

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

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

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

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

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

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

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

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

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

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

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

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

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polynucleotide

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cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agattcagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

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tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly

85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Xaa Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 120
<211> 380
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Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Xaa Xaa Asp Glu His
35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Xaa
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Xaa Leu Gln Leu His Asp Xaa Xaa Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Xaa Xaa Pro Ile Pro
180 185 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Xaa Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val

210 215 220

Xaa Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser Xaa Xaa
225 230 235 240

Xaa Xaa Arg Xaa Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
245 250 255

Xaa Xaa Gln Xaa Val Lys Lys Leu Xaa Glu Pro Pro Pro Xaa Gly Xaa
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

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peptide

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<212> PRT
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polypeptide

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20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val

165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

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

Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu

595 600 605

Ser Pro Gly Lys
610

<210> 123
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 123
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly

145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
    370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
    450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500 505 510

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

Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val

580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 124
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 124
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

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

Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala Asp Thr 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 Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala

130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

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

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 125
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 125
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

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

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

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

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

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

Ser Thr Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
130 135 140

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
145 150 155 160

Ser Tyr Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
165 170 175

Trp Val Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala Asp
180 185 190

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

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

Tyr Cys Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr Trp
225 230 235 240

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
245 250

<210> 126
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 126
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg

195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 127
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 127
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser

420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 128
<211> 617
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 128
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

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

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 129
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 129
Gly His Ala Phe Thr Ser Asp Ser
1 5

<210> 130
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 130
Ile Tyr Pro Arg Ser Gly Asn Pro
1 5

<210> 131
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 131
Asp Tyr Tyr Gly Arg Tyr Phe Asp Val
1 5

<210> 132
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 132
Glu Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala

1 5 10 15

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

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

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

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

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

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

Thr Val Thr Val Ser Ser
115

<210> 133
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 133
Glu Asp Ile Tyr Asn Arg
1 5

<210> 134
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 134
Gly Ala Thr
1

<210> 135
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 135
Gln Gln Tyr Trp Ser Thr Pro Trp Thr
1 5

<210> 136
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 136
Asp Ile Gln Met Thr Gln Ser Ser Phe Ser Phe Ser Val Ser Leu Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100 105

<210> 137
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 137
Gly Tyr Ser Phe Thr Asp Tyr Tyr
1 5

<210> 138
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 138
Ile Tyr Pro Gly Ser Gly Asn Thr
1 5

<210> 139
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 139
Ser Tyr Tyr Tyr Gly Ser Ser Tyr Leu Phe Asp Tyr
1 5 10

<210> 140
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 140
Glu Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
1 5 10 15

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

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

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

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

Gln Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 141
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 141
Gln Ser Ile Gly Thr Ser
1 5

<210> 142
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

peptide

<400> 142
Tyr Ala Ser
1

<210> 143
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 143
Gln Gln Ser Asn Asn Trp Pro Phe Thr
1 5

<210> 144
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 144
Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
1 5 10 15

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

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu 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 Ser
65 70 75 80

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

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

<210> 145
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 145
Gly Tyr Thr Phe Thr Asp Tyr Tyr
1 5

<210> 146
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 146
Ile Asn Pro Asn Asn Gly Tyr Thr
1 5

<210> 147
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 147
Ser Ala Ala Tyr Tyr Val Leu Asp Asp
1 5

<210> 148
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 148
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

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

Tyr Met Asn Trp Val Lys Lys Ser His Gly Arg Ser Leu Glu Trp Ile
35 40 45

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

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

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

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

Ser Val Thr Val Ser Ser
115

<210> 149
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 149
Lys Lys Val Thr Ile Phe Gly Ser Ile Ser Val
1 5 10

<210> 150
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 150
Asn Gly Ala
1

<210> 151
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 151
Leu Gln Asn Lys Glu Val Pro Tyr Thr
1 5

<210> 152
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 152
Asp Ile Val Met Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Lys Ala Thr Ile Ser Cys Lys Ala Ser Lys Lys Val Thr Ile Phe
20 25 30

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

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

Arg Phe Ser Asp Ser Gly Ser Gln Asn Arg Ser Pro Phe Gly Asn Gln
65 70 75 80

Leu Asn Phe Thr Leu Thr Ile Asp Pro Val Glu Ala Asp Asp Ala Ala

85 90 95

Thr Tyr Tyr Cys Leu Gln Asn Lys Glu Val Pro Tyr Thr Phe Gly Gly
100 105 110

Gly Thr Glu Leu Glu Ile Lys
115

<210> 153
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 153
Gly Asp Ser Ile Thr Ser Gly Tyr
1 5

<210> 154
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 154
Ile Ser Tyr Thr Gly Ser Thr
1 5

<210> 155
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 155
Gln Gly Gly Trp Leu Gln Ala Met Asp Tyr
1 5 10

<210> 156

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

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 156
Glu Val Gln Leu Gln Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln
1 5 10 15

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

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

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

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

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

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

Ser Val Thr Val Ser Ser
115

<210> 157
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 157
Gln Ser Leu Leu Tyr Ser Ser Asn Gln Lys Asn Ser
1 5 10

<210> 158
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 158
Trp Ala Ser
1

<210> 159
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 159
Gln Gln Tyr Tyr Gly Tyr Pro Trp Thr
1 5

<210> 160
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 160
Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
1 5 10 15

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

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

Lys

<210> 161
<211> 8
<212> PRT
<213> Mus musculus

<400> 161
Gly Phe Asn Ile Lys Asp Thr Tyr
1 5

<210> 162
<211> 8
<212> PRT
<213> Mus musculus

<400> 162
Ile Asp Pro Ala Asn Asp Asn Thr
1 5

<210> 163
<211> 11
<212> PRT
<213> Mus musculus

<400> 163
Glu Gly Tyr Gly Gly Ser Tyr Gly Glu Gly Tyr
1 5 10

<210> 164
<211> 120
<212> PRT
<213> Mus musculus

<400> 164
Glu Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala

1 5 10 15

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

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

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

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

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

Ala Arg Glu Gly Tyr Gly Gly Ser Tyr Gly Glu Gly Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 165
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 165
Gln Ser Val Ser Asn Asp
1 5

<210> 166
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 166
Gln Gln Asp Tyr Asn Ser Pro Trp Thr
1 5

<210> 167
<211> 107
<212> PRT
<213> Mus musculus

<400> 167
Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
1 5 10 15

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

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

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

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

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

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

<210> 168
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 168
Ile Asp Pro Ala Asn Gly Asn Thr
1 5

<210> 169

<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 169
Pro Phe Asn Tyr Arg Phe Tyr Asp Val Tyr Tyr Phe Asp Tyr
1 5 10

<210> 170
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 170
Glu Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

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

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

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

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

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

Ala Arg Pro Phe Asn Tyr Arg Phe Tyr Asp Val Tyr Tyr Phe Asp Tyr
100 105 110

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

<210> 171
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 171
Ser Ser Val Ser Tyr
1 5

<210> 172
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 172
Asp Thr Ser
1

<210> 173
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 173
Gln Gln Trp Ser Thr Tyr Pro Leu Thr
1 5

<210> 174
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 174
Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly

1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

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

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Leu Ser Arg Met Glu Ala Glu
65 70 75 80

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

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

<210> 175
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 175
Gly Tyr Thr Phe Thr Ser Tyr Val
1 5

<210> 176
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 176
Ile Asn Pro Tyr Asn Asp Gly Ser
1 5

<210> 177
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 177
Gln Thr Leu Asp Phe
1 5

<210> 178
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 178
Glu Val Gln Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Thr
1 5 10 15

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

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

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

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

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

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

Ser Thr

<210> 179
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 179
Glu Ser Val Glu Phe Tyr Gly Thr Thr Leu
1 5 10

<210> 180
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 180
Ala Ala Ser
1

<210> 181
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 181
Gln Gln Ser Arg Lys Val Pro Tyr Thr
1 5

<210> 182
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 182
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 Glu Phe Tyr
20 25 30

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

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

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

<210> 183
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 183
Gly Phe Ser Leu Ser Thr Tyr Gly Leu Gly
1 5 10

<210> 184
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 184
Ile Trp Trp Asn Asp Asp Lys

1 5

<210> 185
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 185
Thr Leu His Tyr Tyr Asp Gly Ile Ala Trp Phe Ala Tyr
1 5 10

<210> 186
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 186
Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser Gln
1 5 10 15

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

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

Trp Leu Ala Asn Ile Trp Trp Asn Asp Asp Lys Phe Tyr Asp Ser Val
50 55 60

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

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

Cys Ala Gln Thr Leu His Tyr Tyr Asp Gly Ile Ala Trp Phe Ala Tyr
100 105 110

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

<210> 187
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 187
His Tyr Val Gly Thr Phe
1 5

<210> 188
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 188
Ser Thr Ser
1

<210> 189
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 189
Gln Gln Tyr Tyr Asn Ser Pro Leu Thr
1 5

<210> 190
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 190
Asp Ile Val Met Thr Gln Ser Gln Asn Phe Met Ser Thr Ser Val Gly
1 5 10 15

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

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

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

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

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

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

<210> 191
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 191
Gly Tyr Thr Phe Thr Ser Asn Trp
1 5

<210> 192
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 192
Ile His Pro Ser Asp Ser Glu Thr
1 5

<210> 193
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 193
Ser Ser Gly Asp Tyr Gly Arg Asp Tyr
1 5

<210> 194
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 194
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 Asn
20 25 30

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

Gly Arg Ile His Pro Ser Asp Ser Glu Thr His Tyr His Gln 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

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

Ala His Ser Ser Gly Asp Tyr Gly Arg Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 195
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 195
Glu Ser Val Asp Ser Tyr Gly Asn Ser Phe
1 5 10

<210> 196
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 196
Leu Ala Ser
1

<210> 197
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 197
Gln Gln Asn Asn Glu Asp Pro Trp Thr
1 5

<210> 198
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 198
Asn 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 Asn Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

<210> 199
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 199
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr 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 Arg Glu Gly Tyr Gly Gly Ser Tyr Gly Glu Gly Tyr Trp Gly Gln
            100 105 110

Gly Thr Leu Val Thr Val Ser Ser
        115 120

<210> 200
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 200
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

Tyr Tyr Ala Ser Ile Arg Phe Thr Gly Ile Pro Ala 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 Val Tyr Tyr Cys Gln Gln Asp Tyr Asn Ser Pro Trp
                85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 201
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 201
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 202
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 202
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly

1 5 10 15

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

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

Tyr Tyr Ala Ser Ile Arg Phe Thr Gly Ile Pro Ala 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 Val Tyr Phe Cys Gln Gln Asp Tyr Asn Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 203
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 203
Gln Gln Asp Tyr Thr Ser Pro Trp Thr
1 5

<210> 204
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 204
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

Tyr Tyr Ala Ser Ile Arg Phe Thr Gly Ile Pro Ala 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 Val Tyr Tyr Cys Gln Gln Asp Tyr Thr Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 205
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 205
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

Tyr Tyr Ala Ser Ile Arg Phe Thr Gly Ile Pro Ala 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 Val Tyr Tyr Cys Gln Gln Asp Tyr Thr Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 206
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 206
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr 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 Arg Glu Gly Tyr Gly Gly Ser Tyr Gly Glu Gly Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

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

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile

245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365

Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 207
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 207
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

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

385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
    610

<210> 208
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 208
gaaattgtga tgacacagag ccctccaacg ctgagcctgt ctcctggcga aagagtgacc 60

ctgagctgta gagccagcca gagcgtgtcc aacgacctga gctggtatca gcagaagcct 120

ggacaggccc ctcggctgct gatctactac gccagcatca gattcacagg catccccgcc 180

agattttccg gcagcggctc tggcacagat ttcaccctga ccataagcag cctgcagcct 240

gaggacttcg ccgtgtacta ctgtcagcag gactacacta gcccctggac ctttggccag 300

ggcaccaagg tggaaatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 209
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 209
gaggtgcagc tggttcagtc tggcgccgaa gtgaaaaagc ctggcgccac cgtgaagatc 60

agctgcaagg tgtccggctt caacatcaag gacacctaca tgcactgggt gcagcaggcc 120

cctggcaaag gacttgaatg gatgggcctg atcgaccccg ccaacgacaa taccatctac 180

gccgagaagt tccagggcag agtgaccatc accgccgaca cctctaccga caccgcctac 240

atggaactga gcagcctgag aagcgaggac accgccgtgt actactgtgc cagagaaggc 300

tacggcggca gctacggcga aggatattgg ggacagggca ccctggtcac cgttagctct 360

gctagcacca agggcccatc cgtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcc 480

tggaactcag gcgctctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacgcc 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtctacaccc tgcccccatc ccgggaggag 1080

atgaccaaga accaggtcag cctgtactgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc taagcttgtc tccgggtaaa 1350

<210> 210
<211> 1836
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 210
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgtcaagt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agagccagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccacag ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 1200

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 1260

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380

tacgccagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1500

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 1560

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1620

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680

cccgtgctgg actccgacgg ctccttcttc ctcaccagca agctcaccgt ggacaagagc 1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctctc cctgtctccg ggtaaa 1836

<210> 211
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 211
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 212
<211> 1836
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 212
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agattcagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 1200

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 1260

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380

tacgccagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1500

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 1560

gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1620

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680

cccgtgctgg actccgacgg ctccttcttc ctcaccagca agctcaccgt ggacaagagc 1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctctc cctgtctccg ggtaaa 1836

<210> 213
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 213
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr 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 Arg Glu Gly Tyr Gly Gly Ser Tyr Gly Glu Gly Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

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

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His

275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 214
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 214
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser

420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

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

Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 215
<211> 1350
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 215
gaggtgcagc tggttcagtc tggcgccgaa gtgaaaaagc ctggcgccac cgtgaagatc 60

agctgcaagg tgtccggctt caacatcaag gacacctaca tgcactgggt gcagcaggcc 120

cctggcaaag gacttgaatg gatgggcctg atcgaccccg ccaacgacaa taccatctac 180

gccgagaagt tccagggcag agtgaccatc accgccgaca cctctaccga caccgcctac 240

atggaactga gcagcctgag aagcgaggac accgccgtgt actactgtgc cagagaaggc 300

tacggcggca gctacggcga aggatattgg ggacagggca ccctggtcac cgttagctct 360

gctagcacca agggcccatc cgtcttcccc ctggcaccct cctccaagag cacctctggg 420

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcc 480

tggaactcag gcgctctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 600

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 660

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 720

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 780

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 840

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacgcc 900

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 960

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1020

aaagccaaag ggcagccccg agaaccacag gtctacaccc tgcccccatc ccgggaggag 1080

atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1140

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1200

ctggactccg acggctcctt cttcctcacc agcaagctca ccgtggacaa gagcaggtgg 1260

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1320

cagaagagcc tctccctgtc tccgggtaaa 1350

<210> 216
<211> 1836
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 216
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agattcagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 1200

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 1260

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380

tacgccagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1500

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 1560

gaggagatga ccaagaacca ggtcagcctg tactgcctgg tcaaaggctt ctatcccagc 1620

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680

cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc 1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctaag cttgtctccg ggtaaa 1836

<210> 217
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 217
Asp Ala Ser Leu Pro Tyr Leu Gln Asp Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

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

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln

100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

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

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Arg Phe Arg Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

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

Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val

530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 218
<211> 1836
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 218
gatgcatctc tgccttacct gcaggatgaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gcccctacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgtcaagt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggcgaatcag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agagccagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccacag ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960

tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatccgtt tccgtatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 1200

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 1260

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380

tacgccagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1500

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 1560

gaggagatga ccaagaacca ggtcagcctg tactgcctgg tcaaaggctt ctatcccagc 1620

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680

cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc 1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctaag cttgtctccg ggtaaa 1836

<210> 219
<211> 612
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 219
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

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

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr
    450   455   460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465   470   475   480

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            500   505   510

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

Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    530   535   540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545   550   555   560

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            580   585   590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        595   600   605

Ser Pro Gly Lys
    610

<210> 220
<211> 1836
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 220
gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cggcggagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga 420

gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480

cctggacact gtctccagct gcacgacagg gctagatctc tggtggtgcc tgcctacgcc 540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ccttctgctt tctgagccac 600

gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660

gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg 720

agattcagag tgcaggccca gagcacaaac gacggcctgg atttccaaga gagccagctg 780

gtcaagaaac tggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca 840

tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca ccccacacac 900

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tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg 1020

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080

gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140

gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 1200

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 1260

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380

tacgccagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1500

atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg 1560

gaggagatga ccaagaacca ggtcagcctg tactgcctgg tcaaaggctt ctatcccagc 1620

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680

cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc 1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctaag cttgtctccg ggtaaa 1836

<210> 221
<211> 330
<212> PRT
<213> Homo sapiens

<400> 221
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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 222
<211> 330
<212> PRT
<213> Homo sapiens

<400> 222
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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 223
<211> 330
<212> PRT
<213> Homo sapiens

<400> 223
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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 224
<211> 330
<212> PRT
<213> Homo sapiens

<400> 224
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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 225
<211> 330
<212> PRT
<213> Homo sapiens

<400> 225
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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 226
<211> 330
<212> PRT
<213> Homo sapiens

<400> 226
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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 227
<211> 330
<212> PRT
<213> Homo sapiens

<400> 227
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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

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

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 228
<211> 326
<212> PRT
<213> Homo sapiens

<400> 228
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg

1 5 10 15

Ser Thr Ser Glu Ser 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 Asn Phe Gly Thr Gln Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
100 105 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
115 120 125

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
130 135 140

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145 150 155 160

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

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
180 185 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
195 200 205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
210 215 220

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

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
245 250 255

Ser Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
260 265 270

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
275 280 285

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
290 295 300

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Pro Gly Lys
325

<210> 229
<211> 377
<212> PRT
<213> Homo sapiens

<400> 229
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
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 Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
100 105 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
115 120 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
130 135 140

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145 150 155 160

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
165 170 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
180 185 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
195 200 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
210 215 220

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225 230 235 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
245 250 255

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
275 280 285

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

290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
305 310 315 320

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
340 345 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375

<210> 230
<211> 327
<212> PRT
<213> Homo sapiens

<400> 230
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Glu Ser 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 Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro

100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

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

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
325

<210> 231
<211> 106
<212> PRT
<213> Homo sapiens

<400> 231
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15

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

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

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 232
<211> 107
<212> PRT
<213> Homo sapiens

<400> 232
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> 233
<211> 105
<212> PRT
<213> Homo sapiens

<400> 233
Gly Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser
1 5 10 15

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

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro
35 40 45

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

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65 70 75 80

Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
85 90 95

Glu Lys Thr Val Ala Pro Thr Glu Cys
100 105

<210> 234

<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 234
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

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

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro

180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 235
<211> 450
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 235
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr 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 Arg Glu Gly Tyr Gly Gly Ser Tyr Gly Glu Gly Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

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

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

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

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp

405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly Lys
450

<210> 236
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Gln or Val

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Glu or Gln

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Leu or Val

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Val or Lys

<220>
<221> MOD_RES
<222> (17)..(17)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (19)..(19)
<223> Thr or Lys

<220>
<221> MOD_RES
<222> (20)..(20)
<223> Leu or Ile

<220>
<221> MOD_RES
<222> (23)..(23)
<223> Thr or Lys

<220>
<221> MOD_RES
<222> (24)..(24)
<223> Ala or Val

<220>
<221> MOD_RES
<222> (38)..(38)
<223> Lys or Gln

<220>
<221> MOD_RES
<222> (40)..(40)
<223> Arg or Ala

<220>
<221> MOD_RES
<222> (42)..(42)
<223> Glu or Gly

<220>
<221> MOD_RES
<222> (43)..(43)
<223> Gln or Lys

<220>
<221> MOD_RES
<222> (48)..(48)
<223> Ile or Met

<220>
<221> MOD_RES
<222> (50)..(50)
<223> Arg or Leu

<220>
<221> MOD_RES
<222> (59)..(59)
<223> Lys or Ile

<220>
<221> MOD_RES
<222> (61)..(61)

<223> Asp or Ala

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Pro or Glu

<220>
<221> MOD_RES
<222> (66)..(66)
<223> Asp or Gly

<220>
<221> MOD_RES
<222> (67)..(67)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (68)..(68)
<223> Ala or Val

<220>
<221> MOD_RES
<222> (76)..(76)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (81)..(81)
<223> Leu or Met

<220>
<221> MOD_RES
<222> (82)..(82)
<223> Arg or Glu

<220>
<221> MOD_RES
<222> (87)..(87)
<223> Thr or Arg

<220>
<221> MOD_RES
<222> (115)..(115)
<223> Thr or Leu

<220>
<221> MOD_RES
<222> (116)..(116)
<223> Leu or Val

<400> 236
Glu Val Gln Leu Xaa Xaa Ser Gly Ala Glu Xaa Xaa Lys Pro Gly Ala

1 5 10 15

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

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

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

Gln Xaa Xaa Xaa Thr Ile Thr Ala Asp Thr Ser Xaa Asp Thr Ala Tyr
65 70 75 80

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

Ala Arg Glu Gly Tyr Gly Gly Ser Tyr Gly Glu Gly Tyr Trp Gly Gln
100 105 110

Gly Thr Xaa Xaa Thr Val Ser Ser
115 120

<210> 237
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ser or Glu

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Thr or Ser

<220>
<221> MOD_RES
<222> (9)..(9)

<223> Lys or Pro

<220>
<221> MOD_RES
<222> (10)..(10)
<223> Phe or Thr

<220>
<221> MOD_RES
<222> (12)..(12)
<223> Leu or Ser

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Val or Leu

<220>
<221> MOD_RES
<222> (15)..(15)
<223> Ala or Pro

<220>
<221> MOD_RES
<222> (17)..(17)
<223> Asp or Glu

<220>
<221> MOD_RES
<222> (21)..(21)
<223> Ile or Leu

<220>
<221> MOD_RES
<222> (22)..(22)
<223> Thr or Ser

<220>
<221> MOD_RES
<222> (24)..(24)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (33)..(33)
<223> Val or Leu

<220>
<221> MOD_RES
<222> (34)..(34)
<223> Ile or Ser

<220>
<221> MOD_RES

<222> (43)..(43)
<223> Ser or Ala

<220>
<221> MOD_RES
<222> (45)..(45)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (58)..(58)
<223> Val or Ile

<220>
<221> MOD_RES
<222> (60)..(60)
<223> Asp or Ala

<220>
<221> MOD_RES
<222> (63)..(63)
<223> Ala or Ser

<220>
<221> MOD_RES
<222> (67)..(67)
<223> Tyr or Ser

<220>
<221> MOD_RES
<222> (73)..(73)
<223> Phe or Leu

<220>
<221> MOD_RES
<222> (76)..(76)
<223> Asn or Ser

<220>
<221> MOD_RES
<222> (77)..(77)
<223> Thr or Ser

<220>
<221> MOD_RES
<222> (78)..(78)
<223> Val or Leu

<220>
<221> MOD_RES
<222> (80)..(80)
<223> Ala or Pro

<220>

<221> MOD_RES
<222> (83)..(83)
<223> Leu or Phe

<220>
<221> MOD_RES
<222> (87)..(87)
<223> Phe or Tyr

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Tyr or Thr

<220>
<221> MOD_RES
<222> (100)..(100)
<223> Gly or Gln

<220>
<221> MOD_RES
<222> (104)..(104)
<223> Leu or Val

<400> 237
Xaa Ile Val Met Thr Gln Xaa Pro Xaa Xaa Leu Xaa Xaa Ser Xaa Gly
1 5 10 15

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

Xaa Xaa Trp Tyr Gln Gln Lys Pro Gly Gln Xaa Pro Xaa Leu Leu Ile
35 40 45

Tyr Tyr Ala Ser Ile Arg Phe Thr Gly Xaa Pro Xaa Arg Phe Xaa Gly
50 55 60

Ser Gly Xaa Gly Thr Asp Phe Thr Xaa Thr Ile Xaa Xaa Xaa Gln Xaa
65 70 75 80

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

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

<210> 238

<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr,
Val, or not present

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Ala or Lys

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Asn or Leu

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Pro or His

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe, Trp, Tyr or Val

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Lys or Asp

<220>
<221> MOD_RES
<222> (42)..(42)
<223> Ala or Arg

<220>
<221> MOD_RES
<222> (44)..(44)
<223> Lys, Arg, or Glu

<220>
<221> MOD_RES
<222> (45)..(45)
<223> Lys, Ala, Arg, or Glu

<220>
<221> MOD_RES
<222> (54)..(54)
<223> Leu or Met

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
<221> MOD_RES
<222> (69)..(69)
<223> Gln or His

<220>
<221> MOD_RES
<222> (78)..(78)
<223> Arg or Lys

<220>
<221> MOD_RES
<222> (80)..(80)
<223> Asp or Pro

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Ala, Glu or Lys

<220>
<221> MOD_RES
<222> (107)..(107)
<223> Gly or Asp

<220>
<221> MOD_RES
<222> (108)..(108)
<223> Gln or His

<220>
<221> MOD_RES
<222> (112)..(112)
<223> Gln, Arg, or Lys

<220>
<221> MOD_RES
<222> (125)..(125)
<223> Ala, Cys, Ile, Ser, Val, or Leu

<220>
<221> MOD_RES
<222> (126)..(126)

<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>
<221> MOD_RES
<222> (150)..(150)
<223> Ala or Val

<220>
<221> MOD_RES
<222> (164)..(164)
<223> Cys or Gly

<220>
<221> MOD_RES
<222> (170)..(170)
<223> Arg or Pro

<220>
<221> MOD_RES
<222> (171)..(171)
<223> Ala or Gly

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Arg, Ile, or Lys

<220>
<221> MOD_RES
<222> (188)..(188)
<223> Gln or Pro

<220>
<221> MOD_RES
<222> (189)..(189)
<223> Arg or Pro

<220>
<221> MOD_RES
<222> (196)..(196)
<223> Ala, Cys, Leu, or Val

<220>
<221> MOD_RES
<222> (213)..(213)
<223> Ala, Cys, Asn, Ser, or Thr

<220>
<221> MOD_RES
<222> (217)..(217)
<223> Leu, Ala, or Val

<220>
<221> MOD_RES

<222> (225)..(225)
<223> Glu or Pro

<220>
<221> MOD_RES
<222> (239)..(239)
<223> His or Pro

<220>
<221> MOD_RES
<222> (240)..(240)
<223> Leu, Asp, Asn, or Tyr

<220>
<221> MOD_RES
<222> (241)..(241)
<223> Arg, Ala, Asp, Leu, Gln, or Tyr

<220>
<221> MOD_RES
<222> (242)..(242)
<223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser,
Val, Trp, or Tyr

<220>
<221> MOD_RES
<222> (244)..(244)
<223> Val, Ile, or Lys

<220>
<221> MOD_RES
<222> (249)..(249)
<223> Thr or Ala

<220>
<221> MOD_RES
<222> (251)..(251)
<223> Asp or Gly

<220>
<221> MOD_RES
<222> (257)..(257)
<223> Glu, Lys, or Pro

<220>
<221> MOD_RES
<222> (258)..(258)
<223> Ser or Cys

<220>
<221> MOD_RES
<222> (260)..(260)
<223> Leu, Asp, Phe, Gln, or Thr

<220>
<221> MOD_RES
<222> (265)..(265)
<223> Val or Phe

<220>
<221> MOD_RES
<222> (270)..(270)
<223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>
<221> MOD_RES
<222> (272)..(272)
<223> Cys or Val

<220>
<221> MOD_RES
<222> (292)..(292)
<223> Trp or Arg

<220>
<221> MOD_RES
<222> (301)..(301)
<223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Thr, Val, Trp, or Tyr

<220>
<221> MOD_RES
<222> (302)..(302)
<223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>
<221> MOD_RES
<222> (325)..(325)
<223> Lys or Val

<220>
<221> MOD_RES
<222> (332)..(332)
<223> Ala, Cys, Ser, or Val

<220>
<221> MOD_RES
<222> (352)..(352)
<223> Cys, Leu, or Val

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Val or Arg

<220>
<221> MOD_RES

<222> (365)..(365)
<223> Leu, Gln, His, Ile, Lys, or Ser

<220>
<223> See specification as filed for detailed description of substitutions and preferred embodiments

<400> 238
Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Xaa Ser Xaa Xaa Asp Glu His
35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Xaa
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Xaa Leu Gln Leu His Asp Xaa Xaa Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Xaa Xaa Pro Ile Pro
180 185 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Xaa Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
210 215 220

Xaa Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser Xaa Xaa
225 230 235 240

Xaa Xaa Arg Xaa Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
245 250 255

Xaa Xaa Gln Xaa Val Lys Lys Leu Xaa Glu Pro Pro Pro Xaa Gly Xaa
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 239
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr,
Val, or not present

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe, Trp, Tyr or Val

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Lys or Asp

<220>
<221> MOD_RES
<222> (42)..(42)
<223> Arg or Ala

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Ala, Glu, or Lys

<220>
<221> MOD_RES
<222> (126)..(126)
<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Arg, Ile, or Lys

<220>
<221> MOD_RES
<222> (242)..(242)
<223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser,
Val, Trp, or Tyr

<220>

<221> MOD_RES
<222> (270)..(270)
<223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>
<221> MOD_RES
<222> (301)..(301)
<223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Thr, Val, Trp, or Tyr

<220>
<221> MOD_RES
<222> (302)..(302)
<223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>
<221> MOD_RES
<222> (332)..(332)
<223> Ala, Cys, Ser, or Val

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Val or Arg

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Leu, Gln, His, Ile, Lys, or Ser

<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 239
Xaa Ala Ser Leu Pro Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Xaa Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Xaa Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
    290   295   300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305   310   315   320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
                325   330   335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
            340   345   350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
        355   360   365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
    370   375   380

<210> 240
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr,
      Val, or not present

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Ala or Lys

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Asn or Leu

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Pro or His

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe, Trp, Tyr or Val

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Lys or Asp

<220>
<221> MOD_RES
<222> (42)..(42)
<223> Ala or Arg

<220>
<221> MOD_RES
<222> (44)..(44)
<223> Lys, Arg, or Glu

<220>
<221> MOD_RES
<222> (45)..(45)
<223> Lys, Ala, Arg, or Glu

<220>
<221> MOD_RES
<222> (54)..(54)
<223> Leu or Met

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
<221> MOD_RES
<222> (69)..(69)
<223> Gln or His

<220>
<221> MOD_RES
<222> (78)..(78)
<223> Arg or Lys

<220>
<221> MOD_RES
<222> (80)..(80)
<223> Asp or Pro

<220>
<221> MOD_RES
<222> (93)..(93)

<223> Ala, Glu or Lys

<220>
<221> MOD_RES
<222> (107)..(107)
<223> Gly or Asp

<220>
<221> MOD_RES
<222> (108)..(108)
<223> Gln or His

<220>
<221> MOD_RES
<222> (112)..(112)
<223> Gln, Arg, or Lys

<220>
<221> MOD_RES
<222> (125)..(125)
<223> Ala, Cys, Ile, Ser, Val, or Leu

<220>
<221> MOD_RES
<222> (126)..(126)
<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>
<221> MOD_RES
<222> (150)..(150)
<223> Ala or Val

<220>
<221> MOD_RES
<222> (164)..(164)
<223> Cys or Gly

<220>
<221> MOD_RES
<222> (170)..(170)
<223> Arg or Pro

<220>
<221> MOD_RES
<222> (171)..(171)
<223> Ala or Gly

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Arg, Ile, or Lys

<220>
<221> MOD_RES

<222> (188)..(188)
<223> Gln or Pro

<220>
<221> MOD_RES
<222> (189)..(189)
<223> Arg or Pro

<220>
<221> MOD_RES
<222> (196)..(196)
<223> Ala, Cys, Leu, or Val

<220>
<221> MOD_RES
<222> (213)..(213)
<223> Ala, Cys, Asn, Ser, or Thr

<220>
<221> MOD_RES
<222> (217)..(217)
<223> Leu, Ala, or Val

<220>
<221> MOD_RES
<222> (225)..(225)
<223> Glu or Pro

<220>
<221> MOD_RES
<222> (239)..(239)
<223> His or Pro

<220>
<221> MOD_RES
<222> (240)..(240)
<223> Leu, Asp, Asn, or Tyr

<220>
<221> MOD_RES
<222> (241)..(241)
<223> Arg, Ala, Asp, Leu, Gln, or Tyr

<220>
<221> MOD_RES
<222> (242)..(242)
<223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser,
Val, Trp, or Tyr

<220>
<221> MOD_RES
<222> (244)..(244)
<223> Val, Ile, or Lys

<220>
<221> MOD_RES
<222> (249)..(249)
<223> Thr or Ala

<220>
<221> MOD_RES
<222> (251)..(251)
<223> Asp or Gly

<220>
<221> MOD_RES
<222> (257)..(257)
<223> Glu, Lys, or Pro

<220>
<221> MOD_RES
<222> (258)..(258)
<223> Ser or Cys

<220>
<221> MOD_RES
<222> (260)..(260)
<223> Leu, Asp, Phe, Gln, or Thr

<220>
<221> MOD_RES
<222> (265)..(265)
<223> Val or Phe

<220>
<221> MOD_RES
<222> (270)..(270)
<223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>
<221> MOD_RES
<222> (272)..(272)
<223> Cys or Val

<220>
<221> MOD_RES
<222> (292)..(292)
<223> Trp or Arg

<220>
<221> MOD_RES
<222> (301)..(301)
<223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Thr, Val, Trp, or Tyr

<220>
<221> MOD_RES
<222> (302)..(302)

<223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>
<221> MOD_RES
<222> (325)..(325)
<223> Lys or Val

<220>
<221> MOD_RES
<222> (332)..(332)
<223> Ala, Cys, Ser, or Val

<220>
<221> MOD_RES
<222> (352)..(352)
<223> Cys, Leu, or Val

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Val or Arg

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Leu, Gln, His, Ile, Lys, or Ser

<220>
<221> MOD_RES
<222> (381)..(390)
<223> This region may encompass one of the following sequences: "GGGGS" or "GGGGSGGGGS" or "EPKSS"

<220>
<223> See specification as filed for detailed description of substitutions and preferred embodiments

<400> 240
Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Xaa Ser Xaa Xaa Asp Glu His
35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Xaa
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Xaa Leu Gln Leu His Asp Xaa Xaa Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Xaa Xaa Pro Ile Pro
180 185 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Xaa Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
210 215 220

Xaa Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser Xaa Xaa
225 230 235 240

Xaa Xaa Arg Xaa Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
245 250 255

Xaa Xaa Gln Xaa Val Lys Lys Leu Xaa Glu Pro Pro Pro Xaa Gly Xaa
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser

275 280 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Xaa Xaa Xaa
370 375 380

Xaa Xaa Xaa Xaa Xaa Xaa Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

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

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 241
<211> 617
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr,
Val, or not present

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe, Trp, Tyr or Val

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Lys or Asp

<220>
<221> MOD_RES
<222> (42)..(42)
<223> Arg or Ala

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Ala, Glu, or Lys

<220>
<221> MOD_RES
<222> (126)..(126)
<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Arg, Ile, or Lys

<220>
<221> MOD_RES
<222> (242)..(242)
<223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser,
Val, Trp, or Tyr

<220>
<221> MOD_RES
<222> (270)..(270)
<223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>
<221> MOD_RES
<222> (301)..(301)
<223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Thr, Val, Trp, or Tyr

<220>
<221> MOD_RES
<222> (302)..(302)
<223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>

<221> MOD_RES
<222> (332)..(332)
<223> Ala, Cys, Ser, or Val

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Val or Arg

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Leu, Gln, His, Ile, Lys, or Ser

<220>
<221> MOD_RES
<222> (381)..(390)
<223> This region may encompass one of the following sequences:
"GGGGS" or "GGGGSGGGGS" or "EPKSS"

<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 241
Xaa Ala Ser Leu Pro Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Xaa Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Xaa Val Thr

115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Xaa Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Xaa Xaa Xaa
370 375 380

Xaa Xaa Xaa Xaa Xaa Xaa Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

545 550 555 560

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

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 242
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 242
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

Tyr Tyr Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala 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 Val Tyr Tyr Cys Gln Gln Asp Tyr Asn Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 243
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 243
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

Tyr Tyr Ala Ser Ile Arg Ala Thr Gly Ile Pro Ala 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 Val Tyr Tyr Cys Gln Gln Asp Tyr Asn Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 244
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 244
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

Tyr Tyr Ala Ser Thr Arg Phe Thr Gly Ile Pro Ala 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 Val Tyr Tyr Cys Gln Gln Asp Tyr Asn Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 245
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 245
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 246
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 246
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

Tyr Tyr Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala 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 Val Tyr Phe Cys Gln Gln Asp Tyr Asn Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 247
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 247
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 248
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 248
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

Tyr Tyr Ala Ser Ile Arg Ala Thr Gly Ile Pro Ala 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 Val Tyr Phe Cys Gln Gln Asp Tyr Asn Ser Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 249
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 249
Glu Ile Val Met Thr Gln Ser Pro Pro Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 250

<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 250
Asp Thr Tyr Met His
1 5

<210> 251
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 251
Arg Ile Asp Pro Ala Asn Asp Asn Thr Lys Tyr Asp Pro Lys Phe Gln
1 5 10 15

Asp

<210> 252
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 252
Leu Ile Asp Pro Ala Asn Asp Asn Thr Ile Tyr Ala Glu Lys Phe Gln
1 5 10 15

Gly

<210> 253
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 253
Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ile
1 5 10

<210> 254
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 254
Tyr Ala Ser Ile Arg Phe Thr
1 5

<210> 255
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 255
Arg Ala Ser Gln Ser Val Ser Asn Asp Leu Ser
1 5 10

<210> 256
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
10xHis tag

<400> 256
His His His His His His His His His His
1 5 10

<210> 257
<211> 15
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> SITE
<222> (1)..(15)
<223> This sequence may encompass 1-5 "Gly Gly Pro"
repeating units

<400> 257
Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Gly Pro
1 5 10 15

<210> 258
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> SITE
<222> (1)..(25)
<223> This sequence may encompass 1-5 "Gly Gly Gly Gly Ser"
repeating units

<400> 258
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 259
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
6xHis tag

<400> 259
His His His His His His

1 5