

SEQUENCE LISTING

<110> ZYMEWORKS INC.

<120> Anti-HER2 Biparatopic Antibody-Drug Conjugates and Methods of Use

<130> V813602WO

<150> 62/642,483
<151> 2018-03-13

<150> 62/658,477
<151> 2018-04-16

<150> 62/743,884
<151> 2018-10-10

<160> 89

<170> PatentIn version 3.5

<210> 1
<211> 217
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Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
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Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
115 120 125

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

130

135

140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 145 150 155 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 165 170 175

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 180 185 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 210 215

<210> 2
 <211> 607
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 <213> Homo sapiens

<400> 2

Thr Gln Val Cys Thr Gly Thr Asp Met Lys Leu Arg Leu Pro Ala Ser
 1 5 10 15

Pro Glu Thr His Leu Asp Met Leu Arg His Leu Tyr Gln Gly Cys Gln
 20 25 30

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

Leu Ser Phe Leu Gln Asp Ile Gln Glu Val Gln Gly Tyr Val Leu Ile
 50 55 60

Ala His Asn Gln Val Arg Gln Val Pro Leu Gln Arg Leu Arg Ile Val
 65 70 75 80

Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu Asp
 85 90 95

Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro Val Thr Gly Ala Ser Pro
 100 105 110

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

Gly Gly Val Leu Ile Gln Arg Asn Pro Gln Leu Cys Tyr Gln Asp Thr
 130 135 140

Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn	Asn	Gln	Leu	Ala	Leu	Thr	145	150	155	160
Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	His	Pro	Cys	Ser	Pro	Met	165	170	175	
Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser	Ser	Glu	Asp	Cys	Gln	Ser	180	185	190	
Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys	Ala	Arg	Cys	Lys	Gly	Pro	195	200	205	
Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys	Ala	Ala	Gly	Cys	Thr	Gly	210	215	220	
Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	His	Phe	Asn	His	Ser	Gly	225	230	235	240
Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	245	250	255	
Phe	Glu	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Ala	Ser	260	265	270	
Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Tyr	Leu	Ser	Thr	Asp	Val	Gly	Ser	275	280	285	
Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln	Glu	Val	Thr	Ala	Glu	Asp	290	295	300	
Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys	Pro	Cys	Ala	Arg	Val	Cys	305	310	315	320
Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu	Val	Arg	Ala	Val	Thr	Ser	325	330	335	
Ala	Asn	Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys	Lys	Ile	Phe	Gly	Ser	Leu	340	345	350	
Ala	Phe	Leu	Pro	Glu	Ser	Phe	Asp	Gly	Asp	Pro	Ala	Ser	Asn	Thr	Ala	355	360	365	
Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe	Glu	Thr	Leu	Glu	Glu	Ile	370	375	380	
Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	Asp	Ser	Leu	Pro	Asp	Leu	385	390	395	400

Ser Val Phe Gln Asn Leu Gln Val Ile Arg Gly Arg Ile Leu His Asn
405 410 415

Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu Gly
420 425 430

Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly Leu Ala Leu Ile His His
435 440 445

Asn Thr His Leu Cys Phe Val His Thr Val Pro Trp Asp Gln Leu Phe
450 455 460

Arg Asn Pro His Gln Ala Leu Leu His Thr Ala Asn Arg Pro Glu Asp
465 470 475 480

Glu Cys Val Gly Glu Gly Leu Ala Cys His Gln Leu Cys Ala Arg Gly
485 490 495

His Cys Trp Gly Pro Gly Pro Thr Gln Cys Val Asn Cys Ser Gln Phe
500 505 510

Leu Arg Gly Gln Glu Cys Val Glu Glu Cys Arg Val Leu Gln Gly Leu
515 520 525

Pro Arg Glu Tyr Val Asn Ala Arg His Cys Leu Pro Cys His Pro Glu
530 535 540

Cys Gln Pro Gln Asn Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp
545 550 555 560

Gln Cys Val Ala Cys Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala
565 570 575

Arg Cys Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp
580 585 590

Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn
595 600 605

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<213> Artificial Sequence

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<400> 3

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Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Thr	Asp	Tyr	20	25	30	
Thr	Met	Asp	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	35	40	45	
Ala	Asp	Val	Asn	Pro	Asn	Ser	Gly	Gly	Ser	Ile	Tyr	Asn	Gln	Arg	Phe	50	55	60	
Lys	Gly	Arg	Phe	Thr	Leu	Ser	Val	Asp	Arg	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	Asn	Leu	Gly	Pro	Ser	Phe	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	100	105	110	
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	115	120	125	
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	130	135	140	
Gly	Cys	Leu	Val	Lys	Gly	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	145	150	155	160
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	165	170	175	
Lys	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	180	185	190	
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	195	200	205	
Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	210	215	220	
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	225	230	235	240
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	245	250	255	

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Val
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Leu
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Leu Thr Trp Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

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tcttgcgccg ctagtggctt cacttttacc gactacacca tggattgggt gcgacaggca 120
cctggaaagg gcctggagtg ggtcgccgat gtgaacccaa atagcggagg ctccatctac 180
aaccagcggg tcaagggccg gttcaccctg tcagtggacc ggagcaaaaa caccctgtat 240

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg 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 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 6
<211> 8
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<220>
<223> Artificial sequence

<400> 6

Gly Phe Thr Phe Thr Asp Tyr Thr
1 5

<210> 7
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 7

Ala Arg Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr
1 5 10

<210> 8
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<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 8

Val Asn Pro Asn Ser Gly Gly Ser
1 5

<210> 9
<211> 214
<212> PRT
<213> Artificial Sequence

<220>

<223> Artificial sequence

<400> 9

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ile Tyr Pro Tyr
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
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<210> 10

<211> 642

<212> DNA
<213> Artificial Sequence

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ggcaaagcac ccaagctgct gatctatagc gcctcctacc ggtataccgg cgtgccctct 180
agattctctg gcagtgggtc aggaacagac ttactctga ccatctctag tctgcagcct 240
gaggatttcg ctacctacta ttgccagcag tactatatct acccatatac ctttggccag 300
gggacaaaag tggagatcaa gaggactgtg gccgctccct ccgtcttcat ttttccccct 360
tctgacgaac agctgaaaag tggcacagcc agcgtggtct gtctgctgaa caatttctac 420
cctcgcgaa ccaaagtga gtggaaggtc gataacgctc tgcagagcgg caacagccag 480
gagtctgtga ctgaacagga cagtaaagat tcaacctata gcctgtcaag cacactgact 540
ctgagcaagg cagactacga gaagcacaaa gtgtatgcct gcgaagtcac acatcagggg 600
ctgtcctctc ctgtgactaa gagctttaac agaggagagt gt 642

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<400> 11
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Ile Gly
20 25 30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ile Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 12
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Artificial sequence

<400> 12

Gln Asp Val Ser Ile Gly
1 5

<210> 13
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 13

Gln Gln Tyr Tyr Ile Tyr Pro Tyr Thr
1 5

<210> 14
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 14
Ser Ala Ser

<210> 15
<211> 222
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 15

Asp Tyr Lys Asp Asp Asp Asp Lys Asp Ile Gln Met Thr Gln Ser Pro
1 5 10 15

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

Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro
35 40 45

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser
50 55 60

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

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

Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val
100 105 110

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

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

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
145 150 155 160

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

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
180 185 190

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
195 200 205

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

<210> 16
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<212> DNA
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<400> 16
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gcttctgtgg gcgatagggt cactattacc tgccgcgcat ctcaggacgt gaacaccgca 120
gtcgcctggt accagcagaa gcctgggaaa gctccaaagc tgctgatcta cagtgcata 180
ttcctgtatt caggagtgcc cagccggttt agcggcagca gatctggcac cgatttcaca 240
ctgactatatt ctagtctgca gcctgaggac tttgccacat actattgcca gcagcactat 300

accacacccc ctacttttcgg ccaggggacc aaagtggaga tcaagcgaac tgtggccgct 360
ccaagtgtct tcattttttcc acccagcgat gaaagactga agtccggcac agcttctgtg 420
gtctgtctgc tgaacaattt ttaccccaga gaggccaaag tgcagtggaa ggtcgacaac 480
gctctgcaga gtggcaacag ccaggagagc gtgacagaac aggattccaa agactctact 540
tatagtctgt caagcaccct gacactgagc aaggcagact acgaaaagca taaagtgtat 600
gcctgtgagg tcacacatca ggggctgtca tcaccagtca ccaaatacatt caatcggggg 660
gagtgc 666

<210> 17
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<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 17

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 18
<211> 222
<212> PRT
<213> Artificial Sequence

<220>
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<400> 18

Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	1	5	10	15
Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	20	25	30	
Ala	Ser	Gln	Asp	Val	Asn	Thr	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	35	40	45	
Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ser	Ala	Ser	Phe	Leu	Tyr	Ser	50	55	60	
Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Thr	Asp	Phe	Thr	65	70	75	80
Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	85	90	95	
Gln	Gln	His	Tyr	Thr	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	100	105	110	
Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	115	120	125	
Ser	Asp	Glu	Arg	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	130	135	140	
Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	145	150	155	160
Ala	Leu	Gln	Ser	Gly	Asn	Ser	Lys	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	165	170	175	
Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Arg	Leu	Thr	Leu	Ser	Lys	Ala	180	185	190	
Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	195	200	205	
Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	210	215	220			

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gtcgcctggt accagcagaa gcctgggaaa gctccaaagc tgctgatcta cagtgcacatca 180
ttcctgtatt caggagtgcc cagccgggtt agcggcagca gatctggcac cgatttcaca 240
ctgactatatt ctagtctgca gcctgaggac tttgccacat actattgcca gcagcactat 300
accacacccc ctacttttcgg ccaggggacc aaagtggaga tcaagcgaac tgtggccgct 360
ccaagtgtct tcatttttcc acccagcgat gaaagactga agtccggcac agcttctgtg 420
gtctgtctgc tgaacaattt ttaccccaga gaggccaaag tgcagtggaa ggtcgacaac 480
gctctgcaga gtggcaacag caaggagagc gtgacagaac aggattccaa agactctact 540
tatagtctgt caagcagact gacactgagc aaggcagact acgaaaagca taaagtgtat 600
gcctgtgagg tcacacatca ggggctgtca tcaccagtca ccaaatcatt caatcggggg 660
gagtgc 666

<210> 20
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<400> 20

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 21
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 21

Gln Asp Val Asn Thr Ala
1 5

<210> 22
<211> 9
<212> PRT
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<220>
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<400> 22

Gln Gln His Tyr Thr Thr Pro Pro Thr
1 5

<210> 23
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<400> 23
Ser Ala Ser

<210> 24
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<400> 24

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

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

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ile Tyr Pro Ala
 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> 25
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 ggcaaagcac ccaagctgct gatctatagc gcctcctacc ggtataccgg cgtgccctct 180
 agattctctg gcagtgggtc aggaacagac ttactctga ccatctctag tctgcagcct 240
 gaggatttcg ctacctacta ttgccagcag tactatatct acccagccac ctttggccag 300
 gggacaaaag tggagatcaa gaggactgtg gccgctccct ccgtcttcat ttttccccct 360
 tctgacgaac agctgaaaag tggcacagcc agcgtggtct gtctgctgaa caatttctac 420

cctcgcggaag ccaaagtgca gtggaaggtc gataacgctc tgcagagcgg caacagccag	480
gagtctgtga ctgaacagga cagtaaagat tcaacctata gcctgtcaag cacactgact	540
ctgagcaagg cagactacga gaagcacaaa gtgtatgcct gcgaagtcac acatcagggg	600
ctgtcctctc ctgtgactaa gagctttaac agaggagagt gt	642

<210> 26
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificial sequence

<400> 26

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

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

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

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

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

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

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys
			100					105		

<210> 27
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificial sequence

<400> 27

Gln	Asp	Val	Ser	Ile	Gly
1				5	

<210> 28
 <211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 28

Gln Gln Tyr Tyr Ile Tyr Pro Ala Thr
1 5

<210> 29
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 29
Ser Ala Ser

<210> 30
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 30

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

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

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

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

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

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met 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	Glu	Val	Thr	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	145	150	155
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
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
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
Val	Tyr	Pro	Pro	Ser	Arg	Asp	Glu	Leu	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 Ala Leu Val 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

<210> 31
 <211> 1347
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial sequence

<400> 31
 gaggtgcagc tggtcgaaag cggaggagga ctggtgcagc caggagggtc actgcgactg 60
 agctgcgcag cttccggctt caacatcaag gacacctaca ttcactgggt ccgccaggct 120
 cctggaaaag gcctggagtg ggtggcacga atctatccaa ctaatggata cacccggtat 180
 gccgactccg tgaagggccg gttcaccatt tctgcagata caagtaaaaa cactgcctac 240
 ctgcagatga acagcctgcg agccgaagat acagccgtgt actattgcag ccgatgggga 300
 ggcgacggct tctacgctat ggattattgg gggcagggaa ccctgggtcac agtgagctcc 360
 gcatcaacaa aggggcctag cgtgtttcca ctggccccct ctagtaaadc cacctctggg 420
 ggaacagcag ccctgggatg tgaggtgacc gactacttcc cagagcccgt cactgtgagc 480
 tggaactccg gcgccctgac atctggggtc catacttttc ctgctgtgct gcagtcaagc 540
 ggctgtaca gcctgtcctc tgtgggtcact gtgccaagtt caagcctggg gactcagacc 600
 tatatctgca acgtgaatca caagccatcc aataccaaag tcgacaagaa agtggaaacc 660
 aagtcttgtg ataaaacaca tacttgcccc ccttgtcctg caccagagct gctgggagga 720
 ccaagcgtgt tcctgtttcc acccaagcct aaagacaccc tgatgattag taggactcca 780
 gaagtcacct gcgtggctgt ggacgtgagc cacgaggacc ccgaagtcaa gttcaactgg 840
 tacgtggatg gcgtcgaggt gcataatgcc aagacaaaac ccaggaggga acagtacaac 900
 tccacttatc gcgtcgtgtc tgtcctgacc gtgctgcacc aggactggct gaacggcaag 960
 gagtataagt gcaaagtgag caataaggct ctgcccgcac ctatcgagaa aacaatttcc 1020

aaggctaaag ggcagcctag agaaccacag gtgtacgtgt accctccatc tagggacgag 1080
 ctgaccaaga accaggtcag tctgacatgt ctggtgaaag ggttctatcc cagcgatatc 1140
 gcagtggagt gggaatccaa tggacagcct gagaacaatt acaagaccac acccctgtg 1200
 ctggactctg atggaagttt cgccctggtg agtaagctga ccgtcgataa atcacggtgg 1260
 cagcagggca acgtgttcag ctgttcagtg atgcacgaag cactgcacaa ccactacacc 1320
 cagaaaagcc tgtccctgtc ccccggc 1347

<210> 32
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificial sequence

<400> 32

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
 20 25 30

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 33
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificial sequence

<400> 33

Gly Phe Asn Ile Lys Asp Thr Tyr
1 5

<210> 34

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial sequence

<400> 34

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr
1 5 10

<210> 35

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial sequence

<400> 35

Ile Tyr Pro Thr Asn Gly Tyr Thr
1 5

<210> 36

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial sequence

<400> 36

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

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

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

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

Lys Gly Arg Phe Thr Phe Ser Val Asp Arg 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 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140

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

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

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

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220

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

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Val
 340 345 350

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

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 385 390 395 400

Asp Ser Asp Gly Ser Phe Ala Leu Val Ser Lys Leu Thr Val Asp Lys
 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

<210> 37
 <211> 1344
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial sequence

<400> 37
 gaggtgcagc tgggtggaatc aggagggggc ctggtgcagc ccggagggtc tctgcgactg 60
 tcatgtgccg cttctggggt cactttcgca gactacacaa tggattgggt gcgacaggcc 120
 cccggaaagg gactggagtg ggtgggcat gtcaacccta attctggcgg gagtatctac 180
 aaccagcggg tcaaggggag attcactttt tcagtggaca gaagcaaaaa caccctgtat 240
 ctgcagatga acagcctgag ggccgaagat accgctgtct actattgcgc tcgcaatctg 300
 ggccccagtt tctactttga ctattggggg cagggaaccc tggtgacagt cagctccgct 360
 agcactaagg ggccttccgt gtttccactg gctccctcta gtaaataccac ctctggaggc 420
 acagctgcac tgggatgtct ggtgaaggat tacttccctg aaccagtcac agtgagttgg 480
 aactcagggg ctctgacaag tggagtccat acttttcccg cagtgtgca gtcaagcgga 540
 ctgtactccc tgtcctctgt ggtcaccgtg cctagttcaa gcctgggcac ccagacatat 600
 atctgcaacg tgaatcacia gccatcaaat acaaaagtcg acaagaaagt ggagcccaag 660
 agctgtgata aaactcatal ctgcccacct tgtccggcgc cagaactgct gggaggacca 720
 agcgtgttcc tgtttccacc caagcctaaa gacaccctga tgatttcccg gactcctgag 780
 gtcacctgcg tggtcgtgga cgtgtctcac gaggaccccg aagtcaagtt caactggtac 840

gtggatggcg tcgaagtgca taatgccaa accaaacccc gggaggaaca gtacaactct 900
acctatagag tcgtgagtgt cctgacagt ctgcaccagg actggctgaa tgggaaggag 960
tataagtgt aagttagcaa caaagccctg cccgccccaa tcgaaaaaac aatctctaaa 1020
gcaaaaggac agcctcgca accacaggtc tacgtctacc ccccatcaag agatgaactg 1080
acaaaaaatc aggtctctct gacatgcctg gtcaaaggat tctacccttc cgacatcgcc 1140
gtggagtggg aaagtaacgg ccagcccag aacaattaca agaccacacc ccctgtcctg 1200
gactctgatg ggagtttcgc tctggtgtca aagctgaccg tcgataaaag ccggtggcag 1260
cagggcaatg tgtttagctg ctccgtcatg cacgaagccc tgcacaatca ctacacacag 1320
aagtccctga gcctgagccc tggc 1344

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

<220>
<223> Artificial sequence

<400> 38

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

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

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

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

Lys Gly Arg Phe Thr Phe Ser Val Asp Arg 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 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 39
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 39

Gly Phe Thr Phe Ala Asp Tyr Thr
1 5

<210> 40
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 40

Ala Arg Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr
1 5 10

<210> 41
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 41

Val Asn Pro Asn Ser Gly Gly Ser
1 5

<210> 42
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 42

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Thr Gly Ser Asp Ile Gln Met
1 5 10 15

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

Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Ile Gly Val Ala Trp Tyr
35 40 45

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

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

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

Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ile Tyr Pro Tyr Thr Phe Gly Gln
100 105 110

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

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

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
145 150 155 160

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

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Glu
180 185 190

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
195 200 205

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
210 215 220

Glu Cys
225

<210> 43
<211> 678
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 43
tatccctacg atgtgcctga ctacgctact ggctccgata tccagatgac ccagtctcca 60
agctccctga gtgcatcagt gggggaccga gtcaccatca catgcaaggc ttcccaggat 120
gtgtctattg gagtcgcatg gtaccagcag aagccaggca aagcacccaa gctgctgata 180
tacagcgct cctaccggta tactggggtg ccttccagat tctctggcag tgggtcagga 240
accgacttta ctctgacat ctctagtctg cagcccaggg atttcgccac ctactattgc 300

cagcagtact atatctaccc ttataccttt ggccagggga caaaagtgga gatcaagagg	360
acagtggccg ctccaagtgt cttcatTTTT ccccttccg acgaagagct gaaaagtgga	420
actgcttcag tggctctgtct gctgaacaat ttctaccccc gcgaagccaa agtgcagtgg	480
aaggctcgata acgctctgca gagcggcaat tccgaggagt ctgtgacaga acaggacagt	540
aaagattcaa cttatagcct gtcaagcaca ctggagctgt ctaaggcaga ctacgagaag	600
cacaaagtgt atgcctgcga agtcacccat caggggctgt cctctcccgt gacaaagagc	660
tttaacagag gagagtgt	678

<210> 44
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificial sequence

<400> 44

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

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

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

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

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

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

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys
			100							105

<210> 45
 <211> 481
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificial sequence

<400> 45

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	1	5	10	15
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Val	Asn	Thr	Ala	20	25	30	
Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	35	40	45	
Tyr	Ser	Ala	Ser	Phe	Leu	Tyr	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	50	55	60	
Ser	Arg	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	65	70	75	80
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	His	Tyr	Thr	Thr	Pro	Pro	85	90	95	
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Gly	Gly	Ser	Gly	Gly	100	105	110	
Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Glu	115	120	125	
Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	130	135	140	
Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Thr	Tyr	145	150	155	160
Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	165	170	175	
Arg	Ile	Tyr	Pro	Thr	Asn	Gly	Tyr	Thr	Arg	Tyr	Ala	Asp	Ser	Val	Lys	180	185	190	
Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	Ala	Tyr	Leu	195	200	205	
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ser	210	215	220	
Arg	Trp	Gly	Gly	Asp	Gly	Phe	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	225	230	235	240
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ala	Glu	Pro	Lys	Ser	Ser	Asp	Lys	245	250	255	

Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	
			260					265					270			
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	
		275					280					285				
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	
	290					295					300					
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	
305					310					315					320	
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	
				325					330					335		
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	
			340					345					350			
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	
		355					360					365				
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	
	370					375					380					
Tyr	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	
385					390					395					400	
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	
				405					410					415		
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	
			420					425					430			
Asp	Glu	Asp	Gly	Ser	Phe	Ala	Leu	Val	Ser	Lys	Leu	Thr	Val	Asp	Lys	
		435					440					445				
Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	
	450					455					460					
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	
465					470					475					480	

Lys

<210> 46
 <211> 1443
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Artificial sequence

<400> 46

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc	60
atcacttgcc gggcaagtca ggacgttaac accgctgtag cttggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctattct gcacccctttt tgtacagtgg ggtcccatca	180
aggttcagtg gcagtcgata tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg caacttacta ctgtcaacag cattacacta cccacccac ttctggccaa	300
gggaccaaag tggagatcaa aggtggttct ggtggtggtt ctggtggtgg ttctggtggt	360
ggttctggtg gtggttctgg tgaagtgcag ctggtggagt ctgggggagg cttggtacag	420
cctggcgggt ccctgagact ctctgtgca gcctctggat tcaacattaa agatacttat	480
atccactggg tccggcaagc tccagggaag ggcctggagt gggtcgcacg tatttatccc	540
acaaatggtt acacacggta tgcggactct gtgaagggcc gattcaccat ctccgcagac	600
acttccaaga acaccgcgta tctgcaaatg aacagtctga gagctgagga cacggccgtt	660
tattactgtt caagatgggg cggagacggt ttctacgcta tggactactg gggccaaggg	720
accctggtca ccgtctctc agccgccgag cccaagagca gcgataagac ccacacctgc	780
cctccctgtc cagctccaga actgctggga ggacctagcg tgttcctgtt tccccctaag	840
ccaaaagaca ctctgatgat ttccaggact cccgaggtga cctgcgtggt ggtggacgtg	900
tctcacgagg accccgaagt gaagttcaac tggtagctgg atggcgtgga agtgcataat	960
gctaagacaa aaccaagaga ggaacagtac aactccactt atcgcgtcgt gagcgtgctg	1020
accgtgctgc accaggactg gctgaacggg aaggagtata agtgcaaagt cagtaataag	1080
gccctgcctg ctccaatcga aaaaaccatc tctaaggcca aaggccagcc aagggagccc	1140
caggtgtaca catacccacc cagcagagac gaactgacca agaaccaggt gtccctgaca	1200
tgtctggtga aaggcttcta tcctagtgat attgctgtgg agtggaatc aaatggacag	1260
ccagagaaca attacaagac cacacctcca gtgctggacg aggatggcag ctctgccctg	1320
gtgtccaagc tgacagtgga taaatctcga tggcagcagg ggaacgtgtt tagttgttca	1380
gtgatgcatg aagccctgca caatcattac actcagaaga gcctgtccct gtctcccggc	1440
aaa	1443

<210> 47

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial sequence

<400> 47

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 48

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial sequence

<400> 48

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 49

<211> 481

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial sequence

<400> 49

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Ser Gly Gly
100 105 110

Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Glu
115 120 125

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
130 135 140

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
145 150 155 160

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

Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys
180 185 190

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

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
450 455 460

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
465 470 475 480

Lys

<210> 50
<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 50
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca ggacgttaac accgctgtag cttggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctattct gcatcctttt tgtacagtgg ggtcccatca 180
aggttcagtg gcagtcgata tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag cattacacta cccacccac ttctggccaa 300
gggaccaaag tggagatcaa aggtggttct ggtggtggtt ctggtggtgg ttctggtggt 360
ggttctggtg gtggttctgg tgaagtgcag ctggtggagt ctgggggagg cttggtacag 420
cctggcggtt ccctgagact ctctgtgca gcctctggat tcaacattaa agatacttat 480
atccactggg tccggcaagc tccagggaag ggctctggagt ggtcgcacg tatttatccc 540
acaaatggtt acacacggtg tgcggactct gtgaagggcc gattcaccat ctccgcagac 600
acttccaaga acaccgcgta tctgcaaatg aacagtctga gagctgagga cacggccggtt 660
tattactggt caagatgggg cggagacggt ttctacgcta tggactactg gggccaaggg 720
accctggtca ccgtctctc agccgccgag cccaagagca gcgataagac ccacacctgc 780
cctccctgtc cagctccaga actgctggga ggacctagcg tggtcctgtt tccccctaag 840
ccaaaagaca ctctgatgat ttccaggact cccgaggtga cctgcgtggt ggtggacgtg 900
tctcacgagg accccgaagt gaagttcaac tgggtacgtg atggcgtgga agtgcataat 960
gctaagacaa aaccaagaga ggaacagtac aactccactt atcgcgtcgt gagcgtgctg 1020
accgtgctgc accaggactg gctgaacggg aaggagtata agtgcaaagt cagtaataag 1080
gccctgcctg ctccaatcga aaaaaccatc tctaaggcca aaggccagcc aagggagccc 1140
caggtgtaca cactgccacc cagcagagac gaactgacca agaaccaggt gtccctgata 1200
tgtctggtga aaggcttcta tcctagtgat attgctgtgg agtgggaatc aaatggacag 1260

ccagagaaca gatacatgac ctggcctcca gtgctggaca gcgatggcag cttcttcctg 1320
tattccaagc tgacagtgga taaatctcga tggcagcagg ggaacgtgtt tagttgttca 1380
gtgatgcatg aagccctgca caatcattac actcagaaga gcctgtccct gtctcccggc 1440
aaa 1443

<210> 51
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 51

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 52
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 52

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 53

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial sequence

<400> 53

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

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

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

Ala Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr Asn Gln Arg Phe
50 55 60

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg 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 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	
	115						120					125				
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	
	130					135					140					
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	
145					150					155					160	
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	
				165					170					175		
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	
			180					185					190			
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	
		195					200					205				
Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	
	210					215					220					
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	
225					230					235					240	
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	
				245					250					255		
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	
			260					265					270			
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	
		275					280					285				
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	
	290					295					300					
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	
305					310					315					320	
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	
				325					330					335		
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Val	
			340					345					350			
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Leu	
		355					360					365				

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Leu Thr Trp Pro Pro Val Leu
 385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

<210> 54
 <211> 1344
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial sequence

<400> 54
 gaagtgcagc tggtcgaatc tggaggagga ctggtgcagc caggagggtc cctgcgccctg 60
 tcttgcgccg ctagtggctt cacttttacc gactacacca tggattgggt gcgacaggca 120
 cctggaaagg gcctggagtg ggtgcgccgat gtgaacccaa atagcggagg ctccatctac 180
 aaccagcggg tcaagggccg gttcaccctg tcagtggacc ggagcaaaaa caccctgtat 240
 ctgcagatga atagcctgcg agccgaagat actgctgtgt actattgcgc ccggaatctg 300
 gggccctcct tctactttga ctattggggg cagggaactc tggtcaccgt gagctccgcc 360
 tccaccaagg gaccttctgt gttcccactg gctccctcta gtaaattccac atctggggga 420
 actgcagccc tgggctgtct ggtgaaggac tacttcccag agcccgtcac agtgtcttgg 480
 aacagtggcg ctctgacttc tgggggtccac acctttcctg cagtgtctgca gtcaagcggg 540
 ctgtacagcc tgtcctctgt ggtcaccgtg ccaagttcaa gcctgggaac acagacttat 600
 atctgcaacg tgaatcacia gccatccaat acaaaagtcg acaagaaagt ggaacccaag 660
 tcttgtgata aaaccatac atgccccctt tgtcctgcac cagagctgct gggaggacca 720
 agcgtgttcc tgtttccacc caagcctaaa gatacactga tgattagtag gacccagaa 780
 gtcacatgcg tggtcgtgga cgtgagccac gaggaccccg aagtcaagtt taactggtac 840
 gtggacggcg tcgaggtgca taatgccaag actaaacca gggaggaaca gtacaacagt 900
 acctatcgcg tcgtgtcagt cctgacagtg ctgcatcagg attggctgaa cgggaaagag 960
 tataagtgca aagtgagcaa taaggctctg cccgcaccta tcgagaaaac aatttccaag 1020
 gcaaaaggac agcctagaga accacaggtg tacgtgctgc ctccatcaag ggatgagctg 1080

acaaagaacc aggtcagcct gctgtgtctg gtgaaaggat tctatccctc tgacattgct 1140
 gtggagtggg aaagtaatgg ccagcctgag aacaattacc tgacctggcc ccctgtgctg 1200
 gactcagatg gcagcttctt tctgtatagc aagctgaccg tcgacaaatc ccggtggcag 1260
 caggggaatg tgtttagttg ttcagtcatg cacgaggcac tgcacaacca ttacaccag 1320
 aagtcactgt cactgtcacc aggg 1344

<210> 55
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificial sequence

<400> 55

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

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

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

Ala Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr Asn Gln Arg Phe
 50 55 60

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg 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 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 56
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificial sequence

<400> 56

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	1	5	10	15
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Thr	Asp	Tyr	20	25	30	
Thr	Met	Asp	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	35	40	45	
Ala	Asp	Val	Asn	Pro	Asn	Ser	Gly	Gly	Ser	Ile	Tyr	Asn	Gln	Arg	Phe	50	55	60	
Lys	Gly	Arg	Phe	Thr	Leu	Ser	Val	Asp	Arg	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	Asn	Leu	Gly	Pro	Ser	Phe	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	100	105	110	
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	115	120	125	
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	130	135	140	
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	145	150	155	160
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	165	170	175	
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	180	185	190	
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	195	200	205	
Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	210	215	220	
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	225	230	235	240
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	245	250	255	

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 325 330 335
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Val
 340 345 350
 Tyr Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 385 390 395 400
 Asp Ser Asp Gly Ser Phe Ala Leu Val Ser Lys Leu Thr Val Asp Lys
 405 410 415
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

<210> 57

<211> 1344

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial sequence

<400> 57

gaagtgcagc tggtcgaatc tggaggagga ctggtgcagc caggagggtc cctg'gcctg 60

tcttgcgccg ctagtggctt cacttttacc gactacacca tggattgggt gcgacaggca 120

cctggaaagg gcctggagtg ggtcgccgat gtgaacccaa atagcggagg ctccatctac 180

aaccagcggg tcaagggccg gttcaccctg tcagtggacc ggagcaaaaa caccctgtat 240

ctgcagatga atagcctgcg agccgaagat actgctgtgt actattgcgc ccggaatctg	300
gggccctcct tctactttga ctattggggg caggggaactc tggtcaccgt gagctccgcc	360
tccaccaagg gaccttctgt gttcccactg gctccctcta gtaaataccac atctggggga	420
actgcagccc tgggctgtct ggtgaaggac tacttcccag agcccgtcac agtgtcttgg	480
aacagtggcg ctctgacttc tgggggtccac acctttcctg cagtgtgca gtcaagcggg	540
ctgtacagcc tgtcctctgt ggtcaccgtg ccaagttcaa gcctgggaac acagacttat	600
atctgcaacg tgaatcacia gccatccaat acaaaagtcg acaagaaagt ggaacccaag	660
tcttgtgata aaaccatac atgccccctt tgtcctgcac cagagctgct gggaggacca	720
agcgtgttcc tgtttccacc caagcctaaa gatacactga tgattagtag gacccagaa	780
gtcacatgcg tggtcgtgga cgtgagccac gaggaccccg aagtcaagtt taactggtac	840
gtggacggcg tcgaggtgca taatgccaag actaaacca gggaggaaca gtacaacagt	900
acctatcgcg tcgtgtcagt cctgacagtg ctgcatcagg attggctgaa cgggaaagag	960
tataagtgca aagtgagcaa taaggctctg cccgcaccta tcgagaaaac aatttccaag	1020
gcaaaaggac agcctagaga accacaggtg tacgtgtatc ctccatcaag ggatgagctg	1080
acaaagaacc aggtcagcct gacttgtctg gtgaaaggat tctatccctc tgacattgct	1140
gtggagtggg aaagtaatgg ccagcctgag aacaattaca agaccacacc ccctgtgctg	1200
gactcagatg gcagcttcgc gctggtgagc aagctgaccg tcgacaaatc ccggtggcag	1260
caggggaatg tgtttagttg ttcagtcatg cacgaggcac tgcacaacca ttacacccag	1320
aagtcactgt cactgtcacc aggg	1344

<210> 58
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificial sequence

<400> 58

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

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

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

Ala	Asp	Val	Asn	Pro	Asn	Ser	Gly	Gly	Ser	Ile	Tyr	Asn	Gln	Arg	Phe
50						55					60				

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg 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 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 59

<211> 475

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial sequence

<400> 59

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu
115 120 125

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
130 135 140

Ala	Ala	Ser	Gly	Phe	Thr	Phe	Thr	Asp	Tyr	Thr	Met	Asp	Trp	Val	Arg	145	150	155	160
Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Asp	Val	Asn	Pro	Asn	165	170	175	
Ser	Gly	Gly	Ser	Ile	Tyr	Asn	Gln	Arg	Phe	Lys	Gly	Arg	Phe	Thr	Leu	180	185	190	
Ser	Val	Asp	Arg	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	195	200	205	
Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asn	Leu	Gly	Pro	210	215	220	
Ser	Phe	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	225	230	235	240
Ser	Ala	Ala	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	245	250	255	
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	260	265	270	
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	275	280	285	
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	290	295	300	
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	305	310	315	320
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	325	330	335	
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	340	345	350	
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	355	360	365	
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Val	Tyr	Pro	Pro	Ser	Arg	Asp	370	375	380	
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	385	390	395	400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
405 410 415

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

Ala Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
435 440 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
450 455 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 60
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 60
gacattcaga tgaccagag ccctagctcc ctgagtgcct cagtcgggga cagggtgact 60
atcacctgca aggcttcaca ggatgtcagc attggcgtgg catggtacca gcagaagcca 120
gggaaagcac ccaagctgct gatctatagc gcctcctaca ggtatacagg cgtgccatcc 180
cgcttctctg gcagtgggtc aggaactgac ttacactga ctatttctag tctgcagccc 240
gaagatttctg ccacatacta ttgccagcag tactatatct acccttatac ttttggccag 300
gggaccaaag tggagattaa gggcggagga ggctccggag gaggagggtc tggaggagga 360
ggaagtgagg tccagctggt ggaatctgga ggaggactgg tgcagccagg agggctccctg 420
aggctgtctt gtgccgctag tggcttcacc ttacagact acacaatgga ttgggtgcgc 480
caggcaccag gaaagggact ggaatgggtc gctgatgtga accctaatac cggaggctcc 540
atctacaacc agcggttcaa aggacgggtc accctgtcag tggaccggag caagaacacc 600
ctgtatctgc agatgaacag cctgagagcc gaggatactg ctgtgtacta ttgcgccagg 660
aatctgggcc caagcttcta ctttgactat tgggggcagg gaacactggt cactgtgtca 720
agcgcagccg aacccaaata ctctgataag actcacacct gccaccttg tccagctcca 780
gagctgctgg gaggacctag cgtgttcctg tttccacca agccaaaaga cactctgatg 840
atttctagaa cccctgaagt gacatgtgtg gtcgtggacg tcagtcacga ggaccccgaa 900
gtcaaattca actggtacgt ggatggcgtc gaggtgcata atgccaagac caaaccgca 960
gaggaacagt acaactcaac ctatcgggtc gtgagcgtcc tgacagtgtc gcatcaggac 1020
tggctgaacg gcaaggagta taagtgcaaa gtgagcaaca aggctctgcc tgcaccaatc 1080

gagaagacca tttccaaggc taaagggcag cccgcgaac ctcaggtcta cgtgtatcct	1140
ccaagccgag atgagctgac aaaaaaccag gtctccctga cttgtctggt gaagggattt	1200
tacccaagtg acatcgcagt ggagtgggaa tcaaattggcc agcccgaataa caattataag	1260
accacacccc ctgtgctgga ctctgatggg agtttcgcac tggctctcaa actgaccgtg	1320
gacaagtctc ggtggcagca gggaaacgtc tttagctggt ccgtgatgca cgaggccctg	1380
cacaatcatt acacacagaa atctctgagt ctgtcacctg gcaag	1425

<210> 61
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificial sequence

<400> 61

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

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

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

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

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

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

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys
			100					105		

<210> 62
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificial sequence

<400> 62

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

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

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

Ala Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr Asn Gln Arg Phe
50 55 60

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg 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 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 63
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 63

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

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

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

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

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

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

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Gly	Gly	Ser	Gly	Gly			100	105	110
Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Glu			115	120	125
Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser			130	135	140
Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Thr	Tyr			145	150	155
Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala			165	170	175
Arg	Ile	Tyr	Pro	Thr	Asn	Gly	Tyr	Thr	Arg	Tyr	Ala	Asp	Ser	Val	Lys			180	185	190
Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	Ala	Tyr	Leu			195	200	205
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ser			210	215	220
Arg	Trp	Gly	Gly	Asp	Gly	Phe	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly			225	230	235
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ala	Glu	Pro	Lys	Ser	Ser	Asp	Lys			245	250	255
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro			260	265	270
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser			275	280	285
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp			290	295	300
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn			305	310	315
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val			325	330	335
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu			340	345	350

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 355 360 365

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Val
 370 375 380

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Leu
 385 390 395 400

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 405 410 415

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Leu Thr Trp Pro Pro Val Leu
 420 425 430

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 435 440 445

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 450 455 460

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 465 470 475 480

<210> 64
 <211> 1440
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial sequence

<400> 64
 gacattcaga tgacacagag ccccagctcc ctgagtgcct cagtcggcga cagggtgact 60
 atcacctgcc gcgcatccca ggatgtcaac accgctgtgg catggtacca gcagaagcct 120
 ggaaaagccc caaagctgct gatctacagc gcttccttcc tgtattctgg cgtgccaaagt 180
 cggttttctg gaagtagatc aggcactgac ttcacactga ctatctctag tctgcagccc 240
 gaagattttg ccacctacta ttgccagcag cactatacca caccctac attcggacag 300
 ggcactaaag tggagattaa gggcgggtca ggcggaggga gcggaggagg gtccggagga 360
 gggctctggag gagggagtgg agaggtccag ctggtggaat ctggaggagg actggtgcag 420
 cctggaggct cactgcgact gagctgtgcc gcttcgggct ttaacatcaa agacacatac 480
 attcattggg tcaggcaggc accaggggaag ggactggaat gggtgggccg catctatccc 540
 acaaatgggt aactcgata tgccgacagc gtgaaaggac ggtttaccat ttctgctgat 600
 accagtaaga acacagcata cctgcagatg aacagcctgc gcgcagagga tacagccgtg 660
 tactattgca gtcgatgggg gggagacggc ttctacgcca tggattattg gggccagggg 720

actctgggtca ccgtgtcaag cgcagccgaa cctaaatcct ctgacaagac ccacacatgc	780
ccaccctgtc ctgctccaga gctgctggga ggaccatccg tgttcctgtt tcctccaaag	840
cctaaagata cactgatgat tagccgcact cccgaagtca cctgtgtggt cgtggacgtg	900
tcccacgagg accccgaagt caagttcaac tgggtacgtgg acggcgtcga ggtgcataat	960
gccaagacta aaccaagaga ggaacagtac aattcaacct atagggtcgt gagcgtcctg	1020
acagtgctgc atcaggattg gctgaacggc aaggagtata agtgcaaagt gtctaacaag	1080
gccctgcccg ctcctatcga gaagactatt agcaaggcaa aagggcagcc acgggaaccc	1140
caggtctacg tgctgcccc tagcagagac gagctgacca aaaaccagggt ctccctgctg	1200
tgtctggtga agggctttta tcctagtgat atcgctgtgg agtgggaatc aaatgggacg	1260
ccagaaaaca attacctgac atggccaccc gtgctggaca gcgatgggtc cttctttctg	1320
tattccaaac tgactgtgga caagtctaga tggcagcagg gaaacgtctt cagctgttcc	1380
gtgatgcacg aggccctgca caatcattac acccagaagt ctctgagtct gtcacccggc	1440

<210> 65
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Artificial sequence

<400> 65

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

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

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

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

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

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

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys
			100					105		

<210> 66
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 66

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 67
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 67

Gln Asp Val Asn Thr Ala
1 5

<210> 68
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 68
Ser Ala Ser

<210> 69
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 69

Gln Gln His Tyr Thr Thr Pro Pro Thr
1 5

<210> 70
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 70

Gly Phe Asn Ile Lys Asp Thr Tyr
1 5

<210> 71
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 71

Ile Tyr Pro Thr Asn Gly Tyr Thr
1 5

<210> 72
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 72

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr
1 5 10

<210> 73
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 73

Val Asn Pro Asn Ser Gly Tyr Ser
1 5

<210> 74
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 74

Gly Phe Thr Phe Gln Asp Tyr Thr
1 5

<210> 75
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 75

Ala Arg Asn Leu Gly Pro Trp Phe Tyr Phe Asp Tyr
1 5 10

<210> 76
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 76

Gln Gln Tyr Tyr Ile Tyr Pro Gly Thr
1 5

<210> 77
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 77

Gly Phe Thr Phe Tyr Asp Tyr Thr
1 5

<210> 78
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 78

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

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

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

Ala Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr Asn Gln Arg Phe
50 55 60

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg 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 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 79
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 79

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 80

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial sequence

<400> 80

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

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

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

Ala Asp Val Asn Pro Asn Ser Gly Tyr Ser Ile Tyr Asn Gln Arg Phe
50 55 60

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg Ser Trp 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 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 81

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial sequence

<400> 81

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 82

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial sequence

<400> 82

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

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

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

Ala Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr Asn Gln Arg Phe
50 55 60

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg 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 Asn Leu Gly Pro Trp Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 83
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 83

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

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

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

Ala Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr Asn Gln Arg Phe
50 55 60

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg 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 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 84
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 84

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 85

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial sequence

<400> 85

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

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

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

Ala Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr Asn Gln Arg Phe
50 55 60

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg Ser Trp 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 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 86
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 86

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

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

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

Ala Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr Asn Gln Arg Phe
50 55 60

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg Ser Trp 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 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 87
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 87

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

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

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

Ala Asp Val Asn Pro Asn Ser Gly Tyr Ser Ile Tyr Asn Gln Arg Phe
50 55 60

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg 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 Asn Leu Gly Pro Trp Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 88

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial sequence

<400> 88

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 89
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial sequence

<400> 89

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

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

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

Ala Asp Val Asn Pro Asn Ser Gly Tyr Ser Ile Tyr Asn Gln Arg Phe
50 55 60

Lys Gly Arg Phe Thr Leu Ser Val Asp Arg 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 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115