

ET-2015-11_ST25
SEQUENCE LISTING

<110> Eureka Therapeutics Inc
 <120> ANTIBODY AGENTS SPECIFIC FOR HUMAN CD19 AND USES THEREOF
 <130> ET-2015-11-WO-PCT
 <140> US 62/240,624
 <141> 2015-10-13
 <160> 302
 <170> PatentIn version 3.5
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 <211> 747
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic Construct

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 <213> Artificial Sequence

<220>
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<400> 2

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			20					25					30		

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
65 70 75 80

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
85 90 95

Ser Ala Gly Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gly Ser
100 105 110

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Leu Glu Met Ala Gln Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
195 200 205

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Tyr Tyr Tyr Ser Arg Leu Asp Tyr Trp Gly
225 230 235 240

Gln Gly Thr Leu Val Thr Val Ser Ser
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<210> 4
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<220>
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Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
 20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
 65 70 75 80

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
 85 90 95

Arg Ala Gly Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Ser
 100 105 110

Arg Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125

Leu Glu Met Ala Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val

130

135

140

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
 145 150 155 160

Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
 165 170 175

Leu Glu Trp Val Ser Gly Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr
 180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
 195 200 205

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 210 215 220

Val Tyr Tyr Cys Ala Arg Tyr Tyr Leu Ser Gln Ile Asp Ser Trp Gly
 225 230 235 240

Gln Gly Thr Leu Val Thr Val Ser Ser
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<210> 5

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic Construct

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gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240
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gtattcggcg gagggaccaa gctgaccgtc ctaggttcta gaggtggtgg tggtagcggc      360
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gtcaccataa ccgcggacac gtctacagac acagcctaca tggagctgag cagcctgaga      660
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<210> 6

<211> 251
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 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 6

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Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
 20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
 65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
 85 90 95

Asn Gly His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105 110

Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 115 120 125

Ser Leu Glu Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val
 130 135 140

Lys Lys Pro Gly Ala Thr Val Lys Ile Ser Cys Lys Val Ser Gly Tyr
 145 150 155 160

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

Gly Leu Glu Trp Met Gly Leu Val Asp Pro Glu Asp Gly Glu Thr Ile
 180 185 190

Tyr Ala Glu Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser
 195 200 205

Thr Asp Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
 210 215 220

Ala Val Tyr Tyr Cys Ala Thr Gly Ile Tyr Ser Arg Pro Leu Gly Tyr
 225 230 235 240

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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<210>	7
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<212>	DNA
<213>	Artificial Sequence

<220>
<223> Synthetic Construct

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gaccgattct	ctgggtccaa	gtctggcacc	tcagcctccc	tggccatcag	tgggctccag		240
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gaggacacgg	ccgtgtatta	ctgtgcgcgc	tctgacggta	aacatttctg	gcagcagtac		720
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<210>	8
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<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic Construct

<400> 8

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

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
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Asn Gly Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Ser
100 105 110

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

Leu Glu Met Ala Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
195 200 205

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Ser Asp Gly Lys His Phe Trp Gln Gln Tyr
225 230 235 240

Asp Ala Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
245 250

<210>	9
<211>	729
<212>	DNA
<213>	Artificial Sequence

<220>
<223> Synthetic Construct

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aggttcagtg	gcagtggatt	tgggacggat	ttcactctca	ccatcagcag	cctgcagcct		240
gaagattttg	cagttttatta	ctgtcaacac	tatttaggta	ccccgtactc	ttttggccag		300
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<210> 10
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 10

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu Glu Met
115 120 125

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

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

Asn Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
165 170 175

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Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
180 185 190

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

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
210 215 220

Cys Ala Arg Met Asn Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
225 230 235 240

Val Ser Ser

<210> 11
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

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<210> 12
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12

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

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

<210> 13
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 <212> DNA
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<223> Synthetic Construct

<400> 13

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<210> 14

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<212> PRT

<213> Artificial Sequence

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

Pro Gln Leu Leu Ile His Leu Gly Ser Asp Arg Ala Ser Gly Val Pro
50          55          60

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

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

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

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Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Leu Glu Met Ala Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val
130 135 140

Lys Lys Ala Gly Ser Ser Val Lys Val Ser Cys Glu Thr Ser Gly Gly
145 150 155 160

Thr Phe Ser Ser Ser Ser Val Asn Trp Val Arg Gln Ala Pro Gly Gln
165 170 175

Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Val Gly Thr Pro Asn
180 185 190

Tyr Ala Gln Lys Phe Gln Asp Arg Val Thr Ile Thr Ala Val Glu Ser
195 200 205

Thr Phe Thr Ala Tyr Met Glu Leu Ser Gly Leu Arg Ser Glu Asp Thr
210 215 220

Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Arg Asp Tyr Met Asp Val
225 230 235 240

Trp Gly Arg Gly Thr Thr Val Thr Val Ser Ser
245 250

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

<220>
<223> Synthetic Construct

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gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccgg 240
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caggaaccc tggtcaccgt ctcctca 747

<210> 16
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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16

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

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

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

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

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Ser Gly Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Ser
100 105 110

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Leu Glu Met Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ile
130 135 140

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Val Ser Ser Asn Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala
180 185 190

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

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
Page 13

210

215

220

Tyr Tyr Cys Ala Arg Gly Gly Phe Gly Ala Glu Phe Asp Tyr Trp Gly
 225 230 235 240

Gln Gly Thr Leu Val Thr Val Ser Ser
 245

<210> 17
 <211> 756
 <212> DNA
 <213> Artificial Sequence

<220>
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 ggtggtggtg gatccctcga gatggccgag gtgcagctgg tggagtctgg aggaggcttg 420
 atccagcctg ggggggtccct gagactctcc tgtgcagcct ctggggtcac cgtcagtagc 480
 aactacatga gctgggtccg ccaggctcca gggaaggggc tggagtgggt ctcagttatt 540
 tatagcggtg gtagcacata ctacgcagac tccgtgaagg gccgattcac catctccaga 600
 gacaattcca agaacacgct gtatcttcaa atgaacagcc tgagagccga ggacacggcc 660
 gtgtattact gtgcgagagg tggattttcg gacgattact atggttcggg gagttatgat 720
 aactggggcc aggggaaccct ggtcaccgtc tcctca 756

<210> 18
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 18

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 1 5 10 15

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

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

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

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu Glu Met
115 120 125

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

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

Asn Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
165 170 175

Val Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
180 185 190

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
195 200 205

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
210 215 220

Ala Arg Gly Gly Ile Ser Asp Asp Tyr Tyr Gly Ser Gly Ser Tyr Asp
225 230 235 240

Asn Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
245 250

<210> 19
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 19
gacatccagt tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

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aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagta ccccttcac tttcggcgga 300
 gggaccaagg tggagatcaa acgttctaga ggtggtggtg gtagcggcgg cggcggctct 360
 ggtggtggtg gatccctcga gatggccgag gtgcagctgg tggagtctgg gggaggcttg 420
 gtccagcctg ggggggtccct gagactctcc tgtgcagcct ctggattcac cgtcagtagc 480
 aactacatga gctgggtccg ccaggctcca gggaaggggc tggagtgggt ctcagttatt 540
 tatagcggtg gtagcacata ctacgcagac tccgtgaagg gccgattcac catctccaga 600
 gacaattcca agaacacgct gtatcttcaa atgaacagcc tgagagctga ggacacggct 660
 gtgtattact gtgcgagaga aagggggatg ggatatgctt ttgatattctg gggccaaggg 720
 acaatgggtca cgcgtctcttc a 741

<210> 20
 <211> 247
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 20

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

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

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

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

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

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

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu Glu Met
 115 120 125

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

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser
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145 150 155 160
 Asn Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 165 170 175
 Val Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 180 185 190
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 195 200 205
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 210 215 220
 Ala Arg Glu Arg Gly Met Gly Tyr Ala Phe Asp Ile Trp Gly Gln Gly
 225 230 235 240
 Thr Met Val Thr Val Ser Ser
 245

<210> 21
 <211> 720
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 21
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 ctggagatta aacgttctag aggtggtggt ggtagcggcg gcggcggtc tggtggtggt 360
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 agctggatcc ggcagcccc agggaagcga ctggagtgga ttgggtgtgc ccattacact 540
 ggggacaccc actacaacc ctccctcaag ggtcgagtca ccatatcact agacacgtcc 600
 atgaaccagt tctccctgag gctgaactct gtgaccgtg cggacacggc cgtctattac 660
 tgtgcgagtt atcatccctt taactactgg ggccagggaa ccctggtcac cgtctcctca 720

<210> 22
 <211> 240
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 22

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

<210> 23

<211> 774

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 23

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ccaggaacgg cccccaaact cctcatctat agtaattatc gccggccctc aggggtccct      180
gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240
tctgacgatg aggctgatta ttactgtgca ctatgggatg acagcctgga tggttatgtc      300
ttcggaaactg ggaccaaggt caccgtccta ggttctagag gtggtggtgg tagcggcggc      360
ggcggctctg gtggtggtgg atccctcgag atggccgagg tccagctggt gcagtctggg      420
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ttcaacgact tctacttaca ctgggtgcga caggcccctg gaaaagggtt tgagtggatg      540
ggacgtattg atcctgaaga tggtaaaaca agatatgcag agaagttcca gggcagactc      600
accattaccg cggacacgtc tacagacact ctttcatatg aactgggcgg cctgacatct      660
gacgacacgg ccgtctatta ctgtacaact gattggggct atagcagttc cctacgtgag      720
gaggacatct ggtacgactg ctggggccag ggaaccctgg tcaccgtctc ctca          774

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<210> 24

<211> 258

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 24

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Thr Lys
20        25        30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65        70        75        80

Ser Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Asp Asp Ser Leu
85        90        95

Asp Gly Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Ser
100       105       110

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Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Leu Glu Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg
130 135 140

Arg Pro Gly Ala Thr Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr
145 150 155 160

Phe Asn Asp Phe Tyr Leu His Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Met Gly Arg Ile Asp Pro Glu Asp Gly Lys Thr Arg Tyr
180 185 190

Ala Glu Lys Phe Gln Gly Arg Leu Thr Ile Thr Ala Asp Thr Ser Thr
195 200 205

Asp Thr Leu Tyr Met Gln Leu Gly Gly Leu Thr Ser Asp Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Thr Thr Asp Trp Gly Tyr Ser Ser Ser Leu Arg Glu
225 230 235 240

Glu Asp Ile Trp Tyr Asp Cys Trp Gly Gln Gly Thr Leu Val Thr Val
245 250 255

Ser Ser

<210> 25
<211> 756
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 25
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cagggccctg tgctggatcat ctattatgat agcgaccggc cctcagggat ccctgagcga 180
ttctctgggt ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg 240
gatgaggccg actattactg tcagggtgtg gatagtagta gtgatcatta tgtcttcgga 300
actgggacca aggtcaccgt cctaggttct agaggtggtg gtggtagcgg cggcggcggc 360
tctggtggtg gtggatccct cgagatggcc gaggtgcagc tgggtgcagtc tggggctgag 420
gtgaagaagc ctgggtcctc ggtgaaggtc tcctgcaagg cttctggagg caccttcagc 480
agctatgcta tcagctgggt gcgacaggcc cctggacaag ggcttgagtg gatgggaggg 540

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atcatcccta tctttggtac agcaaactac gcacagaagt tccagggcag agtcacgatt 600
 accgcggacg aatccacgag cacagcctac atggagctga gcagcctgag atctgaggac 660
 acggccgtgt attactgtgc gagagattat gggtagcgtg actacggtga tgcttttgat 720
 atctggggcc aagggacaat ggtcacgctc tcttca 756

<210> 26
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 26

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

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

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

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

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

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

Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Ser Arg Gly
 100 105 110

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

Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
 130 135 140

Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser
 145 150 155 160

Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
 165 170 175

Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln
 180 185 190

Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr
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195

200

205

Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
 210 215 220

Tyr Cys Ala Arg Asp Tyr Gly Tyr Gly Asp Tyr Gly Asp Ala Phe Asp
 225 230 235 240

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 245 250

<210> 27
 <211> 753
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 27
 tcctatgtgc tgactcagcc accctcgggtg tcagtggccc caggaaagac ggccaggatt 60
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 cagggccctg tgctggctgt ctatgatgat agcgaccggc cctcagggat ccctgagcga 180
 ttctctggct ccaactctgg aaacacggcc accctgacca tcagcagggt cgaagccggg 240
 gatgaggccg actattcctg tcagggtgtgg gatagcagta gtgatcatta tgtcttcgga 300
 cctgggacca aggtcacctg cctaggttct agaggtggtg gtggtagcgg cggcggcggc 360
 tctggtggtg gtggatccct cgagatggcc gaagtgcagc tgggtgcagtc tggagcagag 420
 gtgaaaaagc ccggggagtc tctgaagatc tcctgtaagg gttctggata cagctttacc 480
 agctactgga tcggctgggt gcgccagatg cccgggaaag gcctggagtg gatggggatc 540
 atctatcctg gtgactctga taccagatac agcccgtcct tccaaggcca ggtcaccatc 600
 tcagccgaca agtccatcag caccgcctac ctgcagtggg gcagcctgaa ggcctcggac 660
 accgccatgt attactgtgc gcgcgttggt ggtactatct actctatgca gtacgatgtt 720
 tggggtaag gtactctggt gaccgtctcc tca 753

<210> 28
 <211> 251
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 28

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

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

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

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

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

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

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

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

Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
130 135 140

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr
145 150 155 160

Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
165 170 175

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro
180 185 190

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr
195 200 205

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
210 215 220

Tyr Cys Ala Arg Val Val Gly Thr Ile Tyr Ser Met Gln Tyr Asp Val
225 230 235 240

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
245 250

<210> 29
<211> 780
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 29
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60

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tcagccgaca agtccatcag caccgcctac ctgcagtgga gcagcctgaa ggcctcggac 660
accgccatgt attactgtgc gcgccagggt tggggttggc aggggtggtat gtaccgcgt 720
tctaactggt ggtacaacat ggattcttgg ggtcaaggta ctctggtgac cgtctcctca 780

<210> 30
<211> 260
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 30

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

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

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

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

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

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

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser Arg Gly
100 105 110

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

Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro

130

135

140

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr
 145 150 155 160

Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 165 170 175

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro
 180 185 190

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr
 195 200 205

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 210 215 220

Tyr Cys Ala Arg Gln Val Trp Gly Trp Gln Gly Gly Met Tyr Pro Arg
 225 230 235 240

Ser Asn Trp Trp Tyr Asn Met Asp Ser Trp Gly Gln Gly Thr Leu Val
 245 250 255

Thr Val Ser Ser
 260

<210> 31
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 31
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 ccaggaaagg ctcccaaact cctcatctat tatgatgatc tgctgtcctc aggggtctct 180
 gaccgattct ctgggtccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240
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gattactggg gtcaaggtac tctggtgacc gtctcctca

<210> 32
 <211> 253
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 32

Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
 1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Val Gly Asn Asn
 20 25 30

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

Ile Tyr Tyr Asp Asp Leu Leu Ser Ser Gly Val Ser Asp Arg Phe Ser
 50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
 65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
 85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser
 100 105 110

Arg Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125

Leu Glu Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
 130 135 140

Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser
 145 150 155 160

Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly
 165 170 175

Leu Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr
 180 185 190

Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile
 195 200 205

Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala
 210 215 220

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Met Tyr Tyr Cys Ala Arg Trp Ser Ser Thr Trp Asp Ser Met Tyr Met
225 230 235 240

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
245 250

<210> 33
<211> 756
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 33
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acctgtggag gaaacaacat tggaagtga agtgtgcact ggtaccagca gaagccaggc 120
caggccccta tgggtggcat ctattatgat agcaaccggc cctcagggat ccctgagcga 180
ttctctggct ccaactctgg gaacacggcc accctgaccg tcagcagggt cgaagccgag 240
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ggcggaggga ccaagctgac cgtcctaggt tctagagggt gtggtggtag cggcggcggc 360
ggctctggtg gtggtggatc cctcgagatg gccgaagtgc agctggtgca gtctggagca 420
gaggtgaaaa agcccgggga gtctctgagg atctcctgta agggttcttg atacagcttt 480
accagctact ggatcggctg ggtgcgccag atgcccgga aaggcctgga gtggatgggg 540
atcatctatc ctggtgactc tgataccaga tacagcccgt ccttccaagg ccaggtcacc 600
atctcagccg acaagtccat cagcaccgcc tacctgcagt ggagcagcct gaaggcctcg 660
gacaccgcca tgtattactg tgcgcgcgtt acttactcta tggactctta ctacttcgat 720
tcttggggtc aaggctactc ggtgaccgtc tcctca 756

<210> 34
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34

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

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

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

Tyr Asp Ser Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
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55

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

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

Arg Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser Arg
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu
115 120 125

Glu Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
130 135 140

Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
145 150 155 160

Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu
165 170 175

Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser
180 185 190

Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser
195 200 205

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met
210 215 220

Tyr Tyr Cys Ala Arg Val Thr Tyr Ser Met Asp Ser Tyr Tyr Phe Asp
225 230 235 240

Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
245 250

<210> 35
<211> 780
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 35
ctgcctgtgc ttactcagcc accctcggtg tcagtggccc caggaaagac ggccaggatt 60
acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120
caggcccctg tgctggtcgt ctatgatgat agcgaccggc cctcagggat ccctgagcga 180
ttctctggct ccaactctgg gaacacggcc accctgacca tcaacagggt cgaagccggg 240

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gatgaggccg actattactg tcaggtgtgg gatagtagta gtgattatgt ggtattcggc 300
 ggagggacca agctgaccgt cctaggttct agaggtggtg gtggtagcgg cggcggcggc 360
 tctggtggtg gtggatccct cgagatggcc gaagtgcagc tggatgcagtc tggagcagag 420
 gtgaaaaagc ctggggagtc tctgaagatc tcctgtaagg gttctggata cagctttacc 480
 agctactgga tcggctgggt gcgccagatg cccgggaaag gcctggagtg gatggggatc 540
 atctatcctg gtgactctga taccagatac agcccgtcct tccaaggcca ggtcaccatc 600
 tcagccgaca agtccatcag caccgcctac ctgcagtgga gcagcctgaa ggcctcggac 660
 accgccatgt attactgtgc gcgccagggt tggggttggc aggggtggtat gtaccgcgct 720
 tctaactggt ggtacaacat ggattcttgg ggtcaaggta ctctggtgac tgtctcctca 780

<210> 36
 <211> 260
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 36

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

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

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

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

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

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

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser Arg Gly
 100 105 110

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

Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
 130 135 140

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr
 145 150 155 160

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Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
165 170 175

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro
180 185 190

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr
195 200 205

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
210 215 220

Tyr Cys Ala Arg Gln Val Trp Gly Trp Gln Gly Gly Met Tyr Pro Arg
225 230 235 240

Ser Asn Trp Trp Tyr Asn Met Asp Ser Trp Gly Gln Gly Thr Leu Val
245 250 255

Thr Val Ser Ser
260

<210> 37
<211> 780
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 37
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acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120
caggcccctg tgctggtcgt ctatgatgat agcgaccggc cctcagggat ccctgagcga 180
ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg 240
gatgaggccg actattactg tcagggtgtg gatagtagta gtgattatgt ggtatttggc 300
ggagggacca agctgaccgt cctaggttct agagggtgtg gtggtagcgg cggcggcggc 360
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gtgaaaaagc ccggggagtc tctgaagatc tcctgcaagg gttctggata cagctttacc 480
agcttctgga tcggctgggt gcgccagatg cccgggaaag gcctggagtg gatggggatc 540
atctatcctg gtgactctga taccagatac agcccgtcct tccaaggcca ggtcaccatc 600
tcagccgaca agtccatcag caccgcctac ctgcagtgga gcagcctgaa ggcctcggac 660
accgcgatgt attactgtgt gcgccagggt tggggttggc aggggtggtat gtacccgcgt 720
tctaactggt ggtacaacat ggattcttgg ggtcaaggta ctctggtaac cgtctcctca 780

<210> 38
<211> 260
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 38

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

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

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

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

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

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

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser Arg Gly
100 105 110

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

Met Ala Glu Val Arg Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
130 135 140

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr
145 150 155 160

Ser Phe Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
165 170 175

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro
180 185 190

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr
195 200 205

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
210 215 220

Tyr Cys Val Arg Gln Val Trp Gly Trp Gln Gly Gly Met Tyr Pro Arg
225 230 235 240

Ser Asn Trp Trp Tyr Asn Met Asp Ser Trp Gly Gln Gly Thr Leu Val

Thr Val Ser Ser
260

<210> 39
<211> 780
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 39
ctgcctgtgc tgactcagcc accctcggtg tcagtggccc caggagagac ggccaggatt 60
acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120
caggccccctg tgctggctgt ctatgatgat agcgaccggc cctcagggat ccctgagcga 180
ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg 240
gatgaggccg actattactg tcagggtgtg gatagtagta gtgattatgt ggtattcggc 300
ggagggacca agctgaccgt cctaggttct agaggtggtg gtggtagcgg cggcggcggc 360
tctggtggtg gtggatccct cgagatggca gaagtgcagc tgggtgcagtc tggagcagag 420
gtgaaaaagc ccggggagtc tctgaagatc tcctgtaagg gttctggata cagctttacc 480
agctactgga tcggctgggt gcgccagatg cccgggaaag gcctggagtg gatggggatc 540
atctatcctg gtgactctga taccagatac agcccgtcct tccaaggcca ggtcaccatc 600
tcagccgaca agtccatcag caccgcctac ctgcagtgga gcagcctgaa ggcctcggac 660
accgccatgt attactgtgc gcgccagggt tggggttggc aggggtggtat gtaccgcgt 720
tctaactggt ggtacaacat ggattcttgg ggtcaaggta ctctggtgac cgtctcctca 780

<210> 40
<211> 260
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 40

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

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

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

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

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

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

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser Arg Gly
100 105 110

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

Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
130 135 140

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr
145 150 155 160

Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
165 170 175

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro
180 185 190

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr
195 200 205

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
210 215 220

Tyr Cys Ala Arg Gln Val Trp Gly Trp Gln Gly Gly Met Tyr Pro Arg
225 230 235 240

Ser Asn Trp Trp Tyr Asn Met Asp Ser Trp Gly Gln Gly Thr Leu Val
245 250 255

Thr Val Ser Ser
260

<210> 41
<211> 780
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 41
ctgcctgtgc tgactcagcc accctcggtg tcagtggccc caggaaagac ggccaggatt 60
acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120
caggcccctg tgctggtcgt ctatgatgat agcgaccggc cctcagggat ccctgagcga 180

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ttctctggct ccaactctgg gaacacggcc accctgacca tcagcaggggt cgaagccggg	240
gatgaggccg actattactg tcaggtgtgg gatagtagta gtgattatgt ggtattcggc	300
ggagggacca agctgaccgt cctaggttct agaggtggtg gtggtagcgg cggcggcggc	360
tctggcgggtg gtggatccct cgagatggcc gaagtgcagc tgggtgcagtc tggagcagag	420
gtgaaaaagc ccggggagtc tctgaagatc tcctgtaagg gttctggata cagctttacc	480
agctactgga tcggctgggt gcgccagatg cccgggaaag gcctggagtg gatggggatc	540
atctatcctg gtgactctga taccagatac agcccgtcct tccaaggcca ggtcaccatc	600
tcagccgaca agtccatcag caccgcctac ctgcagtgga gcagcctgaa ggcctcggac	660
accgccatgt attactgtgc gcgccagggt tggggttggc aggggtggtat gtaccgcgt	720
tctaactggt ggtacaactt ggattcttgg ggtcaaggta ctctggtgac cgtctcctca	780

<210> 42
 <211> 260
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 42

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

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

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

Asp	Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe	Ser	Gly	Ser
	50					55					60				

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

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

Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Ser	Arg	Gly
			100					105					110		

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

Met	Ala	Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro
	130					135					140				

Gly	Glu	Ser	Leu	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Ser	Phe	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

145 150 155 160
 Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 165 170 175
 Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro
 180 185 190
 Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr
 195 200 205
 Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 210 215 220
 Tyr Cys Ala Arg Gln Val Trp Gly Trp Gln Gly Gly Met Tyr Pro Arg
 225 230 235 240
 Ser Asn Trp Trp Tyr Asn Leu Asp Ser Trp Gly Gln Gly Thr Leu Val
 245 250 255
 Thr Val Ser Ser
 260

<210> 43
 <211> 780
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 43
 ctgcctgtgc tgactcagcc accctcggtg tcagtggccc caggaaagac ggccaggatt 60
 acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120
 caggccccctg tgctggtcgt ctatgatgat agcgaccggc cctcagggat ccctgagcga 180
 ttctctggct ccaactctgg gaacacggcc accatgacca tcagcagggt cgaagccggg 240
 gatgaggccg actattactg tcagggtgtg gatagtagta gtgattatgt ggtattcggc 300
 ggagggacca agctgaccgt cctaggttct agaggtggtg gtggtagcgg cggcggcggc 360
 tctggtggtg gtggatccct cgagatggcc gaagtgcagc tgggtgcagtc tggagcagag 420
 gtgaaaaagc ccggggagtc tctgaagatc tcctgtaagg gtgctggata cagctttacc 480
 agctactgga tcggctgggt gcgccagatg cccgggaaag gcctggagtg gatggggatc 540
 atctatcctg gtgactctga taccagatac agcccgtcct tccaaggcca ggtcaccatc 600
 tcagccgaca agtccatcag caccgcctac ctgcagtgga gcagcctgaa ggcctcggac 660
 accgccatgt attactgtgc gcgccagggt tggggttggc aggggtggtat gtaccgcgt 720
 tctaactggt ggtacaacat ggattcttgg ggtcaaggta ctctggtgac cgtctcctca 780

<210> 44

<211> 260
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 44

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

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

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

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
      50      55      60

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

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

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser Arg Gly
      100      105      110

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

Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
      130      135      140

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

Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
      165      170      175

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro
      180      185      190

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr
      195      200      205

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
      210      215      220

Tyr Cys Ala Arg Gln Val Trp Gly Trp Gln Gly Gly Met Tyr Pro Arg
225      230      235      240

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Ser Asn Trp Trp Tyr Asn Met Asp Ser Trp Gly Gln Gly Thr Leu Val
245 250 255

Thr Val Ser Ser
260

<210> 45
<211> 780
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 45
ctgcctgtgc tgactcagcc accctcggtg tcagtggccc caggaaagac ggccaggatt 60
acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120
caggccccctg tgctggctgt ctatgatgat agcgaccggc cctcagggat ccctgagcga 180
ttctctggct ccaactctgg gaacatggcc accctgacca tcagcagggt cgaagccggg 240
gatgaggccg actattactg tcaggtgtgg gatagtagta gtgattatgt ggtattcggc 300
ggagggacca agctgaccgt cctaggttct agaggtggtg gtggtagcgg cggcggcggc 360
tctggtggtg gtggatccct cgagatggcc gaagtgcagc tgggtgcagtc tggagcagag 420
gtgaaaaagc ccggggagtc tctgaagatc tcctgtaagg gttctggata cagctttacc 480
agctactgga tcggctgggt gcgccagatg cccgggaaag gcctggagtg gatggggatc 540
atctatcctg gtgactctga taccagatac agcccgtcct tccaaggcca ggtcaccatc 600
tcagccgaca agtccatcag caccgcctac ctgcagtggg gcagcctgaa ggcctcggac 660
accgccatgt attactgtgc gcgccagggt tggggttggc aggggtggtat gtacccgcgt 720
tctaactggt ggtacaacat ggattcttgg ggtcaaggta ctctggtgac cgtctcctca 780

<210> 46
<211> 260
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 46

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

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

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

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
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55

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

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

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser Arg Gly
100 105 110

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

Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
130 135 140

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr
145 150 155 160

Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
165 170 175

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro
180 185 190

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr
195 200 205

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
210 215 220

Tyr Cys Ala Arg Gln Val Trp Gly Trp Gln Gly Gly Met Tyr Pro Arg
225 230 235 240

Ser Asn Trp Trp Tyr Asn Met Asp Ser Trp Gly Gln Gly Thr Leu Val
245 250 255

Thr Val Ser Ser
260

<210> 47
<211> 780
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 47
ctgcctgtgc tgactcagcc accctcggtg tcagtggccc caggaaagac ggccaggatt 60
acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120

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caggccccctg tgctggtcgt ctatgatgat agcaaccggc cctcagggat ccctgagcga	180
ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggg cgaagccggg	240
gatgaggccg actattactg tcaggtgtgg gatagtagta gtgagtatgt ggtattcggc	300
ggagggacca agctgaccgt cctaggttct agaggtggtg gtggtagcgg cggcggcggc	360
tctggtggtg gtggatccct cgagatggcc gaagtgcagc tgggtgcagtc tggagcagag	420
gtgaaaaagc ccggggagtc tctgaagatc tcctgtaagg gttctggata cagctttacc	480
agctactgga tcggctgggt gcgccagatg cccgggaaag gcctggagtg gatggggatc	540
atctatcctg gtgactctga taccagatac agcccgtcct tccaaggcca ggtcaccatc	600
tcagccgaca agtccatcag caccgcctac ctgcagtgga gcagcctgaa ggcctcggac	660
accgccatgt attactgtgc gcgtcaggtt tggggttggc aggggtggtat gtaccgcgt	720
tctaactggt ggtacaacat ggattcttgg ggtcaaggta ctctggtgac cgtctcctca	780

<210> 48
 <211> 260
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 48

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

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

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

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

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

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

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser Arg Gly
 100 105 110

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

Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
 130 135 140

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Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr
145 150 155 160

Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
165 170 175

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro
180 185 190

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr
195 200 205

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
210 215 220

Tyr Cys Ala Arg Gln Val Trp Gly Trp Gln Gly Gly Met Tyr Pro Arg
225 230 235 240

Ser Asn Trp Trp Tyr Asn Met Asp Ser Trp Gly Gln Gly Thr Leu Val
245 250 255

Thr Val Ser Ser
260

<210> 49
<211> 780
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 49
ctgcctgtgc tgactcagcc accctcgatg tcagtggccc caggaaagac ggccaggatt 60
acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120
caggcccctg tgctggctgt ctatgatgat agcgaccggc cctcagggat ccctgagcga 180
ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg 240
gatgaggccg actattactg tcagggtgtgg gatagtagta gtggttatgt ggtattcggc 300
ggagggacca agctgaccgt cctaggttct agaggtggtg gtggttagcgg cggcggcggc 360
tctggtggtg gtggatccct cgagatggcc gaagtgcagc tggatgcagc tggagcagag 420
gtgaaaaagc ccggggagtc tctgaagatc tcctgtaagg gttctggata cagctttacc 480
agctactgga tcggctgggt gcgccagatg cccgggaaag gcctggagtg gatggggatc 540
atctatcctg gtgactctga taccagatac agcccgtcct tccaaggcca ggtcaccatc 600
tcagccgaca agtccatcag caccgcctac ctgcagtggg gcagcctgaa ggcctcggac 660
accgccatgt attactgtgc gcgccagggt tgggggttggc aggggtggtat gtacccgcgt 720
tctaactggt ggtacaacat ggattcttgg ggtcaaggta ctctggtgac cgtctcctca 780

<210> 50
 <211> 260
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 50

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

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

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

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

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

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Gly Tyr
 85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser Arg Gly
 100 105 110

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

Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
 130 135 140

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr
 145 150 155 160

Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 165 170 175

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro
 180 185 190

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr
 195 200 205

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 210 215 220

Tyr Cys Ala Arg Gln Val Trp Gly Trp Gln Gly Gly Met Tyr Pro Arg

225 230 235 240

Ser Asn Trp Trp Tyr Asn Met Asp Ser Trp Gly Gln Gly Thr Leu val
245 250 255

Thr Val Ser Ser
260

<210>	51
<211>	780
<212>	DNA
<213>	Artificial Sequence

<220>
<223> Synthetic Construct

<400>	51						
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caggcccctg	tgctggtcgt	ctacgatgat	agcgaccggc	cctcagggat	ccctgagcga		180
ttctctggct	ccaactctgg	gaacacggcc	accctgacca	tcagcagggg	cgaagccggg		240
gatgaggccg	actattactg	tcagggtgtg	gatagtacta	gtgattatgt	ggtattcggc		300
ggagggacca	agctgaccgt	cctaggttct	agaggtggtg	gtggtagcgg	cggcggcggc		360
tctggtggtg	gtggatccct	cgagatggcc	gaagtgcagc	tggtgcagtc	tggagcagag		420
gtgaaaaagc	ccggggagtt	tctgaagatc	tcctgtaagg	gttctggata	cagcttcacc		480
agctactgga	tcggctgggt	gcgccagatg	cccgggaaag	gcctggagtg	gatggggatc		540
atctatcctg	gtgactctga	taccagatac	agcccgtcct	tccaaggcca	ggtcgccatc		600
tcagccgaca	agtccatcag	caccgcctac	ctgcagtgga	gcagcctgaa	ggcctcggac		660
accgccatgt	attactgtgc	gcgccagggt	tggggttggc	agggtggtat	gtacccgcgt		720
tctaactggt	ggtacaacat	ggattcttgg	ggtcaaggta	ctctggtgac	cgtctcctca		780

<210>	52
<211>	260
<212>	PRT
<213>	Artificial Sequence

<220>
<223> Synthetic Construct

<400> 52

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

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

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

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Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

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

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

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser Arg Gly
100 105 110

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

Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
130 135 140

Gly Glu Phe Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr
145 150 155 160

Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
165 170 175

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro
180 185 190

Ser Phe Gln Gly Gln Val Ala Ile Ser Ala Asp Lys Ser Ile Ser Thr
195 200 205

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
210 215 220

Tyr Cys Ala Arg Gln Val Trp Gly Trp Gln Gly Gly Met Tyr Pro Arg
225 230 235 240

Ser Asn Trp Trp Tyr Asn Met Asp Ser Trp Gly Gln Gly Thr Leu Val
245 250 255

Thr Val Ser Ser
260

<210> 53
<211> 780
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 53
ctgcctgtgc tgactcagcc accctcgggtg tcagtggccc caggaaagac ggccaggatt

60

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acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggg 120
cagggccctg tgctggtcgt ctatgatgat agcgaccggc cctcagggat ccctgagcga 180
ttctctgggt ccaactctgg gaccactgcc accctgacca tcagcagggt cgaagccggg 240
gatgaggccg actattactg tcaggtgtgg gatagtagta gtgattatgt ggtattcggc 300
ggagggacca agctgaccgt cctaggttct agaggtggtg gtggtagcgg cggcggcggc 360
tctggtggtg gtggatccct cgagatggcc gaagtgcagc tagtgcagtc tggagcagag 420
gtgaaaaagc ccggggagtc tctgaagatc tcctgtaagg gttctggata cagctttacc 480
agctactgga tcggctgggt gcgccagatg cccgggaaag gcctggagtg gatggggatc 540
atctatcctg gtgactccga taccagatac agcccgtcct tccaaggcca ggtcaccatc 600
tcagccgaca agtccatcag caccgcctac ctgcagtgga gcagcctgaa ggcctcggac 660
accgccatgt attactgtgc gcgccagggt tggggttggc aggggtggtat gaaccgcgt 720
tctaactggt ggtacaacat ggattcttgg ggtcaaggta ctctggtgac cgtctcctca 780

<210> 54
<211> 260
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 54

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

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

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

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

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

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

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser Arg Gly
100 105 110

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

Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro

130

135

140

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr
 145 150 155 160

Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 165 170 175

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro
 180 185 190

Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr
 195 200 205

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 210 215 220

Tyr Cys Ala Arg Gln Val Trp Gly Trp Gln Gly Gly Met Asn Pro Arg
 225 230 235 240

Ser Asn Trp Trp Tyr Asn Met Asp Ser Trp Gly Gln Gly Thr Leu Val
 245 250 255

Thr Val Ser Ser
 260

<210> 55
 <211> 780
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 55
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 acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc 120
 caggcccctg tgctggtcgt ctatgatgat agcgaccggc cctcagggat ccctgagcga 180
 ttctctggct ccaactctgg gaacacggcc accttgacca tcagcagggt cgaagccggg 240
 gatgaggccg actattactg tcagggtgtg gatagtagta gtgattatgt ggtattcggc 300
 ggagggacca agctgaccgt cctaggttct agaggtggtg gtggtagtgg cggcggcggc 360
 tctggtggtg gtggatccct cgagatggcc gaagtgcagc tgggtgcagtc tggagcagag 420
 gtgaaaaagc ccggggagtc tctgaagatc tcctgtaagg gttctggata cagctttacc 480
 agctactgga tcggctgggt gcgccagatg cccgggaaag gcctggagtg gatggggatc 540
 atctatcctg gtgactctga taccagatac agcccgttct tccaaggcca ggtcaccatc 600
 tcagccgaca agtccatcag caccgcctac ctgcagtgga gcagcctgaa ggcctcggac 660
 accgccatgt attactgtgc gcgccagggt tggggttggc aggggtggtat gtacccgcgt 720

tctaactggt ggtacaacat ggattcttgg ggtcaaggta ctctggtgac cgtctcctca

<210> 56
 <211> 260
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 56

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

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

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

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

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

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

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser Arg Gly
 100 105 110

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

Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro
 130 135 140

Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr
 145 150 155 160

Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 165 170 175

Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro
 180 185 190

Phe Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr
 195 200 205

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 210 215 220

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Tyr Cys Ala Arg Gln Val Trp Gly Trp Gln Gly Gly Met Tyr Pro Arg
225 230 235 240

Ser Asn Trp Trp Tyr Asn Met Asp Ser Trp Gly Gln Gly Thr Leu Val
245 250 255

Thr Val Ser Ser
260

<210> 57
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 57
caggctgtgc tgactcagcc accctcggtg tctgaagccc ccaggcagag ggtcaccatc 60
tcctgttctg gaagcagctc caacgtcggg aataatgctg taaactggta ccagcaggtc 120
ccaggaaagg ctcccaaact cctcatctat tatgatgata tgctgtcctc aggggtctct 180
gaccgattct ctgggtccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240
tctgaggatg aggccgatta ttattgtgca gcatgggatg acagcctgaa tgggtccgga 300
ttcggcggag ggaccaagct gaccgtccta ggttctagag gtggtggtgg tagcggcggc 360
ggcggctctg gtggtggtgg atccctcgag atggccgaag tgcagctggt gcagtccgga 420
gcagaggatg aaaagcccgg ggagtctctg aagatctcct gtaagggttc tggatacagc 480
tttaccagct actggatcgg ctgggtgctg cagatgcccg ggaaaggcct ggagtggatg 540
gggatcatct atcctggtga ctctgatacc agatacagcc cgtccttcca aggccaggtc 600
accatctcag ccgacaagtc catcagcacc gcctacctgc agtggagcag cctgaaggcc 660
tcggacaccg ccatgtatta ctgtgcgcgc tgggtcttctt cttgggactc tatgtacatg 720
gattactggg gtcaaggtag tatggtgacc gtctcctca 759

<210> 58
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 58

Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Val Gly Asn Asn
20 25 30

Ala Val Asn Trp Tyr Gln Gln Val Pro Gly Lys Ala Pro Lys Leu Leu
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35

40

45

Ile Tyr Tyr Asp Asp Leu Leu Ser Ser Gly Val Ser Asp Arg Phe Ser
 50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
 65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
 85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser
 100 105 110

Arg Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125

Leu Glu Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
 130 135 140

Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser
 145 150 155 160

Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly
 165 170 175

Leu Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr
 180 185 190

Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile
 195 200 205

Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala
 210 215 220

Met Tyr Tyr Cys Ala Arg Trp Ser Ser Ser Trp Asp Ser Met Tyr Met
 225 230 235 240

Asp Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 245 250

<210> 59

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 59

caggctgtgc ttactcagcc accctcggtg tctgaagccc ccaggcagag ggtcaccatc 60

tcctgttctg gaaacagctc caacgtcgga aataatgcta taaactggta ccagcaggtc 120

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ccaggaaagg ctcccaaact cctcatctat tatgatgatc tgctgtcctc aggggtctct	180
gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag	240
tctgaggatg aggccgatta ttattgtgca gcatgggatg acagcctgaa tgggtccgga	300
ttcggcggag ggaccaagct gaccgtccta ggttctagag gtggtggtgg tagcggcggc	360
ggcggctctg gtggtggtgg atccctcgag atggccgaag tgcagctggt gcagtctgga	420
gcagagggtg aaaagcccgg ggagtctctg aagatctcct gtaagggttc tggatacagc	480
tttaccagct actggatcgg ctgggtgctg cagatgcccg ggaaaggcct ggagtggatg	540
gggatcatct atcctggtga ctctgatacc agatacagcc cgtccttcca aggccaggtc	600
accatctcag ccgacaagtc catcagcacc gcctacctgc agtggagcag cctgaaggcc	660
tcggacaccg ccatgtatta ctgtgctgctg tgggtcttcta cttgggactc tatgtacatg	720
gaatactggg gtcaaggtag tctggtgacc gtctcctca	759

<210> 60
 <211> 253
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 60

Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
 1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Asn Ser Ser Asn Val Gly Asn Asn
 20 25 30

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

Ile Tyr Tyr Asp Asp Leu Leu Ser Ser Gly Val Ser Asp Arg Phe Ser
 50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
 65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
 85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser
 100 105 110

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125

Leu Glu Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Glu
 130 135 140

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Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser
145 150 155 160

Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly
165 170 175

Leu Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr
180 185 190

Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile
195 200 205

Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala
210 215 220

Met Tyr Tyr Cys Ala Arg Trp Ser Ser Thr Trp Asp Ser Met Tyr Met
225 230 235 240

Glu Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
245 250

<210> 61
<211> 760
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 61
caggctgtgc tgactcagcc accctcggtg tctgaagccc ccaggcagag ggtcaccatc 60
tcctgtttctg gaagcagctc caacgtcgga aataatgctg taaactggta ccagcaggtc 120
ccaggaaagg ctcccaaact cctcatctat tatgatgatc tgctgtcctc aggggtctct 180
gaccgattct ctgggtccaa gtctggcacc tcagcctccc tggccatcag tggggtccag 240
tctgaggatg aggccgatta ttattgtgca gcatgggatg acagcctgaa tgggtccggt 300
ttcggcgag ggaccaagct gaccgtccta gggtctagag gtggtggtgg tagcggcggc 360
ggcggctctg gtggtggtgg atccctcgag atggccgaag tgcagctggt gcagtctgga 420
gcagaggtga aaaagcccgg ggggtctctg aagatctcct gtaagggttc tggatacagc 480
tttaccagct actggatcgg ctgggtgctg cagatgcccg ggaaaggcct ggagtggatg 540
gggatcatct atcctggtga ctctgatacc agatacagcc cgtccttcca aggccaggtc 600
accatctcag ccgacaagtc catcagcacc gcctacctgc agtggagcag cctgaaggcc 660
tcggacaccg ccatgtatta ctgtgcgcgc tgggtcttcta cttgggactc tatgtacatg 720
gattactggg gtcaaggtac tctggtgacc gtctcctcaa 760

<210> 62
<211> 253
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 62

Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Val Gly Asn Asn
20 25 30

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

Ile Tyr Tyr Asp Asp Leu Leu Ser Ser Gly Val Ser Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser
100 105 110

Arg Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Leu Glu Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
130 135 140

Lys Pro Gly Gly Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser
145 150 155 160

Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly
165 170 175

Leu Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr
180 185 190

Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile
195 200 205

Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala
210 215 220

Met Tyr Tyr Cys Ala Arg Trp Ser Ser Thr Trp Asp Ser Met Tyr Met
225 230 235 240

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

<210> 63
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 63
 caggctgtgc tgactcagcc accctcggtg tctgaagccc ccaggcagag ggtcaccatc 60
 tcctgttctg gaagcagctc caacgtcgga aataatgctg taaactggta ccagcaggtc 120
 ccaggaaagg ctcccaaact cctcatctat tatgatgatc agctgtcctc aggggtctct 180
 gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240
 tctgaggatg aggccgatta ttattgtgca gcatgggatg acagcctgaa tgggtccggta 300
 ttcggcggag ggaccaagct gaccgtccta ggttctagag gtggtggtgg tagcggcggc 360
 ggcggctctg gtggtggtgg atccctcgag atggccgaag tgcagctggt gcagtctgga 420
 gcagaggtga aaaagcccgg ggagtctctg aagatctcct gtaagggttc tggatacagc 480
 tttaccagct actggatcgg ctgggtgctg cagatgcccg ggaaaggcct ggagtggatg 540
 gggatcatct atcctggtga ctctgatacc agatacagcc cgtccttcca aggccaggtc 600
 accatctcag ccgacaagtc catcagcacc gcctacctgc agtggagcag cctgaaggcc 660
 tcggacaccg ccatgtatta ctgtgcgcgc tggctcttcta cttgggactc tttgtacatg 720
 gattactggg gtcaaggtac tctggtgacc gtctcctca 759

<210> 64
 <211> 253
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 64
 Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
 1 5 10 15
 Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Val Gly Asn Asn
 20 25 30
 Ala Val Asn Trp Tyr Gln Gln Val Pro Gly Lys Ala Pro Lys Leu Leu
 35 40 45
 Ile Tyr Tyr Asp Asp Gln Leu Ser Ser Gly Val Ser Asp Arg Phe Ser
 50 55 60
 Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
 65 70 75 80

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Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser
100 105 110

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Leu Glu Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
130 135 140

Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser
145 150 155 160

Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly
165 170 175

Leu Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr
180 185 190

Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile
195 200 205

Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala
210 215 220

Met Tyr Tyr Cys Ala Arg Trp Ser Ser Thr Trp Asp Ser Leu Tyr Met
225 230 235 240

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
245 250

<210> 65
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 65
caggctgtgc tgactcagcc accctcgggtg tctgaagccc ccaggcagag ggtcaccatc 60
tcctgttctg gaaacagctc caacgtcgga aataatgctg taaactggta ccagcaggtc 120
ccaggaaagg ctcccaaact tctcatctat tatgatgata tgctgtcctc aggggtctct 180
gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240
tctgaggatg aggccgatta ttattgtgca gcatgggatg acagcctgaa tgggtccggta 300
ttcggcggag ggaccaagct gaccgtccta ggttctagag gtggtggtgg tagcggcggc 360
ggcggctctg gtggtggtgg atccctcgag atggccgaag tgcagctggt gcagtctgga 420

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gcagaggtga aaaagcccg ggagtctctg aagatctcct gtaaggggttc tggatacagc 480
 ttaccagct actggatcgg ctgggtgcgc cagatgcccg ggaaaggcct ggagtggatg 540
 gggatcatct atcctggtga ctctgatacc agatacagcc cgtccttcca aggccaggtc 600
 accatctcag ccgacaagtc catcagcacc gcctacctgc agtggagcag cctgaaggcc 660
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 gattactggg gtcaaggtac tctggtgacc gtctcctca 759

<210> 66
 <211> 253
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 66

Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
 1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Asn Ser Ser Asn Val Gly Asn Asn
 20 25 30

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

Ile Tyr Tyr Asp Asp Leu Leu Ser Ser Gly Val Ser Asp Arg Phe Ser
 50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
 65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
 85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser
 100 105 110

Arg Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125

Leu Glu Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
 130 135 140

Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser
 145 150 155 160

Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly
 165 170 175

Leu Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr

180

185

190

Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile
 195 200 205

Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala
 210 215 220

Met Tyr Tyr Cys Ala Arg Trp Ser Ser Thr Trp Asp Ser Met Tyr Met
 225 230 235 240

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 245 250

<210> 67
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 67
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 ccaggaaagg ctcccaaact cctcatctat tatgatgata tgctgtcctc aggggtctct 180
 gaccgattct ctgggtccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240
 tctgaggatg aggccgatta ttattgtgca gcatgggatg acagcctgaa tgggtccggta 300
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 gcagaggtga aaaagcccgg ggaatctctg aagatctcct gtaagggttc tgcatacagc 480
 tttaccagct actggatcgg ctgggtgctg cagatgcccg ggaaaggcct ggagtggatg 540
 gggatcatct atcctggtga ctctgatacc agatacagcc cgtccttcca aggccaggtc 600
 accatctcag ccgacaagtc catcagcacc gcctacctgc agtggagcag cctgaaggcc 660
 tcggacaccg ccatgtatta ctgtgcgcgc tgggtcttcta cttgggactc tatgtacatg 720
 gattactggg gtctaggtac tctggtgacc gtctcctca 759

<210> 68
 <211> 253
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 68

Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
 1 5 10 15

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Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Val Gly Asn Asn
20 25 30

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

Ile Tyr Tyr Asp Asp Leu Leu Ser Ser Gly Val Ser Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser
100 105 110

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Leu Glu Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
130 135 140

Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Ala Tyr Ser
145 150 155 160

Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly
165 170 175

Leu Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr
180 185 190

Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile
195 200 205

Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala
210 215 220

Met Tyr Tyr Cys Ala Arg Trp Ser Ser Thr Trp Asp Ser Met Tyr Met
225 230 235 240

Asp Tyr Trp Gly Leu Gly Thr Leu Val Thr Val Ser Ser
245 250

<210> 69
<211> 759
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Construct

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<400> 69
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ccaggaaagg ctcccaaact cctcatctat tatgatgatc agctgtcctc aggggtctct 180
gaccgattct ctgggtccaa gtctggcacc tcagcctccc tggccatcag tggggtccag 240
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ttcggcggag ggaccaagct gaccgtccta ggttctagag gtggtggtgg tagcggcggc 360
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gcagaggatg aaaagcccgg ggagtctctg aagatctcct gtaagggttc tggatacagc 480
tttaccagct actggatcgg ctgggtgctc cagatgcccg ggaaaggcct ggagtggatg 540
gggatcatct atcctggtga ctctgatacc agatacagcc cgtccttcca aggccagggt 600
accatctcag ccgacaagtc catcagcacc gcctacctgc agtgagcag cctgaaggcc 660
tcggacaccg ccatgtatta ctgtgcgcgc tgggtcttcta cttgggactc tatgtacatg 720
gattactggg gtcaaggtag tctggtaacc gtctcctca 759

<210> 70
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 70

Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Val Gly Asn Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser
100 105 110

Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115

120

125

Leu Gly Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
 130 135 140

Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser
 145 150 155 160

Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly
 165 170 175

Leu Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr
 180 185 190

Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile
 195 200 205

Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala
 210 215 220

Met Tyr Tyr Cys Ala Arg Trp Ser Ser Thr Trp Asp Ser Met Tyr Met
 225 230 235 240

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 245 250

<210> 71

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 71

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ccaggaaagg ctcccaaact cctcatctat tatgatgatc tgctgtcctc aggggtctct	180
gaccgattct ctgggtccaa gtctggcacc tcagcctccc tggccatcag tgggctccag	240
tctgaggatg aggccgatta ttattgtgca gcatgggatg acagcctgaa tgggtccggta	300
ttcggcgagg ggaccaagct gaccgtccta ggttctagag gtggtggtgg tagcggcggc	360
ggcggctctg gtggtggtgg atccctcgag atggccgaag tgcagctggt gcagtctgga	420
gcagaggtga aaaagcccgg ggagtctctg aagatctcct gtaagggttc tggatacagc	480
tttaccagct actggatcgg ctgggtgctg cagatgcccg ggaaaggcct ggagtggatg	540
gggatcatct atcctggtga ctctgatacc agatacagcc cgtccttcca aggccaggtc	600
accatctcag ccgacaagtc catcagcacc gcctacctgc agtggagcag cctgaaggcc	660
tcggacaccg ccatgtatta ctgtgcgcgc tgggtcttctt cttgggactc tatgtacatg	720

gattactggg gtcaaggtac tctggtgacc gtctcctca

759

<210> 72
 <211> 253
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 72

Gln Ala Val Leu Thr Gln Pro Pro Ser Val Ser Glu Ala Pro Arg Gln
 1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Val Gly Asn Asn
 20 25 30

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

Ile Tyr Tyr Asp Asp Leu Leu Ser Ser Gly Val Ser Asp Arg Phe Ser
 50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
 65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
 85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser
 100 105 110

Arg Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125

Leu Glu Met Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
 130 135 140

Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser
 145 150 155 160

Phe Thr Ser Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly
 165 170 175

Leu Glu Trp Met Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr
 180 185 190

Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile
 195 200 205

Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala
 210 215 220

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Met Tyr Tyr Cys Ala Arg Trp Ser Ser Ser Trp Asp Ser Met Tyr Met
225 230 235 240

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
245 250

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

<220>
<223> Synthetic Construct

<400> 73

Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

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

<220>
<223> Synthetic Construct

<400> 74

Ile Ser Gly Ser Gly Gly Ser Thr
1 5

<210> 75
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 75

Ala Arg Tyr Tyr Tyr Ser Arg Leu Asp Tyr
1 5 10

<210> 76
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 76

Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

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

<220>

<223> Synthetic Construct

<400> 77

Ile Ser Ala Ser Gly Gly Ser Thr
1 5

<210> 78

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 78

Ala Arg Tyr Tyr Leu Ser Gln Ile Asp Ser
1 5 10

<210> 79

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 79

Gly Tyr Thr Phe Thr Asp Tyr Tyr
1 5

<210> 80

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 80

Val Asp Pro Glu Asp Gly Glu Thr
1 5

<210> 81

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 81

Ala Thr Gly Ile Tyr Ser Arg Pro Leu Gly Tyr
1 5 10

<210> 82

<211> 8
 <212> PRT
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<220>
 <223> Synthetic Construct

<400> 82

Gly Phe Thr Phe Ser Ser Tyr Ala
 1 5

<210> 83
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 83

Ile Ser Gly Ser Gly Gly Ser Thr
 1 5

<210> 84
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 84

Ala Arg Ser Asp Gly Lys His Phe Trp Gln Gln Tyr Asp Ala
 1 5 10

<210> 85
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 85

Gly Phe Thr Val Ser Ser Asn Tyr
 1 5

<210> 86
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 86

Ile Ser Gly Ser Gly Gly Ser Thr
 1 5

<210> 87
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 87

Ala Arg Met Asn Ile Asp Tyr
 1 5

<210> 88
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 88

Glu Tyr Ser Phe Ala Ser Tyr Trp
 1 5

<210> 89
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 89

Ile Asp Pro Ser Asp Ser Tyr Thr
 1 5

<210> 90
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 90

Ala Arg Pro Phe Gln Tyr Asp Tyr Gly Gly Tyr Ser Asp Ala Phe Asp
 1 5 10 15

Ile

<210> 91
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 91

Gly Gly Thr Phe Ser Ser Ser Ser
 1 5

<210> 92

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 92

Ile Ile Pro Ile Val Gly Thr Pro
 1 5

<210> 93

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 93

Ala Arg Gly Gly Tyr Arg Asp Tyr Met Asp Val
 1 5 10

<210> 94

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 94

Gly Phe Thr Val Ser Ser Asn Tyr
 1 5

<210> 95

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 95

Ile Tyr Ser Gly Gly Ser Thr
 1 5

<210> 96

<211> 11

<212> PRT

<213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 96

Ala Arg Gly Gly Phe Gly Ala Glu Phe Asp Tyr
 1 5 10

<210> 97
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 97

Gly Phe Thr Val Ser Ser Asn Tyr
 1 5

<210> 98
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 98

Ile Tyr Ser Gly Gly Ser Thr
 1 5

<210> 99
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 99

Ala Arg Gly Gly Ile Ser Asp Asp Tyr Tyr Gly Ser Gly Ser Tyr Asp
 1 5 10 15

Asn

<210> 100
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 100

Gly Phe Thr Val Ser Ser Asn Tyr
 1 5

<210> 101
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 101

Ile Tyr Ser Gly Gly Ser Thr
 1 5

<210> 102
 <211> 12
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 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 102

Ala Arg Glu Arg Gly Met Gly Tyr Ala Phe Asp Ile
 1 5 10

<210> 103
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 103

Gly Val Ser Met Ser Glu Asn Tyr
 1 5

<210> 104
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 104

Ala His Tyr Thr Gly Asp Thr
 1 5

<210> 105
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 105

Ala Ser Tyr His Pro Phe Asn Tyr

1

5

<210> 106
 <211> 8
 <212> PRT
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<220>
 <223> Synthetic Construct

<400> 106

Gly Tyr Thr Phe Asn Asp Phe Tyr
 1 5

<210> 107
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 107

Ile Asp Pro Glu Asp Gly Lys Thr
 1 5

<210> 108
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 108

Thr Thr Asp Trp Gly Tyr Ser Ser Ser Leu Arg Glu Glu Asp Ile Trp
 1 5 10 15

Tyr Asp Cys

<210> 109
 <211> 8
 <212> PRT
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<220>
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<400> 109

Gly Gly Thr Phe Ser Ser Tyr Ala
 1 5

<210> 110
 <211> 8
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 <213> Artificial Sequence

<220>
 <223> Synthetic Construct
 <400> 110

Ile Ile Pro Ile Phe Gly Thr Ala
 1 5

<210> 111
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct
 <400> 111

Ala Arg Asp Tyr Gly Tyr Gly Asp Tyr Gly Asp Ala Phe Asp Ile
 1 5 10 15

<210> 112
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct
 <400> 112

Gly Tyr Ser Phe Thr Ser Tyr Trp
 1 5

<210> 113
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct
 <400> 113

Ile Tyr Pro Gly Asp Ser Asp Thr
 1 5

<210> 114
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct
 <400> 114

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

<210> 115
 <211> 8
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<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 115

Gly Tyr Ser Phe Thr Ser Tyr Trp
1 5

<210> 116

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 116

Ile Tyr Pro Gly Asp Ser Asp Thr
1 5

<210> 117

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 117

Ala Arg Gln Val Trp Gly Trp Gln Gly Gly Met Tyr Pro Arg Ser Asn
1 5 10 15

Trp Trp Tyr Asn Met Asp Ser
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<210> 118

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 118

Gly Tyr Ser Phe Thr Ser Tyr Trp
1 5

<210> 119

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 119

Ile Tyr Pro Gly Asp Ser Asp Thr

1

5

<210> 120
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 120

Ala Arg Trp Ser Ser Thr Trp Asp Ser Met Tyr Met Asp Tyr
 1 5 10

<210> 121
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 121

Gly Tyr Ser Phe Thr Ser Tyr Trp
 1 5

<210> 122
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 122

Ile Tyr Pro Gly Asp Ser Asp Thr
 1 5

<210> 123
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 123

Ala Arg Val Thr Tyr Ser Met Asp Ser Tyr Tyr Phe Asp Ser
 1 5 10

<210> 124
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 124

Gly Tyr Ser Phe Thr Ser Tyr Trp
1 5

<210> 125
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 125

Ile Tyr Pro Gly Asp Ser Asp Thr
1 5

<210> 126
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 126

Ala Arg Gln Val Trp Gly Trp Gln Gly Gly Met Tyr Pro Arg Ser Asn
1 5 10 15

Trp Trp Tyr Asn Met Asp Ser
20

<210> 127
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 127

Gly Tyr Ser Phe Thr Ser Tyr Trp
1 5

<210> 128
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 128

Ile Tyr Pro Gly Asp Ser Asp Thr
1 5

<210> 129
<211> 23
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 129

Ala Arg Gln Val Trp Gly Trp Gln Gly Gly Met Tyr Pro Arg Ser Asn
1 5 10 15

Trp Trp Tyr Asn Met Asp Ser
20

<210> 130

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 130

Gly Tyr Ser Phe Thr Ser Tyr Trp
1 5

<210> 131

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 131

Ile Tyr Pro Gly Asp Ser Asp Thr
1 5

<210> 132

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 132

Ala Arg Gln Val Trp Gly Trp Gln Gly Gly Met Tyr Pro Arg Ser Asn
1 5 10 15

Trp Trp Tyr Asn Met Asp Ser
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<210> 133

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 133

Gly Tyr Ser Phe Thr Ser Tyr Trp
 1 5

<210> 134

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 134

Ile Tyr Pro Gly Asp Ser Asp Thr
 1 5

<210> 135

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 135

Ala Arg Gln Val Trp Gly Trp Gln Gly Gly Met Tyr Pro Arg Ser Asn
 1 5 10 15

Trp Trp Tyr Asn Met Asp Ser
 20

<210> 136

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 136

Gly Tyr Ser Phe Thr Ser Tyr Trp
 1 5

<210> 137

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

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Ala Ala Trp Asp Asp Ser Leu Asn Gly Pro Val
1 5 10

<210> 268

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 268

Ser Ser Asn Val Gly Asn Asn Ala
1 5

<210> 269

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 269

Tyr Asp Asp
1

<210> 270

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 270

Ala Ala Trp Asp Asp Ser Leu Asn Gly Pro Val
1 5 10

<210> 271

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 271

Ser Ser Asn Val Gly Asn Asn Ala
1 5

<210> 272

<211> 3
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<220>
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<400> 272

Tyr Asp Asp
 1

<210> 273
 <211> 11
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<220>
 <223> Synthetic Construct

<400> 273

Ala Ala Trp Asp Asp Ser Leu Asn Gly Pro Val
 1 5 10

<210> 274
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 274

Ser Ser Asn Val Gly Asn Asn Ala
 1 5

<210> 275
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 275

Tyr Asp Asp
 1

<210> 276
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 276

Ala Ala Trp Asp Asp Ser Leu Asn Gly Pro Val
 1 5 10

<210> 277
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 277

Ser Ser Asn Val Gly Asn Asn Ala
 1 5

<210> 278
 <211> 3
 <212> PRT
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<220>
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<400> 278

Tyr Asp Asp
 1

<210> 279
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 279

Ala Ala Trp Asp Asp Ser Leu Asn Gly Pro Val
 1 5 10

<210> 280
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 280

Ser Ser Asn Val Gly Asn Asn Ala
 1 5

<210> 281
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 281

Tyr Asp Asp

1

<210> 282
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 282

Ala Ala Trp Asp Asp Ser Leu Asn Gly Pro Val
 1 5 10

<210> 283
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 283

Ser Ser Asn Val Gly Asn Asn Ala
 1 5

<210> 284
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 284

Tyr Asp Asp
 1

<210> 285
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 285

Ala Ala Trp Asp Asp Ser Leu Asn Gly Pro Val
 1 5 10

<210> 286
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 286

Ser Ser Asn Val Gly Asn Asn Ala
1 5

<210> 287
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 287

Tyr Asp Asp
1

<210> 288
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> misc_feature
<222> (2)..(2)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (4)..(7)
<223> Xaa can be any naturally occurring amino acid

<400> 288

Ile Xaa Pro Xaa Xaa Xaa Xaa Thr
1 5

<210> 289
<211> 556
<212> PRT
<213> Homo sapeins

<400> 289

Met Pro Pro Pro Arg Leu Leu Phe Phe Leu Leu Phe Leu Thr Pro Met
1 5 10 15

Glu Val Arg Pro Glu Glu Pro Leu Val Val Lys Val Glu Glu Gly Asp
20 25 30

Asn Ala Val Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln
35 40 45

Gln Leu Thr Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu
50 55 60

Ser Leu Gly Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ile
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65				70				75				80			
Trp	Leu	Phe	Ile	Phe 85	Asn	Val	Ser	Gln	Gln 90	Met	Gly	Gly	Phe	Tyr 95	Leu
Cys	Gln	Pro	Gly 100	Pro	Pro	Ser	Glu	Lys 105	Ala	Trp	Gln	Pro	Gly 110	Trp	Thr
Val	Asn	Val 115	Glu	Gly	Ser	Gly	Glu 120	Leu	Phe	Arg	Trp	Asn 125	Val	Ser	Asp
Leu	Gly 130	Gly	Leu	Gly	Cys	Gly 135	Leu	Lys	Asn	Arg	Ser 140	Ser	Glu	Gly	Pro
Ser 145	Ser	Pro	Ser	Gly	Lys 150	Leu	Met	Ser	Pro	Lys 155	Leu	Tyr	Val	Trp	Ala 160
Lys	Asp	Arg	Pro	Glu 165	Ile	Trp	Glu	Gly	Glu 170	Pro	Pro	Cys	Leu	Pro 175	Pro
Arg	Asp	Ser	Leu 180	Asn	Gln	Ser	Leu	Ser 185	Gln	Asp	Leu	Thr	Met 190	Ala	Pro
Gly	Ser	Thr 195	Leu	Trp	Leu	Ser	Cys 200	Gly	Val	Pro	Pro	Asp 205	Ser	Val	Ser
Arg	Gly 210	Pro	Leu	Ser	Trp	Thr 215	His	Val	His	Pro	Lys 220	Gly	Pro	Lys	Ser
Leu 225	Leu	Ser	Leu	Glu	Leu 230	Lys	Asp	Asp	Arg	Pro 235	Ala	Arg	Asp	Met	Trp 240
Val	Met	Glu	Thr	Gly 245	Leu	Leu	Leu	Pro	Arg 250	Ala	Thr	Ala	Gln	Asp 255	Ala
Gly	Lys	Tyr	Tyr 260	Cys	His	Arg	Gly	Asn 265	Leu	Thr	Met	Ser	Phe 270	His	Leu
Glu	Ile	Thr 275	Ala	Arg	Pro	Val	Leu 280	Trp	His	Trp	Leu	Leu 285	Arg	Thr	Gly
Gly	Trp 290	Lys	Val	Ser	Ala	Val 295	Thr	Leu	Ala	Tyr	Leu 300	Ile	Phe	Cys	Leu
Cys 305	Ser	Leu	Val	Gly	Ile 310	Leu	His	Leu	Gln	Arg 315	Ala	Leu	Val	Leu	Arg 320
Arg	Lys	Arg	Lys	Arg 325	Met	Thr	Asp	Pro	Thr 330	Arg	Arg	Phe	Phe	Lys 335	Val
Thr	Pro	Pro	Pro	Gly	Ser	Gly	Pro	Gln	Asn	Gln	Tyr	Gly	Asn	Val	Leu

340

345

350

Ser Leu Pro Thr Pro Thr Ser Gly Leu Gly Arg Ala Gln Arg Trp Ala
 355 360 365

Ala Gly Leu Gly Gly Thr Ala Pro Ser Tyr Gly Asn Pro Ser Ser Asp
 370 375 380

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

Pro Glu Glu Glu Glu Gly Glu Gly Tyr Glu Glu Pro Asp Ser Glu Glu
 405 410 415

Asp Ser Glu Phe Tyr Glu Asn Asp Ser Asn Leu Gly Gln Asp Gln Leu
 420 425 430

Ser Gln Asp Gly Ser Gly Tyr Glu Asn Pro Glu Asp Glu Pro Leu Gly
 435 440 445

Pro Glu Asp Glu Asp Ser Phe Ser Asn Ala Glu Ser Tyr Glu Asn Glu
 450 455 460

Asp Glu Glu Leu Thr Gln Pro Val Ala Arg Thr Met Asp Phe Leu Ser
 465 470 475 480

Pro His Gly Ser Ala Trp Asp Pro Ser Arg Glu Ala Thr Ser Leu Gly
 485 490 495

Ser Gln Ser Tyr Glu Asp Met Arg Gly Ile Leu Tyr Ala Ala Pro Gln
 500 505 510

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

Asp Ser Tyr Glu Asn Met Asp Asn Pro Asp Gly Pro Asp Pro Ala Trp
 530 535 540

Gly Gly Gly Gly Arg Met Gly Thr Trp Ser Thr Arg
 545 550 555

<210> 290
 <211> 488
 <212> PRT
 <213> Homo sapiens

<400> 290

Met Pro Pro Pro Arg Leu Leu Phe Phe Leu Leu Phe Leu Thr Pro Met
 1 5 10 15

Glu Val Arg Pro Glu Glu Pro Leu Val Val Lys Val Glu Glu Gly Asp
 20 25 30

Asn Ala Val₃₅ Leu Gln Cys Leu Lys₄₀ Gly Thr Ser Asp Gly₄₅ Pro Thr Gln
 Gln Leu₅₀ Thr Trp Ser Arg Glu₅₅ Ser Pro Leu Lys₆₀ Phe Leu Lys Leu
 Ser Leu Gly Leu Pro Gly₇₀ Leu Gly Ile His Met₇₅ Arg Pro Leu Ala Ile₈₀
 Trp Leu Phe Ile Phe₈₅ Asn Val Ser Gln Gln₉₀ Met Gly Gly Phe Tyr₉₅ Leu
 Cys Gln Pro Gly₁₀₀ Pro Pro Ser Glu Lys₁₀₅ Ala Trp Gln Pro Gly₁₁₀ Trp Thr
 Val Asn Val₁₁₅ Glu Gly Ser Gly Glu₁₂₀ Leu Phe Arg Trp Asn Val Ser Asp₁₂₅
 Leu Gly₁₃₀ Gly Leu Gly Cys Gly₁₃₅ Leu Lys Asn Arg Ser₁₄₀ Ser Glu Gly Pro
 Ser₁₄₅ Ser Pro Ser Gly Lys₁₅₀ Leu Met Ser Pro Lys₁₅₅ Leu Tyr Val Trp Ala₁₆₀
 Lys Asp Arg Pro Glu₁₆₅ Ile Trp Glu Gly Glu₁₇₀ Pro Pro Cys Leu Pro₁₇₅ Pro
 Arg Asp Ser Leu₁₈₀ Asn Gln Ser Leu Ser₁₈₅ Gln Asp Leu Thr Met₁₉₀ Ala Pro
 Gly Ser Thr₁₉₅ Leu Trp Leu Ser Cys₂₀₀ Gly Val Pro Pro Asp₂₀₅ Ser Val Ser
 Arg Gly₂₁₀ Pro Leu Ser Trp Thr₂₁₅ His Val His Pro Lys₂₂₀ Gly Pro Lys Ser
 Leu₂₂₅ Leu Ser Leu Glu Leu₂₃₀ Lys Asp Asp Arg Pro Ala Arg Asp Met Trp₂₄₀
 Val Met Glu Thr Gly₂₄₅ Leu Leu Leu Pro Arg₂₅₀ Ala Thr Ala Gln Asp₂₅₅ Ala
 Gly Lys Tyr Tyr₂₆₀ Cys His Arg Gly Asn₂₆₅ Leu Thr Met Ser Phe₂₇₀ His Leu
 Glu Ile Thr₂₇₅ Ala Arg Pro Val Leu₂₈₀ Trp His Trp Leu Leu₂₈₅ Arg Thr Gly
 Gly Trp₂₉₀ Lys Val Ser Ala Val₂₉₅ Thr Leu Ala Tyr Leu₃₀₀ Ile Phe Cys Leu

Cys Ser Leu Val Gly Ile Leu His Leu Gln Arg Ala Leu Val Leu Arg
305 310 315 320

Arg Lys Arg Lys Arg Met Thr Asp Pro Thr Arg Arg Phe Phe Lys Val
325 330 335

Thr Pro Pro Pro Gly Ser Gly Pro Gln Asn Gln Tyr Gly Asn Val Leu
340 345 350

Ser Leu Pro Thr Pro Thr Ser Gly Leu Gly Arg Ala Gln Arg Trp Ala
355 360 365

Ala Gly Leu Gly Gly Thr Ala Pro Ser Tyr Gly Asn Pro Ser Ser Asp
370 375 380

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

Pro Glu Glu Glu Glu Gly Glu Gly Tyr Glu Glu Pro Asp Ser Glu Glu
405 410 415

Asp Ser Glu Phe Tyr Glu Asn Asp Ser Asn Leu Gly Gln Asp Gln Leu
420 425 430

Ser Gln Asp Gly Ser Gly Tyr Glu Asn Pro Glu Asp Glu Pro Leu Gly
435 440 445

Pro Glu Asp Glu Asp Ser Phe Ser Asn Ala Glu Ser Tyr Glu Asn Glu
450 455 460

Asp Glu Glu Leu Thr Gln Pro Val Ala Arg Thr Met Asp Phe Leu Ser
465 470 475 480

Pro His Gly Ser Ala Trp Asp Pro
485

<210> 291
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> misc_feature
<222> (2)..(8)
<223> X2 is F, G, Y or V, X3 is S or T, X5 is S or T, X7 is N or Y, and
X8 is A, W or Y

<400> 291

Gly Xaa Xaa Phe Xaa Ser Xaa Xaa

1

5

<210> 292
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<220>
 <221> misc_feature
 <222> (2)..(7)
 <223> X2 is S, D or Y, X4 is E, S, G or I, X5 is D, F or V, X6 is G or S, and X7 is K, E, Y, D or T

<400> 292

Ile Xaa Pro Xaa Xaa Xaa Thr
 1 5

<210> 293
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<220>
 <221> misc_feaure
 <222> (4)..(8)
 <223> X4 is I or V, X6 is N, S or T, X7 is N, H or K, X8 is Y, A or T

<400> 293

Ser Ser Asn Xaa Gly Xaa Xaa Xaa
 1 5

<210> 294
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<220>
 <221> misc_feature
 <222> (5)..(5)
 <223> X5 is K or E

<400> 294

Asn Ile Gly Ser Xaa Ser
 1 5

<210> 295
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> X1 is D, E, S, R or Y, X2 is N or D, X3 is N, Y, S or D
 <400> 295

Xaa Xaa Xaa
 1

<210> 296
 <211> 245
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct
 <400> 296

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

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

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

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

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

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

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

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
 115 120 125

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

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
 145 150 155 160

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

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
180 185 190

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

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
210 215 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225 230 235 240

Val Thr Val Ser Ser
245

<210> 297
<211> 6
<212> PRT
<213> Mus musculus

<400> 297

Gln Asp Ile Ser Lys Tyr
1 5

<210> 298
<211> 3
<212> PRT
<213> Mus musculus

<400> 298

His Thr Ser
1

<210> 299
<211> 9
<212> PRT
<213> Mus musculus

<400> 299

Gln Gln Gly Asn Thr Leu Pro Tyr Thr
1 5

<210> 300
<211> 8
<212> PRT
<213> Mus musculus

<400> 300

Gly Val Ser Leu Pro Asp Tyr Gly
1 5

<210> 301
<211> 7

<212> PRT
<213> Mus musculus

<400> 301

Ile Trp Gly Ser Glu Thr Thr
1 5

<210> 302
<211> 14
<212> PRT
<213> Mus musculus

<400> 302

Ala Lys His Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr
1 5 10