

146392033640_Sequence_Listing
SEQUENCE LISTING

<110> GENENTECH, INC. ET AL
LADIWALA, Asif
MCKAY, Patrick A.
FONG, Chris B.

<120> PURIFICATION OF FKPA AND USES THEREOF FOR PRODUCING RECOMBINANT
POLYPEPTIDES

<130> P32953-WO

<140> Not Yet Assigned

<141> Concurrently Herewith

<150> 62/210,378

<151> 2015-08-26

<150> 62/207,910

<151> 2015-08-20

<150> 62/207,908

<151> 2015-08-20

<160> 45

<170> PatentIn version 3.5

<210> 1

<211> 185

<212> PRT

<213> Escherichia coli

<400> 1

Ala	Phe	Ala	Asp	Lys	Ser	Lys	Leu	Ser	Asp	Gln	Glu	Ile	Glu	Gln	Thr
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Leu	Gln	Ala	Phe	Glu	Ala	Arg	Val	Lys	Ser	Ser	Ala	Gln	Ala	Lys	Met
		20						25					30		

Glu	Lys	Asp	Ala	Ala	Asp	Asn	Glu	Ala	Lys	Gly	Lys	Glu	Tyr	Arg	Glu
		35					40					45			

Lys	Phe	Ala	Lys	Glu	Lys	Gly	Val	Lys	Thr	Ser	Ser	Thr	Gly	Leu	Val
		50				55					60				

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Tyr Gln Val Val Glu Ala Gly Lys Gly Glu Ala Pro Lys Asp Ser Asp
65 70 75 80

Thr Val Val Val Asn Tyr Lys Gly Thr Leu Ile Asp Gly Lys Glu Phe
85 90 95

Asp Asn Ser Tyr Thr Arg Gly Glu Pro Leu Ser Phe Arg Leu Asp Gly
100 105 110

Val Ile Pro Gly Trp Thr Glu Gly Leu Lys Asn Ile Lys Lys Gly Gly
115 120 125

Lys Ile Lys Leu Val Ile Pro Pro Glu Leu Ala Tyr Gly Lys Ala Gly
130 135 140

Val Pro Gly Ile Pro Pro Asn Ser Thr Leu Val Phe Asp Val Glu Leu
145 150 155 160

Leu Asp Val Lys Pro Ala Pro Lys Ala Asp Ala Lys Pro Glu Ala Asp
165 170 175

Ala Lys Ala Ala Asp Ser Ala Lys Lys
180 185

<210> 2

<211> 270

<212> PRT

<213> Escherichia coli

<220>

<221> MOD_RES

<222> (239)..(239)

<223> Any amino acid

<400> 2

Met Lys Ser Leu Phe Lys Val Thr Leu Leu Ala Thr Thr Met Ala Val
1 5 10 15

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Ala Leu His Ala Pro Ile Thr Phe Ala Ala Glu Ala Ala Lys Pro Ala
20 25 30

Thr Thr Ala Asp Ser Lys Ala Ala Phe Lys Asn Asp Asp Gln Lys Ser
35 40 45

Ala Tyr Ala Leu Gly Ala Ser Leu Gly Arg Tyr Met Glu Asn Ser Leu
50 55 60

Lys Glu Gln Glu Lys Leu Gly Ile Lys Leu Asp Lys Asp Gln Leu Ile
65 70 75 80

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

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

Ala Gln Ala Lys Met Glu Lys Asp Ala Ala Asp Asn Glu Ala Lys Gly
115 120 125

Lys Glu Tyr Arg Glu Lys Phe Ala Lys Glu Lys Gly Val Lys Thr Ser
130 135 140

Ser Thr Gly Leu Val Tyr Gln Val Val Glu Ala Gly Lys Gly Glu Ala
145 150 155 160

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

Asp Gly Lys Glu Phe Asp Asn Ser Tyr Thr Arg Gly Glu Pro Leu Ser
180 185 190

Phe Arg Leu Asp Gly Val Ile Pro Gly Trp Thr Glu Gly Leu Lys Asn
195 200 205

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Ile Lys Lys Gly Gly Lys Ile Lys Leu Val Ile Pro Pro Glu Leu Ala
 210 215 220

Tyr Gly Lys Ala Gly Val Pro Gly Ile Pro Pro Asn Ser Thr Xaa Val
 225 230 235 240

Phe Asp Val Glu Leu Leu Asp Val Lys Pro Ala Pro Lys Ala Asp Ala
 245 250 255

Lys Pro Glu Ala Asp Ala Lys Ala Ala Asp Ser Ala Lys Lys
 260 265 270

<210> 3
 <211> 813
 <212> DNA
 <213> Escherichia coli

<400> 3
 atgaaatcac tgttttaaagt aacgctgctg gcgaccacaa tggccgttgc cctgcatgca 60
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 ttcaaaaatg acgatcagaa atcagcttat gcaactgggtg cctcgctggg tcgttacatg 180
 gaaaactctc taaaagaaca agaaaaactg ggcatcaaac tggataaaga tcagctgac 240
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 gcggctgata acgaagcaaa aggtaaagag taccgcgaga aatttgccaa agagaaaggt 420
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 ccgaaagaca gcgatactgt tgtagtgaac taaaaggta cgctgatcga cggtaaagag 540
 ttcgacaact cttacacccg tggatgaaccg ctttctttcc gtctggacgg tgttatcccg 600
 ggttggacag aaggcttgaa gaacatcaag aaaggcggta agatcaaact gggtattcca 660
 ccagaactgg cttacggcaa agcgggtgtt ccggggatcc caccgaattc taccctggtg 720

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gatgcgaaaag ccgcagattc tgctaaaaaa taa 813

<210> 4

<211> 132

<212> PRT

<213> Homo sapiens

<400> 4

Met Ala Leu Leu Leu Thr Thr Val Ile Ala Leu Thr Cys Leu Gly Gly
1 5 10 15

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

Ile Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys
35 40 45

Asn Gly Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys
50 55 60

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

Lys Thr Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala
85 90 95

Gly Gln Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala
100 105 110

Gln Phe Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu
115 120 125

Gly Arg Phe Asn
130

<210> 5

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<211> 114

<212> PRT

<213> Homo sapiens

<400> 5

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

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
20 25 30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
35 40 45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
50 55 60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65 70 75 80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
85 90 95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
100 105 110

Phe Asn

<210> 6

<211> 155

<212> PRT

<213> Homo sapiens

<400> 6

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

Leu Glu Ala Ile Val Lys Ala Gly Ile Thr Ile Pro Arg Asn Pro Gly

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20

25

30

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

Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser
50 55 60

Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu
65 70 75 80

Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His
85 90 95

Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser
100 105 110

Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His
115 120 125

Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys
130 135 140

Thr Cys Val Thr Pro Ile Val His His Val Ala
145 150 155

<210> 7

<211> 132

<212> PRT

<213> Homo sapiens

<400> 7

Gly Ile Thr Ile Pro Arg Asn Pro Gly Cys Pro Asn Ser Glu Asp Lys
1 5 10 15

Asn Phe Pro Arg Thr Val Met Val Asn Leu Asn Ile His Asn Arg Asn
20 25 30

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Thr Asn Thr Asn Pro Lys Arg Ser Ser Asp Tyr Tyr Asn Arg Ser Thr
35 40 45

Ser Pro Trp Asn Leu His Arg Asn Glu Asp Pro Glu Arg Tyr Pro Ser
50 55 60

Val Ile Trp Glu Ala Lys Cys Arg His Leu Gly Cys Ile Asn Ala Asp
65 70 75 80

Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln Gln Glu Ile
85 90 95

Leu Val Leu Arg Arg Glu Pro Pro His Cys Pro Asn Ser Phe Arg Leu
100 105 110

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

His His Val Ala
130

<210> 8
<211> 163
<212> PRT
<213> Homo sapiens

<400> 8
Met Thr Val Lys Thr Leu His Gly Pro Ala Met Val Lys Tyr Leu Leu
1 5 10 15

Leu Ser Ile Leu Gly Leu Ala Phe Leu Ser Glu Ala Ala Ala Arg Lys
20 25 30

Ile Pro Lys Val Gly His Thr Phe Phe Gln Lys Pro Glu Ser Cys Pro
35 40 45

Pro Val Pro Gly Gly Ser Met Lys Leu Asp Ile Gly Ile Ile Asn Glu

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50

55

60

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

Pro Trp Asn Tyr Thr Val Thr Trp Asp Pro Asn Arg Tyr Pro Ser Glu
85 90 95

Val Val Gln Ala Gln Cys Arg Asn Leu Gly Cys Ile Asn Ala Gln Gly
100 105 110

Lys Glu Asp Ile Ser Met Asn Ser Val Pro Ile Gln Gln Glu Thr Leu
115 120 125

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

Lys Val Leu Val Thr Val Gly Cys Thr Cys Val Thr Pro Val Ile His
145 150 155 160

His Val Gln

<210> 9

<211> 133

<212> PRT

<213> Homo sapiens

<400> 9

Arg Lys Ile Pro Lys Val Gly His Thr Phe Phe Gln Lys Pro Glu Ser
1 5 10 15

Cys Pro Pro Val Pro Gly Gly Ser Met Lys Leu Asp Ile Gly Ile Ile
20 25 30

Asn Glu Asn Gln Arg Val Ser Met Ser Arg Asn Ile Glu Ser Arg Ser
35 40 45

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Thr Ser Pro Trp Asn Tyr Thr Val Thr Trp Asp Pro Asn Arg Tyr Pro
50 55 60

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

Gln Gly Lys Glu Asp Ile Ser Met Asn Ser Val Pro Ile Gln Gln Glu
85 90 95

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

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

Ile His His Val Gln
130

<210> 10

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 10

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

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

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

Ala Met Ile Trp Gly Asp Gly Lys Ile Val Tyr Asn Ser Ala Leu Lys
50 55 60

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 11
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 11
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ser Val Ser Leu Gly
1 5 10 15

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

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

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

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

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Asn Asn

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85

90

95

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

<210> 12

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 12

Ala Tyr Ser Val Asn
 1 5

<210> 13

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 13

Met Ile Trp Gly Asp Gly Lys Ile Val Tyr Asn Ser Ala Leu Lys Ser
 1 5 10 15

<210> 14

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 14

Asp Gly Tyr Tyr Pro Tyr Ala Met Asp Asn
 1 5 10

<210> 15

<211> 15

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<212> PRT

<213> Artificial Sequence

<220>

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<400> 15

Arg	Ala	Ser	Lys	Ser	Val	Asp	Ser	Tyr	Gly	Asn	Ser	Phe	Met	His
1				5					10				15	

<210> 16

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 16

Leu	Ala	Ser	Asn	Leu	Glu	Ser
1			5			

<210> 17

<211> 9

<212> PRT

<213> Artificial Sequence

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<400> 17

Gln	Gln	Asn	Asn	Glu	Asp	Pro	Arg	Thr
1			5					

<210> 18

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 18

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

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

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

Ala Met Ile Trp Gly Asp Gly Lys Ile Val Tyr Asn Ser Ala Leu Lys
50 55 60

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

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

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

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

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

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

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

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

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

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

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

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

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

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

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

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440

<210> 19

<211> 445

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 19

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

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

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

Ala Met Ile Trp Gly Asp Gly Lys Ile Val Tyr Asn Ser Ala Leu Lys
50 55 60

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

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

Gly Asp Gly Tyr Tyr Pro Tyr Ala Met Asp Asn Trp Gly Gln Gly Ser

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100

105

110

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

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

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

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

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

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

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

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

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

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu

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290

295

300

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

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

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
355 360 365

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

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

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

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 20

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 20

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

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

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

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

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

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

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

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

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

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His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205

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

<210> 21
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic construct

<400> 21
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15

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

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

Ser Gly Ile Asn Trp Ser Ser Gly Gly Ile Gly Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Asp Ile Gly Gly Phe Gly Glu Phe Tyr Trp Asn Phe Gly Leu
 100 105 110

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

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<210> 22

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 22

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

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

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

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

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

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

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

<210> 23

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 23

Asp Tyr Ala Met His

146392033640_Sequence_Listing

1 5

<210> 24
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic construct

<400> 24
 Gly Ile Asn Trp Ser Ser Gly Gly Ile Gly Tyr Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> 25
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic construct

<400> 25
 Asp Ile Gly Gly Phe Gly Glu Phe Tyr Trp Asn Phe Gly Leu
 1 5 10

<210> 26
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic construct

<400> 26
 Arg Ala Ser Gln Ser Val Arg Ser Tyr Leu Ala
 1 5 10

<210> 27
 <211> 7

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<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 27

Asp Ala Ser Asn Arg Ala Thr

1 5

<210> 28

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 28

Gln Gln Arg Ser Asn Trp Pro Pro Ala Thr

1 5 10

<210> 29

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 29

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

1 5 10 15

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

20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Gly Ile Asn Trp Ser Ser Gly Gly Ile Gly Tyr Ala Asp Ser Val

50 55 60

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

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

Ala Arg Asp Ile Gly Gly Phe Gly Glu Phe Tyr Trp Asn Phe Gly Leu
100 105 110

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
130 135 140

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

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

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

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

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
210 215 220

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly
225 230 235 240

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

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

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

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

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

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

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

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

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

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Arg Leu Thr Val Asp
405 410 415

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

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

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Gly

<210> 30

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 30

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

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

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

Ser Gly Ile Asn Trp Ser Ser Gly Gly Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Asp Ile Gly Gly Phe Gly Glu Phe Tyr Trp Asn Phe Gly Leu
100 105 110

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
130 135 140

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

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

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

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

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
210 215 220

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly
225 230 235 240

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

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

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

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

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

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

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

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

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

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

Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Arg Leu Thr Val Asp
405 410 415

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

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

Gly Lys
450

<210> 31
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 31
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1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Tyr

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20

25

30

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

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

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

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

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

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

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys

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210

215

<210> 32
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 32
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ccaggcaagg ccctggagtg gctggccatg atctggggcg acggcaagat cgtgtacaac 180
agcgccctga agagccgcct gaccatcagc aaggacacca gcaagaacca ggtgggtgctg 240
accatgacca acatggaccc agtggacacc gccacctact actgcgccgg cgacggctac 300
taccatacgc ccatggacaa ctggggccag ggcagcctgg tgaccgtgag cagc 354

<210> 33
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 33
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atcaactgcc gcgccagcaa aagcgtggac agctacggca acagcttcat gcaactggat 120
cagcagaagc caggccagcc acccaagctg ctgatctacc tggccagcaa cctggagagc 180
ggcgtgccag accgcttcag cggcagcggc agcggcaccg acttcaccct gaccatcagc 240
tctctgcagg ccgaggatgt ggccgtgtac tactgccagc agaacaacga ggacccacgc 300
accctcgggtg gcggtaccaa ggtggagatc aaa 333

<210> 34

146392033640_Sequence_Listing

<211> 1332

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 34

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acctgcaccg tcagcggctt cagcctgagc gcctacagcg tgaactggat ccgccagcca	120
ccaggcaagg ccctggagtg gctggccatg atctggggcg acggcaagat cgtgtacaac	180
agcgccctga agagccgcct gaccatcagc aaggacacca gcaagaacca ggtggtgctg	240
accatgacca acatggaccc agtggacacc gccacctact actgcgccgg cgacggctac	300
taccatacag ccatggacaa ctggggccag ggcagcctgg tgaccgtgag cagcgcttcc	360
accaagggcc catcggctct cccctggca ccctgctccc gcagtacttc tgagtccaca	420
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac	480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccgctg tcctacagtc ctcaggactc	540
tactccctca gcagcgtggt gactgtgccc tctagcagct tgggcaccaa gacctacag	600
tgcaacgtgg atcacaagcc cagcaacacc aaggaggaca aacgcgttga gtccaaatat	660
ggtcccccat gcccaccatg cccagcacct gagttcctgg ggggaccatc agtcttcctg	720
ttcccccaa aaccaagga cactctcatg atctcccga cccctgaggt cacgtgcgtg	780
gtggtggacg tgagccagga agaccccgag gtccagttca actggtacgt ggatggcgtg	840
gaggtgcata atgccaagac aaagccgcgg gaggagcagt tcaacagcac gtaccgtgtg	900
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaacg gcaaggagta caagtgaag	960
gtctccaaca aaggcctccc gtcctccatc gagaaaacca tctccaaagc caaagggcag	1020
ccccgagagc cacaggtgta caccctgccc ccatcccagg aggagatgac caagaaccag	1080
gtcagcctgt ggtgcctggt caaaggcttc taccacagcg acatcgccgt ggagtgggag	1140
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc	1200

146392033640_Sequence_Listing

tccttcttcc tctacagcag gctaaccgtg gacaagagca ggtggcagga ggggaatgtc	1260
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacacagaa gagcctctcc	1320
ctgtctctgg gt	1332

<210> 35

<211> 1338

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 35

gaagttaccc tgcgcgagag cggcccagcc ctggtgaagc caaccagac cctgaccctg	60
acctgcaccg tcagcggcctt cagcctgagc gcctacagcg tgaactggat ccgccagcca	120
ccaggcaagg ccctggagtg gctggccatg atctggggcg acggcaagat cgtgtacaac	180
agcgccctga agagccgcct gaccatcagc aaggacacca gcaagaacca ggtggtgctg	240
accatgacca acatggaccc agtggacacc gccacctact actgcgccgg cgacggctac	300
taccatacgc ccatggacaa ctggggccag ggcagcctgg tgaccgtgag cagcgcttcc	360
accaagggcc catcggcttt cccctggca ccctgctccc gcagtacttc tgagtccaca	420
gcggcccttg gctgccttgt caaggactac ttccccgaac cggtgacggt gtcgtggaac	480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc	540
tactccctca gcagcgtggt gactgtgccc tctagcagct tgggcaccaa gacctacag	600
tgcaacgtgg atcacaagcc cagcaacacc aagggtggaca aacgcgttga gtccaaatat	660
ggtcccccat gcccaccatg cccagcacct gagttcctgg ggggaccatc agtcttcctg	720
ttccccccaa aaccaagga cactctcatg atctcccga cccctgaggt cacgtgcgtg	780
gtggtggacg tgagccagga agaccccgag gtccagttca actggtacgt ggatggcgtg	840
gaggtgcata atgccaagac aaagccgcgg gaggagcagt tcaacagcac gtaccgtgtg	900
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaacg gcaaggagta caagtgcaag	960

146392033640_Sequence_Listing

gtctccaaca aaggcctccc gtcctccatc gagaaaacca tctccaaagc caaagggcag	1020
ccccgagagc cacaggtgta caccctgccc ccatcccagg aggagatgac caagaaccag	1080
gtcagcctgt ggtgcctggt caaaggcttc taccacagcg acatcgccgt ggagtgggag	1140
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc	1200
tccttcttcc tctacagcag gctaaccgtg gacaagagca ggtggcagga ggggaatgtc	1260
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacacagaa gagcctctcc	1320
ctgtctctgg gtaaataa	1338

<210> 36

<211> 657

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 36

gatatcgtgc tgacccagag cccagacagc ctgtctgtga gcctgggcga gcgcgccacc	60
atcaactgcc gcgccagcaa aagcgtggac agctacggca acagcttcat gacttggtat	120
cagcagaagc caggccagcc acccaagctg ctgatctacc tggccagcaa cctggagagc	180
ggcgtgccag accgcttcag cggcagcggc agcggcaccg acttcaccct gaccatcagc	240
tctctgcagg ccgaggatgt ggccgtgtac tactgccagc agaacaacga ggacccacgc	300
accttcggtg gcggtacca ggtggagatc aaacgaactg tggctgcacc atctgtcttc	360
atcttcccg ccatctgatga gcagttgaaa tctggaactg cttctgttgt gtgcctgctg	420
aataacttct atccccgtga ggccaaagta cagtgggaagg tggataacgc cctccaatcg	480
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc	540
agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc	600
acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgttaa	657

<210> 37

146392033640_Sequence_Listing

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 37

gaagtgcagc tggaggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc	60
tcctgtgcag cctctggatt cacctttgat gattatgccca tgcactgggt ccggcaagct	120
ccagggaagg gcctggagtg ggtctcaggc attaatgga gcagtgggtg cataggctat	180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat	240
ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aagagatatc	300
gggggggttcg gggagtttta ctggaacttc ggtctctggg gccgtggcac cctggtcact	360
gtctcctca	369

<210> 38

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 38

gaaatttgtt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc	60
ctctcctgca gggccagtca gagggttaga agctacttag cctggtacca acagaaacct	120
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc	180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct	240
gaagattttg cagtttatta ctgtcagcag cgtagcaact ggcctccggc cactttcggc	300
ggagggacca aggtggagat caaa	324

<210> 39

<211> 1347

<212> DNA

146392033640_Sequence_Listing

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 39

gaagtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc	60
tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct	120
ccagggaagg gcctggagtg ggtctcaggc attaattgga gcagtgggtg cataggctat	180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat	240
ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aagagatatc	300
gggggggttcg gggagtttta ctggaacttc ggtctctggg gccgtggcac cctggtcact	360
gtctcctcag cctccaccaa gggcccatcg gtcttcccc tggcaccctg ctcccgcagt	420
acttctgagt ccacagcggc cctgggctgc ctgggtcaagg actacttccc cgaaccgggtg	480
acgggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta	540
cagtcctcag gactctactc cctcagcagc gtgggtgactg tgccctctag cagcttgggc	600
accaagacct acacgtgcaa cgtggatcac aagcccagca acaccaagggt ggacaaacgc	660
gttgagtcca aatatgggtcc cccatgcccc ccatgcccag cacctgagtt cctgggggga	720
ccatcagtct tcctgttccc cccaaaaccc aaggacactc tcatgatctc ccggaccct	780
gaggtcacgt gcgtgggtgg ggacgtgagc caggaagacc ccgaggtcca gttcaactgg	840
tacgtggatg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagttcaac	900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaacggcaag	960
gagtacaagt gcaaggctct caacaaaggc ctcccgtcct ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agagccacag gtgtacaccc tgcccccatc ccaggaggag	1080
atgaccaaga accaggctcag cctgagctgc gctgtcaaag gcttctaccc cagcgacatc	1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1200
ctggactccg acggctcctt cttcctcggt agcaggctaa ccgtggacaa gagcagggtg	1260

146392033640_Sequence_Listing

caggagggga atgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacaca 1320
cagaagagcc tctccctgtc tctgggt 1347

<210> 40

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 40

gaagtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatgcc a tgactgggt ccggcaagct 120
ccaggggaagg gcctggagtg ggtctcaggt attaattgga gcagtgggtg cataggctat 180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aagagatatc 300
gggggggttcg gggagtttta ctggaacttc ggtctctggg gccgtggcac cctggtcact 360
gtctcctcag cctccaccaa gggcccatcg gtcttcccc tggcaccctg ctcccgcagt 420
acttctgagt ccacagcggc cctgggctgc ctgggtcaagg actacttccc cgaaccgggtg 480
acgggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 540
cagtcctcag gactctactc cctcagcagc gtgggtgactg tgccctctag cagcttgggc 600
accaagacct acacgtgcaa cgtggatcac aagcccagca acaccaaggt ggacaaacgc 660
gttgagtcca aatatgggtcc cccatgcccc ccatgcccag cacctgagtt cctgggggga 720
ccatcagtct tcctgttccc cccaaaaccc aaggacactc tcatgatctc ccggaccctt 780
gaggtcacgt gcgtgggtgg ggacgtgagc caggaagacc ccgaggtcca gttcaactgg 840
tacgtggatg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagttcaac 900
agcacgtacc gtgtgggtcag cgtcctcacc gtctgcacc aggactgggt gaacggcaag 960
gagtacaagt gcaaggctct caacaaaggc ctcccgctct ccatcgagaa aaccatctcc 1020

146392033640_Sequence_Listing

aaagccaaag ggcagccccg agagccacag gtgtacaccc tgcccccatc ccaggaggag	1080
atgaccaaga accagggtcag cctgagctgc gctgtcaaag gcttctaccc cagcgacatc	1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1200
ctggactccg acggctcctt cttcctcgtt agcaggctaa ccgtggacaa gagcagggtg	1260
caggagggga atgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacaca	1320
cagaagagcc tctccctgtc tctgggtaaa taa	1353

<210> 41

<211> 648

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 41

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc	60
ctctcctgca gggccagtca gagtgttaga agctacttag cctggtacca acagaaacct	120
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc	180
aggttcagtg gcagtgggtc tgggacagac ttcacttca ccatcagcag cctagagcct	240
gaagattttg cagtttatta ctgtcagcag cgtagcaact ggcctccggc cactttcggc	300
ggagggacca aggtggagat caaacgaact gtggctgcac catctgtctt catcttcccg	360
ccatctgatg agcagttgaa atctggaact gcttctgttg tgtgcctgct gaataacttc	420
tatccccgtg aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc	480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg	540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag	600
ggcctgagct cgcccgtcac aaagagcttc aacagggggag agtggttaa	648

<210> 42

<211> 1347

<212> DNA

146392033640_Sequence_Listing

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 42

gaagttcagc	tggttgaaag	cggtaggtgt	ctggttcagc	ctggctcgtag	cctgcgtctg	60
agctgtgcag	caagcgggtt	tacctttgat	gattatgcca	tgcatagggt	tcgtcaggca	120
ccgggttaaag	gtctggaatg	ggtagcgggt	attaattgga	gcagcgggtg	tattggttat	180
gcagatagcg	ttaaagggtc	ttttaccatt	agccgtgata	atgccaaaaa	tagcctgtac	240
ctgcagatga	atagtctgcg	tgcaagaagat	accgcactgt	attattgtgc	acgtgatatt	300
ggtaggtttt	gcgaattcta	ttggaatttt	ggctctgtgg	gtcgtggcac	cctgggttacc	360
gtagcagcgc	cctccaccaa	gggcccacgc	gtcttcccc	tggcaccctg	ctcccgagct	420
acttctgagt	ccacagcggc	cctgggctgc	ctgggtcaagg	actacttccc	cgaaccgggtg	480
acgggtgtcgt	ggaactcagg	cgccctgacc	agcggcgtgc	acaccttccc	ggctgtccta	540
cagtcctcag	gactctactc	cctcagcagc	gtgggtgactg	tgccctctag	cagcttgggc	600
accaagacct	acacgtgcaa	cgtggatcac	aagcccagca	acaccaaggt	ggacaaacgc	660
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tacgtggatg	gcgtggaggt	gcataatgcc	aagacaaagc	cgcgggagga	gcagttcaac	900
agcacgtacc	gtgtgggtcag	cgtcctcacc	gtcctgcacc	aggactggct	gaacggcaag	960
gagtacaagt	gcaagggtctc	caacaaaggc	ctcccgctct	ccatcgagaa	aacctctctc	1020
aaagccaaag	ggcagccccg	agagccacag	gtgtacaccc	tgcccccatc	ccaggaggag	1080
atgaccaaga	accagggtcag	cctgagctgc	gctgtcaaag	gcttctaccc	cagcgacatc	1140
gccgtggagt	gggagagcaa	tgggcagccg	gagaacaact	acaagaccac	gcctcccgtg	1200
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146392033640_Sequence_Listing

caggagggga atgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacaca 1320
 cagaagagcc tctccctgtc tctgggt 1347

<210> 43
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic construct

<400> 43
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 agctgtgcag caagcgggtt tacctttgat gattatgcc a tgcatgggt tcgtcaggca 120
 ccgggttaaag gtctggaatg ggtagcgggt attaattgga gcagcgggtg tattggttat 180
 gcagatagcg ttaaagggtc ttttaccatt agccgtgata atgccaaaaa tagcctgtac 240
 ctgcagatga atagtctgcg tgcagaagat accgcactgt attattgtgc acgtgatatt 300
 ggtggttttg gcgaattcta ttggaatttt ggtctgtggg gtcgtggcac cctggttacc 360
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146392033640_Sequence_Listing

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