

SEQUENCE LISTING

<110> Giver, Lorraine Joan
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 Zhu, Jun
 Behrouzian, Behnaz
 Grate, John H.
 Lalonde, James

<120> Compositions and Methods for Producing Stereoisomerically Pure Statins and Synthetic Intermediates Therefor

<130> 376247-012WO

<140> PCT/US2007/080125

<141> 2007-10-01

<150> US 60/848,951

<151> 2006-10-02

<160> 366

<210> 1

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 1

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agtctggttg aacaaatcgt gtatgcgttg aaactgcggg ggattatcca catcgacgcc 180
gcgagatatt atcgcaccta ccgggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggaaggctc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
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gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
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gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tggaagcata ttctccgctg ggcccgtgca agaagaaaac cgcgaggat 660
gacagccaac cattttttga gtaagtcaaa gaattgagcg aaaaatacat caaatccgag 720
gccagatca tctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
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<210> 2

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 2

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20      25      30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35      40      45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50      55      60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65      70      75      80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85      90      95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100     105     110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115     120     125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130     135     140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
145     150     155     160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165     170     175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180     185     190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195     200     205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210     215     220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Ile Lys Ser Glu
225     230     235     240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245     250     255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260     265     270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275     280     285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290     295     300
Tyr Asn Tyr Ala Ala Gln Lys Val
305     310
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<210> 3

<211> 762

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 3

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tccgatgtag gtgaaaaggc cgccaaatca gtaggcactc cggatcagat tcagtttttt 180
cagcacgatt catccgatga agatggctgg acgaaactgt tcgacgccac cgagaaagca 240
ttcggcccgg ttagcacctt agtgaacaat gcagggattg cagttaacaa aagcggttgaa 300
gaaactacca cggccgaatg gcgtaaactg ctggccgtta atotggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcataaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgagggggt cgtaggcgat ccgagcctgg gggcatacaa cgtttccaag 480
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ggggcgggtac gtatcatgtc gaaaagcgca gcgctggatt ggcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggctat atcaagaccc cgctgggtcga tgatctgccg 600
ggtgctgagg aagcgatgtc acagcgtacg aaaaccctta tgggccacat tggcgaaccg 660
aatgacatcg catatatctg tgtgtacctg gcactctaat aatcgaaatt tgcgacgggt 720
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<210> 4
 <211> 253
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 4

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

<210> 5
 <211> 1050
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 5

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atgaaagcca ttcagtacac tcgtatcggt gcggaaccag aactgactga aatccogaag 60
ccggaaccgg gcccgggcga agtactgctg gaagtcacgg cagctggcgt gtgccattcc 120

```

```

gatgatttca ttatgtctpt gccggaagaa cagtacacct acggcctgcc gctgacctg 180
ggatcatgaag gtgctggtaa agttgccgca gttggcgaag gtgttgaagg gttggatatt 240
ggcaccaatg tggttgtgta cggcccatgg ggttgtggca actgttggca ttgcagtcag 300
ggcctggaga actattgtct ccgtgcgcag gaactgggta ttaaccggcc tggctctgggt 360
gctccggggg ctttggcaga atttatgatt gtcgactcac cacgtcattt ggtcccgatt 420
ggcgatttag accctgttaa aactgttccg ttgactgatg cgggcctgac cccataccat 480
gcaatcaaac gctccctgcc gaaactgcgc ggcggtcttt atgcagtagt gatcggtacg 540
ggtggcctgg gccacgtggc tatccaactg ctgcgtcatt tatctgctgc aacgggtgac 600
gccttggacg tttctgccga taaactggaa ctggctacca aagtcggcgc acatgaagta 660
gtcctgtctg ataaagatgc agcggagaat gtgcgtaaaa ttactggtag ccaaggtgca 720
gcttgggtgt tggattttgt gggctatcag cctaccattg acaccgccat ggcagtggcg 780
ggcgtgggct ctgacgtcac cattgttggg atcgggtgat gccaggcaca tgcgaaagtt 840
ggtttcttcc agagtcttta tgaggcatcg gttacgggtac cttattgggg cgctcgtaat 900
gaactgatcg aattgatcga tctggcgcgt gctgggtattt tcgacattgc cgttgagacc 960
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<210> 6

<211> 349

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 6

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Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr
1           5           10           15
Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
          20           25           30
Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
        35           40           45
Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly
       50           55           60
Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
      65           70           75           80
Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
          85           90           95
His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
        100          105          110
Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
       115          120          125
Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
      130          135          140
Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
     145          150          155          160
Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
        165          170          175
Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
       180          185          190
His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
      195          200          205
Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
     210          215          220
Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala
    225          230          235          240
Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
        245          250          255
Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
      260          265          270

```

Asp	Gly	Gln	Ala	His	Ala	Lys	Val	Gly	Phe	Phe	Gln	Ser	Pro	Tyr	Glu
	275						280				285				
Ala	Ser	Val	Thr	Val	Pro	Tyr	Trp	Gly	Ala	Arg	Asn	Glu	Leu	Ile	Glu
	290					295					300				
Leu	Ile	Asp	Leu	Ala	His	Ala	Gly	Ile	Phe	Asp	Ile	Ala	Val	Glu	Thr
305					310					315				320	
Phe	Ser	Leu	Asp	Asn	Gly	Ala	Glu	Ala	Tyr	Arg	Arg	Leu	Ala	Ala	Gly
			325						330					335	
Thr	Leu	Ser	Gly	Arg	Ala	Val	Val	Val	Pro	Gly	Leu				
			340					345							

<210> 7
 <211> 1050
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 7

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aaaaatgacg	gtttgctgaa	gaagttcaag	tccaaccoga	atctgagcat	ggaaattgtg	180
gaagatattg	cggcaccaaa	cgccttcgat	aaagtattcc	agaaacatgg	taaagaaatt	240
aaagtgggcc	tgcatatcgc	gtccccgggc	catttcaaca	ctaccgattt	cgaaaaagac	300
ttactgatcc	cggcggtaaa	cggtaacaaa	tctattttgg	aagcaattaa	gaactatgcc	360
gcagacaccg	tggaaaaagt	ggttattact	tcactctgtg	ccgcgttggc	ctctccgggt	420
gatatgaaag	ataccagctt	cgtgggttaac	gaagaatcct	ggaataaaga	cacctgggaa	480
tcgtgtcagg	cgaatgctgt	gtccgcttat	tgcggttcta	aaaaattcgc	agagaaaacg	540
gcgtgggact	tcttggaaga	aaaccagagc	agcattaaat	ttactctgtc	cacgattaac	600
ccaggcttcg	tttttggtcc	gcagctgttc	gccgactcct	tgcgcaatgg	tattaactct	660
agcagtgcga	ttattgcaaa	cctgggtgtc	tataaattag	gggataactt	ctacaattat	720
agcggcccg	ttatcgacgt	ccgtgacgtt	tccaaagctc	atctgctggc	atttgagaaa	780
cctgaatgcg	ccggtcagcg	cctgtttctg	tgcgaggata	tggtctgttc	ccaggaagcc	840
ctggacattc	tgaacgaaga	atttcacacg	ctgaagggca	agatcgcaac	gggcgaacct	900
ggcagcggct	cgaccttcct	gactaaaaat	tggtgcaaat	gcgacaatcg	taaaactaaa	960
aacttgctgg	gcttcacagt	caacaaattc	cgcgactgca	ttgtcgatac	tgctccocag	1020
ttgctggaag	tgcaaagcaa	aagctaatga				1050

<210> 8
 <211> 349
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 8

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

<210> 10
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 10

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Met Pro Ala Thr Leu Lys Asn Ser Ser Ala Thr Leu Lys Leu Asn Thr
1          5          10          15
Gly Ala Ser Ile Pro Val Leu Gly Phe Gly Thr Trp Arg Ser Val Asp
20          25          30
Asn Asn Gly Tyr His Ser Val Ile Ala Ala Leu Lys Ala Gly Tyr Arg
35          40          45
His Ile Asp Ala Ala Ala Ile Tyr Leu Asn Glu Glu Glu Val Gly Arg
50          55          60
Ala Ile Lys Asp Ser Gly Val Pro Arg Glu Glu Ile Phe Ile Thr Thr
65          70          75          80
Lys Leu Trp Gly Thr Glu Gln Arg Asp Pro Glu Ala Ala Leu Asn Lys
85          90          95
Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Met His
100         105         110
Trp Pro Val Pro Leu Lys Thr Asp Arg Val Thr Asp Gly Asn Val Leu
115         120         125
Cys Ile Pro Thr Leu Glu Asp Gly Thr Val Asp Ile Asp Thr Lys Glu
130         135         140
Trp Asn Phe Ile Lys Thr Trp Glu Leu Met Gln Glu Leu Pro Lys Thr
145         150         155         160
Gly Lys Thr Lys Ala Val Gly Val Ser Asn Phe Ser Ile Asn Asn Ile
165         170         175
Lys Glu Leu Leu Glu Ser Pro Asn Asn Lys Val Val Pro Ala Thr Asn
180         185         190
Gln Ile Glu Ile His Pro Leu Leu Pro Gln Asp Glu Leu Ile Ala Phe
195         200         205
Cys Lys Glu Lys Gly Ile Val Val Glu Ala Tyr Ser Pro Phe Gly Ser
210         215         220
Ala Asn Ala Pro Leu Leu Lys Glu Gln Ala Ile Ile Asp Met Ala Lys
225         230         235         240
Lys His Gly Val Glu Pro Ala Gln Leu Ile Ile Ser Trp Ser Ile Gln
245         250         255
Arg Gly Tyr Val Val Leu Ala Lys Ser Val Asn Pro Glu Arg Ile Val
260         265         270
Ser Asn Phe Lys Ile Phe Thr Leu Pro Glu Asp Asp Phe Lys Thr Ile
275         280         285
Ser Asn Leu Ser Lys Val His Gly Thr Lys Arg Val Val Asp Met Lys
290         295         300
Trp Gly Ser Phe Pro Ile Phe Gln
305         310

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<210> 11
 <211> 1032
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 11

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accgaagcct tcggttaacaa cccgaaattt agcatggaag tgggtgctga tattagcaaa 180
ctggatgcct tcgatcatgt attccagaaa catggttaaag atattaaaaat cgtcctgcat 240
accgcgtccc cgttttgttt cgatattacc gattccgaac gtgacttact gatccccggc 300
gtaaacgggtg tcaaagggtat tttgcacagt attaagaaat atgccgcaga cagcgtggaa 360
cgcgtgggtt tgacttcac ttaacgcgcg gtatttgata tggcgaagga aaacgataag 420
agcctgacct tcaacgaaga atcctggaat ccggcgacct ggaatcgtg tcagagtgat 480
ccggtgaacg cttattgcgg ttctaaaaaa ttcgcagaga aagcagcgtg ggaattcttg 540
gaagaaaacc gtgatagcgt gaaatttgag ctgacagcgg tcaaccaggt ttacgttttt 600
ggtccgcaga tgttcgataa agatgttaaa aaacacttga acaccagctg cgaactgggtg 660
aactctctga tgcattctgag ccctgaagat aaaattccgg aactgttttg cgtttacatc 720
gacgtccgtg acgttgcgaa agctcatctg gttgcatttc agaaacgtga aacaatcgg 780
cagcgcctga tctgttcgga ggcacgtttc acgatgcagg acgttctgga cattctgaac 840
gaagactttc cagtactgaa gggcaatata ccggtcggca agcctggcag cggcgccacc 900
cataatactc tgggcgccac cctggacaat aaaaaaagca aaaaattgct gggcttcaaa 960
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<210> 12

<211> 343

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 12

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

```

Glu	Thr	Ile	Gly	Gln	Arg	Leu	Ile	Val	Ser	Glu	Ala	Arg	Phe	Thr	Met
		260						265					270		
Gln	Asp	Val	Leu	Asp	Ile	Leu	Asn	Glu	Asp	Phe	Pro	Val	Leu	Lys	Gly
	275						280					285			
Asn	Ile	Pro	Val	Gly	Lys	Pro	Gly	Ser	Gly	Ala	Thr	His	Asn	Thr	Leu
	290					295					300				
Gly	Ala	Thr	Leu	Asp	Asn	Lys	Lys	Ser	Lys	Lys	Leu	Leu	Gly	Phe	Lys
305				310					315					320	
Phe	Arg	Asn	Leu	Lys	Glu	Thr	Ile	Asp	Asp	Thr	Ala	Ser	Gln	Ile	Leu
			325					330						335	
Lys	Phe	Glu	Gly	Arg	Ile										
		340													

<210> 13
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 13
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 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
 cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaaccac cgaggaggca 240
 ttgggcccggt ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttcc 360
 ggcaccpgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgagggggt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcaactgaa ggactacgat 540
 gtgcgtgtca acacagtaca tccgggctat atcaagaccc cgctgggtcga tgatctggaa 600
 ggtgctgagg aaatgatgtc acagcgtacg aaaaccoccta tgggcacat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcctctgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 14
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 14
 Met Thr Asp Arg Leu Lys Gly Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
 65 70 75 80
 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Val Ser
 85 90 95
 Lys Ser Val Glu Asp Thr Thr Thr Glu Trp Arg Lys Leu Leu Ser
 100 105 110

Val	Asn	Leu	Asp	Gly	Val	Phe	Phe	Gly	Thr	Arg	Leu	Gly	Ile	Gln	Arg
	115						120					125			
Met	Lys	Asn	Lys	Gly	Leu	Gly	Ala	Ser	Ile	Ile	Asn	Met	Ser	Ser	Ile
	130					135					140				
Glu	Gly	Phe	Val	Gly	Asp	Pro	Thr	Leu	Gly	Ala	Tyr	Asn	Ala	Ser	Lys
145					150					155					160
Gly	Ala	Val	Arg	Ile	Met	Ser	Lys	Ser	Ala	Ala	Leu	Asp	Cys	Ala	Leu
				165					170					175	
Lys	Asp	Tyr	Asp	Val	Arg	Val	Asn	Thr	Val	His	Pro	Gly	Tyr	Ile	Lys
			180					185					190		
Thr	Pro	Leu	Val	Asp	Asp	Leu	Glu	Gly	Ala	Glu	Glu	Met	Met	Ser	Gln
		195					200					205			
Arg	Thr	Lys	Thr	Pro	Met	Gly	His	Ile	Gly	Glu	Pro	Asn	Asp	Ile	Ala
	210					215					220				
Trp	Ile	Cys	Val	Tyr	Leu	Ala	Ser	Asp	Glu	Ser	Lys	Phe	Ala	Thr	Gly
225					230					235					240
Ala	Glu	Phe	Val	Val	Asp	Gly	Gly	Tyr	Thr	Ala	Gln				
				245					250						

<210> 15
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 15
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattggc 60
 atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtacgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
 gcggacggtc tggatatagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatccttg tggaagcata ttctccgtcg ggcccgtgac agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
 gccagatca tcttgccgtg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcatttagca tgctcagaac ctgttttctt togacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 16
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 16
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr

35	40	45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp	Ala Ala Glu Ile Tyr	
50	55	60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser	Leu Thr Glu Lys Pro	
65	70	75
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser	Pro Gln Ile Lys Met	
85	90	95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Ile Ala	Leu Lys Lys Met Gly	
100	105	110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser	Pro Phe Val Ser Lys	
115	120	125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp	Lys Asp Met Glu Gln	
130	135	140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly	Val Ser Asn Phe Ala	
145	150	155
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala	Glu Val Lys Pro Gln	
165	170	175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln	Asn Gln Thr Pro Gly	
180	185	190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu	Val Glu Ala Tyr Ser	
195	200	205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln	Asp Asp Ser Gln Pro	
210	215	220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys	Tyr Ile Lys Ser Glu	
225	230	235
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg	Gly Val Leu Pro Val	
245	250	255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp	Ala Gln Asn Leu Phe	
260	265	270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys	Ile Thr Glu Leu Gly	
275	280	285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn	Lys Leu Tyr Gly Lys	
290	295	300
Tyr Asn Tyr Ala Ala Gln Lys Val		
305	310	

<210> 17
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 17
 atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaaatccc ggcgattgcc 60
 atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgcggg ggattatcca catcgacgcc 180
 gggagattt atcgcaccta ccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgcgtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgctg ggcccgtgca agaagaaaac cgcgcaggat 660
 gacagtcaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
 gccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac caactottca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttccct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900

ttgtatggca aatataacta cgccgcccag aaagtgtaat ga

942

<210> 18

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 18

Met	Ser	Phe	His	Gln	Gln	Phe	Phe	Thr	Leu	Asn	Asn	Gly	Asn	Lys	Ile		
1				5					10					15			
Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Arg	Trp	Tyr	Lys	Asn	Glu		
			20					25					30				
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr		
		35					40					45					
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Ile	Tyr		
	50					55				60							
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro		
65				70					75						80		
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met		
			85					90						95			
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Arg		
			100				105						110				
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Leu	His	Ser	Pro	Phe	Val	Ser	Lys		
	115					120						125					
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln		
	130					135					140						
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr		
145				150					155					160			
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln		
			165				170						175				
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly		
		180					185						190				
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser		
	195					200						205					
Pro	Leu	Gly	Pro	Leu	Gln	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro		
	210				215						220						
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Ile	Lys	Ser	Glu		
225				230					235					240			
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val		
			245					250						255			
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe		
		260					265						270				
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly		
	275					280					285						
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys		
	290				295					300							
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val										
305					310												

<210> 19

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 19

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atgtcttttc atcaacagtt tttcacgctg aataacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg atcaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcgagagatt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcgacaggtc tggatttagc attgaagaaa atgggtaccg attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tctctgcgtg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcctgta ctggaataaa 900
ttgtatggca aatataactc cgccgccagc aaagtgtaat ga 942
```

<210> 20

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 20

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

Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Ser	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 21
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 21
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatgggca ctggtacacg ttggtataaa aatgaagaaa ctgaocgcgac cttctccaat 120
 agtctggttg agcaaatcgt gtatgcgttg aaactgccgg ggattatcca catogacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatattggagc agttatataa aactggtaaa gctaaaaaca tcgggggttc caatttcgca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tgggaagcata ttctccgtcg ggcccgctgc agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcgggtgtg tgccagttac cacctottca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctcggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccagc aaagtgtaat ga 942

<210> 22
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 22
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Met Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys

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

<210> 23
 <211> 939
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 23
 atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcgga ctggtacacg ttggtataaa aatgaagaaa ctgaacgogac cttotccaat 120
 agtctggttg aacaaatogt gtatgcgttg aaactgccgg ggattatoca catcgacgoc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aaactcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatattcttg tggaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
 gccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct gggtctggat catgaaccgc tgogcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaa 939

<210> 24
 <211> 312
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 24

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
20      25      30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35      40      45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50      55      60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65      70      75      80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85      90      95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100     105     110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115     120     125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130     135     140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
145     150     155     160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165     170     175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180     185     190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195     200     205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210     215     220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Ile Lys Ser Glu
225     230     235     240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245     250     255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260     265     270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275     280     285
Leu Asp His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290     295     300
Tyr Asn Tyr Ala Ala Gln Lys Val
305      310
```

<210> 25

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 25

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atgtcttttt accaacagtt tttaacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatoca catcgacgco 180
gcggagattt atcgcaocta cccggaagtg ggtaaagcac tgcccoctgac ogaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatotg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcgca 480
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gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgc agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcttgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<210> 26

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 26

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Met Ser Phe His Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Asn Glu
20     25     30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35     40     45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50     55     60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65     70     75     80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85     90     95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100    105    110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115    120    125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130    135    140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
145    150    155    160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165    170    175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180    185    190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195    200    205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210    215    220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Ile Lys Ser Glu
225    230    235    240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245    250    255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260    265    270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275    280    285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290    295    300
Tyr Asn Tyr Ala Ala Gln Lys Val
305    310

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<210> 27
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 27
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 atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttotccaat 120
 agtctggttg agcaaatacg gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagatct atcgcaccta cccggaagtg ggtaaagcac tgccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tgggaagcata ttctccgctg ggcccgctgc agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
 gccagatca tctcgcgctg ggctactaaa cgcggtgccc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcc tgcacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcctgta ctggaataaa 900
 ttgtatggca aatataacaa cgccgccag aaagtgtaat ga 942

<210> 28
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 28
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser

195	200	205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro		
210	215	220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Ile Lys Ser Glu		
225	230	235
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Ala Leu Pro Val		
245	250	255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe		
260	265	270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly		
275	280	285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys		
290	295	300
Tyr Asn Asn Ala Ala Gln Lys Val		
305	310	

<210> 29
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 29
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 agtctggttg aacaaatcgt gcatgcgttg aaactgcggg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcgca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgctg ggcccgtgca agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtaagtcaaa gaattgagcg aaaaatacat caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcgggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcc tgcacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 30
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 30
 Met Ser Phe His Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val His
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60

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

<210> 31

<211> 936

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 31

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atcatcgcca ctggtacacg ttggtataaa aatgaagaaa ctgacgogac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgcogg ggattatcca catcgacacc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca toggggtttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tggaaagcata ttctccgctg ggcccgtgc agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtaagtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccgatca tcttgcgctg ggtcactaaa cgoggtgtgc tgccagttac cacctottca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tgacctgac agcggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtg 936

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<210> 32
 <211> 312
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 32
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Thr Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Ile Lys Ser Glu
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 33
 <211> 936
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 33
 atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60

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agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
gcggacggtc tggatttagc attgaagaaa atgggtacag gttatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttt caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctg agaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gccagatca tctctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagoga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcgctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtg 936

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<210> 34

<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 34

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
          20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
          35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
          50          55          60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
          85          90          95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
          100          105          110
Thr Gly Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
          115          120          125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
          130          135          140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
145          150          155          160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
          165          170          175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
          180          185          190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
          195          200          205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
          210          215          220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Ile Lys Ser Glu
225          230          235          240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
          245          250          255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
          260          265          270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly

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	275		280		285										
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290				295						300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 35
 <211> 936
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 35
 atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcgaggc ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac ctctctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgcggg ggattatcca catcgacgccc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgccctcgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcgca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaagt caaccagatt 540
 gagttctctc cgctcctgca aaaccaaaca ccaggtattt ataaattctg tcaggagcac 600
 gatatcctgg tgggaagcata ttctccgctg ggcccgtgc agaagaaaac ogcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
 gccagatca tcttgogctg ggtcactaaa cgcgggtgtg tgccagttac caactcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccagc aaagtg 936

<210> 36
 <211> 312
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 36
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140

Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Ala	
145					150					155					160	
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln	
				165					170						175	
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Leu	Leu	Gln	Asn	Gln	Thr	Pro	Gly	
			180					185					190			
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser	
	195						200					205				
Pro	Leu	Gly	Pro	Leu	Gln	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro	
	210					215					220					
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Ile	Lys	Ser	Glu	
225					230					235					240	
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val	
				245					250					255		
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe	
			260				265						270			
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly	
		275					280					285				
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys	
	290					295					300					
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val									
305					310											

<210> 37

<211> 936

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 37

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agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatoca catogaagcc 180
gcgagagatt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatattcttg tggaagcata ttctccgctg ggcccgtgc agaagaaaac cgogcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatcogag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgaactgac agcgggaagag 840
gttgataaaa tcacggagct ggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtg 936

```

<210> 38

<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 38

Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile


```

gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
goccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttccct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggag catgaaccgc tgcgcgtgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtg 936

```

<210> 40
 <211> 312
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 40

Met	Ser	Phe	His	Gln	Gln	Phe	Phe	Thr	Leu	Asn	Asn	Gly	Asn	Lys	Ile
1				5					10					15	
Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Arg	Trp	Tyr	Lys	Asn	Glu
			20					25					30		
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr
		35					40					45			
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Ile	Tyr
	50					55				60					
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro
65					70					75				80	
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met
				85					90					95	
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly
			100					105					110		
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Leu	His	Ser	Pro	Phe	Val	Ser	Lys
		115					120					125			
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln
	130					135					140				
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Ala
145					150				155					160	
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
				165					170					175	
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
		180						185					190		
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
	195						200					205			
Pro	Leu	Gly	Pro	Leu	Gln	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210					215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Ile	Lys	Ser	Glu
225					230					235				240	
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
				245					250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Val	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 41
 <211> 936
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 41

```
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac caaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgtctc agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccgatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tcgcgttgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtg 936
```

<210> 42

<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 42

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

Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Ile	Lys	Ser	Glu
225					230					235					240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
				245						250					255
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
				260					265					270	
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280						285		
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 43

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 43

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctcctat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcgagagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttctctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ctctccgctg ggcccgtctc agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgtgcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgctg ggtaactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tcgcgctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<210> 44

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 44

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

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

<210> 45

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 45

```

atgtcttttc accaacagtt ttacacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgogac ctctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgcogg ggattatcca catcgacgc 180
gcggagattt atcgaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagoot 240
cgtaacgcga tttttctgac ggataaatat tctcgcgaga ttaaaatgag tgactccoot 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgttgc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tgggggttgc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctcgcgtg ggcccgctgc ataagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gccagatca tcttgcgctg ggtcaactaa cgcgggtgtg tgccagttac cactcttca 780
aagcctcagc gcattagcga tgcacagaac ctgttttcoo tgcacctgac agcgggaagag 840
gttgataaaa tcacggagtt gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

```

<210> 46

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 46

```
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
          20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
          35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
          50          55          60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
          85          90          95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
          100          105          110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
          115          120          125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
          130          135          140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
145          150          155          160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
          165          170          175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
          180          185          190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
          195          200          205
Pro Leu Gly Pro Leu His Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
          210          215          220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Ile Lys Ser Glu
225          230          235          240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
          245          250          255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
          260          265          270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
          275          280          285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
          290          295          300
Tyr Asn Tyr Ala Ala Gln Lys Val
305          310
```

<210> 47

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 47

```
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgaacgac cttotocaat 120
agtctggttg aacaaatcgt gtatgogttg aaactgcogg ggattatoca catogacgcc 180
gcggagattt atcgcaccta ccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
```

```

cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgctgc agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccgatca tcctgcgctg gatcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctgaa catgaaccgc tcgcctgtga ctggaataaa 900
ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

```

<210> 48

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 48

```

Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
20        25        30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35        40        45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50        55        60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65        70        75        80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85        90        95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100       105       110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115       120       125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130       135       140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
145       150       155       160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165       170       175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180       185       190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195       200       205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210       215       220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Ile Lys Ser Glu
225       230       235       240
Ala Gln Ile Ile Leu Arg Trp Ile Thr Lys Arg Gly Val Leu Pro Val
245       250       255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260       265       270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275       280       285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290       295       300

```

Tyr Asn Tyr Ala Ala Gln Lys Val
305 310

<210> 49

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 49

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcgcagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatggtga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgatcctgca aaaccaaact ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gccagatca tctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cactcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tcgacctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942
```

<210> 50

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 50

```
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Gln Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
145 150 155 160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
```


gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 54
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 54
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val His
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Ile Lys Ser Glu
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 55
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 55

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatgggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agcctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catogaagcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgaactccct 300
gtggacggtc tggatttagc attgaagaaa atgcgtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtctc agaagaaaac cgcgcaggat 660
gacagtcaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gccagatca tcttgcgctg ggctactaaa cgcggtgtgc tgccagttac cactcttca 780
aagcctcagc gcattagcga tgcacagaac ctgttttctt tcgaactgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcgctgta ctggaataaa 900
ttgtatggca aatataactc cgccgccagc aaagtgtaat ga 942
```

<210> 56

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 56

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

				245					250					255			
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe		
			260					265					270				
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly		
		275					280					285					
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys		
	290					295					300						
Tyr	Asn	Ser	Ala	Ala	Gln	Lys	Val										
305					310												

<210> 57
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 57
 atgtcttttc atcaacagtt cttcacgctg aataacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gottagaaga ggcttggaaa 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttogca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttctctga aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatacttg tggaagcata ttctccgctg ggcccgctgc agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
 gccagatca tctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctottca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataactc cgcgcgccag aaagtgtaat ga 942

<210> 58
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 58
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110

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

<210> 59
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 59
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgogac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg gaactgcogg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatotg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatatggagc agttatataa aactggtaaa gctaaaaaca tcggggtttc caatttgcga 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatacttg tggaagcata ttctccgctg ggcccgctgc agaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcctgcgctg ggctactaaa cgcgggtgtg tgccagttac cacctottca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcctgtga ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

<210> 60
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 60

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20     25     30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35     40     45
Ala Leu Glu Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50     55     60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65     70     75     80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85     90     95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100    105    110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115    120    125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130    135    140
Leu Tyr Lys Thr Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
145    150    155    160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165    170    175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180    185    190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195    200    205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210    215    220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225    230    235    240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245    250    255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260    265    270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275    280    285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290    295    300
Tyr Asn Tyr Ala Ala Gln Lys Val
305    310
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<210> 61

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 61

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atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggogattgcc 60
atcatcgga ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac ctctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catgcacacc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgcacctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcgggcggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgttgc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
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gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttccctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctgc agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tccctgcgctg ggtcactaaa cgcgggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttctcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct ggggtctggaa catgaaccgc tcgcgctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<210> 62

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 62

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Met Ser Phe His Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
20     25     30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35     40     45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Thr Ala Glu Ile Tyr
50     55     60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65     70     75     80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85     90     95
Ser Asp Ser Pro Ala Gly Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100    105    110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115    120    125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130    135    140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
145    150    155    160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165    170    175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180    185    190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195    200    205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210    215    220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225    230    235    240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245    250    255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260    265    270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275    280    285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290    295    300
Tyr Asn Tyr Ala Ala Gln Lys Val
305    310

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<210> 63
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 63
atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgcggg ggattatoca catogaagcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatc 540
gagttctctc cgttctctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcgtc agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcgctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 64
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 64
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
145 150 155 160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165 170 175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180 185 190

50	Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro	55	60
65	Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met	70	75
	85	90	95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly	100	105	110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys	115	120	125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln	130	135	140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr	145	150	155
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln	165	170	175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly	180	185	190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser	195	200	205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro	210	215	220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Ile Lys Ser Glu	225	230	235
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val	245	250	255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe	260	265	270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly	275	280	285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys	290	295	300
Tyr Asn Tyr Ala Ala Gln Lys Val	305	310	

<210> 67
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 67
 atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctgggtg agcaaatcgt gtatgcgttg aaactaccgg ggattatcca catcgacacc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttggttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caattttgca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatc 540
 gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tgggaagcata ttctccgctg ggcccgctgc agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcctgcgctg ggtaactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 68
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 68
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Thr Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 69
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 69

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atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaaatccc ggcgattgcc 60
atcatgggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg agcaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacacc 180
gcgagagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccct 300
gcgacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aacggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggagcata ttctccgctg ggcccgtgc agaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct ggtcttgaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtacggca aatataacta cgccgccag aaagtgtaat ga 942

```

<210> 70

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 70

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Met Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
          20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
          35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Thr Ala Glu Ile Tyr
          50          55          60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
          85          90          95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
          100          105          110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
          115          120          125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
          130          135          140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
145          150          155          160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
          165          170          175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
          180          185          190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
          195          200          205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
          210          215          220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225          230          235          240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
          245          250          255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
          260          265          270

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Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275 280 285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290 295 300
Tyr Asn Tyr Ala Ala Gln Lys Val
305 310

<210> 71
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 71
atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgco 60
atcatcggca ctggtacagc ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgaotccoct 300
gcggacggto tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgc agaagaaaac cgcacaggat 660
gacagtcaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tccctgcgctg ggctactaaa cgcgggtgtg tgcagttac cacctcttca 780
aggccccagc gcattagcga tgctcagaac ctgttttctc tcgacotgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 72
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 72
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Asn Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln

130		135		140
Leu Tyr Lys Ser Gly	Lys Ala Lys Asn Ile Gly	Val Ser Asn Phe Thr		
145	150	155		160
Val Glu Asp Leu Gln Arg	Ile Leu Lys Val Ala Glu Val Lys Pro Gln			
	165	170		175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly				
	180	185		190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser				
	195	200		205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro				
	210	215		220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Ile Lys Ser Glu				
225	230	235		240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val				
	245	250		255
Thr Thr Ser Ser Arg Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe				
	260	265		270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly				
	275	280		285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys				
	290	295		300
Tyr Asn Tyr Ala Ala Gln Lys Val				
305	310			

<210> 73
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 73
 atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggogattgcc 60
 atcatgggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgccctgac cgaagagcct 240
 cgtaacgcga tttttctgac ggataaatat totccgcaga ttaaaatgag tgactccctt 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatacctg tggaagcata ttctccgctg ggcccgtgc agaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcgggtgoc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcctgtga ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 74
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 74

Met	Ser	Phe	His	Gln	Gln	Phe	Phe	Thr	Leu	Asn	Asn	Gly	Asn	Lys	Ile
1			5						10					15	
Pro	Ala	Ile	Ala	Ile	Met	Gly	Thr	Gly	Thr	Arg	Trp	Tyr	Lys	Asn	Glu
			20					25					30		
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr
		35					40					45			
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Ile	Tyr
	50					55					60				
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro
65					70					75					80
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met
				85					90					95	
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly
			100					105					110		
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Leu	His	Ser	Pro	Phe	Val	Ser	Lys
		115					120					125			
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln
	130					135					140				
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Ala
145					150					155					160
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
				165					170					175	
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
		180						185					190		
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
	195						200					205			
Pro	Leu	Gly	Pro	Leu	Gln	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210					215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225					230					235					240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Ala	Leu	Pro	Val
				245					250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 75

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 75

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatgggca ctggtacacg ttggtataaa aatgaagaaa ctgacgogac cttctccaat 120
agtctggttg atcaaatcgt gtatgcgttg aaactgccgg ggattatcca catogaogcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggottaa gottagaaga ggcttgga 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatc 540
gagttctctc cgttctctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600

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gatatcctgg tggaagcata ttctccgctg ggcccgcctgc agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctgcaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<210> 76

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 76

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Met Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
      20      25      30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Asp Gln Ile Val Tyr
      35      40      45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
      50      55      60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65      70      75      80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
      85      90      95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
      100     105     110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
      115     120     125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
      130     135     140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
145     150     155     160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
      165     170     175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
      180     185     190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
      195     200     205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210     215     220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225     230     235     240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
      245     250     255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
      260     265     270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
      275     280     285
Leu Gln His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
      290     295     300
Tyr Asn Tyr Ala Ala Gln Lys Val
305      310

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<210> 77

<211> 942

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 77
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgaccta cccggaagtg ggtaaagcac tgccoctgac cgaaaagcct 240
cgtaacgca tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gottagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gotaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttctctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgtgca agaagaaaac cgcgcaggat 660
gacagtcaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gccagatca tcttgcgctg ggtcactaaa cgcgggtgtgc tgccagttac cacctottca 780
aagcctcagc gcattagcga tgcctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggat catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 78
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 78
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145 150 155 160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165 170 175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180 185 190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195 200 205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro

210		215		220
Phe Phe Glu Tyr Val	Lys Glu Leu Ser Glu	Lys Tyr Ile Lys Ser Glu		
225	230	235		240
Ala Gln Ile Ile Leu	Arg Trp Val Thr	Lys Arg Gly Val Leu	Pro Val	
	245	250		255
Thr Thr Ser Ser Lys	Pro Gln Arg Ile	Ser Asp Ala Gln	Asn Leu Phe	
	260	265		270
Ser Phe Asp Leu Thr	Ala Glu Glu Val	Asp Lys Ile Thr	Glu Leu Gly	
	275	280		285
Leu Asp His Glu Pro	Leu Arg Leu Tyr	Trp Asn Lys	Leu Tyr Gly Lys	
	290	295		300
Tyr Asn Tyr Ala Ala	Gln Lys Val			
305	310			

<210> 79
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 79
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 atcatgggca ctggtacacg ttggtataaa aatgaagaaa ctgacgogac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatoca catcgacgcc 180
 gcgagagatt atcgcaccta cccggaagtg ggtaaagcac tgccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctcgcaga ttaaaatgag tgactccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttt caatttgcga 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tgggaagcata ttctcgcgtg ggcccgtgca agaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcttgcgctg ggtaactaaa cggggtgtgc tgccagttac caactottca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct gggctctggat catgaacggc tgcgccctgta ctggaataaa 900
 ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 80
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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

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

<210> 81
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 81
 atgtcttttt accaacagtt ttccaogctg aacaaogggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaag ttggtataaa aatgaagaaa ctgacgogac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgcccttgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
 gcggacggtc tggatttagc attgaagaaa atgcgtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatattgagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatacttg tggaaagcata ttctccgctg ggcccgtgc agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
 gccagatca tcttgccgtg ggtcactaaa cgcgggtgtg tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcctgtga ctggaataaa 900
 ttgtatggca aatataactc cgcgcgccag aaagtgtaat ga 942

<210> 82
 <211> 313

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 82
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Arg
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145 150 155 160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165 170 175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180 185 190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195 200 205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210 215 220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Ile Lys Ser Glu
225 230 235 240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245 250 255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260 265 270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275 280 285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290 295 300
Tyr Asn Ser Ala Ala Gln Lys Val
305 310

<210> 83
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 83
atgtctttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatgggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg agcaaatcgt gtatgcgttg aaactgcggg ggattatcca catcgacgcc 180

```

gcgagagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctggc cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcgagcggtc tggatttagc attgaagaaa atgcgtacag attatggtga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgca agaagaaaac cgcgcaggat 660
gacagtcaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gccagatca tctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgcgcccgag aaagtgtaat ga 942

```

<210> 84

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 84

```

Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Met Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
20     25     30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35     40     45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50     55     60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Ala Glu Lys Pro
65     70     75     80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85     90     95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Arg
100    105    110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115    120    125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130    135    140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145    150    155    160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165    170    175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180    185    190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195    200    205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210    215    220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Ile Lys Ser Glu
225    230    235    240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245    250    255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260    265    270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275    280    285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys

```

290
Tyr Asn Tyr Ala Ala Gln Lys Val
305 310

300

<210> 85
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 85
atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatgggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg agcaaatcgt gtatgcgttg aaactgcogg ggattatcca catcgacgcc 180
gcgagagatt atcgcaccta cccggaagtg ggtaaagcac tgccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaagatgag tgactccct 300
gcgacgggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcctaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttt caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tgggaagcgt ttctccgctg ggcccgtctc agaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggctactaaa cgoggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 86
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 86
Met Ser Phe His Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Met Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
145 150 155 160

Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 87
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 87
 atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacacg ttggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgcgag ggattatcca catcgacgac 180
 gcggagattt atcgaccta cccggaagtg ggtaaagcac tgccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctcgcaga ttaaaatgag tgactccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aaactcaggt caaccagatc 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tgggaagcata ttctccgctg ggcgcgctgc agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tctcagaac ctgttttctc tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct ggtctggaa catgaaccgc tcgcctgtga ctggaataaa 900
 ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 88
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 88
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Ser Glu


```

aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

```

<210> 90
<211> 313
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic Construct

```

```

<400> 90
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
20      25      30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35      40      45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Thr Ala Glu Ile Tyr
50      55      60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65      70      75      80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85      90      95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100     105     110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115     120     125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130     135     140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
145     150     155     160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165     170     175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180     185     190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195     200     205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210     215     220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Thr Lys Ser Glu
225     230     235     240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245     250     255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260     265     270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275     280     285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290     295     300
Tyr Asn Tyr Ala Ala Gln Lys Val
305     310

```

```

<210> 91
<211> 942
<212> DNA
<213> Artificial Sequence

```

<220>

<223> Synthetic Construct

<400> 91

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atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcgcca ctggtacacg ttggtataaa aatgaagaaa ctgacggac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgacaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggaaggctc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgtgc agaagaaaac cgcgaggat 660
gacagtcaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tctgctgctg gggtactaaa cgcgggtgtg tgcagttac cacctcttca 780
aagccccagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctgga catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataactc cgccgccag aaagtgtgat ga 942
```

<210> 92

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 92

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

Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
				245					250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
				260				265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275				280						285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Ser	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 93

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 93

atgtcttttc	accaacagtt	tttcacgctg	aacaacggca	ataaaatccc	ggcgattgcc	60
atcatcggca	ctggtacacg	ttggtataaa	aatgaagaaa	ctgacgcgac	cttctccaat	120
agtctggttg	aacaaatcgt	gtatgcgttg	aaactgccgg	ggattatcca	catcgacgcc	180
gcggagattt	atcgcaccta	cccgagggtg	ggtaaagcac	tgtccctgac	cgaaaagcct	240
cgtaacgcga	tttttctgac	ggataaatat	tctccgcaga	ttaaaatgag	tgactccoct	300
gcggacggtc	tggatttagc	attgaagaaa	atgggtacag	attatgttga	tttatactcg	360
ttacattccc	cgtttgtttc	gaaggaagtg	aatggcttaa	gcttagaaga	ggcttggaaa	420
gatatggagc	agttatacag	aagtggtaaa	gctaaaaaca	tcgggggtttc	caatttcaca	480
gtggaagacc	tgcaacgtat	cctgaaagtc	gctgaagtta	agcctcaggt	caaccagatt	540
gagttctctc	cgttctctgca	aaaccaaaaca	ccaggcattt	ataaattctg	tcaggagcac	600
gatatcctgg	tggaagcata	ttctccgctg	ggcccgtctc	agaagaaaac	cgcgaggat	660
gacagccaac	cattttttga	gtacgtcaaa	gaattgagcg	aaaaatacaa	caaattccgag	720
gccagatca	tcttgccgtg	ggctactaaa	cgcggtgtgc	tgccagttac	cacctcttca	780
aagcctcagc	gcattagcga	tgctcagaac	ctgttttctt	tcgacctgac	agcggaagag	840
gttgataaaa	tcacggagct	gggtctggaa	catgagcgcg	tgcgctgtga	ctggaataaa	900
ttgtatggca	aatataactc	cgccgcccag	aaagtgtaat	ga		942

<210> 94

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 94

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

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

<210> 95
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 95
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoot 300
 gcggacggtc tggattttagc attgaagaaa atgggtacag attatggtga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggottggaaa 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttt caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cactcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 96
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 96

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
      20      25      30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
      35      40      45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
      50      55      60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65      70      75      80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
      85      90      95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
      100     105     110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
      115     120     125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
      130     135     140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145     150     155     160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
      165     170     175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
      180     185     190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
      195     200     205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
      210     215     220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225     230     235     240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
      245     250     255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
      260     265     270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
      275     280     285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
      290     295     300
Tyr Asn Tyr Ala Ala Gln Lys Val
305      310
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<210> 97

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 97

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atgtctttttc accaacagtt tttaacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgcogg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgccctgac cgaaaggcct 240
cggaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
gcggacggtc tggatttagc attgaagaaa atgggtaccg attatgttga tttatatctg 360
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<210> 99
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 99
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc ttggtacaaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg agcaaatcgt gtatgcgttg aaactgocgg ggattatcca catcgacgcc 180
gcgagatatt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggaaggctc tggatttagc attgaagaaa atgcgtacag attatggtga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggottggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgctgc agaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 100
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 100
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Asn Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Arg
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145 150 155 160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165 170 175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly

Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Thr	Ala	Glu	Ile	Tyr
50						55					60				
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro
65					70					75					80
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met
				85					90					95	
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly
			100					105					110		
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Leu	His	Ser	Pro	Phe	Val	Ser	Lys
		115					120					125			
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln
	130					135					140				
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Ala
145					150					155					160
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
				165					170					175	
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
			180					185					190		
Ile	Tyr	Arg	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
	195						200					205			
Pro	Leu	Gly	Pro	Leu	Gln	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210					215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225					230					235					240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
				245					250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 103

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 103

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atgtcttttc accaacagtt tttaacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtagcgcttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggacggtc tggatttagc actgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacotcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tggaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gccagatca tcttgcgctg ggtcactaaa cgcgggtgtg tgccagttac cactcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaacgcg tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<210> 104
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 104
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Ile Lys Ser Glu
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 105
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 105

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtcctggtg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcgagaggtt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac caaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcgacaggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggagcata ttctccgttg ggcccgtgc ggaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tctcgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcttgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942
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<210> 106

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 106

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


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

<210> 109
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 109
 atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacacg ttggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tgggaagcata ttctccgctg ggcccgtgca agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacac caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcgggtgtg tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tcgcctgtga ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 110
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 110

```
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Ser Glu
20      25      30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35      40      45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50      55      60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65      70      75      80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85      90      95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100     105     110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115     120     125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130     135     140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
145     150     155     160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165     170     175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180     185     190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195     200     205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210     215     220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Thr Lys Ser Glu
225     230     235     240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245     250     255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260     265     270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275     280     285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290     295     300
Tyr Asn Tyr Ala Ala Gln Lys Val
305      310
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<210> 111

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 111

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atgtctttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta ccggaagtg ggtaaagcac tgccoctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
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gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctcogctg ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccgatca tcctgcgctg ggctactaaa cgcgggtgtg tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcctgtga ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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<210> 112

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 112

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50          55          60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85          90          95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100         105         110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115         120         125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130         135         140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145         150         155         160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165         170         175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180         185         190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195         200         205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210         215         220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225         230         235         240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245         250         255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260         265         270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275         280         285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290         295         300
Tyr Asn Tyr Ala Ala Gln Lys Val
305          310

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<210> 113

<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 113
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgcggg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgtctc agaagaaaac cgcgcaggat 660
gacagccaac catttttttg gtacgtcaaa gaattgggcg aaaaatacaa caaatccgag 720
gcccagatca tctctgcgctg ggtaactaaa cgcgggtgtg tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccagc aaagtgtaat ga 942

<210> 114
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 114
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145 150 155 160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165 170 175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180 185 190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195 200 205

Pro	Leu	Gly	Pro	Leu	Gln	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
210						215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Gly	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225					230					235					240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
				245					250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 115
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 115
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgatgcgac cttctocaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacaa attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tctcgcgctg gatcactaaa cgcgggtgtg tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 116
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 116
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro

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

<210> 117
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 117
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggogattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgogac cttctocaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatoca catcgacgcc 180
 gcggagattt atcgcaccta ccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tggaagctta ttctccgctg ggcccgtgc agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcctgcgctg ggtaactaaa cgcggtgcgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaacgc tcgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 118

<211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 118
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Ala Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 119
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 119
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgogac cttctccaat 120

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agtctgtttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgoc 180
gcgagagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccoct 300
gcgagacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgttcc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttcc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttccctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgc agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctottca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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<210> 120

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 120

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20        25        30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Phe Glu Gln Ile Val Tyr
35        40        45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50        55        60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65        70        75        80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85        90        95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100       105       110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115       120       125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130       135       140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145       150       155       160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165       170       175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180       185       190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195       200       205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210       215       220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225       230       235       240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245       250       255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260       265       270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275       280       285

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Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 121
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 121
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggogattgcc 60
 atcatcgga ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctgggtg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatgggttaa gottagaaga ggcttggaaa 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gatttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatattcctg tggaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacatcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tctcgcgctg ggctactaaa cgcggtgtgc tgcagttac caoctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaacogo tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 122
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 122
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr

145		150		155		160									
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
		165		170		175									
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
		180		185		190									
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
	195				200						205				
Pro	Leu	Gly	Pro	Leu	Gln	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210				215						220				
Phe	Phe	Glu	Tyr	Ile	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225				230					235						240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
		245						250						255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
		260						265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
	275					280					285				
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290				295					300					
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305				310											

<210> 123
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 123
 atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcgga ctggtacaaa atggtataaa aatgaagaaa ctgaacgcac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgcgg ggattatcca catogaagcc 180
 gcggagattt atcgaccta cccggaagtg ggtaaagcac tgtccctgac cgaagagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccccc 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatcta 360
 ttacattccc cgcttggttc gaaggaagtg aatgggttaa gcttagaaga ggcttgga 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gaggttcttc cgttcctgca aaaccaaaca ccaggcattt ataaattctg ccaggagcac 600
 gatattcctg tggaagcata ttctccgtg ggcccgtgc agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccag 720
 gccagatca tctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cactottca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgatctgac agcggagag 840
 gttgataaaa tcacggagct ggtcttgaa catgaacgc tgccgctgta ctggaataaa 900
 ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 124
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 124
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15

<220>

<223> Synthetic Construct

<400> 127

```
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccactg ggcccgtctc agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
atgcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942
```

<210> 128

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 128

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

225		230		235		240									
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
		245		250		255									
Thr	Thr	Ser	Ser	Met	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
		260		265		270									
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275		280		285									
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290			295		300									
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305				310											

<210> 129
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 129

```

atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctocaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catogacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatggtga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttt caatttctcg 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaataccg gaaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagoga tgcacagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tcgcctgtga ctggaataaa 900
ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942
  
```

<210> 130
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 130

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

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

<210> 131
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 131
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggga ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac ottctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatoca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacgggtc tggatttagc attgaagaaa atgggtacag attatggtga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttctcc 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccagc aaagtgtaat ga 942

<210> 132
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 132

```
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
      20      25      30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
      35      40      45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
      50      55      60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65      70      75      80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
      85      90      95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
      100      105      110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
      115      120      125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130      135      140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ser
145      150      155      160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
      165      170      175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
      180      185      190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195      200      205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210      215      220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Gly Lys Ser Glu
225      230      235      240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
      245      250      255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260      265      270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275      280      285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290      295      300
Tyr Asn Tyr Ala Ala Gln Lys Val
305      310
```

<210> 133

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 133

```
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgocgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctcgcgaga ttaaaatgag tgactccoct 300
```

```

gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcagc 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctgc agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacca aaaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt togacctgac agcggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

```

<210> 134

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 134

```

Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
      20      25      30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
      35      40      45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
      50      55      60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65      70      75      80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
      85      90      95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
      100     105     110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
      115     120     125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
      130     135     140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ser
145     150     155     160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
      165     170     175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
      180     185     190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
      195     200     205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
      210     215     220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Gln Lys Ser Glu
225     230     235     240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
      245     250     255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
      260     265     270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
      275     280     285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290     295     300
Tyr Asn Tyr Ala Ala Gln Lys Val

```

<210> 135
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 135
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcgga ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtocatgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gottagaaga ggcttgga 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgctg ggcccgtgca agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 136
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 136
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Met Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175

Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
			180					185					190		
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
		195					200					205			
Pro	Leu	Gly	Pro	Leu	Gln	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210					215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225					230					235					240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
				245					250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 137
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 137
 atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggogattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgaacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgaagcc 180
 gcggagatat atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
 gatatggagc agttatacaa acgtggtaaa gctaaaaaca tcgggggttt caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatccttg tggaagcata ttctccgctg ggcccgtgc agaagaaaac cggcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctt togaactgac agcggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 138
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 138
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr

35	40	45
Ala Leu Lys Leu Pro Gly Ile	Ile His Ile Asp	Ala Ala Glu Ile Tyr
50	55	60
Arg Thr Tyr Pro Glu Val Gly	Lys Ala Leu Ser	Leu Thr Glu Lys Pro
65	70	75
Arg Asn Ala Ile Phe Leu Thr	Asp Lys Tyr Ser	Pro Gln Ile Lys Met
85	90	95
Ser Asp Ser Pro Ala Asp Gly	Leu Asp Leu Ala	Leu Lys Lys Met Gly
100	105	110
Thr Asp Tyr Val Asp Leu Tyr	Leu Leu His Ser	Pro Phe Val Ser Lys
115	120	125
Glu Val Asn Gly Leu Ser Leu	Glu Glu Ala Trp	Lys Asp Met Glu Gln
130	135	140
Leu Tyr Lys Arg Gly Lys Ala	Lys Asn Ile Gly	Val Ser Asn Phe Thr
145	150	155
Val Glu Asp Leu Gln Arg Ile	Leu Lys Val Ala	Glu Val Lys Pro Gln
165	170	175
Val Asn Gln Ile Glu Phe Ser	Pro Phe Leu Gln	Asn Gln Thr Pro Gly
180	185	190
Ile Tyr Lys Phe Cys Gln Glu	His Asp Ile Leu	Val Glu Ala Tyr Ser
195	200	205
Pro Leu Gly Pro Leu Gln Lys	Lys Thr Ala Gln	Asp Asp Ser Gln Pro
210	215	220
Phe Phe Glu Tyr Val Lys Glu	Leu Ser Glu Lys	Tyr Asn Lys Ser Glu
225	230	235
Ala Gln Ile Ile Leu Arg Trp	Val Thr Lys Arg	Gly Val Leu Pro Val
245	250	255
Thr Thr Ser Ser Lys Pro Gln	Arg Ile Ser Asp	Ala Gln Asn Leu Phe
260	265	270
Ser Phe Asp Leu Thr Ala Glu	Glu Val Asp Lys	Ile Thr Glu Leu Gly
275	280	285
Leu Glu His Glu Pro Leu Arg	Leu Tyr Trp Asn	Lys Leu Tyr Gly Lys
290	295	300
Tyr Asn Tyr Ala Ala Gln Lys	Val	
305	310	

<210> 139
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 139
 atgtcttttc accaacagtt ttctacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta ccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatccttg tggaagcata ttctcogctg ggcccgtgac agaagaaaac cgcgaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaaaccgag 720
 gccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcc tgcacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900

ttgtatggca aatataacta cgccgccag aaagtgtaat ga

942

<210> 140

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 140

Met	Ser	Phe	His	Gln	Gln	Phe	Phe	Thr	Leu	Asn	Asn	Gly	Asn	Lys	Ile	
1				5					10					15		
Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Lys	Trp	Tyr	Lys	Asn	Glu	
			20					25					30			
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr	
		35					40					45				
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Ile	Tyr	
	50					55				60						
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro	
65				70						75					80	
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met	
				85					90					95		
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly	
			100					105					110			
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Leu	His	Ser	Pro	Phe	Val	Ser	Lys	
	115						120					125				
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln	
	130					135					140					
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr	
145				150					155						160	
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln	
				165				170						175		
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly	
			180					185					190			
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser	
	195						200					205				
Pro	Leu	Gly	Pro	Leu	Gln	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro	
	210					215					220					
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Thr	Glu	
225					230					235					240	
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val	
				245					250					255		
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe	
			260				265						270			
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly	
		275					280					285				
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys	
	290					295					300					
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val									
305					310											

<210> 141

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 141

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgaacgcac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcgagagattt atcgcaccta cccggaagtg ggtaaagcac tgccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcgatggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctcgcgtg ggcccgtgc agaagaaaaa cgcgcaggat 660
gacagacacc cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tctgcgcgtg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctcggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942
```

<210> 142

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 142

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

Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 143
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 143
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgaacgogac cttctccaac 120
 agtctggttg aacaaatctt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tgggaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgcaggat 660
 gtcagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcttgcgctg ggtcactaaa cgcgggtgtg tgccagttac cacctottca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 144
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 144
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Leu Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys

<400> 146

```
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20      25      30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35      40      45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50      55      60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65      70      75      80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85      90      95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100     105     110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115     120     125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130     135     140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145     150     155     160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165     170     175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180     185     190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195     200     205
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210     215     220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225     230     235     240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245     250     255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260     265     270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275     280     285
Leu Glu His Glu Pro Leu Arg Gln Tyr Trp Asn Lys Leu Tyr Gly Lys
290     295     300
Tyr Asn Tyr Ala Ala Gln Lys Val
305      310
```

<210> 147

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 147

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atgtcttttt accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgogac ottctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgcggg ggattatoca catcgacgcc 180
gcggagattt atcgaccta cccggaagtg ggtaaagcac tgccctgac cgaagagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caattttctc 480
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```

gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aaccccaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgct ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgctgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<210> 148

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 148

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20     25     30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35     40     45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50     55     60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65     70     75     80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85     90     95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100    105    110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115    120    125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130    135    140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ser
145    150    155    160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165    170    175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180    185    190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195    200    205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210    215    220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225    230    235    240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245    250    255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260    265    270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275    280    285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290    295    300
Tyr Asn Tyr Ala Ala Gln Lys Val
305    310

```

<210> 149
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 149
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg agcaaatcgt gcatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcgagagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcgacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttggttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tctgogctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 150
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 150
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val His
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145 150 155 160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165 170 175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180 185 190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser

195	200	205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro		
210	215	220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu		
225	230	235
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val		
245	250	255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe		
260	265	270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly		
275	280	285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys		
290	295	300
Tyr Asn Tyr Ala Ala Gln Lys Val		
305	310	

<210> 151
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 151
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 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctgggtg aacaaatcgt gtacgcgttg gagctgccgg gaattatoca catcgaogcc 180
 gcggaggttt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tgggaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
 gccagatca tcctgcgctg ggtaactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 152
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 152
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Glu Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Val Tyr
 50 55 60

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

<210> 153

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 153

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atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgcggg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctcgcgaga ttaaaatgag tgactccoct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaacg ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ctctccgctg ggcccgtgac ggatgaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gagttgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcgggtgtg tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tcgcgctgta ctggaataaa 900
ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

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<210> 154
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 154
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Ser Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Arg Met Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 155
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 155
 atgtcttttc accaacagtt ttacacgctg aacaacggca ataaaatccc ggcgattgcc 60

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atcatcggca ctggtacagc ctggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgcogg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gottagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagctc 600
gatatecttg tggaagcata ttctccgtg ggcccgtgc gggagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tctcgcgctg ggtcactaaa cgcggtgtgc tgccagttac caoctttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctcggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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<210> 156

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 156

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
20        25        30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35        40        45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50        55        60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65        70        75        80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85        90        95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100       105       110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115       120       125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130       135       140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145       150       155       160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165       170       175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180       185       190
Ile Tyr Lys Phe Cys Gln Glu Leu Asp Ile Leu Val Glu Ala Tyr Ser
195       200       205
Pro Leu Gly Pro Leu Arg Glu Lys Thr Ala Gln Asp Asp Ser Gln Pro
210       215       220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225       230       235       240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245       250       255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260       265       270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly

```

	275		280		285
Leu	Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys	Leu Tyr Gly Lys			
	290		295		300
Tyr Asn Tyr Ala Ala Gln Lys Val					
305		310			

<210> 157
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 157
 atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc ctggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctgggtg aacaaatcgt gtatgcgttg aaactgcggg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttggttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatattcctg tggaagcata ttctcgcgtg ggcccgctgc ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgcacagaac ctgttttctt tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaacgcg tcgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagaataat ga 942

<210> 158
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 158
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140

Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr
145					150					155					160
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
			165						170					175	
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
			180					185					190		
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
	195						200					205			
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210					215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225					230					235					240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
				245					250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260				265						270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Glu								
305					310										

<210> 159

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 159

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agtctgggtg agcaaatcgt gtatgcgttg aaactgcggg ggattatoca cgtcgacggc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaagagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatctctg tggaagcata ttctccgctg ggcccgctgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtaactaaa cgcgggtgtg tgccagttac caactottca 780
aagcctcagc gcgttagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccagc aaagtgtaat ga 942

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<210> 160

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 160

Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile

1		5		10		15									
Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Lys	Trp	Tyr	Lys	Ser	Glu
		20						25					30		
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr
		35					40					45			
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Val	Asp	Ala	Ala	Glu	Ile	Tyr
	50					55					60				
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro
65					70					75				80	
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met
				85					90					95	
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly
			100					105					110		
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Leu	His	Ser	Pro	Phe	Val	Ser	Lys
		115					120					125			
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln
	130					135					140				
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr
145					150				155					160	
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
				165				170						175	
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
		180						185					190		
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
	195						200					205			
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210					215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225					230					235				240	
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
				245					250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Val	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 161

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 161

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atcatcggca ctggtacagc ctggtataaa agtgaagaaa ctgacgogac cttctccaat 120
agtctgggtg aacaaatcgt gcatgcgttg aaactgccgg ggattatoca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgctgc ggaagaaaac cgcgcaggat 660

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<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 163

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtcctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagatttt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgaotcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccagacattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactgaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgcacagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942
```

<210> 164

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 164

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

Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225 230 235 240
Ala Gln Ile Ile Leu Arg Trp Val Thr Glu Arg Gly Val Leu Pro Val
245 250 255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260 265 270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275 280 285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290 295 300
Tyr Asn Tyr Ala Ala Gln Lys Val
305 310

<210> 165
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 165
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagggtt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgcttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttt caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcttgccgtg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct ggtcttgaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 166
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 166
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Val Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 168

```
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20     25     30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35     40     45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50     55     60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65     70     75     80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85     90     95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100    105    110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115    120    125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130    135    140
Leu Tyr Lys Ser Gly Lys Ala Arg Asn Ile Gly Val Ser Asn Phe Thr
145    150    155    160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165    170    175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180    185    190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195    200    205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210    215    220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225    230    235    240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245    250    255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260    265    270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275    280    285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290    295    300
Tyr Asn Tyr Ala Ala Gln Lys Val
305    310
```

<210> 169

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 169

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atgtctttt accaacagtt tttaacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc ctggtataaa agtgaagaaa ctgaacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
```

```

cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcgagacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
goccagatca tctcgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctcggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

```

<210> 170

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 170

```

Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
20        25        30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35        40        45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50        55        60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65        70        75        80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85        90        95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100       105       110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115       120       125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130       135       140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145       150       155       160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165       170       175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180       185       190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195       200       205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210       215       220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225       230       235       240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245       250       255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260       265       270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275       280       285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290       295       300

```

Tyr Asn Tyr Ala Ala Gln Lys Val
305 310

<210> 171
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 171
atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcgga ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggacagtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgctgtttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcctgtga ctggaataaa 900
ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 172
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 172
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Ser Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145 150 155 160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln

Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr
		35					40					45			
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Thr	Ala	Glu	Ile	Tyr
	50					55					60				
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro
	65				70					75					80
Arg	Asn	Ala	Val	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met
			85						90					95	
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly
			100					105					110		
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Leu	His	Ser	Pro	Phe	Val	Ser	Lys
		115					120					125			
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln
	130					135					140				
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr
	145				150					155					160
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
				165					170					175	
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
			180					185					190		
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
	195						200					205			
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210					215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
	225				230					235					240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
				245					250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 175

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 175

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgct ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaataccg caaatccgag 720
gccagatca tcttgcgctg ggtcactaaa cgcgggtgtg tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840

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gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataactc tgccgcccag aaagtgtaat ga 942

<210> 176
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 176
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Arg Lys Ser Glu
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Ser Ala Ala Gln Lys Val
 305 310

<210> 177
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 177

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc ctggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgcttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgagagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcttgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tcgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccagc aaagtgtaat ga 942
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<210> 178

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 178

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

				245					250					255					
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe				
			260					265					270						
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly				
		275					280					285							
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys				
	290					295					300								
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val												
305					310														

<210> 179

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 179

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcgcca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catogaagcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc gggtatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccogag 720
gccagatca tcttgccgtg ggtcactaaa cgcggtgtgc tgccagttac cacctottca 780
aagcctcagc gcattagcga tgcacagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcaoggagct gggtctggaa catgaaccgc tcgcctgtga ctggaataaa 900
ttgtatggca aatataacta cgccgccagc aaagtgtaat ga 942

```

<210> 180

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 180

Met	Ser	Phe	His	Gln	Gln	Phe	Phe	Thr	Leu	Asn	Asn	Gly	Asn	Lys	Ile				
1			5					10					15						
Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Lys	Trp	Tyr	Lys	Asn	Glu				
		20					25					30							
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr				
	35					40					45								
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Ile	Tyr				
	50			55			60												
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro				
65			70				75							80					
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met				
		85				90							95						
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly				
		100				105						110							

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

<210> 181
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 181
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttt caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgctg ggcccgctgc ggaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacga caaatccgag 720
 gcccgatca tcttgccgtg ggtcactaaa cgcgggtgtg tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 182
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 182

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20     25     30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35     40     45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50     55     60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65     70     75     80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85     90     95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100    105    110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Phe Val Ser Lys
115    120    125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130    135    140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145    150    155    160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165    170    175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180    185    190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195    200    205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210    215    220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asp Lys Ser Glu
225    230    235    240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245    250    255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260    265    270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275    280    285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290    295    300
Tyr Asn Tyr Ala Ala Gln Lys Val
305    310
```

<210> 183

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 183

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atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca cattgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaggcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tccccgcaga ttaaaatgag tgactccoct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
```

```

gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctgc ggaagaaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcgctgta ctggaataaa 900
ttgtatggca aatataactc tgccgcccag aaagtgtaat ga 942

```

<210> 184

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 184

```

Met Ser Phe His Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Ser Glu
20     25     30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35     40     45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50     55     60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65     70     75     80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85     90     95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100    105    110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115    120    125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130    135    140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145    150    155    160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165    170    175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180    185    190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195    200    205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210    215    220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225    230    235    240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245    250    255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260    265    270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275    280    285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290    295    300
Tyr Asn Ser Ala Ala Gln Lys Val
305    310

```

<210> 185
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 185
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgcggg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatccttg tggaaagcata ttctccgctg ggcccgtctg ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcttgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgcgcccag aaagtgtaat ga 942

<210> 186
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 186
 Met Ser Phe His Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190

```

<400> 188
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Ser Glu
          20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
          35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr

```

50	55	60
Arg Thr Tyr Pro Glu Val	Gly Lys Ala Leu Ser	Leu Thr Lys Lys Pro
65	70	75
Arg Asn Ala Ile Phe Leu Thr	Asp Lys Tyr Ser	Pro Gln Ile Lys Met
85	90	95
Ser Asp Ser Pro Ala Asp	Gly Leu Asp Leu Ala	Leu Lys Lys Met Gly
100	105	110
Thr Asp Tyr Val Asp Leu Tyr	Leu Leu His Ser	Pro Phe Val Ser Lys
115	120	125
Glu Val Asn Gly Leu Ser	Leu Glu Glu Ala Trp	Lys Asp Met Glu Gln
130	135	140
Leu Tyr Lys Ser Gly Lys	Ala Lys Asn Ile Gly	Val Ser Asn Phe Thr
145	150	155
Val Glu Asp Leu Gln Arg	Ile Leu Lys Val Ala	Glu Val Lys Pro Gln
165	170	175
Val Asn Gln Ile Glu Phe	Ser Pro Phe Leu Gln	Asn Gln Thr Pro Gly
180	185	190
Ile Tyr Lys Phe Cys Gln	Glu His Asp Ile Leu	Val Glu Ala Tyr Ser
195	200	205
Pro Leu Gly Pro Leu Arg	Lys Lys Ala Ala Gln	Asp Asp Gly Gln Pro
210	215	220
Phe Phe Glu Tyr Val Lys	Glu Leu Ser Glu Lys	Tyr Asn Lys Ser Glu
225	230	235
Ala Gln Ile Ile Leu Arg	Trp Val Thr Lys Arg	Gly Val Leu Pro Val
245	250	255
Thr Thr Ser Ser Lys Pro	Gln Arg Ile Ser Asp	Ala Gln Asn Leu Phe
260	265	270
Ser Phe Asp Leu Thr Ala	Glu Glu Val Asp Lys	Ile Thr Glu Leu Gly
275	280	285
Leu Glu His Glu Pro Leu	Arg Leu Tyr Trp Asn	Lys Leu Tyr Gly Lys
290	295	300
Tyr Asn Tyr Ala Ala Gln	Lys Val	
305	310	

<210> 189
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 189
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa gtggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatccttg tggaagcata ttctccgctg ggcccgtg gcgaagaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
 gccagatca tcttgccgtg ggtcactaaa cgcgggtgtg tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 190
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 190
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Gly Lys Ser Glu
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 191
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 191

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atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcgagagattt atcgcaccta cccggaagtg ggtaaagcac tgcacctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcgacggttc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccatc ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgatatggca aatataacta cgccgccag aaagtgtaat ga 942

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<210> 192

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 192

```

Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
          20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
          35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
          50          55          60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
          85          90          95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
          100         105         110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
          115         120         125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
          130         135         140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145         150         155         160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
          165         170         175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
          180         185         190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
          195         200         205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser His Pro
210         215         220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225         230         235         240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
          245         250         255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260         265         270

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Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
		290				295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 193
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 193
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catogaagcc 180
 gcgagagatt atcgcaccta ccggaagtg ggtaaagcac tgtccctgac caaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
 gcgacaggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatattgagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tgggaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tctcgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttatatggca aatataactc tgccgcccg aaagtgtaat ga 942

<210> 194
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 194
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Lys Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln

130		135		140
Leu Tyr Lys Ser Gly	Lys Ala Lys Asn Ile Gly	Val Ser Asn Phe Thr		
145	150	155	160	
Val Glu Asp Leu Gln Arg	Ile Leu Lys Val Ala Glu	Val Lys Pro Gln		
	165	170	175	
Val Asn Gln Ile Glu Phe	Ser Pro Phe Leu Gln	Asn Gln Thr Pro Gly		
	180	185	190	
Ile Tyr Lys Phe Cys Gln	Glu His Asp Ile Leu	Val Glu Ala Tyr Ser		
	195	200	205	
Pro Leu Gly Pro Leu Arg	Lys Lys Thr Ala Gln	Asp Asp Ser Gln Pro		
	210	215	220	
Phe Phe Glu Tyr Val Lys	Glu Leu Ser Glu Lys	Tyr Asn Lys Ser Glu		
225	230	235	240	
Ala Gln Ile Ile Leu Arg	Trp Val Thr Lys Arg	Gly Val Leu Pro Val		
	245	250	255	
Thr Thr Ser Ser Lys Pro	Gln Arg Ile Ser Asp	Ala Gln Asn Leu Phe		
	260	265	270	
Ser Phe Asp Leu Thr Ala	Glu Glu Val Asp Lys	Ile Thr Glu Leu Gly		
	275	280	285	
Leu Glu His Glu Pro Leu	Arg Leu Tyr Trp Asn	Lys Leu Tyr Gly Lys		
	290	295	300	
Tyr Asn Ser Ala Ala Gln	Lys Val			
305	310			

<210> 195
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 195
 atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgccc 60
 atcatcgcca ctggtacagc ctggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatattgagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttctctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatattcttg tggaaagcata ttctccgctg ggcccgctgc ggaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcttgcgctg ggtcactaaa cgcgggtgtg tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcc tgcacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccagc aaagtgtaat ga 942

<210> 196
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 196

Met	Ser	Phe	His	Gln	Gln	Phe	Phe	Thr	Leu	Asn	Asn	Gly	Asn	Lys	Ile
1			5						10					15	
Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Ala	Trp	Tyr	Lys	Ser	Glu
		20						25					30		
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr
		35					40					45			
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Ile	Tyr
	50					55					60				
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro
65				70						75					80
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met
			85						90					95	
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly
			100					105					110		
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Ile	His	Ser	Pro	Phe	Val	Ser	Lys
		115					120					125			
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln
	130					135					140				
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr
145				150					155						160
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
			165					170						175	
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
		180						185					190		
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
		195					200					205			
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210					215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225				230						235					240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
			245						250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
		260						265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 197

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 197

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgoc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaacct cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttggc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtttgtttc gaaggaagtg aatggcctaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600

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gatatcctgg tggaagcata ttctccgctg ggcccgcgtgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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<210> 198

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 198

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50          55          60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65          70          75          80
Arg Asp Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85          90          95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100         105         110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Phe Val Ser Lys
115         120         125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130         135         140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145         150         155         160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165         170         175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180         185         190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195         200         205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210         215         220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225         230         235         240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245         250         255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260         265         270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275         280         285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290         295         300
Tyr Asn Tyr Ala Ala Gln Lys Val
305         310

```

<210> 199

<211> 942

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 199
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgaagcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgtg gcgagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tcgcgctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 200
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 200
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Ser Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Phe Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145 150 155 160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165 170 175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180 185 190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195 200 205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro

210		215		220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu				
225		230		235
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val				240
		245		250
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe				255
		260		265
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly				270
		275		280
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys				285
		290		295
Tyr Asn Tyr Ala Ala Gln Lys Val				300
305		310		

<210> 201
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 201
 atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
 attatcggca ctggtacaaa gtggtataaaa agtgaagaaa ctgacgogac cttctccaat 120
 agtctgggtg aacaaatcgt gtatgcgttg aaactgcggg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcatth ataaattctg tcaggagcac 600
 gatatcctgg tgggaagcata ttctccgctg ggcccgotgc ggaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
 gccagatca tcttgcgctg ggtaactaaa cgcgggtgtg tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 202
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 202
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Ser Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80

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

<210> 203
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 203
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggogactgcc 60
 attatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtacgcgttg aaactgccgg ggattatoca catogaogcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtocotgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
 gccagatca tcctgcgctg ggtaactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tcgcctgtga ctggaataaa 900
 ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 204
 <211> 313

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 204
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Thr Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Ser Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145 150 155 160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165 170 175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180 185 190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195 200 205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210 215 220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Gly Lys Ser Glu
225 230 235 240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245 250 255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260 265 270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275 280 285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290 295 300
Tyr Asn Tyr Ala Ala Gln Lys Val
305 310

<210> 205
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 205
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggogattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgcggg ggattatoca catcgacgcc 180

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gcgagggttt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggaacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctcggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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<210> 206

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 206

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20        25        30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35        40        45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Val Tyr
50        55        60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65        70        75        80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85        90        95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100       105       110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115       120       125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130       135       140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145       150       155       160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165       170       175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180       185       190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195       200       205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210       215       220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225       230       235       240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245       250       255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260       265       270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275       280       285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys

```

290
Tyr Asn Tyr Ala Ala Gln Lys Val
305 310

300

<210> 207
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 207
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgaacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg gaactgccgg ggattatcca catcgacgcc 180
gcgagatatt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttggttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tctcgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctottca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctgaa catgaaccgc tgcgctgta ctggaataaa 900
ttgtatggca gatataacta cgccgccag aaagtgtaat ga 942

<210> 208
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 208
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Ser Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Glu Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145 150 155 160

Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
				165					170					175	
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
			180					185					190		
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
		195					200					205			
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210					215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225					230					235					240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
				245					250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Arg
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 209
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 209
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatogt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaagagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
 gcggacggto tggattttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgctg ggcccgcgtc ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaataccg caaatccgag 720
 gccagatca tccctgcgtg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 210
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 210
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Ser Glu

<220>
<223> Synthetic Construct

<400> 213
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc ctggtataaa agtgaagaaa ctgacgcgac ctctctccaat 120
agtctgggtg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatggtga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgtgct ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaataccg caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgccgtga ctggaataaa 900
ttgtatggca aatataacta cgcgcccgag aaagtgtaat ga 942

<210> 214
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 214
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145 150 155 160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165 170 175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180 185 190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195 200 205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210 215 220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Arg Lys Ser Glu
225 230 235 240

Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
				245					250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275				280						285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 215
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 215
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac caaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgctg ggcccgtctg ggaagagAAC cgcgaggat 660
 gacagccaac cattctttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagoga tgctcagaac ctgttttctt togacctgac agcggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 216
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 216
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Lys Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly

<220>

<223> Synthetic Construct

<400> 218

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
      20      25      30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
      35      40      45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
      50      55      60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65      70      75      80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
      85      90      95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
      100     105     110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
      115     120     125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
      130     135     140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145     150     155     160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
      165     170     175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
      180     185     190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
      195     200     205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
      210     215     220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Gly Lys Ser Glu
225     230     235     240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
      245     250     255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
      260     265     270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
      275     280     285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
      290     295     300
Tyr Asn Tyr Ala Ala Gln Lys Val
305      310
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<210> 219

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 219

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atgtcttttt accaacagtt tttaacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattgtcca catcgacgcc 180
gcggagattt atcgcaccta ccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
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<210> 221
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 221
 atgtcttttt accaacagtt tttcacactg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagggtt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttggttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gotgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tggaaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tctgocgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 222
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 222
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Ser Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Val Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly

			180					185					190				
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser		
		195					200					205					
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro		
		210				215					220						
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu		
225					230					235					240		
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val		
			245						250					255			
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe		
		260						265					270				
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly		
		275					280					285					
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys		
	290					295					300						
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val										
305					310												

<210> 223
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 223
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcgga ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
 gcggacggtc tggattttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta agcctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctcgcgtg ggcccgctgc ggaagaaaac cgcgcaggat 660
 gacagccaac cattctttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcttgccgtg ggtcactaga cgcgggtgtg tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatacaacta cgccgccag aaagtgtaat ga 942

<210> 224
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 224
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45

Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Ile	Tyr
50						55					60				
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro
65					70					75					80
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met
				85					90					95	
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly
			100					105					110		
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Leu	His	Ser	Pro	Phe	Val	Ser	Lys
		115					120					125			
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln
		130				135					140				
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr
145					150					155					160
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
				165					170					175	
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
			180					185					190		
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
		195					200					205			
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
		210				215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225					230					235					240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Arg	Arg	Gly	Val	Leu	Pro	Val
				245					250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
		290				295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 225

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 225

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaaggg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcatttagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tcgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<210> 226
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 226
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Gly Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 227
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 227

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtcctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcttgccgtg ggtcactaaa cgcggcgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942
```

<210> 228

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 228

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

			260					265					270				
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly		
		275					280					285					
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys		
	290					295					300						
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val										
305					310												

<210> 229
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 229
 atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatoca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgccctcgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttggttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccatata ccaggcattt ataaattctg tcaggagcac 600
 gatattcctg tggaagcata ttctccgctg ggcgcgctgc ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tctcgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgcacagaac ctgttttctc tcgaacctgac agcgggaagag 840
 gttgataaaa tcacggagcg ggtctggaa catgaaccgc tcgcgctgta ctggaataag 900
 ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 230
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 230
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125

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

<210> 231
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 231
 atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgcgag ggattatcca catogacgcc 180
 gcggagattt atgcaccta cccggaagtg ggtaaaccac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatggtga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 ggtatcctgg tggaaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
 gccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcgctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 232
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 232

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
      20      25      30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
      35      40      45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
      50      55      60
Arg Thr Tyr Pro Glu Val Gly Lys Pro Leu Ser Leu Thr Glu Lys Pro
65      70      75      80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
      85      90      95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
      100     105     110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
      115     120     125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
      130     135     140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145     150     155     160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
      165     170     175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
      180     185     190
Ile Tyr Lys Phe Cys Gln Glu His Gly Ile Leu Val Glu Ala Tyr Ser
      195     200     205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
      210     215     220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Gly Lys Ser Glu
225     230     235     240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
      245     250     255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
      260     265     270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
      275     280     285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
      290     295     300
Tyr Asn Tyr Ala Ala Gln Lys Val
305      310
```

<210> 233

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 233

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atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgcogg ggattatcca catogaogcc 180
gcgagagatt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
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gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacca cgccgccag aaagtgtaat ga 942

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<210> 234

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 234

```

Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50          55          60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85          90          95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100         105         110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115         120         125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130         135         140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145         150         155         160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165         170         175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180         185         190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195         200         205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210         215         220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225         230         235         240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245         250         255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260         265         270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275         280         285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290         295         300
Tyr Asn His Ala Ala Gln Lys Val
305          310

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<210> 235

<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 235
atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattggc 60
atcatcggca ctggtacaaa atggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttctctgca aaaccaaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgcctgc ggaagaaaac cgcgcaggat 660
gacagccaac catttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcttgcgctg ggtcactaaa cgcgggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtttgga catgaaccgc tcgcgctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 236
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 236
Met Ser Phe His Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Ser Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Phe Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145 150 155 160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165 170 175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180 185 190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195 200 205

Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
210						215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225					230					235					240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
				245					250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 237
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 237
 atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcgcca ctggtacaaa gtggtataaa agtgaagaaa ctgacggcgc cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgtttggttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttctcc 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgctg ggcccgtg gcgaagaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcttgccgtg ggtaactaaa cgcgggtgtg tgccagttac cacctottca 780
 aagcctcagc gcattagcga tgcacagaac ctgttttctc tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct ggtcttgga catgaacgcg tcgcgcctgt ctggaataaa 900
 ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 238
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 238
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Ser Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro

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

<210> 239

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 239

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgacggcag cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aagctgccgg ggattatcca catogacgcc 180
gcggagattt atcgcaccta cccggaagtg ggcaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatattggagc agttatacaa aaccggtaaa gctaaaaaca tcgggggttt caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccgatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggag catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataactc tgccgccagc aaagtgtaat ga 942

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<210> 240

<211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 240
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Ser Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Thr Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Ser Ala Ala Gln Lys Val
 305 310

<210> 241
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 241
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120

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agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgoc 180
gcgagagatt atcgcaccta ccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcgagcggtc tggatttagc attgaagaaa atgggtacgg attatgttga tttatatctg 360
attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttctcc 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgct ggaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgcccagaac ctgttttctc tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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<210> 242

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 242

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20        25        30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35        40        45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50        55        60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65        70        75        80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85        90        95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100       105       110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Phe Val Ser Lys
115       120       125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130       135       140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ser
145       150       155       160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165       170       175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180       185       190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195       200       205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210       215       220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225       230       235       240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245       250       255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260       265       270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275       280       285

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Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 243
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 243
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggogattgcc 60
 atcatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgoc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac caaaaagcct 240
 cgtaacgoga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgttgc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatctcctgg tggaagcata ttctccgctg ggcccactgc ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
 gccagatca tcttgccgtg ggctactaaa cgcggtgtgc tgccagttac cacctottca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataactc tgccgcccgag aaagtgtaat ga 942

<210> 244
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 244
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Ser Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Lys Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr

145		150		155		160									
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
		165		170		175									
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
		180		185		190									
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
		195		200		205									
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
		210		215		220									
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Gly	Lys	Ser	Glu
225				230		235									240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
		245		250		255									
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
		260		265		270									
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275		280		285									
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
		290		295		300									
Tyr	Asn	Ser	Ala	Ala	Gln	Lys	Val								
305				310											

<210> 245
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 245
 atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcgga ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgcgag ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaagagcct 240
 cgtaacgcga tttttctgac ggataaatat tctcgcgaga ttaaaatgag tgactccctt 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgtttggtac gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatccttg tggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tctgcgctg ggtcactaaa cgcggtgtgc tgcagttac cactottca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct ggtcttgaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 246
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 246
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15

Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Lys	Trp	Tyr	Lys	Ser	Glu
			20					25					30		
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr
		35					40					45			
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Ile	Tyr
	50				55					60					
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro
65					70				75						80
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met
				85					90					95	
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly
			100					105					110		
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Ile	His	Ser	Pro	Phe	Val	Thr	Lys
		115					120					125			
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln
	130					135					140				
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr
145					150					155					160
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
				165				170						175	
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
			180					185					190		
Ile	Cys	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
	195						200					205			
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210					215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225					230					235					240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
				245					250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 247

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 247

```

atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc ctggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta ccgggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttctcc 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720

```

```

gccagatca tctgcgctg ggtcactaaa cgcgggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<210> 248
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 248

Met	Ser	Phe	His	Gln	Gln	Phe	Phe	Thr	Leu	Asn	Asn	Gly	Asn	Lys	Ile	1	5	10	15
Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Ala	Trp	Tyr	Lys	Ser	Glu	20	25	30	
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr	35	40	45	
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Ile	Tyr	50	55	60	
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro	65	70	75	80
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met	85	90	95	
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly	100	105	110	
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Ile	His	Ser	Pro	Phe	Val	Ser	Lys	115	120	125	
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln	130	135	140	
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Ser	145	150	155	160
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln	165	170	175	
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly	180	185	190	
Ile	Cys	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser	195	200	205	
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro	210	215	220	
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu	225	230	235	240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val	245	250	255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe	260	265	270	
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly	275	280	285	
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys	290	295	300	
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val	305	310										

<210> 249
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 249

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg aacaaatcgt gtacgcgttg aagctgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtttgtttc gaaggaagtg aatggcttaa gottagaaga ggcttggaag 420
gatatggagc agttatacaa aaccggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgctgc ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccgatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctottca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgaacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgogcctgta ctggaataaa 900
ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942
```

<210> 250

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 250

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

225		230		235		240									
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
		245		250		255									
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
		260		265		270									
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275		280		285									
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
		290		295		300									
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305				310											

<210> 251
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 251

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atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta ccggaagtg ggcaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatggtga tttatatctg 360
attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtctg ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
gccagatca tcttgcgctg ggtaactaaa cgcggtgtgc tgccagttac cactcttcca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct ggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccagc aaagtataat ga 942
  
```

<210> 252
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 252

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

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

<210> 253

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 253

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggacggtc tggatatagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttctcc 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac cactcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct ggtctgggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccagc aaagtgtaat ga 942

```

<210> 254

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 254

```
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Ser Glu
20      25      30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35      40      45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50      55      60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65      70      75      80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85      90      95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Ile Ala Leu Lys Lys Met Gly
100      105      110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Phe Val Ser Lys
115      120      125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130      135      140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ser
145      150      155      160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165      170      175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180      185      190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195      200      205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210      215      220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225      230      235      240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245      250      255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260      265      270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275      280      285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290      295      300
Tyr Asn Tyr Ala Ala Gln Lys Val
305      310
```

<210> 255

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 255

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atgtctttt accaacagtt ttacacgtg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc ctggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtacgcgttg aagctgcggg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
```

```

gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttctcc 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<210> 256

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 256

```

Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50          55          60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85          90          95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100          105          110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Phe Val Ser Lys
115          120          125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130          135          140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ser
145          150          155          160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165          170          175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180          185          190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195          200          205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210          215          220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225          230          235          240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245          250          255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260          265          270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275          280          285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290          295          300
Tyr Asn Tyr Ala Ala Gln Lys Val

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<210> 257
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 257
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtacgcgttg aagctgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
 gcggacggtc tggaatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgtttgtttc gaaggaagtg aatgggttaa gcttagaaga ggcttgga 420
 gatatggagc agttatacaa aaccggtaaa gctaaaaaca tcgggggttt caattttctc 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgctg ggcccgtg gcgaagaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctt togacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 258
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 258
 Met Ser Phe His Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Ser Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Thr Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ser
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175

Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
		180						185					190		
Ile	Cys	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
	195						200					205			
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210					215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225					230					235					240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
			245						250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 259

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 259

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcgagagatt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgct ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcttgccgtg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttccct tcgacctgac agcgggaagag 840
gttgataaaa tcaccgagct gggtctggaa catgaaccgc tcgcgctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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<210> 260

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 260

Met	Ser	Phe	His	Gln	Gln	Phe	Phe	Thr	Leu	Asn	Asn	Gly	Asn	Lys	Ile
1			5						10					15	
Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Ala	Trp	Tyr	Lys	Ser	Glu
			20					25					30		
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr

35	40	45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp	Ala Ala Glu Ile Tyr	
50	55	60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser	Leu Thr Glu Lys Pro	
65	70	75
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser	Pro Gln Ile Lys Met	
85	90	95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala	Leu Lys Lys Met Gly	
100	105	110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser	Pro Leu Val Ser Lys	
115	120	125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp	Lys Asp Met Glu Gln	
130	135	140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly	Val Ser Asn Phe Thr	
145	150	155
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala	Glu Val Lys Pro Gln	
165	170	175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln	Asn Gln Thr Pro Gly	
180	185	190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu	Val Glu Ala Tyr Ser	
195	200	205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln	Asp Asp Ser Gln Pro	
210	215	220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys	Tyr Asn Lys Ser Glu	
225	230	235
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg	Gly Val Leu Pro Val	
245	250	255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp	Ala Gln Asn Leu Phe	
260	265	270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys	Ile Thr Glu Leu Gly	
275	280	285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn	Lys Leu Tyr Gly Lys	
290	295	300
Tyr Asn Tyr Ala Ala Gln Lys Val		
305	310	

<210> 261

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 261

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atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaaatccc ggogattgcc 60
atcatcgcca ctggtacagc gtggtataaa agtgaagaaa ctgacgogac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta ccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctc 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgcgtgtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt acaaattctg tcaggagcac 600
gatatccttg tggaagcata ttctccgctg ggcccgtg ggaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcttgcgctg ggtcactaaa cgoggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900

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ttgtatggca aatataacta cgccgccag aaagtgtaat ga

942

<210> 262

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 262

Met	Ser	Phe	His	Gln	Gln	Phe	Phe	Thr	Leu	Asn	Asn	Gly	Asn	Lys	Ile	
1				5					10					15		
Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Ala	Trp	Tyr	Lys	Ser	Glu	
			20					25					30			
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr	
		35					40					45				
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Ile	Tyr	
	50					55				60						
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro	
65					70					75					80	
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met	
				85					90					95		
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly	
			100				105						110			
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Leu	His	Ser	Pro	Leu	Val	Ser	Lys	
		115					120					125				
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln	
	130					135					140					
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr	
145					150				155						160	
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Arg	Val	Ala	Glu	Val	Lys	Pro	Gln	
				165				170						175		
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly	
			180					185					190			
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser	
		195					200					205				
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro	
	210					215					220					
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu	
225					230					235					240	
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val	
				245					250					255		
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe	
			260					265					270			
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly	
		275					280					285				
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys	
	290					295					300					
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val									
305					310											

<210> 263

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 263

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atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcgagagatt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
gcgagcggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt acaaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgctgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaataccg caaatccgag 720
gccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942
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<210> 264

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 264

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

Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 265

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 265

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atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggogattgcc 60
atcatcggca ctggtacaaa atggtataaa agtgaagaaa ctgacgagac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgocgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaagtg aatggcctaa gcttagaaga ggcttggaaa 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgac ggatgaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcttgcgctg ggtcactaaa cgcgggtgtg tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccagc aaagtgtaat ga 942

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<210> 266

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 266

Met	Ser	Phe	His	Gln	Gln	Phe	Phe	Thr	Leu	Asn	Asn	Gly	Asn	Lys	Ile
1			5					10					15		
Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Lys	Trp	Tyr	Lys	Ser	Glu
			20					25					30		
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr
		35					40					45			
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Ile	Tyr
	50					55					60				
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro
65				70						75				80	
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met
			85					90						95	
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly
			100					105					110		
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Ile	His	Ser	Pro	Leu	Val	Ser	Lys

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

<210> 267
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 267
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 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta ccoggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgttcgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatattggagc agttatacaa aaccggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgcgtgtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt acaaattctg tcaggagcac 600
 gatatacttg tggaagcata ttctccgctg ggcccgtgtc ggaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
 gccagatca tctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cactcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 268
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 268

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
20      25      30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35      40      45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50      55      60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65      70      75      80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85      90      95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100     105     110
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115     120     125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130     135     140
Leu Tyr Lys Thr Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145     150     155     160
Val Glu Asp Leu Gln Arg Ile Leu Arg Val Ala Glu Val Lys Pro Gln
165     170     175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180     185     190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195     200     205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210     215     220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225     230     235     240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245     250     255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260     265     270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275     280     285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290     295     300
Tyr Asn Tyr Ala Ala Gln Lys Val
305      310
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<210> 269

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 269

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atgtctttttc accaacagtt tttaacgctg aacaacggca ataaaatccc ggcgattgcc 60
accatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac ctctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcgagagatt atgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggaaggctc tggatttagc attgaagaaa atgggtacag attatgttg tttatatctg 360
attcattccc cgtagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
```

```

gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt acaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgct ggaagaaaac cgcgccaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<210> 270

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 270

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Thr Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50          55          60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85          90          95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100         105         110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
115         120         125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130         135         140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145         150         155         160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165         170         175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180         185         190
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195         200         205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210         215         220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225         230         235         240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245         250         255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260         265         270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275         280         285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290         295         300
Tyr Asn Tyr Ala Ala Gln Lys Val
305         310

```

<210> 271
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 271
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatcctgg tgggaagcata ttctccgctg ggcccgtctg ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaataccg caaatccgag 720
 gccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 272
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 272
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Leu Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser

195	200	205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro		
210	215	220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Arg Lys Ser Glu		
225	230	235
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val		
245	250	255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe		
260	265	270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly		
275	280	285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys		
290	295	300
Tyr Asn Tyr Ala Ala Gln Lys Val		
305	310	

<210> 273
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 273
 atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgogac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgttagtctt gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaaca ccaggcattt acaaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgctg ggcccgtg gcgaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
 gccagatca tcctgogctg ggtaactaaa cgoggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tcgcgctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

<210> 274
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 274
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60

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

<210> 275

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 275

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atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgogac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatoca catcgacgcc 180
gcgagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat totccgcaga ttaaaatgag tgactcccct 300
gcgacgggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtg gcgaagaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccgatca tcctgcgctg ggtaactaaa cgcgggtgtg tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcgctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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<210> 276
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 276
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 277
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 277
 atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60

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atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta ccoggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgtg ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcttgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctcggaa catgaaccgc tcgcgctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<210> 278
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 278

Met	Ser	Phe	His	Gln	Gln	Phe	Phe	Thr	Leu	Asn	Asn	Gly	Asn	Lys	Ile	1	5	10	15
Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Ala	Trp	Tyr	Lys	Pro	Glu	20	25	30	
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr	35	40	45	
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Ile	Tyr	50	55	60	
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro	65	70	75	80
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met	85	90	95	
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly	100	105	110	
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Ile	His	Ser	Pro	Leu	Val	Ser	Lys	115	120	125	
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln	130	135	140	
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr	145	150	155	160
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln	165	170	175	
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly	180	185	190	
Ile	Cys	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser	195	200	205	
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro	210	215	220	
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu	225	230	235	240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val	245	250	255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe	260	265	270	
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly				

Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr
145					150					155					160
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
				165					170						175
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Leu	Leu	Gln	Asn	Gln	Thr	Pro	Gly
			180					185					190		
Ile	Cys	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
	195						200					205			
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210					215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225					230					235					240
Ala	Gln	Val	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
				245					250						255
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Asp	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 281

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 281

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atgtcttttc accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
accctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt gcaaattctg tcagcaaacac 600
gacatcctgg tggaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tctgcgctg ggtcactaaa cgcggtgtgc tgccagttac caoctottca 780
aagcctcagc gcattagcga tgctcagaac atcttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctgaa catgaacgcg tcgcgctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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<210> 282

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 282

Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile

1		5		10		15									
Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Ala	Trp	Tyr	Lys	Ser	Glu
		20				25							30		
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Thr	Leu	Val	Glu	Gln	Ile	Val	Tyr
		35				40						45			
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Ile	Tyr
	50				55					60					
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro
65				70					75					80	
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met
			85					90					95		
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly
		100					105					110			
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Ile	His	Ser	Pro	Leu	Val	Ser	Lys
	115					120						125			
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln
	130					135					140				
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr
145				150				155						160	
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
			165				170						175		
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
	180						185					190			
Ile	Cys	Lys	Phe	Cys	Gln	Gln	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
	195				200						205				
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210				215						220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225				230					235					240	
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
		245					250						255		
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Ile	Phe
		260					265					270			
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
	275					280					285				
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290				295					300					
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305				310											

<210> 283

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 283

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atgtcttttc accaagaatt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
accctggttg aacaattagt gtatgcgttg aaactgccgg gggttatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatotg 360
attcattccc cgttagtttc gaaggaagtg aatggottaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaac ccaggcattt gcaaattctg tcagcaaacac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660

```

```

gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<210> 284
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 284

Met	Ser	Phe	His	Gln	Glu	Phe	Phe	Thr	Leu	Asn	Asn	Gly	Asn	Lys	Ile	1	5	10	15
Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Ala	Trp	Tyr	Lys	Ser	Glu	20	25	30	
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Thr	Leu	Val	Glu	Gln	Leu	Val	Tyr	35	40	45	
Ala	Leu	Lys	Leu	Pro	Gly	Val	Ile	His	Ile	Asp	Ala	Ala	Glu	Ile	Tyr	50	55	60	
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro	65	70	75	80
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met	85	90	95	
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly	100	105	110	
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Ile	His	Ser	Pro	Leu	Val	Ser	Lys	115	120	125	
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln	130	135	140	
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr	145	150	155	160
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln	165	170	175	
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly	180	185	190	
Ile	Cys	Lys	Phe	Cys	Gln	Gln	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser	195	200	205	
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro	210	215	220	
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu	225	230	235	240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val	245	250	255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe	260	265	270	
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly	275	280	285	
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys	290	295	300	
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val	305	310										

<210> 285
 <211> 942
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 285

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atgtcttttc accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctocaat 120
acctgggttg aacaattagt gtatgcgttg aaactgccgg ggattatcca catogaagcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ctgcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagg agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcagcaacac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccogag 720
gcccagatca tccctgocgtg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac atcttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct ggtcttgaa catgaaccgc tcgcctgtga ctggaataaa 900
ttgtatggca aatataacta cgcgcccag aaagtgtaat ga 942
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<210> 286

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 286

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

Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Thr	Glu
225					230					235					240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
				245					250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Ile	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280						285		
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 287
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 287

atgtcttttc	accaagaatt	tttcacgctg	aacaacggca	ataaaatccc	ggcgattgcc	60
atcatcggca	ctggtacagc	gtggtataaa	agtgaagaaa	ctgacgcgac	cttctccaat	120
agtctggttg	aacaattagt	gtatgcgttg	aaactgccgg	ggattatcca	catcgacgcc	180
gcggagattt	atcgcaccta	cccggaagtg	ggtaaagcac	tgtocttgac	cgaaaagcct	240
cgtaacgcga	tttttctgac	ggataaatat	tctccgcaga	ttaaaatgag	tgactccctt	300
gcggacggtc	tggatttagc	attgaagaaa	atgggtacag	attatgttga	tttatatctg	360
attcattccc	cgttagtttc	gaaggaagtg	aatggcttaa	gcttagaaga	ggcttggaaa	420
gatatggagc	agttatacaa	aagtggtaaa	gctaaaaaca	tcgggggttc	caatttcaca	480
gtggaagacc	tgcaacgtat	cctgaaagtc	gctgaagtta	aacotcaggt	caaccagatt	540
gagttctctc	cgttcctgca	aaaccaaaca	ccaggcattt	gcaaattctg	tcaggagcac	600
gatatcctgg	tggaagcata	ttctccgctg	ggcccgtctc	ggaagaaaac	cgcgcaggat	660
gacagccaac	cattttttga	gtacgtcaaa	gaattgagcg	aaaaatacaa	taaaaccgag	720
gccagatct	tactgcgctg	ggctactaaa	cgcggtgtgc	tgccagttac	cacctcttca	780
aagcctcagc	gcattagcga	tgctcagaac	ctgttttcct	tcgacctgac	agcggaagag	840
gttgataaaa	tcacggagct	gggtctggaa	catgaaccgc	tgcgccctgta	ctggaataaa	900
ttgtatggca	aatataacta	cgccgcccag	aaagtgtaat	ga		942

<210> 288
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 288

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

```
<210> 290
<211> 313
<212> PRT
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<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 290

```
Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
          20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
          35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
          50          55          60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
          85          90          95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
          100          105          110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
          115          120          125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
          130          135          140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145          150          155          160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
          165          170          175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
          180          185          190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
          195          200          205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
          210          215          220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Thr Glu
225          230          235          240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
          245          250          255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
          260          265          270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
          275          280          285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
          290          295          300
Tyr Asn Tyr Ala Ala Gln Lys Val
305          310
```

<210> 291

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 291

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atgtcttttt accaagaatt tttaacgctg aacaacggca ataaaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
accctggttg aacaaatcgt gtatgcgttg aaactgcggg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta ccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
```

```

cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctgc ggaagaaaac cgcgcaggat 660
gacagccaac catitttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac atcttttctt tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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<210> 292

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 292

```

Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
          20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Thr Leu Val Glu Gln Ile Val Tyr
          35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
          50          55          60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
          85          90          95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
          100          105          110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
          115          120          125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
          130          135          140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145          150          155          160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
          165          170          175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
          180          185          190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
          195          200          205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
          210          215          220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225          230          235          240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
          245          250          255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Ile Phe
          260          265          270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
          275          280          285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
          290          295          300

```

Tyr Asn Tyr Ala Ala Gln Lys Val
305 310

<210> 293
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 293
atgtcttttt accaagaatt ttctacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtctt gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttt caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcc agaaatacaa taaaaccgag 720
gccagatca tctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aaacctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaacgc tcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgcgcgcag aaagtgtaat ga 942

<210> 294
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 294
Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145 150 155 160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln

				165					170					175			
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly		
			180					185					190				
Ile	Cys	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser		
		195					200					205					
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro		
	210					215					220						
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Gln	Lys	Tyr	Asn	Lys	Thr	Glu		
225					230					235					240		
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val		
			245					250					255				
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe		
			260					265					270				
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly		
		275					280					285					
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys		
	290					295					300						
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val										
305					310												

<210> 295
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 295
 atgtcttttt accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcgga ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca cctggaagcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ctgcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaaca ccaggcattt gcaaattctg tcagcaaacac 600
 gatatacttg tggaagcata ttctccgctg ggcccgtgct ggaagaaaac cgcgaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
 gccagatct tactgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 296
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 296
 Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
 20 25 30

Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr
	35						40					45			
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Leu	Asp	Ala	Ala	Glu	Ile	Tyr
	50					55					60				
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro
	65				70					75					80
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met
			85						90					95	
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly
			100					105					110		
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Leu	His	Ser	Pro	Leu	Val	Ser	Lys
	115						120					125			
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln
	130					135					140				
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr
	145				150					155					160
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
			165					170						175	
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
	180							185					190		
Ile	Cys	Lys	Phe	Cys	Gln	Gln	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
	195						200					205			
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210					215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
	225				230					235					240
Ala	Gln	Ile	Leu	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
			245						250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
	275						280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 297

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 297

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atgtcttttc accaagaatt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaattagt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctc 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtagtttgc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcagcaaacac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgct ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
gccagatct tactgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctottca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc togacctgac agcgggaagag 840

```

gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

<210> 298
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 298
 Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Leu Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Cys Lys Phe Cys Gln Gln His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Thr Glu
 225 230 235 240
 Ala Gln Ile Leu Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 299
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 299

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atgtcttttc accaagaatt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcgga ctggtacagc gtggtataaa agtgaagaaa ctgacgogac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgcogg ggattatcca cctggacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttatcac ggataaatat tctccgcaga ttaaaatgag tgactccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aaactcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtg gcgaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
gccagatct tactgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctottca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctcggaa catgaaccgc tcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgcgcgccag aaagtgtaat ga 942
```

<210> 300

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 300

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

				245					250					255			
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe		
			260					265					270				
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly		
		275					280					285					
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys		
	290					295					300						
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val										
305					310												

<210> 301

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 301

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atgtcttttc accaagaatt ttccacgctg aacaacggca ataaaatccc ggogattgcc 60
atcatcgcca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaattagt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcgagagatt atcgcaccta cccggaagtg ggtaaagcac tgcacctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcgacaggto tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtagtttcc gaaggaagtg aatgggttaa gcttagaaga ggcttggaaa 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgctgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
gccagatca tcttgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<210> 302

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 302

Met	Ser	Phe	His	Gln	Glu	Phe	Phe	Thr	Leu	Asn	Asn	Gly	Asn	Lys	Ile		
1			5					10					15				
Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Ala	Trp	Tyr	Lys	Ser	Glu		
		20					25					30					
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Leu	Val	Tyr		
		35				40					45						
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Ile	Tyr		
	50				55			60									
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro		
65			70				75						80				
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met		
		85				90						95					
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly		
		100				105					110						

<223> Synthetic Construct

<400> 304

```
Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
20      25      30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35      40      45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50      55      60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65      70      75      80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85      90      95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100     105     110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
115     120     125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130     135     140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145     150     155     160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165     170     175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180     185     190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195     200     205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210     215     220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225     230     235     240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245     250     255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Ile Phe
260     265     270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275     280     285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290     295     300
Tyr Asn Tyr Ala Ala Gln Lys Val
305      310
```

<210> 305

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 305

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atgtcttttc accaagaatt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcgga ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaattagt gtatgcgttg aaactgccgg ggattatcca cctggacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
```

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gatatggagg agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccgatca tctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcgctgta ctggaataaa 900
ttgtatggca aatataacta cgccaccag aaagtgtaat ga 942

```

<210> 306

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 306

```

Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
20     25     30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Leu Val Tyr
35     40     45
Ala Leu Lys Leu Pro Gly Ile Ile His Leu Asp Ala Ala Glu Ile Tyr
50     55     60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65     70     75     80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85     90     95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100    105    110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
115    120    125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Glu
130    135    140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145    150    155    160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165    170    175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180    185    190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195    200    205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210    215    220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225    230    235    240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245    250    255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260    265    270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275    280    285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290    295    300
Tyr Asn Tyr Ala Thr Gln Lys Val
305    310

```

<210> 307
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 307
 atgtcttttc accaagaatt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac ctctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgcgag ggattatoca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctcgcaga ttaaaatgag tgactccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgttagtctt gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatatggagg agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tggaaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcagcaacac 600
 gatatcctgg tggaaagcata ttctcgcgtg ggcccgctgc ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
 gccagatct tactgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgcacagaac ctgttttctt tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tcgcctgta ctggaataaa 900
 ttgtatggca aacataacta cgcgcgccag aaagtgtaat ga 942

<210> 308
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 308
 Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Glu
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Glu Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190

Ile	Cys	Lys	Phe	Cys	Gln	Gln	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser		
	195						200					205					
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro		
	210					215					220						
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Thr	Glu		
225					230					235					240		
Ala	Gln	Ile	Leu	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val		
			245						250						255		
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe		
			260					265						270			
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly		
		275					280					285					
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys		
	290					295					300						
His	Asn	Tyr	Ala	Ala	Gln	Lys	Val										
305					310												

<210> 309
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 309
 atgtcttttc accaagaatt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcgcca ctggtacagc gtggtataaa agtgaagaaa ctgacgogac cttotccaat 120
 accctggttg aacaattagt gtatgcgttg aaactgcggg ggattatcca catcgacgcc 180
 gcggagattt atcgcacota ccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
 gcggacgggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
 gccagatca tctgcgctg ggtcactaaa cgoggtgtgc tgccagttac cacctottca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccagc aaagtataat ga 942

<210> 310
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 310
 Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Thr Leu Val Glu Gln Leu Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr

50	55	60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro		
65	70	75
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met		80
	85	90
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly		95
	100	105
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys		110
	115	120
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln		125
	130	135
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr		140
145	150	155
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln		160
	165	170
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly		175
	180	185
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser		190
	195	200
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro		205
	210	215
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu		220
225	230	235
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val		240
	245	250
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe		255
	260	265
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly		270
	275	280
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys		285
	290	295
Tyr Asn Tyr Ala Ala Gln Lys Val		300
305	310	

<210> 311
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 311
 atgtcttttc accaagaatt ttacacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgogac cttctccaat 120
 accctggttg aacaattagt gtatgcgttg aaactgccgg ggattatoca catcgacgcc 180
 gcgagatttt atcgcaccta cccggaagtg ggtaaagcac tgccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctecgcta ggccogctgc ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcoo tcgacotgac agcggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaacgcg tcgcgctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 312
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 312
 Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Thr Leu Val Glu Gln Leu Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 313
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 313

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atgtcttttc accaagaatt tttcacgctg aacaacggca ataaaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaattagt gtatgcgttg aaactgcogg ggattatcca catcgacgcc 180
gcggagatth atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaagagcct 240
cgtaacgcga tttttatcac ggataaatat tctccgcaga ttaaaatgag cgactccccct 300
goggaacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtthc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgcta ggcccgctgc ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaacogag 720
gcccagatca tcttgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccagc aaagtataat ga 942

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<210> 314

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 314

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Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
20        25        30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Leu Val Tyr
35        40        45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50        55        60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65        70        75        80
Arg Asn Ala Ile Phe Ile Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85        90        95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100       105       110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
115       120       125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130       135       140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145       150       155       160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165       170       175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180       185       190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195       200       205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210       215       220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Thr Glu
225       230       235       240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245       250       255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260       265       270

```

Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 315
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 315
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcgga ctggtacagc gtggtataaa cccgaagaaa ctgaogcgac cttctccaat 120
 agtctgggtg aacaaatcgt gtatgcgttg aaactgccgg ggattatoca catcgacgoc 180
 gcggagtggg atcgcaccta cccggaagtg ggtaaagcac tgccoctgac cgaagagcct 240
 cgtaacgcga tttttctgac ggataaatat tctcgcgaga ttaaaatgag tgactccoct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgtiga tttatatctg 360
 attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gatttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctcgcgtg ggcccgctgc ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
 gccagatca tctgcgcgtg ggtaactaaa cgcgggtgtg tgccagttac caccctottca 780
 aagcctcagc gcattagoga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct ggggtctggaa catgaacgc tgccgctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 316
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 316
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Trp Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln

130		135		140
Leu Tyr Lys Ser Gly	Lys Ala Lys Asn Ile Gly	Val Ser Asn Phe Thr		
145	150	155		160
Val Glu Asp Leu Gln Arg	Ile Leu Lys Val Ala Glu	Val Lys Pro Gln		
	165	170		175
Val Asn Gln Ile Glu Phe Ser Pro Phe	Leu Gln Asn Gln Thr Pro Gly			
	180	185		190
Ile Cys Lys Phe Cys Gln Glu His Asp	Ile Leu Val Glu Ala Tyr Ser			
	195	200		205
Pro Leu Gly Pro Leu Arg Lys Lys Thr	Ala Gln Asp Asp Ser Gln Pro			
	210	215		220
Phe Phe Glu Tyr Val Lys Glu Leu Ser	Glu Lys Tyr Asn Lys Ser Glu			
225	230	235		240
Ala Gln Ile Ile Leu Arg Trp Val Thr	Lys Arg Gly Val Leu Pro Val			
	245	250		255
Thr Thr Ser Ser Lys Pro Gln Arg Ile	Ser Asp Ala Gln Asn Leu Phe			
	260	265		270
Ser Phe Asp Leu Thr Ala Glu Glu Val	Asp Lys Ile Thr Glu Leu Gly			
	275	280		285
Leu Glu His Glu Pro Leu Arg Leu Tyr	Trp Asn Lys Leu Tyr Gly Lys			
	290	295		300
Tyr Asn Tyr Ala Ala Gln Lys Val				
305	310			

<210> 317

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 317

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atgtcttttc accaacagtt ttacacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcgga cttgtacagc gtggtataaa cccgaagaaa ctgacgogac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatoca catcgacggc 180
gcggagtggg atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaagagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctc 300
gcggacgggc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaagtg aatgggttaa gcttagaaga ggcttggaag 420
gatattggag agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgctgc ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcttgcgctg ggtaactaaa cgcgggtgtg tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccagc aaagtgtaat ga 942

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<210> 318

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 318

Met	Ser	Phe	His	Gln	Gln	Phe	Phe	Thr	Leu	Asn	Asn	Gly	Asn	Lys	Ile	
1				5					10					15		
Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Ala	Trp	Tyr	Lys	Pro	Glu	
			20					25					30			
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr	
		35					40					45				
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Trp	Tyr	
	50					55				60						
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro	
65				70					75					80		
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met	
				85					90					95		
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly	
			100					105					110			
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Ile	His	Ser	Pro	Leu	Val	Ser	Lys	
	115						120						125			
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln	
	130					135					140					
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr	
145					150				155					160		
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln	
				165				170						175		
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly	
	180							185					190			
Ile	Cys	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser	
	195						200					205				
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro	
	210					215					220					
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu	
225					230				235						240	
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val	
				245					250					255		
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe	
		260						265					270			
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly	
		275					280					285				
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys	
	290					295					300					
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val									
305					310											

<210> 319

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 319

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atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttctctgca aaaccaaaaca ccaggcattt gcaaattctg tcaggagcac 600

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gatatacctgg tggaagcata ttctccgctg ggcccgcgtgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccgatca tctgcgctg ggctactaaa cgcggtgtgc tgccagttac caoctottca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tgcacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaacgcg tgcgcctgtg gtggaataaaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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<210> 320

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 320

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50          55          60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85          90          95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100         105         110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
115         120         125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130         135         140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145         150         155         160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165         170         175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180         185         190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195         200         205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210         215         220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225         230         235         240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245         250         255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260         265         270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275         280         285
Leu Glu His Glu Pro Leu Arg Leu Trp Trp Asn Lys Leu Tyr Gly Lys
290         295         300
Tyr Asn Tyr Ala Ala Gln Lys Val
305          310

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<210> 321

<211> 942

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 321
atgtcttttc accaacagtt tttcacgctg aacaaaggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgaacgcac cttctocaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgcggg ggattatcca catcgacgcc 180
gcggagagtt atcgcaccta cccggaagtg ggtaaagcac tgcacctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtagtttgc gaaggaagtg aatggcttaa gcttagaaga ggcttgaaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgcctgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tccctgcctg ggtcactaaa cgcgggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
aggtatggca aatataacta cgccgccagc aaagtgtaat ga 942

<210> 322
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 322
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145 150 155 160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165 170 175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180 185 190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195 200 205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro

210		215		220
Phe Phe Glu Tyr Val	Lys Glu Leu Ser Glu	Lys Tyr Asn Lys Ser Glu		
225	230	235	240	
Ala Gln Ile Ile Leu	Arg Trp Val Thr	Lys Arg Gly Val Leu	Pro Val	
	245	250	255	
Thr Thr Ser Ser Lys	Pro Gln Arg Ile	Ser Asp Ala Gln	Asn Leu Phe	
	260	265	270	
Ser Phe Asp Leu Thr	Ala Glu Glu Val	Asp Lys Ile Thr	Glu Leu Gly	
	275	280	285	
Leu Glu His Glu Pro	Leu Arg Leu Tyr	Trp Asn Lys Arg	Tyr Gly Lys	
	290	295	300	
Tyr Asn Tyr Ala Ala	Gln Lys Val			
305	310			

<210> 323
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 323
 atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgttagtctt gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttt caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatcctgg tggaaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
 gccagatca tcttgcgctg ggctactaaa cgcgggtgtg tgccagttac cactcttca 780
 aagcctcagc gcattagcga tgcctcagaac ctgttttctt tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaacgcg tgogcctgta ctggaataaa 900
 aagtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

<210> 324
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 324
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80

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

<210> 325

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 325

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atgtcttttc accaacagtt tttaacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcgga ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgcogg ggattatcca catcgacgcc 180
gcggagtggg atcgcaccta cccggaagtg ggtaaagcac tgccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctcgcgaga ttaaaatgag tgactccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtagtttgc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gotgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaacaaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgctgc ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcttgccgtg ggtaactaaa cgcgggtgtg tgccagttac cactotcca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct ggtctggaa catgaaccgc tcgcgctgtg gtggaataaa 900
ttgtatggca aatataacta cgccgccagc aaagtgtaat ga 942

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<210> 326

<211> 313

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 326
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Trp Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145 150 155 160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165 170 175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180 185 190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195 200 205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210 215 220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225 230 235 240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245 250 255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260 265 270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275 280 285
Leu Glu His Glu Pro Leu Arg Leu Trp Trp Asn Lys Leu Tyr Gly Lys
290 295 300
Tyr Asn Tyr Ala Ala Gln Lys Val
305 310

<210> 327
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 327
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180

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gcgaggatggg atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccoct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttitga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcctgcgctg gggtcactaaa cgcgggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tcgcctgtg gtggaataaa 900
aagtatggca aatataacta cgccgccag aaagtgtaat ga 942

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<210> 328

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 328

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
          20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
          35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Trp Tyr
          50          55          60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
          85          90          95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
          100         105         110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
          115         120         125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
          130         135         140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145         150         155         160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
          165         170         175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
          180         185         190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
          195         200         205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
          210         215         220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225         230         235         240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
          245         250         255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
          260         265         270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
          275         280         285
Leu Glu His Glu Pro Leu Arg Leu Trp Trp Asn Lys Lys Tyr Gly Lys

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290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 329
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 329
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 atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
 agtctgggtg aacaattagt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagtggt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttatcac ggataaatat tctccgcaga ttaaaatgag cgactccoct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgttagtttc gaaggaagtg aatggcttaa gottagaaga ggcttggaaa 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgcta ggcccgtctg ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtataat ga 942

<210> 330
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 330
 Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Leu Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Trp Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Ile Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160

Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
				165					170					175	
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
			180					185					190		
Ile	Cys	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
		195					200					205			
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210					215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Thr	Glu
225					230					235					240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
			245						250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 331
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 331
 atgtctttt accaacagtt tttcacgctg aacaaoggoa ataaaatccc ggcgattgcc 60
 atcatcgga ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagtggt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctcgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatggtga tttatatctg 360
 attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgaaa 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaatctctg tcaggagcac 600
 gatatcctgg tggaagcata ttctcgcgtg ggcccgtgac ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
 gccagatca tcttgcgctg ggtcactaaa cgcgggtgtg tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgtg gtggaataaa 900
 gcgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

<210> 332
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 332
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu


```

aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgtg gtggaataaa 900
tcgtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<210> 334
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 334

Met	Ser	Phe	His	Gln	Gln	Phe	Phe	Thr	Leu	Asn	Asn	Gly	Asn	Lys	Ile
1				5					10					15	
Pro	Ala	Ile	Ala	Ile	Ile	Gly	Thr	Gly	Thr	Ala	Trp	Tyr	Lys	Pro	Glu
			20					25					30		
Glu	Thr	Asp	Ala	Thr	Phe	Ser	Asn	Ser	Leu	Val	Glu	Gln	Ile	Val	Tyr
		35					40					45			
Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Trp	Tyr
	50					55				60					
Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro
65				70					75					80	
Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met
			85					90					95		
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly
			100				105					110			
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Ile	His	Ser	Pro	Leu	Val	Ser	Lys
		115				120						125			
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln
	130					135					140				
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr
145				150					155					160	
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln
			165					170					175		
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly
		180						185					190		
Ile	Cys	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser
	195					200						205			
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
	210				215						220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225				230					235					240	
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
			245					250					255		
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
		260					265					270			
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
	275					280						285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Trp	Trp	Asn	Lys	Ser	Tyr	Gly	Lys
	290				295					300					
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val								
305					310										

<210> 335
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 335

```
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaaatccc ggcgattgcc 60
atcatcgcca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcgagagtgt atcgcaccta ccggaagtg ggtaaagcac tgccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccct 300
gcgacgggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tctcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct ggtctggaa catgaaccgc tcgcctgtg gtggaataaa 900
gagtatggca aatataacta cgccgccag aaagtgtaat ga 942
```

<210> 336

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 336

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

Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245 250 255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260 265 270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275 280 285
Leu Glu His Glu Pro Leu Arg Leu Trp Trp Asn Lys Glu Tyr Gly Lys
290 295 300
Tyr Asn Tyr Ala Ala Gln Lys Val
305 310

<210> 337

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 337

```

atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcgagatggg atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgct ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcttgcgctg ggctactaaa cgcggtgtgc tgccagttac caoctottca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgtg gtggaataaa 900
ccttatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

<210> 338

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 338

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

<220>

<223> Synthetic Construct

<400> 340

```
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
20      25      30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35      40      45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Trp Tyr
50      55      60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65      70      75      80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85      90      95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100     105     110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
115     120     125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130     135     140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145     150     155     160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165     170     175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180     185     190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195     200     205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210     215     220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225     230     235     240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245     250     255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260     265     270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275     280     285
Leu Glu His Glu Pro Leu Arg Leu Trp Trp Asn Lys Gln Tyr Gly Lys
290     295     300
Tyr Asn Tyr Ala Ala Gln Lys Val
305      310
```

<210> 341

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 341

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atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgoc 60
atcatcgcca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttotccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgocgg ggattatcca catcgacgcc 180
gcggagtggg atcgcaccta ccggaagtg ggtaaagcac tgccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
```

```

attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctgc ggaagaaaaa cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tctgcgctg ggtcactaaa cgcgggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ttggaataaa 900
gagtatggca aatataacta cgcgcgccag aaagtgtaat ga 942

```

<210> 342

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 342

```

Met Ser Phe His Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
20     25     30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35     40     45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Trp Tyr
50     55     60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65     70     75     80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85     90     95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100    105    110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
115    120    125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130    135    140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145    150    155    160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165    170    175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180    185    190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195    200    205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210    215    220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225    230    235    240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245    250    255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260    265    270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275    280    285
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Glu Tyr Gly Lys
290    295    300
Tyr Asn Tyr Ala Ala Gln Lys Val
305    310

```

<210> 343
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 343
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggogattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
ggtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagtggt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtctt gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttt caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccgatca tctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tcgcctgta ctggaataaa 900
gcgtatggca aatataacta cgcgcccgag aaagtgtaat ga 942

<210> 344
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 344
Met Ser Phe His Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1 5 10 15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
20 25 30
Glu Thr Asp Ala Thr Phe Ser Asn Gly Leu Val Glu Gln Ile Val Tyr
35 40 45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Trp Tyr
50 55 60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65 70 75 80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85 90 95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100 105 110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
115 120 125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130 135 140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145 150 155 160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165 170 175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly

			180					185					190				
Ile	Cys	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser		
		195					200					205					
Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro		
		210				215					220						
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu		
225					230					235					240		
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val		
			245						250					255			
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe		
		260						265					270				
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly		
		275					280					285					
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Ala	Tyr	Gly	Lys		
	290					295					300						
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val										
305					310												

<210> 345
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 345
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggogattgcc 60
 atcatcgcca ctggtacagc gtggtataaa ccogaagaaa ctgacgogac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgocgg ggattatcca catcgacgcc 180
 gcggagtggc atcgcaccta ccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatccttg tggaagcata ttctccgctg ggcccgctgc ggaagaaaac cgcgaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
 gccagatca tcttgcgctg ggtcactaaa cgoggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgtt ttggaataaa 900
 gagtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 346
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 346
 Met Ser Phe His Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45

[illegible]

<210> 348
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 348
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Trp Tyr
 50 55 60
 Gly Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Trp Trp Asn Lys Gln Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 349
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 349

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaaatccc ggcgattgcc 60
atcatcgcca ctggtacagc gtggtataaa ccogaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcgagatggg attcgacctt cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcgacaggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcttgccgtg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggcctggaa catgaaccgc tgcgcctgtg gtggaataaa 900
cagtatggca aatataacta cgccgccag aaagtgtaat ga 942
```

<210> 350

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 350

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


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

<210> 353
 <211> 943
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 353
 atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcgga ctggtacagc gtggtataaa ccgaagaaa ctgacgogac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgoc 180
 gcggagtggt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaagagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacgggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgtagtttgc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatattcctg tggaagcata ttctccgctg ggcccgctgc ggaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
 gccagatca tctgctgctg ggtcactaaa ccgggtgtgc tgccagttac cacctottca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgaacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggcctggaa catgaaccgc tgcgcctgtg gtggaataaa 900
 cagtatggca aatataacta cgccgccga gaaagtgtaa tga 943

<210> 354
 <211> 314
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 354

```
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Trp Tyr
50          55          60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85          90          95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100         105         110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
115         120         125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130         135         140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145         150         155         160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165         170         175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180         185         190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195         200         205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210         215         220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225         230         235         240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245         250         255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260         265         270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275         280         285
Leu Glu His Glu Pro Leu Arg Leu Trp Trp Asn Lys Gln Tyr Gly Lys
290         295         300
Tyr Asn Tyr Ala Ala Arg Glu Ser Val Met
305          310
```

<210> 355

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 355

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atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgaacgagac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgcogg ggattatcca catcgacgcc 180
gcgagatggt atcgcaacct cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggaacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
```

```

gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgc ggaagaaaac cacgcaggat 660
gacagccaac cttttttga gtaagtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccgatca tcctgcgctg ggtcactaaa cgcgggtgtg tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgaacctgac agcgggaagag 840
gttgataaaa tcacggagct gggcctggaa catgaaccgc tcgcctgtg gtggaataaa 900
cagtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<210> 356

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 356

```

Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
          20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
          35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Trp Tyr
          50          55          60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
          85          90          95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
          100         105         110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
          115         120         125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
          130         135         140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145         150         155         160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
          165         170         175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
          180         185         190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
          195         200         205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Thr Gln Asp Asp Ser Gln Pro
          210         215         220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225         230         235         240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
          245         250         255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
          260         265         270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
          275         280         285
Leu Glu His Glu Pro Leu Arg Leu Trp Trp Asn Lys Gln Tyr Gly Lys
          290         295         300
Tyr Asn Tyr Ala Ala Gln Lys Val
305          310

```

<210> 357

<211> 943
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 357
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
 agtctgggtg aacaaatcgt gtatgcgttg aaactgocgg ggattatcca catcgacgcc 180
 gcggagtggg atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatcctgg tgggaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggcctggaa catgaaccgc tgccgctgtg gtggaataaa 900
 cagtatggca aatataacta cgcgcgccca gaaagtgtaa tga 943

<210> 358
 <211> 314
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 358
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Trp Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205

Pro	Leu	Gly	Pro	Leu	Arg	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro
210						215					220				
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
225					230					235					240
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val
				245					250					255	
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe
			260					265					270		
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly
		275					280					285			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Trp	Trp	Asn	Lys	Gln	Tyr	Gly	Lys
	290					295					300				
Tyr	Asn	Tyr	Ala	Ala	Pro	Glu	Ser	Val	Met						
305					310										

<210> 359
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 359
 atgtcttttc accaagaatt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcgcca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaattagt gtatgcgttg aaactgocgg ggattatoca catcgacgcc 180
 gcggagtggg atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttatcac ggataaatat tctccgcaga ttaaaatgag cgaactccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgcta ggcccgctgc ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
 gccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctgga catgaaccgc tcgcgcctgta ctggaataaa 900
 gagtatggca aatataacta cgccgccagc aaagtataat ga 942

<210> 360
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 360
 Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Leu Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Trp Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro

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

<210> 361
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 361
 atgtcttttc accaagaatt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcgcca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaattagt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttatcac ggataaatat tctccgcaga ttaaaatgag cgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgttagtttc gaaggaagtg aatggcttaa gottagaaga ggcttggaaa 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatattcctg tggaagcata ttctccgcta ggcccgtgct ggaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
 gccagatca tctctgcgtg ggtcactaaa cgcgggtgtg tgccagttac cactcttca 780
 aagcctcagc gcattagoga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgtg gtggaataaa 900
 ttgtatggca aatataacta cgccgccagc aaagtataat ga 942

<210> 362

<211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 362
 Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Leu Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Ile Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Thr Glu
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Trp Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 363
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 363
 atgtcttttc accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120

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agtcctggttg aacaattagt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagtggt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttatcac ggataaatat tctccgcaga ttaaaatgag cgactccoct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcatccc cgtagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgcta ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac caoctttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggctctgaa catgaaccgc tcgcctgtg gtggaataaa 900
ttgtatggca aatataacta cgcgccag aaagtataat ga 942

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<210> 364

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 364

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Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
          20          25          30
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Leu Val Tyr
          35          40          45
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Trp Tyr
          50          55          60
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65          70          75          80
Arg Asn Ala Ile Phe Ile Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
          85          90          95
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
          100          105          110
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
          115          120          125
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
          130          135          140
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145          150          155          160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
          165          170          175
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
          180          185          190
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
          195          200          205
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
          210          215          220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Thr Glu
225          230          235          240
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
          245          250          255
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
          260          265          270
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
          275          280          285

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Leu Glu His Glu Pro Leu Arg Leu Trp Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 365
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 365
 atgtcttttt accaagaatt ttctacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaattagt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagtggg atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttatcac ggataaatat tctccgcaga ttaaaatgag cgactccct 300
 gcggacggto tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgtagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatcctgg tggaagcata ttctccgcta ggcccgtgc ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
 gccagatca tctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cactcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct ggtcttgaa catgaaccgc tgcgcctgtg gtggaataaa 900
 cagtatggca aatataacta cgccgccag aaagtataat ga 942

<210> 366
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 366
 Met Ser Phe His Gln Glu Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Leu Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Trp Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Ile Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr

[illegible]