

SEQUENCE LISTING



159159

<110> Giver, Lorraine Joan
Newman, Lisa Marie
Mundorff, Emily
Huisman, Gjal't W.
Jenne, Stephane J.
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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agtctgggtg	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	cgittgtttc	gaaggaagtg	aatggcttaa	gcttagaaga	ggcttggaag	420
gatattggagc	agttatacaa	aagtggtaaa	gctaaaaaca	tcgggggttc	caatttcgca	480
gtggaagacc	tgcaacgtat	cctgaaagtc	gctgaagtta	aacctcaggt	caaccagatt	540
gagttctctc	cgttcctgca	aaaccaaaca	ccaggcattt	ataaattctg	tcaggagcac	600
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gacagccaac	cattttttga	gtacgtcaaa	gaattgagcg	aaaaatacat	caaatccgag	720
gcccagatca	tcctgcgctg	ggctactaaa	cgcggtgtgc	tgccagttac	cacctcttca	780
aagcctcagc	gcattagcga	tgctcagaac	ctgttttcct	tcgacctgac	agcggaagag	840
gttgataaaa	tcacggagct	gggtctggaa	catgaaccgc	tgcgcctgta	ctggaataaa	900
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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



G00002

SeqList.TXT

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      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
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

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<210> 3
<211> 762
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetic Construct

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cagcacgatt catccgatga agatggctgg acgaaactgt tcgacgccac cgagaaagca 240
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atgagcagta ttgaggggtt cgtaggcgat ccgagcctgg gggcatacaa cgcttccaag 480
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gtgcgtgtca acacagtaca tccgggctat atcaagaccc cgctggtcga tgatctgccg 600
ggtgctgagg aagcgatgtc acagcgtagc aaaacccta tgggccacat tggcgaaaccg 660
aatgacatcg catatatctg tgtgtacctg gcatctaata aatcgaaatt tgcgacgggt 720
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<210> 4
<211> 253
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Construct

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SeqList.TXT

<400> 4

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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

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<210> 5

<211> 1050

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 5

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gatgatttca ttatgtctct gccggaagaa cagtacacct acggcctgcc gctgaccctg 180
ggtcatgaag gtgctggtaa agttgccgca gttggcgaag gtgttgaagg gttggatatt 240
ggcaccaatg tggttgtgta cggcccatgg ggttgtggca actggttgga ttgcagtcag 300
ggcctggaga actattgctc ccgtgcgcag gaactgggta ttaaccgcc tggctctgggt 360
gctccggggg ctttggcaga atttatgatt gtcgactcac cacgtcattt ggtcccatt 420
ggcgatttag accctgttaa aactgttccg ttgactgatg cgggcctgac cccataccat 480
gcaatcaaac gtcacctgcc gaaactgcgc ggcggtcttt atgcagtagt gatcggtagc 540
ggtggcctgg gccacgtggc tatccaactg ctgctcatt tatctgctgc aacggtgac 600
gccttggacg tttctgccga taaactggaa ctggctacca aagtcggcgc acatgaagta 660
gtcctgtctg ataaagatgc agcggagaat gtgcgtaaaa ttactggtag ccaaggtgca 720
gctttgggtg tggattttgt gggctatcag cctaccattg acaccgccat ggcagtggcg 780
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ggtttcttcc agagtcctta tgaggcatcg gttacggtag cttattgggg cgctcgtaat 900
gaactgatcg aattgatcga tctggcgcac ctggttattt tcgacattgc cgttgagacc 960
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1050

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<210> 6

<211> 349

<212> PRT

SeqList.TXT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 6

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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 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

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<210> 7

<211> 1050

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 7

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aaaaatgacg gtttgctgaa gaagttcaag tccaaccgga atctgagcat ggaaattgtg 180
gaagatattg cggcaccaaa cgccttcgat aaagtattcc agaaacatgg taaagaaatt 240
aaagtgggtc tgcatatcgc gtccccggtc catttcaaca ctaccgattt cgaaaaagac 300
ttactgatcc cggcggtaaa cggtaccaa tctattttgg aagcaattaa gaactatgcc 360
gcagacaccg tggaaaaaagt ggttattact tcatctgttg ccgcgttggc ctctccgggt 420

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SeqList.TXT

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gcgtgggact tcttgaaga aaaccagagc agcattaaat ttactctgtc cacgattaac 600
ccaggcttcg ttttgggtcc gcagctgttc gccgactcct tgcgcaatgg tattaactct 660
agcagtgcga ttattgcgaa cctgggtgtcg tataaattag gggataactt ctacaattat 720
agcggcccggt ttatcgacgt ccgtgacgtt tccaaagctc atctgctggc atttgagaaa 780
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<210> 8
 <211> 349
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 8

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			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
				85				90					95		
Phe	Glu	Lys	Asp	Leu	Leu	Ile	Pro	Ala	Val	Asn	Gly	Thr	Lys	Ser	Ile
			100				105					110			
Leu	Glu	Ala	Ile	Lys	Asn	Tyr	Ala	Ala	Asp	Thr	Val	Glu	Lys	Val	Val
		115					120					125			
Ile	Thr	Ser	Ser	Val	Ala	Ala	Leu	Ala	Ser	Pro	Gly	Asp	Met	Lys	Asp
	130				135						140				
Thr	Ser	Phe	Val	Val	Asn	Glu	Glu	Ser	Trp	Asn	Lys	Asp	Thr	Trp	Glu
145					150				155					160	
Ser	Cys	Gln	Ala	Asn	Ala	Val	Ser	Ala	Tyr	Cys	Gly	Ser	Lys	Lys	Phe
				165				170						175	
Ala	Glu	Lys	Thr	Ala	Trp	Asp	Phe	Leu	Glu	Glu	Asn	Gln	Ser	Ser	Ile
			180				185					190			
Lys	Phe	Thr	Leu	Ser	Thr	Ile	Asn	Pro	Gly	Phe	Val	Phe	Gly	Pro	Gln
	195						200					205			
Leu	Phe	Ala	Asp	Ser	Leu	Arg	Asn	Gly	Ile	Asn	Ser	Ser	Ser	Ala	Ile
	210				215					220					
Ile	Ala	Asn	Leu	Val	Ser	Tyr	Lys	Leu	Gly	Asp	Asn	Phe	Tyr	Asn	Tyr
225					230				235					240	
Ser	Gly	Pro	Phe	Ile	Asp	Val	Arg	Asp	Val	Ser	Lys	Ala	His	Leu	Leu
				245				250						255	
Ala	Phe	Glu	Lys	Pro	Glu	Cys	Ala	Gly	Gln	Arg	Leu	Phe	Leu	Cys	Glu
			260					265					270		
Asp	Met	Phe	Cys	Ser	Gln	Glu	Ala	Leu	Asp	Ile	Leu	Asn	Glu	Glu	Phe
		275					280					285			
Pro	Gln	Leu	Lys	Gly	Lys	Ile	Ala	Thr	Gly	Glu	Pro	Gly	Ser	Gly	Ser
	290				295						300				
Thr	Phe	Leu	Thr	Lys	Asn	Cys	Cys	Lys	Cys	Asp	Asn	Arg	Lys	Thr	Lys
305					310					315					320
Asn	Leu	Leu	Gly	Phe	Gln	Phe	Asn	Lys	Phe	Arg	Asp	Cys	Ile	Val	Asp
				325					330					335	
Thr	Ala	Ser	Gln	Leu	Leu	Glu	Val	Gln	Ser	Lys	Ser				
			340					345							

SeqList.TXT

<210> 9
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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 gcggcgctga aagcggggta ccgtcatatc gatgctgcgg ccatctatct gaatgaagaa 180
 gaagtcggcc gtgcgatcaa ggactccggt gttcctcgtg aagaaatttt tattaccacc 240
 aaactgtggg gcaccgaaca acgcgatcca gaagcagccc tgaacaaatc tctgaaacgt 300
 ctgggtctgg actatgtgga cctgtatctg atgcactggc cggtcctctt gaaaacagac 360
 cgtgtaactg acggtaacgt cctgtgcatc ccgaccctgg aagatggcac cgtggacatc 420
 gataccaaag agtgggaattt tattaaaaac tgggaaactga tgcaggaatt gccgaaaact 480
 ggtaagacca aagccgtcgg tgtgtccaat ttttccatca acaatatcaa agaactgctg 540
 gaatcgccaa ataacaaggc cgttccagca accaatcaga tcgagattca tccgttgctg 600
 ccgcaggatg aattaatcgc cttttgtaaa gaaaaaggca ttgtggtcga agcatatagc 660
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 gtattggcca agtccgtaaa tccggagcgt atcgtgtcga actttaagat ttttaccctg 840
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<210> 10
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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 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 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

SeqList.TXT

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

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

<220>
 <223> Synthetic Construct

<400> 11
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 gaagaaaacc gtgatagcgt gaaatttgag ctgacagcgg tcaaccagcgt ttacgttttt 600
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<210> 12
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 12
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 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

SeqList.TXT

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
 atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggatatcgg 60
 ttggcaatcg cccataaatt tctagaggag ggtgcgaaag tagttattac tggtcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
 cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
 ttccggcccg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
 ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgagggggt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgcgtgtca acacagtaca tccgggctat atcaagacct cgctgggtcga tgatctggaa 600
 ggtgctgagg aaatgatgtc acagcgtacg aaaaccctta tgggccacat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcatctgacg 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

SeqList.TXT

```

65          70          75          80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Val Ser
      85
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
      100
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
      115
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
      130
Glu Gly Phe Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
      145
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
      165
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Tyr Ile Lys
      180
Thr Pro Leu Val Asp Asp Leu Glu Gly Ala Glu Glu Met Met Ser Gln
      195
Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
      210
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
      225
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
      245

```

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

<220>
 <223> Synthetic Construct

```

<400> 15
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg aacaaatcgt gtacgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatatagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tggaaagcata ttctccgctg ggcccgcctg agaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag 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
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
      35
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
      40

```

SeqList.TXT

```

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

<220>
 <223> Synthetic Construct

```

<400> 17
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg 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
gcggacgggc tggatttagc attgaagaaa atgcgtagac attatgttga tttatatctg 360
ttacattccc cgtttggttc gaaggaagtg aatggcctaa gcttagaaga ggcttggaag 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tgaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgcaggat 660
gacagtcaac cttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cactcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

<210> 18
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>

SeqList.TXT

<223> Synthetic Construct

<400> 18

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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 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
agtctggttg atcaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtaccg attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatacctg tggaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840

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SeqList.TXT

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

<210> 20
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 20
 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 ctgacgcgac cttctccaat 120
 agtctggttg agcaaatacgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240

SeqList.TXT

```

cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatataa aactggtaaa gctaaaaaca tcgggggtttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tggaagcata ttctccgctg ggcccgcctg agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgccctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag 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

SeqList.TXT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 23

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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
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 ggcttggaag 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 ggcccgcctg agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggctctggat catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccagc aaagtgttaa 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

```

SeqList.TXT

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
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 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 tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gaggttcttc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatattcctgg tgggaagcata ttctccgctg ggcccgcctg agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
 gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 26
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 26
 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

SeqList.TXT

```

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

<220>
 <223> Synthetic Construct

```

<400> 27
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg agcaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagatct 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
gatatacctg tggaagcata ttctccgctg ggcccgcctg agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgcgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacaa cgccgcccag aaagtgtaat ga 942

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<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

```

SeqList.TXT

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      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 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
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc ttggtacaaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gcatgctgtg 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 ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tggaagcata ttctccgctg ggcccgcgtc agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

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

<220>
 <223> Synthetic Construct

```

<400> 30
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

```

SeqList.TXT

```

      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
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> 31
<211> 936
<212> DNA
<213> Artificial Sequence

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```

<220>
<223> Synthetic Construct

```

```

<400> 31
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacacc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac 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 tcgggggttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tgggaagcata ttctccgctg ggcccgcgtc agaagaaaac cgcgcaggat 660
gacagccaac cttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtg 936

```

```

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

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SeqList.TXT

<220>

<223> Synthetic Construct

<400> 32

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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 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

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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
gcggagattt atcgcaccta cccggaagtg ggtaaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag gttatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcctaa 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 tggaaagcata ttctccgctg ggcccgtgc agaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720

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SeqList.TXT

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gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtg 936

```

<210> 34
 <211> 312
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 34

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
		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

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac ctctccaat 120

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SeqList.TXT

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agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggttacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaagt caaccagatt 540
gagttctctc cgctcctgca aaaccaaaca ccagggtattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctgc agaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggaagag 840
gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtg 936

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<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

SeqList.TXT

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

<220>
 <223> Synthetic Construct

<400> 37
 atgtcttttt accaacagtt tttcacgctg 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 gaagggaagt aatggcctaa gcttagaaga ggcttggaag 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatattcctg tgggaagcata ttctccgctg ggcccgtgc agaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
 gcccgataga tcctgcgctg ggctactaaa cgcgggtgtc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag 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
 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 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
 Page 22

[illegible]

<220>
<223> Synthetic Construct

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

<220>
<223> Synthetic Construct

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SeqList.TXT

```

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
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agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac caaaaagcct 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 tcgggggttt caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac caccctctca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcttgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag 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

```

[illegible]

<210> 43
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 43							
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atcatcggca	ctggtagacg	ttgggtataaa	aatgaagaaa	ctgacgcgac	cttctcctat	120	
agtctggttg	aacaaatcgt	gtatgcggtg	aaactgcggc	ggattattcca	catcgacgcc	180	
cgggagattt	atcgccacct	cccggaagtg	ggtaaagcac	tgtccctgac	cgaaaagcct	240	
cgtaacgcga	tttttctgac	ggataaatat	tctccgcaga	ttaaaatgag	tgactccctt	300	
gcggacggtc	tggatttagc	attgaagaaa	atgggtacag	attatgttga	tttatatctg	360	
ttacattccc	cgtttgtttc	gaagggaagt	aatggcttaa	gcttagaaga	ggcttggaag	420	
gatatgggag	agttatacaa	aagtggtaaa	gctaaaaaca	tcgggggttc	caattttcga	480	
gtggaagacc	tgcacagtat	cttgaagctc	gctgaagtta	aacctcaggt	caaccagatt	540	
gagttctctc	cgttccctga	aaaccaaaca	ccaggcattt	ataaattctg	tcaggagcac	600	
gatatcctgg	tgggaagcata	ctctccgctg	ggcccgtctc	agaagaaaac	cgcgagggat	660	
gacagccaac	cattttttga	gtacgtcaaa	gaattgtgct	aaaaatacat	caaattccgag	720	
gcccagatca	tcctgcgctg	ggtcactaaa	cgcggtgtgc	tgccagttac	cacctcttca	780	
aagccctcag	gcatttagcga	tgctcagaac	ctgttttctc	tcgacctgac	agcgggaagag	840	
ttgtataaaa	tcacggagct	gggtctggaa	catgaaccgc	tgcgcctgta	ctggaataaa	900	
ttgtatggca	aatataacta	cgccgcccaq	aaagtgtaat	ga		942	

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<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

SeqList.TXT

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      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

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<400> 45
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atcatcgga ctggtacacg 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 gcttagaaga ggcttggaag 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgac ataagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagtt gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<210> 46
 <211> 313

SeqList.TXT

<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

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agtctgggtg	aacaaatcgt	gtatgcggtg	aaactgccgg	ggattatcca	catcgacgcc	180
gcggagattt	atcgcaccta	cccgaagtg	ggtaaagcac	tgctccctgac	cgaaaagcct	240
cgtaacgcga	tttttctgac	ggataaatat	tctccgcaga	ttaaaatgag	tgactcccct	300
gcggacggtc	tggatttagc	attgaagaaa	atgggtacag	attatgttga	tttatatctg	360
ttacattccc	cgtttggttc	gaaggaagtg	aatggcttaa	gcttagaaga	ggcttgga	420
gatattggagc	agttatacaa	aagtggtaaa	gctaaaaaca	tcgggggttc	caatttcgca	480
gtggaagacc	tgcaacgtat	cctgaaagtc	gctgaagtta	aacctcaggt	caaccagatt	540
gagttctctc	cgttcctgca	aaaccaaaca	ccaggcattt	ataaattctg	tcaggagcac	600

SeqList.TXT

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gatatcctgg  tggaagcata  ttctccgctg  ggcccgtgc  agaagaaaac  cgcgaggat  660
gacagccaac  cattttttga  gtacgtcaaa  gaattgagcg  aaaaatacat  caaatccgag  720
gcccgatca   tcctgcgctg  gatcactaaa  cgcggtgtgc  tgccagttac  cacctcttca  780
aagcctcagc  gcattagcga  tgctcagaac  ctgttttcct  tcgacctgac  agcggaagag  840
gttgataaaa  tcacggagct  gggctctggaa  catgaaccgc  tgcgcctgta  ctggaataaa  900
ttgtatggca  aatataacta  cgccgccag   aaagtgaat   ga              942

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<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

SeqList.TXT

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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 attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcctaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgatcctgca aaaccaaact ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tgaagcata ttctccgctg ggcccgcctg agaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcgggtgtg tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<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
			165					170					175		
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Ile	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											

SeqList.TXT

<210> 51
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga ttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcgca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cattcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tgggaagcata ttctccgctg ggcccgcctgc agaagaaaac cgcgaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
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<210> 52
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 52
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 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

SeqList.TXT

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

<210> 53
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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 agtctggttg aacaaatcgt gcatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
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 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
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 gatattcttg tgaagcata ttctccgctg ggcccgcctg agaagaaaac cgcgcaggat 660
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<210> 54
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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 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

SeqList.TXT

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

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

<220>
 <223> Synthetic Construct

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<400> 55
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agcctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
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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 tggaagcata ttctccgctg ggcccgcgtc agaagaaaac cgcgcaggat 660
gacagtcaac cttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
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ttgtatggca aatataactc cgccgcccg aaagtgtaat ga 942

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<210> 56
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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<400> 56
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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

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SeqList.TXT

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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		
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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										
					310												
305																	

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

<220>
 <223> Synthetic Construct

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 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaagggaagt aatggcttaa gcttagaaga ggcttggaaa 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
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 aagcctcagc gcattagcga tgctcagaac ctgttttctt tgcacctgac agcgggaagag 840
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 ttgtatggca aatataactc cgccgcccag 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
 Page 33

SeqList.TXT

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

<220>
 <223> Synthetic Construct

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 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
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SeqList.TXT

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

<220>
 <223> Synthetic Construct

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 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
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 290 295 300
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<210> 61
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
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 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
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SeqList.TXT

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<210> 62
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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 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

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

<220>
 <223> Synthetic Construct

SeqList.TXT

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<400> 63
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaaatccc ggcgattgcc 60
atcatcggga ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaataat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgittgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatc 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tggaagcata ttctccgctg ggcccgcgtc agaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggcttgga catgaaccgc tgcgcctgta 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
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 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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SeqList.TXT

305

310

<210> 65
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 65
 atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc ttggtacaaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gcatgcgttg 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 aatggcctaa 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 tgggaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgcaggat 660
 gacagtcaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

<210> 66
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 66
 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

SeqList.TXT

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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

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<400> 69
atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatgggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg agcaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacacc 180
gcgagagatt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggaaggct 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
gatatccttg tgggaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa 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
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

```

SeqList.TXT

65	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
					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
							215					220				
	Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu
						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								
						310										
	305															

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

<220>
 <223> Synthetic Construct

<400> 71
 atgtcttttc accaacagtt tttcacgctg aacaacggca 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 gcttagaaga ggcttggaag 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatacctg tggaaacata ttctccgctg ggcccgcctg agaagaaaac cgcacaggat 660
 gacagtcaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cactcttca 780
 aggccccagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
 gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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

<220>
 <223> Synthetic Construct

SeqList.TXT

<400> 72

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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 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

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatgggca ctggtacacg 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 gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaac ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tggaagcata ttctccgctg ggcccgcctg agaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgcgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccagc aaagtgtaat ga 942

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SeqList.TXT

<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
 atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatgggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg atcaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacgggtc tggattttagc attgaagaaa atgggtacag attatgttga tttatatctg 360

SeqList.TXT

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ttacattccc cgtttgtttc gaaggaagtg aatggcctaa gcttagaaga ggcttgga 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatc 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatattcctgg tggaagcata ttctccgctg ggcccgtgc agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 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

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										

<210> 77
 <211> 942
 <212> DNA
 <213> Artificial Sequence

SeqList.TXT

<220>

<223> Synthetic Construct

<400> 77

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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
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 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 ggcccgcctg agaagaaaac cgcgcaggat 660
gacagtcaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct ggggtctggat catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

<210> 78

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 78

```

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 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

```

SeqList.TXT
300

290 295
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
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatgggca ctggtacacg ttggtataaa 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 aatggcttaa gcttagaaga ggcttggaaa 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgc agaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggat catgaaccgc tcgcgcctga ctggaataaa 900
ttgtatggca aatataacta cgccgcccgag 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

SeqList.TXT

```

      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 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
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg 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 atgcgtagag attatggtga 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 aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcgtc agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctgga catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataactc cgccgcccag 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

```

SeqList.TXT

```

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
atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatgggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg agcaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctggc cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgcgtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcagg caaccagatt 540
gagttctctc cgttcctgca aaaccaaa caaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctcgtg ggcccgtgc agaagaaaac cgcgaggat 660
gacagtcaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgtg ggtcactaaa cgcggtgtgc tgccagttac cacccllcca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag 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

```

SeqList.TXT

```

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

```

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

<220>
 <223> Synthetic Construct

```

<400> 85
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatgggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg agcaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaagatgag tgactcccct 300
gcggacgggtc 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
gatatccttg tggaagcgta ttctccgctg ggcccgtgc agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcc tgcacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

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

<220>

SeqList.TXT

<223> Synthetic Construct

<400> 86

```

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 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

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga ttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatc 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840

```

SeqList.TXT

gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag 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
 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 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> 89
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 89
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctgggtt aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacacc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240

SeqList.TXT

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cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacgggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaagggaagt atgggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctg agaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacac caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<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

SeqList.TXT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 91

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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
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaaagt aatggcctaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgcgtc agaagaaaac cgcgcaggat 660
gacagtcaac catTTTTTga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagccccagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataactc cgccgcccag 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

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SeqList.TXT

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 cccggagggtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
 gatattggagc agttatacag aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta agcctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatacttg tgggaagcata ttctccgctg ggcccgcctgc agaagaaaac cgcgaggat 660
 gacagccaac cttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gcccgatca tcctgcgctg gggtactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct ggggtctggaa catgagccgc tgcgcctgta 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

SeqList.TXT

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      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

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

<220>
 <223> Synthetic Construct

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<400> 95
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcacctt cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc 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 aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tggaagcata ttctccgctg ggcccgtgc agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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

<220>
 <223> Synthetic Construct

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<400> 96
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 Leu His Ser Pro Phe Val Ser Lys

```

SeqList.TXT

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      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> 97
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 97
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 cgaaaggcct 240
cggaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtaccg 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
gatattcttg tgaagcata ttctccgctg ggcccgcctg agaagaaaac cgcgcaggat 660
gacagtcaac cttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<210> 98
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 98
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

```

SeqList.TXT

```

      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 Arg 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> 99
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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<400> 99
atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc ttggtacaaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg agcaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
gcggacggtc 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 tggaagcata ttctccgctg ggcccgtgc agaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcc tgcacctgac agcggaagag 840
gttgataaaa tcacggagct ggtctggaa catgaaccgc tgcgctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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

SeqList.TXT

<220>

<223> Synthetic Construct

<400> 100

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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 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 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> 101

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 101

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atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacacc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaagagcct 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 caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aaccccaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaac ccaggcattt atagattctg tcaggagcac 600
gatatccttg tggaagcata ttctccgctg ggcccgtgca agaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720

```

SeqList.TXT

```

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

```

<210> 102
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 102

```

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
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 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

```

atgtcttttc accaacagtt ttacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120

```

SeqList.TXT

```

agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc actgaagaaa 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 aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgcctg agaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcgggtgtg tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

<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

SeqList.TXT

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

<220>
 <223> Synthetic Construct

<400> 105
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagggtt 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
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatattcctg tgggaagcata ttctccgttg ggcccgcgtc ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
 gccagatca tcttgccgtg ggtcactaaa cgcggtgtgc tgccagttac cactcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcttgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 106
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 106
 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

SeqList.TXT

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> 107
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 107
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg gaactgccgg 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
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcgca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta agcctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gtaaattctg tcaggagcac 600
 gatatcctgg tgggaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
 gccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

<210> 108
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 108
 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 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 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

SeqList.TXT

```

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 tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacacg ttggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg 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
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgc agaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacac caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta 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

```

SeqList.TXT

```

      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> 111
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 111
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggga ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctgggtt 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 caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tggaaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgaat ga 942

```

<210> 112
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 112
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

```

SeqList.TXT

```

      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 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> 113

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 113

```

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 tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcctaa gcttagaaga ggcttggaag 420
gatattggac agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tggaagcata ttctccgctg ggcccgcgtc agaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgggcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcgt tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

<210> 114

<211> 313

SeqList.TXT

<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

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<210> 115

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 115

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgatgacgac ctctccaat 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 tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600

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SeqList.TXT

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gatatcctgg tggaagcata ttctccgctg ggcccgcgtgc agaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg gatcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcaag gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgaat ga 942

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<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

SeqList.TXT

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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 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
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagctta ttctccgctg ggcccgcctgc agaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgcgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<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										

SeqList.TXT

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

<220>
 <223> Synthetic Construct

<400> 119
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 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctgtttg 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
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tggaaagcata ttctccgctg ggcccgcctg agaagaaaac cgcgaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 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> 120
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 120
 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

SeqList.TXT

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

<220>
 <223> Synthetic Construct

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<400> 121
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atcatcggca 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 aatggcttaa gcttagaaga ggcttggaaa 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tggaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacatcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacccttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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

<220>
 <223> Synthetic Construct

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<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

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SeqList.TXT

				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

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agtcctggtg	aacaaatcgt	gtatgcgttg	aaactgccgg	ggattatcca	catcgacgcc	180
gcggagattt	atcgcaccta	cccgggaagt	ggtaaagcac	tgtccctgac	cgaaaagcct	240
cgtaacgcga	tttttctgac	ggataaatat	tctccgcaga	ttaaaatgag	tgactccctt	300
gcggacggtc	tggatttagc	attgaagaaa	atgggtacag	attatgttga	tttatatcta	360
ttacattccc	cgcttggttc	gaagggaagt	aatggcctta	gcttagaaga	ggcttggaag	420
gatatggagc	agttatacaa	aagtggtaaa	gctaaaaaca	tcgggggttc	caatttcaca	480
gtggaagacc	tgcaacgtat	cctgaaagtc	gctgaagtta	aacctcaggt	caaccagatt	540
gagttctctc	cgttctctga	aaaccaaaca	ccaggcattt	ataaattctg	ccaggagcac	600
gatatcctgg	tggaagcata	ttctccgctg	ggcccgcctg	agaagaaaac	cgcgagagat	660
gacagccaac	cattttttga	gtacgtcaaa	gaattgagcg	aaaaatacaa	caaatccgag	720
gcccagatca	tcctgcgctg	ggctactaaa	cgcggtgtgc	tgccagttac	cacctcttca	780
aagcctcagc	gcattagcga	tgctcagaac	ctgttttcct	tcgatctgac	agcgggaagag	840
gttgataaaa	tcacggagct	gggtctggaa	catgaaccgc	tgcgctgta	ctggaataaa	900
ttgtatggca	aatataacta	cgccgcccag	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		
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	

Sequence 1																		
				85									90					95
Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly			
Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Leu	His	Ser	Pro	Leu	Val	Ser	Lys			
Glu	Val	Asn	Gly	Leu	Ser	Leu	Glu	Glu	Ala	Trp	Lys	Asp	Met	Glu	Gln			
Leu	Tyr	Lys	Ser	Gly	Lys	Ala	Lys	Asn	Ile	Gly	Val	Ser	Asn	Phe	Thr			
Val	Glu	Asp	Leu	Gln	Arg	Ile	Leu	Lys	Val	Ala	Glu	Val	Lys	Pro	Gln			
Val	Asn	Gln	Ile	Glu	Phe	Ser	Pro	Phe	Leu	Gln	Asn	Gln	Thr	Pro	Gly			
Ile	Tyr	Lys	Phe	Cys	Gln	Glu	His	Asp	Ile	Leu	Val	Glu	Ala	Tyr	Ser			
Pro	Leu	Gly	Pro	Leu	Gln	Lys	Lys	Thr	Ala	Gln	Asp	Asp	Ser	Gln	Pro			
Phe	Phe	Glu	Tyr	Val	Lys	Glu	Leu	Ser	Glu	Lys	Tyr	Asn	Lys	Ser	Glu			
Ala	Gln	Ile	Ile	Leu	Arg	Trp	Val	Thr	Lys	Arg	Gly	Val	Leu	Pro	Val			
Thr	Thr	Ser	Ser	Lys	Pro	Gln	Arg	Ile	Ser	Asp	Ala	Gln	Asn	Leu	Phe			
Ser	Phe	Asp	Leu	Thr	Ala	Glu	Glu	Val	Asp	Lys	Ile	Thr	Glu	Leu	Gly			
Leu	Glu	His	Glu	Pro	Leu	Arg	Leu	Tyr	Trp	Asn	Lys	Leu	Tyr	Gly	Lys			
Tyr	Asn	Tyr	Ala	Ala	Gln	Lys	Val				300							

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<210> 125
<211> 942
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic Construct

<400> 125						
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agtctggttg	aacaaatcgt	gtatgcgttg	aaactgcggc	ggattattcca	catcgacgcc	180
cgcgagattt	atcgaccta	cccggaagtg	ggtaaagcac	tgtccctgac	cgagaagcct	240
cgtaaacgca	tttttctgac	ggataaatat	tctccgcaga	ttaaaatgag	tgactccctt	300
gcggacggtc	tggatttagc	attgaagaaa	atgggtacag	attatgttga	tttatatctg	360
atacattccc	cgtttgtttc	gaaggaagtg	aatggcttaa	gcttagaaga	ggcttggaag	420
gatatggagc	agttatacaa	aagtggtaaa	gctaaaaaca	tcggggtttc	caattttcac	480
gtggaagacc	tgcacagtat	ctgaaagtc	cgtaagttta	aacctcaggt	caaccagatt	540
gagttctctc	cgttcctgca	aacccaaca	caggcgattt	ataaattctg	tcaggagcac	600
gatatcctgg	tggaagcata	ttctccgctg	ggcccgctgc	agaagaaaac	cgcgagggat	660
gacagccaac	cattttttga	gtacgtcaaa	gaattgagcg	aaaaatacaa	caaattccgag	720
gcccagatca	tcctgcgcgt	ggtcactaaa	cgcggtgtgc	tgccagttac	cacctcttca	780
aagcctcagc	gcatttagcga	tgctcagaac	ctgtttttct	tcgacctgac	agcgggaagag	840
ttgtataaaa	tcacggagct	gggtctggaa	catgaaccgc	tgcgcctgta	ctggaataaa	900
gtgtatggca	aatataacta	gcgcgccag	aaagtgtaat	ga		942

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<210> 126
<211> 313
<212> PRT
<213> Artificial Sequence
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<220>
<223> Synthetic Construct

<400> 126
Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile

SeqList.TXT

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Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Phe Val Ser Lys
115
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195
Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275
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

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<210> 127

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 127

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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 tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tggaagcata ttctccactg ggcccgtgac agaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcgggtgtg tgccagttac cacctcttca 780
atgcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggaagag 840
gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
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SeqList.TXT

<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
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 atcatcggca ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctgggtg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacgggtc tggatttagc attgaagaaa atgggtacag attatgttga ttatatctg 360
 ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttctcg 480

SeqList.TXT

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gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
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gatatcctgg tggaagcata ttctccgctg ggcccgcctgc agaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaataccg gaaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<210> 130

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 130

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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 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

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<210> 131

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

SeqList.TXT

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<400> 131
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atcatcgga ctggtacacg 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 gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttctcc 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcttgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgac agaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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

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<220>
<223> Synthetic Construct

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<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

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305

310

<210> 133
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 133
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 atcatcgga ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcgagagatt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttggttc gaaggaagtg aatggcctaa gcttagaaga ggcttggaag 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcagc 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tgggaagcata ttctccgctg ggcccgcctc agaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacca aaaatccgag 720
 gccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct gggctctgga catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag 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 Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Gln Lys Ser Glu

SeqList.TXT

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

<220>
 <223> Synthetic Construct

<400> 135
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 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccatgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
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 gatatccttg tggaaagcata ttctccgctg ggcccgcctgc agaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
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<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

SeqList.TXT

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					165					170					175		
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				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

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agtctggttg	aacaaatcgt	gtatgcgttg	aaactgccgg	ggattatcca	catcgacgcc	180
gcggagatat	atcgcaccta	cccggaagtg	ggtaaagcac	tgtccctgac	cgaaaagcct	240
cgtaacgcga	tttttctgac	ggataaatat	tctccgcaga	ttaaaatgag	tgactcccct	300
gcggacggtc	tggatttagc	attgaagaaa	atgggtacag	attatgttga	tttatacttg	360
ttacattccc	cgtttggttc	gaaggaagtg	aatggcttaa	gcttagaaga	ggcttggaag	420
gatatggagc	agttatacaa	acgtggtaaa	gctaaaaaca	tcgggggttc	caatttcaca	480
gtggaagacc	tgcaacgtat	cctgaaagtc	gctgaagtta	aacctcaggt	caaccagatt	540
gagttctctc	cgttcctgca	aaaccaaaca	ccaggcattt	ataaattctg	tcaggagcac	600
gatatccttg	tggaagcata	ttctccgctg	ggcccgtgct	agaagaaaac	cgcgaggat	660
gacagccaac	cattttttga	gtacgtcaaa	gaattgagcg	aaaaatacaa	caaattccga	720
gcccagatca	tcctgcgctg	ggtcactaaa	cgcggtgtgc	tgccagttac	cacctcttca	780
aagcctcagc	gcattagcga	tgctcagaac	ctgttttcct	tcgacctgac	agcggaagag	840
gttgataaaa	tcacggagct	gggtctggaa	catgaaccgc	tgcgctgta	ctggaataaa	900
ttgtatggca	aatataacta	cgccgcccag	aaagtgtaat	ga		942

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

<220>
 <223> Synthetic Construct

<400> 138

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	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

SeqList.TXT

65	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					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								
						310										
	305															

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

<220>
 <223> Synthetic Construct

<400> 139
 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 tgactccctt 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaagggaagtg aatggcctaa 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 agaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaaaccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

<210> 140
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

SeqList.TXT

<400> 140

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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 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

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<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 ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggatggtc 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 aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgcctg agaagaaaac cgcgcaggat 660
gacagacacc ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggctactaaa cgcgggtgtg tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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SeqList.TXT

<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 ctgacgcgac cttctccaac 120
 agtctggttg aacaaatctt 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

SeqList.TXT

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ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 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 agaagaaaac cgcgcaggat 660
gtcagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctcggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgaat ga 942

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<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
		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	Val	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> 145
 <211> 942
 <212> DNA
 <213> Artificial Sequence

SeqList.TXT

<220>

<223> Synthetic Construct

<400> 145

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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 tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcctaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgcctgc agaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctggttttct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctcggaa catgaaccgc tgcgccagta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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<210> 146

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 146

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Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
1      5      10
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

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SeqList.TXT
300

290
Tyr Asn Tyr Ala Ala Gln
305 310

295
Lys Val

<210> 147
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 147
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca 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 tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgittgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttctcc 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aaccccaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgcgtc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 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
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

SeqList.TXT

210		215		220
Phe	Phe Glu Tyr Val Lys	Glu Leu Ser Glu Lys	Tyr Asn Lys Ser Glu	
225		230		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
 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 caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatacttg tgggaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgaggat 660
 gacagccaac ctttttttga 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 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

SeqList.TXT

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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 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

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<400> 151
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtacgcgttg gagctgccgg gaattatcca catcgacgcc 180
gcggagggtt 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 ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaac ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac cttttttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
gccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

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

<220>
 <223> Synthetic Construct

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<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

```

SeqList.TXT

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      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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atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggga ctggtacaaa gtggtataaaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg 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 aatggcctaa gcttagaaga ggcttggaag 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaacg ccaggcattt ataaattctg tcaggagcac 600
gatatacctg tgggaagcata ctctccgctg ggcccgcctg ggatgaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gagttgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

<210> 154

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

SeqList.TXT

<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

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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 tgactccctt 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcctaa gcttagaaga ggcttggaag 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagctc 600
gatattcctg tggaagcata ttctccgctg ggcccgcgtc gggagaaaac cgcgacggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cactcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggaagag 840

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SeqList.TXT

gttgataaaa tcacggagct gggctctggaa catgaaccgc tgccgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgaat ga 942

<210> 156
 <211> 313
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic Construct

<400> 156
 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 tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc ctggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctgggtg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240

SeqList.TXT

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cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacgggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcctaa 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 ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctgga catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagaataat ga 942

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<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

SeqList.TXT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 159

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg agcaaatcgt gtatgcgttg aaactgccgg ggattatcca cgtcgacgcc 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 aatggcctaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccgatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcgttagcga tgcctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<210> 160

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 160

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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 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

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SeqList.TXT

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
 atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcgga ctggtacagc ctggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gcatgcgttg 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 cgtttggttc gaagggaagt aatggcttaa gcttagaaga ggcttggaag 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttt caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatattcctg tggaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgaagag 840
 gttgataaaa tcacggagct ggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag aaagtgaat ga 942

<210> 162
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 162
 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 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

SeqList.TXT

```

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> 163
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 163
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca 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 tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgittgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcttgca aaaccaaaca ccagacattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggctactgaa cgcggtgtgc tgccagttac cacccttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgaat 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

```

SeqList.TXT

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      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
atcatcggga ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtcctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagggttt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgcttggttc gaagggaagt aatggcctaa 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 ggcccgcgtc ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag 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

```

SeqList.TXT

```

      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 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      180
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
      185      190      195
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
      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> 167
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 167
atgtcttttt 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 tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctagaaaca tcgggggttt caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaac ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgaggat 660
gacagccaac cgttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<210> 168
 <211> 313
 <212> PRT
 <213> Artificial Sequence

SeqList.TXT

<220>

<223> Synthetic Construct

<400> 168

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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 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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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 cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaac ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgat 720

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SeqList.TXT

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gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagccctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct ggtctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag 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 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
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 Page 98

SeqList.TXT

```

agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacagtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaaagt aatggcctaa 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 ggcccgtgc ggaagaaaac cgcgaggat 660
gacagccaac cttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgcctgttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgaat ga 942

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<210> 172

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 172

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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 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
      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> 173

SeqList.TXT

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

<220>
 <223> Synthetic Construct

<400> 173
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacacc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcgg 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 caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatcctgg tggaaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gcccatgatc tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac caccctctca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

<210> 174
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 174
 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 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

SeqList.TXT

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
 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 ggataaata tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttggttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 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 ggcccgcctg ggaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaataccg caaatccgag 720
 gccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggagag 840
 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

SeqList.TXT

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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

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

<220>
 <223> Synthetic Construct

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<400> 177
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcgga 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 tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgagagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tgaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag 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

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[illegible]

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<210> 179
<211> 942
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic Construct

<400>	179						
atgtcttttc	accaacagtt	tttcacgctg	aacaacggca	ataaaatccc	ggcgattgcc	60	
atcatcggca	ctggtacaaa	atggtataaa	aatgaagaaa	ctgacgcgac	cttctccaat	120	
agtctggttg	aacaatatcgt	gtatgcgttg	aaactgcggc	ggattattcca	catcgacgc	180	
cgggagattt	atcgcaccta	cccggaagt	ggtaaagcac	tgtccctgac	cgaaaagcct	240	
cgtaaacgca	tttttctgac	ggataaatat	tctccgcaga	ttaaaatgag	tgactccctt	300	
gcggacggct	tggatttagc	attgaagaaa	atgggtacag	attatgttga	tgatatcttg	360	
ttacattccc	cgtttgtttc	gaaggaagt	aatggcttaa	gcttagaaga	ggcttgga	420	
gatatggagc	ggttatatac	aagtggtaaa	gctaaaaaca	tcgggggttc	caatttcaca	480	
gtggaagacc	tgcaacgtat	cctgaaagtc	gctgaagtta	aacctcaggt	caaccagatt	540	
gagttctctc	cgttcctgca	aaaccaaaaca	ccaggcattt	ataaattctg	tcaggagcac	600	
gatatcctgg	tggaagcata	ttctccgctg	ggcccgtgc	ggaagaaaac	cgcgaggat	660	
gacagccaac	cattttttga	gtacgtcaaa	gaattgagcg	aaaaatacaa	caaattccgag	720	
gcccagatca	tcctgcgcgt	ggtcactaaa	cgcggtgtgc	tgccagttac	cacctcttca	780	
aagccctcagc	gcatttagcga	tgctcagaac	ctgttttccg	tcgacctgac	agcgggaagag	840	
gttgataaaa	tcacggagct	gggtctggaa	cattgaaccgc	tgcgccgtga	ctggaataaa	900	
ttgtatggca	aatataacta	cgccgcccag	aaagtgtaat	ga		942	

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<210> 180
<211> 313
<212> PRT
<213> Artificial Sequence
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<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

SeqList.TXT

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

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcgga ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac ctctccaat 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 aatggcctta gcttagaaga ggcttggaag 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tgaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgaggat 660
gacagccaac cttttttga gtacgtcaaa gaattgagcg aaaaatacga caaatccgag 720
gccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

<210> 182

<211> 313

SeqList.TXT

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 182
 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
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc 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 tgactccctt 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 aacctcagg caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600

SeqList.TXT

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gatatcctgg tggagcata ttctccgctg ggcccgcctgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccgatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataactc tgccgcccag aaagtgtaat ga 942

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<210> 184
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 184
 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 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

SeqList.TXT

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atgggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgacaccta 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 tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatccttg tgggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<210> 186

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 186

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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 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

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SeqList.TXT

<210> 187
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 187
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 atcatcggca ctggtacaaa atggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgaccta cccggaagtg ggtaaagcac tgtccctgac caaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgtttgtttc gaaggaaagt aatggcttaa gcttagaaga ggcttggaag 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatattcctg tggaagcata ttctccgctg ggcccgcctg ggaagaaagc cgcgcaggat 660
 gacggccaac catTTTTTga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggagag 840
 gttgataaaa tcacggagct ggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

<210> 188
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<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 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 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
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val

SeqList.TXT

245
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275
 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

<210> 189

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 189

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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 tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga 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 ataaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cactcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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<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

SeqList.TXT

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

<220>
 <223> Synthetic Construct

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<400> 191
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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 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
gatatccttg tgggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccatc ctttttttga 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 aatataacta cgccgcccag 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

```

SeqList.TXT

				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				
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	catcgacgcc	180
gcggagattt	atcgaccta	cccgggaagt	ggtaaagcac	tgtccctgac	caaaaagcct	240
cgtaacgcga	tttttctgac	ggataaatat	tctccgcaga	ttaaaatgag	tgactccctt	300
gcggacggtc	tggatttagc	attgaagaaa	atgggtacag	attatgttga	tttatatctg	360
ttacattccc	cgtttggttc	gaagggaagt	aatggcttaa	gcttagaaga	ggcttggaag	420
gatatggagc	agttatacaa	aagtggtaaa	gctaaaaaca	tcgggggttc	caatttcaca	480
gtggaagacc	tgcaacgtat	cctgaaaagtc	gctgaagtta	aacctcaggt	caaccagatt	540
gagttctctc	cgttcctgca	aaaccaaaca	ccaggcattt	ataaattctg	tcaggagcac	600
gatatacctg	tgggaagcata	ttctccgctg	ggcccgcctg	ggaagaaaac	cgcgaggat	660
gacagccaac	cattttttga	gtacgtcaaa	gaattgagcg	aaaaatacaa	caaattccag	720
gcccagatca	tcctgcgctg	ggtcactaaa	cgcggtgtgc	tgccagttac	cacctcttca	780
aagcctcagc	gcattagcga	tgctcagaac	ctgttttctt	tcgacctgac	agcggaagag	840
gttgataaaa	tcacggagct	gggtctggaa	catgaaccgc	tgcgccctga	ctggaataaa	900
ttatatggca	aataataact	tgccgcccat	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

SeqList.TXT

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1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Lys Trp Tyr Lys Asn Glu
20
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Lys Lys Pro
65
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
290
Tyr Asn Ser Ala Ala Gln Lys Val
305
310

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<210> 195

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 195

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atgtcttttc accaacagtt ttccacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc ctggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gctgagattt atcgaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gctgacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtttggttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tgggaagcata ttctccgctg ggcccgcgtg 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 aatataacta cgccgcccag aaagtgtaat ga 942

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SeqList.TXT

<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
 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 tgactcccct 300
 gcggacggtc tggatttggc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgtttgtttc gaaggaagtg aatggcctaa gcttagaaga ggcttggaag 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480

SeqList.TXT

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gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<210> 198
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 198
 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 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

SeqList.TXT

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<400> 199
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atcatcggga ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaata tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgittgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct ggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

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

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<220>
<223> Synthetic Construct

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<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    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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SeqList.TXT

305

310

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

<220>
 <223> Synthetic Construct

<400> 201
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 attatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaaagcac 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 tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gaggttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatatccttg tgggaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
 gacagccaac cttttttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag 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

SeqList.TXT

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 ggcgactgcc 60
 attatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtacgcgttg 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
 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 ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
 gccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag 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

SeqList.TXT

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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

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<400> 205
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctgggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagggttt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgittgtttc gaaggaagtg aatggcctaa gcttagaaga ggcttggaag 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatccttg tggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatcac tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

<210> 206
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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<400> 206
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

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SeqList.TXT

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65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
115
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275
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

```

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

<220>
 <223> Synthetic Construct

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<400> 207
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg gaactgccgg 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 ggcttggaag 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 ggcccgtctg 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 gggctctgga catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca gatataacta cgccgcccag aaagtgtaat ga 942

```

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

<220>
 <223> Synthetic Construct

SeqList.TXT

<400> 208

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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 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

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 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 tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaac ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgcctgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaataaccg caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctgaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgaat ga 942

```

SeqList.TXT

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

<220>
 <223> Synthetic Construct

<400> 211
 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 tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360

SeqList.TXT

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ttacattccc cgtttgtttc gaaggaagtg aatggccttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccagacattt ataaattctg tcaggagcac 600
gatatccttg 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 agcggaagag 840
gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataactc tgccgcccaa aaagtgtaat ga 942

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<210> 212

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 212

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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 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 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

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<210> 213

<211> 942

<212> DNA

<213> Artificial Sequence

SeqList.TXT

<220>

<223> Synthetic Construct

<400> 213

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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 cgtttgtttc 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 tggaaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaataccg caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa gcgggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag 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

```

SeqList.TXT
300

290 295
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
atcatcgga 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 tgactccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgittgtttc 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
gatatcctgg tggaaagcata ttctccgctg ggcccgtgc ggaagagaac cgcgcaggat 660
gacagccaac cattctttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag 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
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 Arg Thr Ala Gln Asp Asp Ser Gln Pro

SeqList.TXT

```

      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> 217
 <211> 942
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Construct

```

<400> 217
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 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 aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaagcata ctctccgctg ggcccgtgac ggaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagtac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

<210> 218
 <211> 313
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic Construct

```

<400> 218
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

```

SeqList.TXT

```

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> 219
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 219
atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattgtcca 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 gaagggaagt aatgggctta 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 ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggctcggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgaat ga 942

```

<210> 220
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 220
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 Val His Ile Asp Ala Ala Glu Ile Tyr

```

SeqList.TXT

```

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          100
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
105          110          115          120
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
125          130          135          140
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
145          150          155          160
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
165          170          175          180
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
185          190          195          200
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
205          210          215          220
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
225          230          235          240
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
245          250          255          260
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
265          270          275          280
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
285          290          295          300
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
305          310
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
310          315          320          325
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
325          330          335          340
Tyr Asn Tyr Ala Ala Gln Lys Val
340          345          350          355

```

<210> 221
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 221
atgtcttttc 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 cgtttgtttc gaaggaagtg aatggcctaa gcttagaaga ggcttggaag 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 cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggctctgga catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgaat ga 942

```

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

<220>

SeqList.TXT

<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

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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 tgactccctt 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatattgagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta agcctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgcaggat 660
gacagccaac cattctttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccgatca tcctgcgctg ggtcactaga cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840

```

SeqList.TXT

gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatacaacta cgccgcccag 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 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
 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

SeqList.TXT

```

cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacgggc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttggttc gaaggaaggg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttccctga aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccg 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
agtctgggtg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc 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 tgggaagcata ttctccgctg ggcccgcgtc ggaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggcgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
gttgataaaa tcacggagct ggtctgggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag 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

```

SeqList.TXT

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 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 cgtttggttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccataca ccaggcattt ataaattctg tcaggagcac 600
 gatatccttg tgggaagcata ttctccgctg ggcccgcgtg ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcgggtgtg tgccagttac cacctctca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagcg ggtctggaa catgaaccgc tgcgcctgta ctggaataag 900
 ttgtatggca aatataacta cgccgcccag 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

SeqList.TXT

```

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 tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa atggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaaccac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc 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 aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
ggatctcttg tgggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

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

<220>
 <223> Synthetic Construct

```

<400> 232
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

```

SeqList.TXT

```

      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
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 tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaaagt 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 ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacca cgccgcccag aaagtgtaat ga 942

```

<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

```

SeqList.TXT

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

<210> 235
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 235
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 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 cgtttggttc 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
 gatatacttg tgaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgcaggat 660
 gacagccaac cttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcctgcgctg ggctactaaa cgcgggtgtg tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtttgga catgaaccgc tgcgctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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

SeqList.TXT

<220>

<223> Synthetic Construct

<400> 236

```

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 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

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaaagcac 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 caatttctcc 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaacaaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720

```

SeqList.TXT

```

gccagatca tcctgcgctg ggtcactaaa cgcgggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tgcacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag 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 ttctacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120

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SeqList.TXT

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gcggagattt atcgacaccta cccggaagtg ggcaaagcac 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 aaccggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgcctg 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 gggctctggag 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	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

SeqList.TXT

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

<220>
 <223> Synthetic Construct

<400> 241
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 atcatcggca 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 tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacgg attatgttga tttatatctg 360
 attcattccc cgtttgtttc 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 tgggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgcccagaac ctgttttcct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

<210> 242
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 242
 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

SeqList.TXT

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

<220>
 <223> Synthetic Construct

<400> 243
 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 caaaaagcct 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 tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaaca ccaggcattt ataaattctg tcaggagcac 600
 gatattcctg tgggaagcata ttctccgctg ggcccactgc ggaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacgg caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataactc tgccgcccag 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

SeqList.TXT

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<210> 245
<211> 942
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic Construct

<400>	245					
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agtctgggtt	aacaaatcgt	gtatgcgttg	aaactgccgg	ggattattcca	catcgacgcc	180
gcggagattt	atcgcacctt	cccggaagt	ggtaaagcac	tgtccctgac	cgaaaagcct	240
cgtaacgcga	tttttctgac	ggataaaat	tctccgcaga	ttaaaatgag	tgactccccc	300
gcggacggtc	tggatttagc	attgaagaaa	atgggtacag	attatgttga	tttatatctg	360
attcattccc	cgtttgttac	gaagggaagt	aatggcttaa	gcttagaaga	ggcttggaag	420
gatatggagc	agttatacaa	aagtggtaaa	gctaaaaaca	tcgggggttc	caatttcaca	480
gtggaagacc	tgcaacgtat	cctgaaagtc	gctgaagtta	aacctcaggt	caaccagatt	540
gagtttctct	cgttcctgca	aaaccaaaca	ccaggcattt	gcaaatctct	tcaggagcac	600
gatatcctgg	tggaagcata	ttctccgctg	ggccccgtgc	ggaagaaaac	cgcgagggat	660
gacagccaac	cattttttga	gtacgtcaaa	gaattgagcg	aaaaatacaa	caaatccgag	720
gcccagatca	tcttcgctg	ggtcactaaa	cgcggttgct	tgccagttac	cacctcttca	780
aagcctcagc	gcattagcga	tgctcagaac	ctgttttctc	tcgacctgac	agcgaagag	840
gttgataaaa	tcacggagct	gggtctggaa	catgaaccgc	tcgcctgta	ctggaataaa	900
ttgtatggca	aatataacta	cggccgccag	aaagtgtaat	ga		942

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

SeqList.TXT

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      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

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<210> 247
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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<400> 247
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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
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
gatatccttg tggagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cactcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct ggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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

<220>
 <223> Synthetic Construct

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<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

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SeqList.TXT

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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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atcatcggga	ctggtacaaa	gtggtataaa	agtgaagaaa	ctgacgcgac	cttctccaat	120
agtctggttg	aacaaatcgt	gtacgcgttg	aagctgcccgg	ggattatcca	catcgacgcc	180
gcggagattt	atcgcaccta	cccggagtg	ggtaaagcac	tgtccctgac	cgaaaagcct	240
cgtaacgcga	tttttctgac	ggataaatat	tctccgcaga	ttaaaatgag	tgactcccct	300
gcggacgggtc	tggatttagc	attgaagaaa	atgggtacag	attatgttga	tttatatctg	360
attcattccc	cgtttgtttc	gaaggaagtg	aatggcttaa	gcttagaaga	ggcttggaaa	420
gatatggagc	agttatacaa	aaccggtaaa	gctaaaaaca	tcgggggttc	caatttcaca	480
gtggaagacc	tgcaacgtat	cctgaaaagtc	gctgaagtta	aacctcaggt	caaccagatt	540
gagttctctc	cgttcctgca	aaaccaaaca	ccaggcattt	gcaaattctg	tcaggagcac	600
gatatacctg	tgggaagcata	ttctccgctg	ggcccgcctg	ggaagaaaac	cgcgagggat	660
gacagccaac	cattttttga	gtacgtcaaa	gaattgagcg	aaaaatacaa	caaattccag	720
gcccagatca	tcctgcgctg	ggctactaaa	cgcggtgtgc	tgccagttac	cacctcttca	780
aagcctcagc	gcattagcga	tgctcagaac	ctgttttctt	tcgacctgac	agcgggaagag	840
gttgataaaa	tcacggagct	gggtctggaa	catgaaccgc	tgcgccctgta	ctggaataaa	900
ttgtatggca	aataataacta	cgccgcccag	aaagtgtaat	ga		942

<210> 250

<211> 313

SeqList.TXT

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 250

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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 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 tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggcaaagcac 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 cgttcctgca aaaccaaaaca ccaggcattt gcaaattctg tcaggagcac 600

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SeqList.TXT

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gatatcctgg  tggaagcata  ttctccgctg  ggcccgtgc  ggaagaaaac  cgcgcaggat  660
gacagccaac  ctttttttga  gtacgtcaaa  gaattgagcg  aaaaatacgg  caaatccgag  720
gcccagatca  tcctgcgctg  ggctactaaa  cgcggtgtgc  tgccagttac  cacctcttca  780
aagccitcagc  gcattagcga  tgctcagaac  ctgttttcct  tcgacctgac  agcgggaagag  840
gttgataaaa  tcacggagct  gggctctggaa  catgaaccgc  tgcgcctgta  ctggaataaa  900
ttgtatggca  aatataacta  cgccgcccag  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

SeqList.TXT

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacaaa gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatatagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtttggttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttctcc 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaatctctg tcaggagcac 600
gatatccttg tggaaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag 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

```

SeqList.TXT

<210> 255
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 255
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc ctggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtacgcgttg aagctgccgg 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 aatggcctaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttctcc 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 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    180
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
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

```

SeqList.TXT

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> 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 gtacgcgctg aagctgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggttacag attatgttga tttatatctg 360
 attcattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
 gatattggagc agttatacaa aaccggtaaa gctaaaaaca tcgggggttc caatttctcc 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatccttg tggaaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa caaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccg aaagtgtaat ga 942

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

<220>
 <223> Synthetic Construct

<400> 258
 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 Ser
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln

SeqList.TXT

```

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> 259
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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<400> 259
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggga 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 tgactccctt 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgttagtttc gaagggaagt aatggcctta gcttagaaga ggcttggaag 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 ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccgatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<210> 260
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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<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      80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met

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SeqList.TXT

				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	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> 261
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 261
 atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctgggtt aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 ttacattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttt caatttcaca 480
 gtggaagacc tgcaacgtat cctgcgtgtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaaca ccaggcattt acaaatcttg tcaggagcac 600
 gatattcctg tggaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgcctcagaac ctgttttcct tcgacctgac agcggagag 840
 gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 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

SeqList.TXT

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1          5          10          15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Ser Glu
20
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
35
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
50
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100
Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Leu Val Ser Lys
115
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145
Val Glu Asp Leu Gln Arg Ile Leu Arg Val Ala Glu Val Lys Pro Gln
165
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275
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

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<210> 263

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 263

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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 aatggcctaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt acaaattctg tcaggagcac 600
gatatccttg tgaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaataccg caaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggagag 840
gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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SeqList.TXT

<210> 264
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 264
 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
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 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 ttatatctg 360
 attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480

SeqList.TXT

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gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctgc ggatgaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

<210> 266
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 266

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

SeqList.TXT

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<400> 267
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 cgttcgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aaccggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgcgtgtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt acaaattctg tcaggagcac 600
gatatcctgg tggagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

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

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<220>
<223> Synthetic Construct

```

```

<400> 268
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

<210> 269
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 269
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
accatcgga cttgtacagc 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 cgttagtttc gaagggaagt aatggcctaa gcttagaaga ggcttggaag 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 ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctgga 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
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 Ser Gln Pro
210      215      220
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu

```

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

<220>
<223> Synthetic Construct

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

<220>
<223> Synthetic Construct

Page 156

SeqList.TXT

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145      150      155      160
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Arg Lys Ser Glu
225
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275
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

```

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

<220>
 <223> Synthetic Construct

<400> 273

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaaagcac 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 acaaattctg tcaggagcac 600
gatatccttg tggaaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagcaaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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

<220>
 <223> Synthetic Construct

<400> 274

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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

```

SeqList.TXT

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65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
      85
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
      100
Thr Asp Tyr Val Asp Leu Tyr Leu His Ser Pro Leu Val Ser Lys
      115
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
      130
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
      145
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
      165
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
      180
Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
      195
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
      210
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
      225
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
      245
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
      260
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
      275
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

```

<210> 275
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 275
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 ggataaata tctccgcaga ttaaaatgag tgactcccct 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 cgttcctgca aaaccaaaac ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

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

<220>
 <223> Synthetic Construct

SeqList.TXT

<400> 276

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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 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 tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgacaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc 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
gatatccttg tgggaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

SeqList.TXT

<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
 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> 279
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 279
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaaatccc ggcggctcgcc 60
 atcatcgcca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg atcaaatcgt gtatgcgttg aaactgccgg ggatcatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtcgtgcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggaattagc attgaagaaa atgggtacag attatgttga tttatatctg 360

SeqList.TXT

```

attcattccc cgtagtttc gaaggaagtg aatggcctaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgctcctgca aaaccaaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgcctgc ggaagaaaac cgcgagcat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccgagtgga tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggac catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccagc aaagtgtaat ga 942

```

<210> 280

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 280

```

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

SeqList.TXT

<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 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 tcagcaacac 600
gacatcctgg tgggaagcata ttctccgctg ggcccgcctgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac atcttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<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

```

SeqList.TXT
300

290 295
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
atgtcttttt accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggga ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
accctgggtg aacaattagt gtatgcgttg aaactgccgg gggttatcca catcgacgcc 180
gcggagattt atcgaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaaagt aatggcttaa gcttagaaga ggcttggaag 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcagcaacac 600
gatatccttg tgggaagcata ttctccgctg ggcccgcgtc ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag 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 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

SeqList.TXT

```

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
atgtcttttc accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
accctggttg aacaattagt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta ccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ctgcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagg agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcagcaacac 600
gatatccttg tggaaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
gccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac atcttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccagc aaagtgtaat ga 942

```

<210> 286
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 286
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

```

SeqList.TXT

```

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 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
gatatccttg tggaaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
gccagatct tactgcgctg ggtcactaaa cgcggtgtgc tgccagttac cactcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta 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

```

SeqList.TXT

```

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
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> 289
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 289
atgtcttttt accaagaatt 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
attcattccc 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
gatatccttg tggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tacgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgaat ga 942

```

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

<220>

SeqList.TXT

<223> Synthetic Construct

<400> 290

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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 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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atgtcttttc accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
accctgggtg 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 cgttagtttc gaaggaagtg aatggcctaa 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 ggcccgtgc ggaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccgatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac atcttttctc tcgacctgac agcgggaagag 840

```

SeqList.TXT

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

<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
 atgtcttttc accaagaatt 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

SeqList.TXT

```

cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgtagtttc 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
gatattcctgg tgggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcc agaaatacaa taaaaccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aaacctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag 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

SeqList.TXT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 295

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atgtcttttc accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca cctggacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacgggtc tggattttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ctgcattccc cgttagtttc gaaggaagtg aatggcctaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcagcaacac 600
gatatcctgg tggaagcata ttctccgtgc ggcccgtgc ggaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatct tactgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta 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

```

SeqList.TXT

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
 atgtcttttt accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 agtctgggtg aacaattagt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 cgcgacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgtagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttt caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcagcaacac 600
 gatatcctgg tggaagcata ttctccgctg ggcccgtgc ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
 gccagatctt tactgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag aaagtgaat 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

SeqList.TXT

```

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
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
atgtcttttc accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca cctggacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttatcac ggataaatat tctccgcaga ttaaaatgag tgactcccct 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 aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
gcccagatct tactgcgctg ggtcactaaa cgcgggtgtc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccg 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

```

SeqList.TXT

```

      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

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<210> 301
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 301
atgtcttttc accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg aacaattagt 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 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
gatatccttg tgggaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac caccctctca 780
aagcctcagc gcattagcga tgtcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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<210> 302
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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<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

```

SeqList.TXT

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      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

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<210> 303
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 303
atgtcttttt accaagaatt tttcacgctg aacaacggca ataaaaatccc 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 cgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc 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
gatatacctg tggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac atcttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<210> 304
 <211> 313
 <212> PRT
 <213> Artificial Sequence

SeqList.TXT

<220>

<223> Synthetic Construct

<400> 304

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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
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 tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca 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 attatggtga tttatatctg 360
attcattccc cgtagtttgc gaagggaagt aatgggctta gcttagaaga ggcttggaag 420
gatatggagg 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 cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgat 720

```

SeqList.TXT

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gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccacccag 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

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atgtcttttc accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120

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SeqList.TXT

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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 cgtagtttcc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagg agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
gtggaagacc tggaaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcagcaacac 600
gatatcctgg tggaaagcata ttctccgctg ggcccgtgct ggaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
gcccagatct tactgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aacataacta cgccgcccag 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

SeqList.TXT

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

<220>
 <223> Synthetic Construct

<400> 309
 atgtcttttt accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 accctggttg aacaattagt 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 cgttagtttc gaagggaagt aatggcctaa 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 tgggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
 gcccgataga tcctgcgctg ggctactaaa cgcgggtgtg tgccagttac cacctcttca 780
 aagccitacg gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgccag 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 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 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

SeqList.TXT

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

<220>
 <223> Synthetic Construct

<400> 311
 atgtcttttc accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc gtggtataaa agtgaagaaa ctgacgcgac cttctccaat 120
 accctgggtg aacaattagt 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
 attcattccc cgttagtttc gaaggaagtg aatggcctaa gcttagaaga ggcttggaag 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatcctgg tggaaagcata ttctccgcta ggcccgcctg ggaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
 gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag 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

SeqList.TXT

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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

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

<220>
 <223> Synthetic Construct

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<400> 313
atgtcttttc accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaattagt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttatcac ggataaatat tctccgcaga ttaaaatgag cgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaagggaagt 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 tgaagcata ttctccgcta ggcccgtgc ggaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtataat ga 942

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<210> 314
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 314
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

```

SeqList.TXT

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      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
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
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

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<400> 315
atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagtggt atcgcaccta cccggaagtg ggtaaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaata tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaac ccaggcattt gcaaattctg tcaggagcac 600
gatatccttg tggaaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<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

```

SeqList.TXT

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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 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 tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcgga ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagtggg 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 ggcttggaag 420
gatattggac agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatattcttg tggaaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcag tgcacagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct ggggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<210> 318

<211> 313

SeqList.TXT

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 318

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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 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> 319
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 319

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atgtcttttc accaacagtt tttcacgctg 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 cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatattgagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600

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SeqList.TXT

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gatatcctgg  tggaagcata  ttctccgctg  ggcccgcgtgc  ggaagaaaac  cgcgcaggat  660
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gcccagatca  tcctgcgctg  ggtcactaaa  cgcggtgtgc  tgccagttac  cacctcttca  780
aagcctcagc  gcattagcga  tgctcagaac  ctgttttcct  tcgacctgac  agcggaagag  840
gttgataaaa  tcacggagct  gggctctggaa  catgaaccgc  tgcgcctgtg  gtggaataaa  900
ttgtatggca  aatataacta  cgccgcccag  aaagtgtaat  ga              942

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<210> 320
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 320
 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

<210> 321
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 321

SeqList.TXT

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgacaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttccctga aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tgggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
aggtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<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

SeqList.TXT

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

<220>
 <223> Synthetic Construct

<400> 323
 atgtcttttc accaacagtt tttcacgctg 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 ggcttggaag 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc 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 tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 aagtatggca aatataacta cgccgcccag 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

250

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SeqList.TXT

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

<220>
 <223> Synthetic Construct

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<400> 327
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg 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 ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagtttcttc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatacttg tggaaagcata ttctccgctg ggcccgtgac ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcctgcgctg gggtactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgtg gtggaataaa 900
aagtatggca aatataacta cgccgcccag aaagtgtaat ga 942

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<210> 328
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 328
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

```

SeqList.TXT

			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		
		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
 atgtcttttc accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaattagt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagtggg atcgaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttatcac ggataaatat tctccgcaga ttaaaatgag cgactcccct 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 aacctcaggt caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatacttg tggaagcata ttctccgcta ggcccgtgc ggaagaaaac cgcgcaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
 gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cactcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
 ttgtatggca aatataacta cgccgcccag 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

SeqList.TXT

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1      5      10      15
Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Ala Trp Tyr Lys Pro Glu
20
Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Leu Val Tyr
35
Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Trp Tyr
50
Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
65
Arg Asn Ala Ile Phe Ile Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
85
Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
100
Thr Asp Tyr Val Asp Leu Tyr Leu Ile His Ser Pro Leu Val Ser Lys
115
Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
130
Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145
Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
165
Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
180
Ile Cys Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
195
Pro Leu Gly Pro Leu Arg Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
210
Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Asn Lys Thr Glu
225
Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
245
Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
260
Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
275
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

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

<220>
 <223> Synthetic Construct

```

<400> 331
atgtcttttt accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagtggt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtctc 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 ggcccgcgtc ggaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgtg gtggaataaa 900
gcgtatggca aatataacta cgccgccag aaagtgtaat ga 942

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SeqList.TXT

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

<210> 333
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 333
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg 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 aatggcctaa gcttagaaga ggcttggaag 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480

SeqList.TXT

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gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatacctgg tggaagcata ttctccgctg ggcccgcctgc ggaagaaaac cgcgaggat 660
gacagccaac catTTTTTga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgtg gtggaataaa 900
tcgtatggca aatataacta cgccgcccag 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

SeqList.TXT

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<400> 335
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctgggtg aacaaatcgt gtatgcgttg aaactgccgg 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 ggcttggaag 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 ggcccgcgtc ggaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgtg gtggaataaa 900
gagtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

```

<210> 336
<211> 313
<212> PRT
<213> Artificial Sequence

```

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<220>
<223> Synthetic Construct

```

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<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 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

```

SeqList.TXT

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
 gcggagtggt atcgcaccta cccggaagtg ggtaaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
 attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
 gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaaagtc gctgaagtta aacctcaggt caaccagatt 540
 gagtctcttc cgttcctgca aaaccaaaca ccaggcattt gcaaatcttg tcaggagcac 600
 gatatccttg tggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
 gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
 gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
 gttgataaaa tcacggagct ggtcttgga 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
 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

SeqList.TXT

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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

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<210> 341
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

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<400> 341
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg 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 ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatccttg tgggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cactcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ttggaataaa 900
gagtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<210> 342
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

```

<400> 342
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

```

SeqList.TXT

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65          70          75          80
Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
Ser Asp Ser Pro 85 Ala Asp Gly Leu Asp 90 Leu Ala Leu Lys Lys 95 Met Gly
Thr Asp Tyr Val 100 Asp Leu Tyr Leu 105 Ile His Ser Pro Leu Val Ser Lys
Glu Val Asn Gly Leu Ser Leu 120 Glu Glu Ala Trp Lys 125 Asp Met Glu Gln
Leu Tyr Lys Ser Gly Lys 135 Ala Lys Asn Ile Gly Val Ser Asn Phe Thr
145 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
Val Asn Gln Ile 165 Glu Phe Ser Pro Phe 170 Leu Gln Asn Gln Thr Pro Gly
Ile Cys Lys Phe Cys Gln Glu His 185 Asp Ile Leu Val Glu Ala Tyr Ser
Pro Leu Gly Pro Leu Arg Lys 200 Lys Thr Ala Gln Asp Asp Ser Gln Pro
Phe Phe Glu Tyr Val Lys 215 Glu Leu Ser Glu Lys Tyr Asn Lys Ser Glu
225 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys 235 Arg Gly Val Leu Pro Val
Thr Thr Ser Ser Lys Pro Gln Arg Ile 250 Ser Asp Ala Gln Asn Leu Phe
Ser Phe Asp Leu Thr Ala Glu Glu Val 265 Asp Lys Ile Thr Glu Leu Gly
Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys 285 Glu Tyr Gly Lys
Tyr Asn Tyr Ala Ala Gln Lys Val 300
305          310

```

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

<220>
 <223> Synthetic Construct

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<400> 343
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
ggtctgggtg aacaaatcgt gtatgcgttg aaactgccgg 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 cgtagtttgc 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
gatatacctg tggaagcata ttctccgctg ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
gcgtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

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

<220>
 <223> Synthetic Construct

SeqList.TXT

<400> 344

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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 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

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg 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 ggcttggaaa 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 ggcccgcctg ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgtt ttggaataaa 900
gagtatggca aatataacta cgccgcccag aaagtgtaat ga 942

```

SeqList.TXT

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

<220>
 <223> Synthetic Construct

<400> 346
 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 Phe Trp Asn Lys Glu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 347
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 347
 atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
 agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagtggg atggaacctt cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
 gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360

SeqList.TXT

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attcattccc cgtagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttgga 420
gatattggagc 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 cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggcctggaa catgaaccgc tgcgcctgtg gtggaataaa 900
cagtatggca aatataacta cgccgccag aaagtgtaat ga 942

```

<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

SeqList.TXT

<220>

<223> Synthetic Construct

<400> 349

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atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagtggg atttcgacct cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc 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 ttctccgctg ggcccgcctg ggaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct 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

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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
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
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

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SeqList.TXT
300

290
Tyr Asn Tyr Ala Ala Gln Lys Val
305 310

<210> 351
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 351
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgtgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagtggg atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactccctt 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc 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
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggcctggaa catgaaccgc tgcgcctgtg gtggaataaa 900
cagtatggca aatataacta cgccgcccag aaagtgtaat ga 942

<210> 352
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 352
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 Val 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

SeqList.TXT

210		215		220
Phe	Phe Glu Tyr Val	Lys Glu Leu Ser Glu	Lys Tyr Asn Lys Ser Glu	
225		230		240
Ala	Gln Ile Ile Leu	Arg Trp Val Thr	Lys Arg Gly Val Leu Pro Val	
		245		255
Thr	Thr Ser Ser Lys	Pro Gln Arg Ile	Ser Asp Ala Gln Asn Leu Phe	
		260		270
Ser	Phe Asp Leu Thr	Ala Glu Glu Val	Asp Lys Ile Thr Glu Leu Gly	
		275		285
Leu	Glu His Glu Pro	Leu Arg Leu Trp	Trp Asn Lys Gln Tyr Gly Lys	
		290		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

atgtcttttc	accaacagtt	tttcacgctg	aacaacggca	ataaaatccc	ggcgattgcc	60
atcatcgga	ctggtacagc	gtggtataaa	cccgaagaaa	ctgacgcgac	cttctccaat	120
agtctggttg	aacaaatcgt	gtatgcgttg	aaactgccgg	ggattatcca	catcgacgcc	180
gcggagtgg	atcgcaccta	cccgggaagt	ggtaaagcac	tgtccctgac	cgaaaagcct	240
cgtaacgcga	tttttctgac	ggataaatat	tctccgcaga	ttaaaatgag	tgactcccct	300
gcggacggtc	tggattttagc	attgaagaaa	atgggtacag	attatgttga	tttatatctg	360
attcattccc	cgttagtttc	gaaggaagt	aatggcctta	gcttagaaga	ggcttggaaa	420
gatatggagc	agttatacaa	aagtggtaaa	gctaaaaaca	tcgggggttc	caatttcaca	480
gtggaagacc	tgcaacgtat	cctgaaagtc	gctgaagtta	aaacctcagg	caaccagatt	540
gagttctctc	cgttcctgca	aaaccaaaca	ccaggcattt	gcaaattctg	tcaggagcac	600
gatatcctgg	tggaagcata	ttctccgctg	ggcccgcctg	ggaagaaaac	cgcgaggat	660
gacagccaac	cattttttga	gtacgtcaaa	gaattgagcg	aaaaatacaa	taaattccgag	720
gcccagatca	tcctgcgctg	ggctactaaa	cgcggtgtgc	tgccagttac	cacctcttca	780
aagcctcagc	gcattagcga	tgctcagaac	ctgttttcct	tcgacctgac	agcgggaagag	840
gttgataaaa	tcacggagct	gggcctggaa	catgaaccgc	tgcgccctgtg	gtggaataaa	900
cagtatggca	aatataacta	cgccgcccga	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

SeqList.TXT

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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

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<400> 355
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctgggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagtggt 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 ggcttggaag 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaatctg tcaggagcac 600
gatatccttg tggaagcata ttctccgctg ggcccgtgac ggaagaaaac cacgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggagag 840
gttgataaaa tcacggagct gggcctggaa catgaaccgc tgcgcctgtg gtggaataaa 900
cagtatggca aatataacta cgccgccag aaagtgtaat ga 942

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<210> 356
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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<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

```

SeqList.TXT

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

```

<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
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg 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 ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaac ccaggcattt gcaaatcttg tcaggagcac 600
gatatccttg tggaagcata ttctccgtgc ggcccgtgac ggaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaatccgag 720
gcccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcgggaagag 840
gttgataaaa tcacggagct gggcctggaa catgaaccgc tgcgcctgtg gtggaataaa 900
cagtatggca aatataacta cgccgcccc aagaagtgtg tga 943

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

<220>

SeqList.TXT

<223> Synthetic Construct

<400> 358

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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 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

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atgtcttttc accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcgcca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctgggttg aacaattagt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagtggt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttatcac ggataaatat tctccgcaga ttaaaatgag cgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaagtg aatggcctaa gcttagaaga ggcttggaag 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcaca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt gcaaattctg tcaggagcac 600
gatatcctgg tggaaagcata ttctccgcta ggcccgtgc ggaagaaaac cgcgaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
gcccgatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttctt tcgacctgac agcgggaagag 840

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SeqList.TXT

gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgta ctggaataaa 900
gagtatggca aatataacta cgccgcccag 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 tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaattagt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240

SeqList.TXT

```

cgtaacgcga tttttatcac ggataaatat tctccgcaga ttaaaatgag cgactcccct 300
gcggacgggc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtctc 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 tggaagcata ttctccgcta ggcccgcgtc ggaagaaaac cgcgcaggat 660
gacagccaac ctttttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagccctcagc gcattagcga tgctcagaac ctgttttctc tcgacctgac agcggagag 840
gttgataaaa tcacggagct ggtctgggaa catgaaccgc tgcgcctgtg gtggaataaa 900
ttgtatggca aatataacta cgccgccagc aaagtataat ga 942

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<210> 362

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 362

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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 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

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atgtcttttc accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcgcca 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 cgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
attcattccc cgttagtttc gaaggaaagt aatggcctaa 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 tggaaagcata ttctccgcta ggcccgtgc ggaagaaaac cgcgcaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgtg gtggaataaa 900
ttgtatggca aatataacta cgccgccag aaagtataat ga 942

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<210> 364

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 364

```

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 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

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SeqList.TXT

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

<220>
 <223> Synthetic Construct

<400> 365
 atgtcttttc accaagaatt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
 atcatcggca ctggtacagc gtggtataaa cccgaagaaa ctgacgcgac cttctccaat 120
 agtctgggtg aacaattagt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
 gcggagtggg atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
 cgtaacgcga tttttatcac ggataaata tctccgcaga ttaaaatgag cgactcccct 300
 gcggacgggc tggatttagc attgaagaaa atgggcttaa gcttagaaga ggcttggaaa 420
 attcattccc cgttagtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaaa 420
 gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggtttc caatttcaca 480
 gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcagg caaccagatt 540
 gagttctctc cgttcctgca aaaccaaaaca ccaggcattt gcaaattctg tcaggagcac 600
 gatatacctg tggaagcata ttctccgcta ggcccgtgc ggaagaaaac cgcgaggat 660
 gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacaa taaaaccgag 720
 gccagatca tcctgcgctg ggctactaaa cgcggtgtgc tgccagttac cactcttca 780
 aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
 gttgataaaa tcacggagct gggctctggaa catgaaccgc tgcgcctgtg gtggaataaa 900
 cagtatggca aatataacta cgccgcccag 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
 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

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Tyr
305