

SEQUENCE LISTING

<110> Yang, Zhi-Yong
 Nabel, Gary J.
 Xu, Ling
 Wei, Ronnie
 Qui, Huawei
 Beninga, Jochen
 Kruip, Jochen
 Rao, Ercole
 Leuschner, Wulf Dirk
 Beil, Christian
 Lange, Christian
 Connors, Mark
 Mascola, John R.
 Koup, Richard A.
 Huang, Jinghe
 Doria-Rose, Nicole A.
 Zhou, Tongqing
 Kwong, Peter D.
 Kwon, Young Do
 Pegu, Amarendra

<120> TRISPECIFIC AND/OR TRIVALENT BINDING
 PROTEINS FOR PREVENTION OR TREATMENT OF HIV INFECTION

<130> 183952027041

<140> Not Yet Assigned

<141> Concurrently Herewith

<160> 526

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 1

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			20					25				30			
Thr	Leu	Asn	Trp	Ile	Arg	Leu	Ala	Pro	Gly	Lys	Arg	Pro	Glu	Trp	Met

4. 183952027041SEQLIST.TXT

[illegible]

450

<210> 2
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 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 2
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 Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Val Ile Tyr Ser
 35 40 45
 Gly Ser Thr Arg Ala Ala Gly Ile Pro Asp Arg Phe Ser Gly Ser Arg
 50 55 60
 Trp Gly Pro Asp Tyr Asn Leu Thr Ile Ser Asn Leu Glu Ser Gly Asp
 65 70 75 80
 Phe Gly Val Tyr Tyr Cys Gln Gln Tyr Glu Phe Phe Gly Gln Gly Thr
 85 90 95
 Lys Val Gln Val Asp Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
 100 105 110
 Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
 115 120 125
 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
 130 135 140
 Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
 145 150 155 160
 Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
 165 170 175
 Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
 180 185 190
 Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
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 Glu Cys
 210

<210> 3
 <211> 611
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 3
 Glu Val Arg Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

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	20							25					30		
Trp	Met	Thr	Trp	Val	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
	35						40					45			
Gly	Arg	Ile	Thr	Gly	Pro	Gly	Glu	Gly	Trp	Ser	Val	Asp	Tyr	Ala	Glu
	50					55					60				
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Thr	Lys	Asn	Thr
65					70				75					80	
Leu	Tyr	Leu	Glu	Met	Asn	Asn	Val	Arg	Thr	Glu	Asp	Thr	Gly	Tyr	Tyr
				85					90					95	
Phe	Cys	Ala	Arg	Thr	Gly	Lys	Tyr	Tyr	Asp	Phe	Trp	Ser	Gly	Tyr	Pro
			100					105					110		
Pro	Gly	Glu	Glu	Tyr	Phe	Gln	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Ile
	115						120					125			
Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Gln	Val	His	Leu	Thr	Gln	Ser	Gly
	130					135					140				
Pro	Glu	Val	Arg	Lys	Pro	Gly	Thr	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala
145					150					155					160
Pro	Gly	Asn	Thr	Leu	Lys	Thr	Tyr	Asp	Leu	His	Trp	Val	Arg	Ser	Val
				165					170					175	
Pro	Gly	Gln	Gly	Leu	Gln	Trp	Met	Gly	Trp	Ile	Ser	His	Glu	Gly	Asp
	180							185					190		
Lys	Lys	Val	Ile	Val	Glu	Arg	Phe	Lys	Ala	Lys	Val	Thr	Ile	Asp	Trp
	195						200					205			
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	210					215					220				
Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Gly	Ser	Lys	His	Arg	Leu
225					230					235					240
Arg	Asp	Tyr	Ala	Leu	Tyr	Asp	Asp	Asp	Gly	Ala	Leu	Asn	Trp	Ala	Val
				245					250					255	
Asp	Val	Asp	Tyr	Leu	Ser	Asn	Leu	Glu	Phe	Trp	Gly	Gln	Gly	Thr	Ala
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Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Ala	Ser	Thr	Lys	Gly	Pro
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Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
	290					295					300				
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
305					310					315					320
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
				325					330					335	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
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Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
		355					360					365			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser
	370					375					380				
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
385					390					395					400
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
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His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
      435      440      445
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
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Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465      470      475      480
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
      485      490      495
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
      500      505      510
Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
      515      520      525
Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
      530      535      540
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545      550      555      560
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
      565      570      575
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
      580      585      590
Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu
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Ser Pro Gly
      610

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<210> 4

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 4

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

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

<210> 5

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 5

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cctg	gcaagc	ggcct	gagtg	gatg	gggatg	ctga	agccta	gagg	cggagc	cgtga	actac	180	
gccag	acctc	tgcag	ggcag	agtg	accatg	accc	gggacg	tgtac	agcga	tacc	gccttc	240	
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aact	gcgact	acaact	ggga	cttc	gagcac	tggg	gcagag	gcac	ccctgt	gatc	gtgtca	360	
agcg	cgctga	ccaagg	ggccc	cagc	gtgttc	cctc	tggccc	ctag	cagcaa	gagc	acatct	420	
ggcg	gaacag	ccgc	ccctggg	ctgc	ctctgtg	aagg	actact	ttcc	cagagc	cgtg	accgtg	480	
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agcg	gcctgt	acag	cctgag	cagc	gtcgtg	acag	tgccca	gcag	ctctct	gggc	acccag	600	
acct	acatct	gcaac	gtgaa	ccaca	agccc	agca	acacca	aggt	ggacaa	gaag	gtgaa	660	
ccca	agagct	gcga	caagac	ccac	acctgt	cccc	cttgtc	ctgc	ccccga	actg	ctggga	720	
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aacagcacct accgggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc 960
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<210> 6

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 6

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gccccagac tcgtgatcta cagcggcagc acaagagccg ccggaatccc cgatagattc 180
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aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
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<210> 7

<211> 1833

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

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ccaggtaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctggtccgtg 180
gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
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acacagagcg gacccgaagt gcggaagcct ggcacctctg tgaagggtgc ctgcaaggcc 480
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cccgtgctgg actccgacgg ctcttcttc ctctactcaa aactcaccgt ggacaagagc 1740
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<210> 8

<211> 1014

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 8

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tacgtgcaga agcccggcag atccccccag ctgctgatct acctggccag cagcagagcc 180
agcggcgtgc ccgatagatt ttctggcagc ggcagcgaca aggacttcac cctgaagatc 240
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tggacctttg gccagggcac caaggtggac atcaaggaca aaaccatac cgcatccgaa 360
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<210> 9

<211> 451

<212> PRT

<213> Artificial Sequence

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<220>

<223> Synthetic Construct

<400> 9

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		20						25					30		
Ile	Leu	Phe	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Val
		35					40					45			
Gly	Trp	Ile	Lys	Pro	Gln	Tyr	Gly	Ala	Val	Asn	Phe	Gly	Gly	Gly	Phe
	50					55				60					
Arg	Asp	Arg	Val	Thr	Leu	Thr	Arg	Asp	Val	Tyr	Arg	Glu	Ile	Ala	Tyr
65					70				75						80
Met	Asp	Ile	Arg	Gly	Leu	Lys	Pro	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Asp	Arg	Ser	Tyr	Gly	Asp	Ser	Ser	Trp	Ala	Leu	Asp	Ala	Trp
			100					105					110		
Gly	Gln	Gly	Thr	Thr	Val	Val	Val	Ser	Ala	Ala	Ser	Thr	Lys	Gly	Pro
	115						120					125			
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
	130					135					140				
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
145					150				155						160
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
			165						170					175	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
		180						185					190		
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
	195						200					205			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser
	210					215					220				
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
225					230				235						240
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
			245					250					255		
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
			260					265					270		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
	275						280					285			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
	290					295					300				
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
305					310				315						320
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro
				325					330					335	
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
			340					345					350		
Val	Cys	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val
	355						360					365			
Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val

4.__183952027041SEQLIST.TXT

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      370      375      380
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385      390      395      400
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
      405      410      415
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
      420      425      430
Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu
      435      440      445
Ser Pro Gly
      450

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<210> 10

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 10

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

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4.__183952027041SEQLIST.TXT

<210> 11

<211> 611

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 11

Glu	Val	Arg	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	Pro	Gly	Gly	1	5	10	15
Ser	Leu	Arg	Leu	Ser	Cys	Ser	Ala	Ser	Gly	Phe	Asp	Phe	Asp	Asn	Ala	20	25	30	
Trp	Met	Thr	Trp	Val	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	35	40	45	
Gly	Arg	Ile	Thr	Gly	Pro	Gly	Glu	Gly	Trp	Ser	Val	Asp	Tyr	Ala	Glu	50	55	60	
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Thr	Lys	Asn	Thr	65	70	75	80
Leu	Tyr	Leu	Glu	Met	Asn	Asn	Val	Arg	Thr	Glu	Asp	Thr	Gly	Tyr	Tyr	85	90	95	
Phe	Cys	Ala	Arg	Thr	Gly	Lys	Tyr	Tyr	Asp	Phe	Trp	Ser	Gly	Tyr	Pro	100	105	110	
Pro	Gly	Glu	Glu	Tyr	Phe	Gln	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Ile	115	120	125	
Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Gln	Val	His	Leu	Thr	Gln	Ser	Gly	130	135	140	
Pro	Glu	Val	Arg	Lys	Pro	Gly	Thr	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	145	150	155	160
Pro	Gly	Asn	Thr	Leu	Lys	Thr	Tyr	Asp	Leu	His	Trp	Val	Arg	Ser	Val	165	170	175	
Pro	Gly	Gln	Gly	Leu	Gln	Trp	Met	Gly	Trp	Ile	Ser	His	Glu	Gly	Asp	180	185	190	
Lys	Lys	Val	Ile	Val	Glu	Arg	Phe	Lys	Ala	Lys	Val	Thr	Ile	Asp	Trp	195	200	205	
Asp	Arg	Ser	Thr	Asn	Thr	Ala	Tyr	Leu	Gln	Leu	Ser	Gly	Leu	Thr	Ser	210	215	220	
Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Gly	Ser	Lys	His	Arg	Leu	225	230	235	240
Arg	Asp	Tyr	Ala	Leu	Tyr	Asp	Asp	Asp	Gly	Ala	Leu	Asn	Trp	Ala	Val	245	250	255	
Asp	Val	Asp	Tyr	Leu	Ser	Asn	Leu	Glu	Phe	Trp	Gly	Gln	Gly	Thr	Ala	260	265	270	
Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Ala	Ser	Thr	Lys	Gly	Pro	275	280	285	
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	290	295	300	
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	305	310	315	320
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	325	330	335	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr				

4. __183952027041SEQLIST.TXT

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          340          345          350
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
          355          360          365
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
          370          375          380
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385          390          395          400
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
          405          410          415
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
          420          425          430
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
          435          440          445
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
          450          455          460
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465          470          475          480
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
          485          490          495
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
          500          505          510
Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
          515          520          525
Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
          530          535          540
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545          550          555          560
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
          565          570          575
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
          580          585          590
Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu
          595          600          605
Ser Pro Gly
          610

```

<210> 12

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 12

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Asp Phe Val Leu Thr Gln Ser Pro His Ser Leu Ser Val Thr Pro Gly
 1          5          10          15
Glu Ser Ala Ser Ile Ser Cys Lys Ser Ser His Ser Leu Ile His Gly
          20          25          30
Asp Arg Asn Asn Tyr Leu Ala Trp Tyr Val Gln Lys Pro Gly Arg Ser
          35          40          45

```

4. __183952027041SEQLIST.TXT

Pro Gln Leu Leu Ile Tyr Leu Ala Ser Ser Arg Ala Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Asp Lys Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Thr Glu Asp Val Gly Thr Tyr Tyr Cys Met Gln Gly
 85 90 95
 Arg Glu Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
 100 105 110
 Asp Lys Thr His Thr Ala Ser Glu Leu Thr Gln Asp Pro Ala Val Ser
 115 120 125
 Val Ala Leu Lys Gln Thr Val Thr Ile Thr Cys Arg Gly Asp Ser Leu
 130 135 140
 Arg Ser His Tyr Ala Ser Trp Tyr Gln Lys Lys Pro Gly Gln Ala Pro
 145 150 155 160
 Val Leu Leu Phe Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp
 165 170 175
 Arg Phe Ser Gly Ser Ala Ser Gly Asn Arg Ala Ser Leu Thr Ile Thr
 180 185 190
 Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Arg Asp
 195 200 205
 Lys Ser Gly Ser Arg Leu Ser Val Phe Gly Gly Gly Thr Lys Leu Thr
 210 215 220
 Val Leu Asp Lys Thr His Thr Arg Thr Val Ala Ala Pro Ser Val Phe
 225 230 235 240
 Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
 245 250 255
 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
 260 265 270
 Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
 275 280 285
 Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
 290 295 300
 Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
 305 310 315 320
 Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
 325 330 335
 Glu Cys

<210> 13

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 13

agagcccacc tgggtgcagtc tggcaccgcc atgaagaaac caggcgcctc tgtgcgggtg 60
 tcctgtcaga caagcggcta caccttcacc gccacatcc tgttctggtt ccggcaggcc 120
 cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180

4. __183952027041SEQLIST.TXT

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ggcggaggct tccgggatag agtgaccctg acccgggacg tgtaccgca gatcgctac 240
atggacatcc ggggcctgaa gcccgatgac accgccgtgt actactgagc cagagacaga 300
agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtggtggtg 360
tctgccgcct ctacaaaggg ccccgagctg ttccctctgg cccctagcag caagagcaca 420
tctggcggaa cagccgccct gggctgcctc gtgaaggact actttcccga gcccgtagacc 480
gtgtcctgga attctggcgc cctgaccagc ggcgtgcaca cttttccagc tgtgctgcag 540
tccagcggcc tgtacagcct gagcagcgtc gtgacagtgc ccagcagctc tctgggcacc 600
cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagaagggtg 660
gaaccacaaga gctgcgacaa gaccacacac tggtccccctt gtcctgcccc cgaactgctg 720
ggaggccctt ccgtgttcct gttcccccca aagcccaagg acaccctgat gatcagccgg 780
acccccgaag tgacctgctg ggtggtggat gtgtcccacg aggacctga agtgaagttc 840
aattggtacg tggacggcgt ggaagtgcac aacgccaaga ccaagccaag agaggaacag 900
tacaacagca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ctggctgaac 960
ggcaaagagt acaagtgaac ggtgtccaac aaggccctgc ctgcccccat cgagaaaacc 1020
atcagcaagg ccaaggcca gccccgcgaa cccaggtgt gcacactgcc cccaagcagg 1080
gacgagctga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccctcc 1140
gatatcgccg tggaatggga gagcaacggc cagcccgaga acaactacaa gaccaccccc 1200
cctgtgctgg acagcgacgg ctattcttc ctggtgtcca agctgacagt ggacaagtcc 1260
cggtggcagc agggcaacgt gttcagctgc tccgtgctgc acgaggccct gcacagccac 1320
tacaccaga agtccctgag cctgagcccc ggc 1353

```

<210> 14

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 14

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tacatccacg tgaccagag ccccgagcag ctgtccgtgt ccatcggcga cagagtgacc 60
atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgccagc 180
agatthttccg gcagcggctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacgggtggc cgctcccagc gtgttcattt tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgaccc accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630

```

<210> 15

<211> 1833

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 15

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gaggttagac tggtggagtc aggagggggg cttgtgaagc ccggtgggtc tctccgcctg 60

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4. __183952027041SEQLIST.TXT

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agctgttctg cctccggctt tgatttcgat aacgcctgga tgacctgggt caggcagcct 120
ccaggtaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctggtccgtg 180
gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
acaggcaa at actacgactt ctggtccggc tatccccctg gcgaggaata ttttcaagac 360
tggggtcagg gaacccttgt tatcgtgtcc tccgacaaaa cccataccca ggtgcacctg 420
acacagagcg gacccgaagt gcggaagcct ggcacctctg tgaaggtgtc ctgcaaggcc 480
cctggcaaca ccctgaaaac ctacgacctg cactgggtgc gcagcgtgcc aggacaggga 540
ctgcagtgga tgggctggat cagccacgag ggcgacaaga aagtgatcgt ggaacggttc 600
aaggccaaag tgaccatcga ctgggacaga agcaccaaca ccgcctacct gcagctgagc 660
ggcctgacct ctggcgatac cgccgtgtac tactgcgcca agggcagcaa gcaccggctg 720
agagactacg ccctgtacga cgatgacggc gccctgaact gggccgtgga tgtggactac 780
ctgagcaacc tgggaattctg gggccagggc acagccgtga ccgtgtcatc tgataagacc 840
cacaccgctt ccaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc 900
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 960
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag 1020
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 1080
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 1140
gagcccaa at cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 1200
gggggaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctcccgg 1260
accctgagg tcacatgctg ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320
aactggtatg ttgacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag 1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440
ggcaaggagt acaagtgaac ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1500
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatgccgg 1560
gatgagctga ccaagaatca agtcagcctg tggtgcctgg taaaaggctt ctatcccagc 1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680
cccgtgctgg actccgacgg ctcttcttct ctctactcaa aactcaccgt ggacaagagc 1740
aggtggcagc aggggaacgt cttctcatgc tccgtgctgc atgaggctct gcacagccac 1800
tacacgcaga agagcctctc cctgtctccg ggt 1833

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<210> 16

<211> 1014

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 16

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gacttcgtgc tgacccagag ccctcacagc ctgagcgtga cacctggcga gagcgccagc 60
atcagctgca agagcagcca ctccctgatc cacggcgacc ggaacaacta cctggcttgg 120
tacgtgcaga agcccgagcag atccccccag ctgctgatct acctggccag cagcagagcc 180
agcggcgtgc ccgatagatt ttctggcagc ggcagcgaca aggacttcac cctgaagatc 240
agccgggtgg aaaccgagga cgtgggcacc tactactgta tgcagggcag agagagcccc 300
tggacctttg gccagggcac caaggtggac atcaaggaca aaaccatac cgcattccgaa 360
ctgactcagg accctgccgt ctctgtggca ctgaagcaga ctgtgactat tacttgccga 420
ggcgactcac tgcggagcca ctacgcttcc tggtatcaga agaaaccgg ccaggcacct 480
gtgctgctgt tctacggaaa gaacaatagg ccatctggca tccccgaccg ctttcttggc 540
agtgcacag ggaaccgagc cagtctgacc attaccggcg cccaggctga ggacgaagcc 600
gattactatt gcagctcccg ggataagagc ggctccagac tgagcgtgtt cggaggagga 660
actaaactga ccgtcctcga taagacctat accgtacgg tggccgctcc cagcgtgttc 720

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4.__183952027041SEQLIST.TXT

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atctttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 780
aacaacttct acccccgcgga ggccaaagtg cagtgggaagg tggacaacgc cctgcagagc 840
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 900
agcaccctga cactgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 960
acccaccagg gcctgtctag ccccgtgacc aagagcttca accggggcga gtgt 1014

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<210> 17

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 17

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

4. __183952027041SEQLIST.TXT

```

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

```

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

<220>
 <223> Synthetic Construct

```

<400> 18
Tyr Ile His Val Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ile Gly
1          5          10          15
Asp Arg Val Thr Ile Asn Cys Gln Thr Ser Gln Gly Val Gly Ser Asp
20          25          30
Leu His Trp Tyr Gln His Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
35          40          45
His His Thr Ser Ser Val Glu Asp Gly Val Pro Ser Arg Phe Ser Gly
50          55          60
Ser Gly Phe His Thr Ser Phe Asn Leu Thr Ile Ser Asp Leu Gln Ala
65          70          75          80
Asp Asp Ile Ala Thr Tyr Tyr Cys Gln Val Leu Gln Phe Phe Gly Arg
85          90          95
Gly Ser Arg Leu His Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
100         105         110
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
115         120         125
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
130         135         140
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
145         150         155         160

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4.__183952027041SEQLIST.TXT

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
165 170 175
Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
180 185 190
Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
195 200 205
Glu Cys
210

<210> 19
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 19
Gln Val His Leu Thr Gln Ser Gly Pro Glu Val Arg Lys Pro Gly Thr
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Pro Gly Asn Thr Leu Lys Thr Tyr
20 25 30
Asp Leu His Trp Val Arg Ser Val Pro Gly Gln Gly Leu Gln Trp Met
35 40 45
Gly Trp Ile Ser His Glu Gly Asp Lys Lys Val Ile Val Glu Arg Phe
50 55 60
Lys Ala Lys Val Thr Ile Asp Trp Asp Arg Ser Thr Asn Thr Ala Tyr
65 70 75 80
Leu Gln Leu Ser Gly Leu Thr Ser Gly Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Gly Ser Lys His Arg Leu Arg Asp Tyr Ala Leu Tyr Asp Asp
100 105 110
Asp Gly Ala Leu Asn Trp Ala Val Asp Val Asp Tyr Leu Ser Asn Leu
115 120 125
Glu Phe Trp Gly Gln Gly Thr Ala Val Thr Val Ser Ser Asp Lys Thr
130 135 140
His Thr Glu Val Arg Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro
145 150 155 160
Gly Gly Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Asp
165 170 175
Asn Ala Trp Met Thr Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu
180 185 190
Trp Val Gly Arg Ile Thr Gly Pro Gly Glu Gly Trp Ser Val Asp Tyr
195 200 205
Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys
210 215 220
Asn Thr Leu Tyr Leu Glu Met Asn Asn Val Arg Thr Glu Asp Thr Gly
225 230 235 240
Tyr Tyr Phe Cys Ala Arg Thr Gly Lys Tyr Tyr Asp Phe Trp Ser Gly
245 250 255
Tyr Pro Pro Gly Glu Glu Tyr Phe Gln Asp Trp Gly Gln Gly Thr Leu

4. __183952027041SEQLIST.TXT

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                260                265                270
Val Ile Val Ser Ser Asp Lys Thr His Thr Ala Ser Thr Lys Gly Pro
                275                280                285
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
                290                295                300
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
305                310                315                320
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                325                330                335
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
                340                345                350
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
                355                360                365
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
                370                375                380
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385                390                395                400
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                405                410                415
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
                420                425                430
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
                435                440                445
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
                450                455                460
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                470                475                480
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                485                490                495
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
                500                505                510
Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
                515                520                525
Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
                530                535                540
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545                550                555                560
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                565                570                575
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
                580                585                590
Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu
                595                600                605
Ser Pro Gly
                610

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<210> 20

<211> 338

<212> PRT

<213> Artificial Sequence

4.__183952027041SEQLIST.TXT

<220>

<223> Synthetic Construct

<400> 20

Ala	Ser	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Lys	Gln
1				5				10						15	
Thr	Val	Thr	Ile	Thr	Cys	Arg	Gly	Asp	Ser	Leu	Arg	Ser	His	Tyr	Ala
		20					25					30			
Ser	Trp	Tyr	Gln	Lys	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Leu	Phe	Tyr
		35					40				45				
Gly	Lys	Asn	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser
	50					55				60					
Ala	Ser	Gly	Asn	Arg	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu
65					70				75						80
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ser	Ser	Arg	Asp	Lys	Ser	Gly	Ser	Arg
			85						90					95	
Leu	Ser	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Asp	Lys	Thr
			100					105					110		
His	Thr	Asp	Phe	Val	Leu	Thr	Gln	Ser	Pro	His	Ser	Leu	Ser	Val	Thr
		115					120					125			
Pro	Gly	Glu	Ser	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	His	Ser	Leu	Ile
	130					135					140				
His	Gly	Asp	Arg	Asn	Asn	Tyr	Leu	Ala	Trp	Tyr	Val	Gln	Lys	Pro	Gly
145					150					155					160
Arg	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Ala	Ser	Ser	Arg	Ala	Ser	Gly
			165						170					175	
Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Asp	Lys	Asp	Phe	Thr	Leu
			180					185					190		
Lys	Ile	Ser	Arg	Val	Glu	Thr	Glu	Asp	Val	Gly	Thr	Tyr	Tyr	Cys	Met
		195					200					205			
Gln	Gly	Arg	Glu	Ser	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Asp
	210					215					220				
Ile	Lys	Asp	Lys	Thr	His	Thr	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe
225					230					235					240
Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val
			245						250					255	
Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp
		260						265					270		
Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr
		275					280					285			
Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr
	290					295					300				
Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val
305					310					315					320
Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly
			325						330					335	

Glu Cys

<210> 21

<211> 1353

4.__183952027041SEQLIST.TXT

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 21

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agagcccacc tgggtgcagtc tggcaccgcc atgaagaaac caggcgcctc tgtgcgggtg 60
tcctgtcaga caagcggcta caccttcacc gccacatcc tgttctgggt ccggcaggcc 120
cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
ggcggaggct tccgggatag agtgaccctg acccgggacg tgtaccgcga gatcgctac 240
atggacatcc ggggcctgaa gcccgatgac accgccgtgt actactgcgc cagagacaga 300
agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtggtggtg 360
tctgccgcct ctacaaaggg cccagcgtg ttccctctgg ccctagcag caagagcaca 420
tctggcggaa cagccgccct gggctgcctc gtgaaggact actttcccga gcccgtagcc 480
gtgtcctgga attctggcgc cctgaccagc ggctgtgcaca cttttccagc tgtgctgcag 540
tccagcggcc tgtacagcct gagcagcgtc gtgacagtgc ccagcagctc tctgggcacc 600
cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagaaggtg 660
gaaccaaga gctgcgacaa gaccacacc tgtccccctt gtcctgcccc cgaactgctg 720
ggaggccctt cgtgttccct gttccccca aagcccaagg acaccctgat gatcagccgg 780
acccccgaag tgacctgcgt ggtggtggat gtgtcccacg aggacctga agtgaagttc 840
aattggtacg tggacggcgt ggaagtgcac aacgccaaga ccaagccaag agaggaacag 900
tacaacagca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ctggctgaac 960
ggcaaagagt acaagtgcaa ggtgtccaac aaggccctgc ctgcccccat cgagaaaacc 1020
atcagcaagg ccaaggcca gccccgcgaa cccaggtgtg gcacactgcc cccaagcagg 1080
gacgagctga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccctcc 1140
gatatcgccg tggaatggga gagcaacggc cagcccgaga acaactaaa gaccaccccc 1200
cctgtgctgg acagcgacgg ctcatcttc ctggtgtcca agctgacagt ggacaagtcc 1260
cgggtggcagc agggcaacgt gttcagctgc tccgtgctgc acgaggccct gcacagccac 1320
tacaccaga agtccctgag cctgagcccc ggc 1353

```

<210> 22

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 22

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tacatccacg tgacccagag cccagcagc ctgtccgtgt ccatcggcga cagagtgacc 60
atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgcccagc 180
agattttccg gcagcggctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accaggccct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcagatgt 630

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4.__183952027041SEQLIST.TXT

<210> 23
 <211> 1833
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 23
 caggtgcacc tgacacagag cggacccgaa gtgcggaagc ctggcacctc tgtgaagggtg 60
 tcctgcaagg cccctggcaa caccctgaaa acctacgacc tgcactgggt gcgcagcgtg 120
 ccaggacagg gactgcagtg gatgggctgg atcagccacg agggcgacaa gaaagtgatc 180
 gtggaacggg tcaaggccaa agtgaccatc gactgggaca gaagcaccaa caccgcctac 240
 ctgcagctga gcggcctgac ctctggcgat accgccgtgt actactgcgc caagggcagc 300
 aagcaccggc tgagagacta cgccctgtac gacgatgacg gcgccctgaa ctgggcccgtg 360
 gatgtggact acctgagcaa cctggaattc tggggccagg gcacagccgt gaccgtgtca 420
 tctgacaaaa cccataccga ggttagactg gtggagtcag gaggggggct tgtgaagccc 480
 ggtgggtctc tccgcctgag ctgttctgcc tccggctttg atttcgataa cgcctggatg 540
 acctgggtca ggcagcctcc aggttaaggga ctggagtggg tgggaagaat cacaggtcca 600
 ggcgagggct ggtccgtgga ctacgcgga tctgttaaag ggcggtttac aatctcaagg 660
 gacaatacca agaatacctt gtatttggag atgaacaacg tgagaactga agacaccgga 720
 tattacttct gtgccagaac aggcaaatac tacgacttct ggtccggcta tccccctggc 780
 gaggaatatt ttcaagactg gggtcaggga acccttggtt tcgtgtcctc cgataagacc 840
 cacaccgctt ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 900
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 960
 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 1020
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 1080
 cagacctaca tctgcaacgt gaatcacaa cccagcaaca ccaaggtgga caagaaagt 1140
 gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 1200
 gggggaccgt cagtcttctt cttcccccca aaaccaagg acaccctcat gatctcccgg 1260
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320
 aactggtatg ttgacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380
 tacaacagca cgtaccgtgt ggtcagcgtc ctaccgtcc tgcaccagga ctggctgaat 1440
 ggcaaggagt acaagtcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1500
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc ccatgcccgg 1560
 gatgagctga ccaagaatca agtcagcctg tgggtgcctg taaaaggctt ctatcccagc 1620
 gacatgcggc tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680
 cccgtgctgg actccgacgg ctcttcttct ctctactcaa aactcaccgt ggacaagagc 1740
 aggtggcagc aggggaacgt cttctcatgc tccgtgctgc atgaggctct gcacagccac 1800
 tacacgcaga agagcctctc cctgtctccg ggt 1833

<210> 24
 <211> 1014
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 24
 gcatccgaac tgactcagga ccctgccgtc tctgtggcac tgaagcagac tgtgactatt 60
 acttgccgag gcgactcact gcggagccac tacgttctt ggtatcagaa gaaacccggc 120

4. __183952027041SEQLIST.TXT

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caggcacctg tgctgctgtt ctacggaaag aacaataggc catctggcat ccccgaccgc 180
ttttctggca gtgcatcagg gaaccgagcc agtctgacca ttaccggcgc ccaggctgag 240
gacgaagccg attactattg cagctcccgg gataagagcg gctccagact gagcgtgttc 300
ggaggaggaa ctaaactgac cgtcctcgac aaaaccata ccgacttcgt gctgaccag 360
agccctcaca gcctgagcgt gacacctggc gagagcgcca gcatcagctg caagagcagc 420
cactccctga tccacggcga ccggaacaac tacctggctt ggtacgtgca gaagcccggc 480
agatccccc agctgctgat ctacctggcc agcagcagag ccagcggcgt gcccgataga 540
ttttctggca gcggcagcga caaggacttc accctgaaga tcagccgggt ggaaaccgag 600
gacgtgggca cctactactg tatgcagggc agagagagcc cctggacctt tggccagggc 660
accaaggtgg acatcaagga taagacccat acccgtaggg tggccgctcc cagcgtgttc 720
atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 780
aacaacttct acccccgcga ggccaaagtg cagtgggaagg tggacaacgc cctgcagagc 840
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 900
agcaccctga cactgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 960
accaccagg gcctgtctag ccccgtagcc aagagcttca accggggcga gtgt 1014

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<210> 25

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 25

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

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210	215	220
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly		
225	230	235
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met		
	245	250
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His		
	260	265
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val		
	275	280
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr		
	290	295
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly		
305	310	315
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile		
	325	330
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val		
	340	345
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser		
	355	360
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu		
	370	375
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro		
385	390	395
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val		
	405	410
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met		
	420	425
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser		
	435	440
Pro Gly		445
450		

<210> 26

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 26

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly		
1	5	10
Glu Thr Ala Ile Ile Ser Cys Arg Thr Ser Gln Tyr Gly Ser Leu Ala		
	20	25
Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Val Ile Tyr Ser		
	35	40
Gly Ser Thr Arg Ala Ala Gly Ile Pro Asp Arg Phe Ser Gly Ser Arg		
	50	55
Trp Gly Pro Asp Tyr Asn Leu Thr Ile Ser Asn Leu Glu Ser Gly Asp		
65	70	75
		80

4.__183952027041SEQLIST.TXT

Phe	Gly	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Glu	Phe	Phe	Gly	Gln	Gly	Thr
			85						90					95	
Lys	Val	Gln	Val	Asp	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe
			100					105						110	
Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val
		115					120					125			
Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp
	130					135					140				
Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr
145					150					155					160
Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr
				165					170					175	
Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val
			180					185					190		
Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly
		195					200						205		
Glu	Cys														
	210														

<210> 27

<211> 611

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 27

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

4. 183952027041SEQLIST.TXT

Lys	Lys	Val	Ile	Val	Glu	Arg	Phe	Lys	Ala	Lys	Val	Thr	Ile	Asp	Trp
		195					200					205			
Asp	Arg	Ser	Thr	Asn	Thr	Ala	Tyr	Leu	Gln	Leu	Ser	Gly	Leu	Thr	Ser
		210				215					220				
Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Gly	Ser	Lys	His	Arg	Leu
225					230					235					240
Arg	Asp	Tyr	Ala	Leu	Tyr	Asp	Asp	Asp	Gly	Ala	Leu	Asn	Trp	Ala	Val
				245					250					255	
Asp	Val	Asp	Tyr	Leu	Ser	Asn	Leu	Glu	Phe	Trp	Gly	Gln	Gly	Thr	Ala
			260					265					270		
Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Ala	Ser	Thr	Lys	Gly	Pro
		275					280					285			
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
		290				295					300				
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
305				310					315						320
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
			325						330					335	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
			340					345					350		
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
		355					360					365			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser
		370				375					380				
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
385				390					395						400
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
			405						410					415	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
			420					425					430		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
		435					440					445			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
		450				455					460				
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
465				470					475						480
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro
			485						490					495	
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
			500					505					510		
Val	Tyr	Thr	Leu	Pro	Pro	Cys	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val
		515					520					525			
Ser	Leu	Trp	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val
		530				535									

595
Ser Pro Gly
610

600

605

<210> 28
<211> 338
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 28
Asp Phe Val Leu Thr Gln Ser Pro His Ser Leu Ser Val Thr Pro Gly
1 5 10 15
Glu Ser Ala Ser Ile Ser Cys Lys Ser Ser His Ser Leu Ile His Gly
20 25 30
Asp Arg Asn Asn Tyr Leu Ala Trp Tyr Val Gln Lys Pro Gly Arg Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Leu Ala Ser Ser Arg Ala Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Asp Lys Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Thr Glu Asp Val Gly Thr Tyr Tyr Cys Met Gln Gly
85 90 95
Arg Glu Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
100 105 110
Asp Lys Thr His Thr Ala Ser Glu Leu Thr Gln Asp Pro Ala Val Ser
115 120 125
Val Ala Leu Lys Gln Thr Val Thr Ile Thr Cys Arg Gly Asp Ser Leu
130 135 140
Arg Ser His Tyr Ala Ser Trp Tyr Gln Lys Lys Pro Gly Gln Ala Pro
145 150 155 160
Val Leu Leu Phe Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp
165 170 175
Arg Phe Ser Gly Ser Ala Ser Gly Asn Arg Ala Ser Leu Thr Ile Thr
180 185 190
Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Arg Asp
195 200 205
Lys Ser Gly Ser Arg Leu Ser Val Phe Gly Gly Gly Thr Lys Leu Thr
210 215 220
Val Leu Asp Lys Thr His Thr Arg Thr Val Ala Ala Pro Ser Val Phe
225 230 235 240
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
245 250 255
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
260 265 270
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
275 280 285
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
290 295 300

4. __183952027041SEQLIST.TXT

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
 305 310 315 320
 Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
 325 330 335
 Glu Cys

<210> 29
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 29
 cagggtgcagc tgggtgcagtc tggcggccag atgaagaaac ccggcgagag catgcggatc 60
 agctgcagag ccagcggcta cgagttcatc gactgcaccc tgaactggat cagactggcc 120
 cctggcaagc ggcctgagtg gatgggatgg ctgaagccta gaggcggagc cgtgaactac 180
 gccagacctc tgcagggcag agtgaccatg acccgggacg tgtacagcga taccgccttc 240
 ctggaactgc ggagcctgac cgtggatgat accgccgtgt acttctgcac ccggggcaag 300
 aactgcgact acaactggga cttcgagcac tggggcgagag gcacccctgt gatcgtgtca 360
 agcgcgtcga ccaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 420
 ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccagacc cgtgaccgtg 480
 tcctggaatt ctggcgccct gaccagcggc gtgcacacct ttccagctgt gctgcagtcc 540
 agcggcctgt acagcctgag cagcgtcgtg acagtgccca gcagctctct gggcacccag 600
 acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 660
 cccaagagct gcgacaagac ccacacctgt ccccttgctc ctgccccga actgctggga 720
 ggcccttccg tgttcctgtt cccccaaag cccaaggaca ccctgatgat cagccggacc 780
 cccgaagtga cctgcgtggt ggtggatgtg tcccacgagg accctgaagt gaagttcaat 840
 tggtagctgg acggcgtgga agtgcacaac gccaaagaca agccaagaga ggaacagtac 900
 aacagcacct accgggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc 960
 aaagagtaca agtgcaaggt gtccaacaag gccctgcctg ccccatcga gaaaaccatc 1020
 agcaaggcca agggccagcc ccgcgaacc caggtgtgca cactgcccc aagcagggac 1080
 gagctgacca agaaccaggt gtccctgagc tgtgccgtga aaggcttcta cccctccgat 1140
 atcgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cccccccct 1200
 gtgctggaca gcgacggctc attcttctg gtgtccaagc tgacagtgga caagtcccgg 1260
 tggcagcagg gcaacgtgtt cagctgtctc gtgatgcacg aggccctgca caaccactac 1320
 acccagaagt ccctgagcct gagccccggc 1350

<210> 30
 <211> 630
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 30
 gagatcgtgc tgacacagag ccctggcacc ctgagcctgt ctccaggcga gacagccatc 60
 atcagctgcc ggacaagcca gtacggcagc ctggcctggt atcagcagag gcctggacag 120

4. __183952027041SEQLIST.TXT

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gccccagac tcgtgatcta cagcggcagc acaagagccg ccggaatccc cgatagattc 180
agcggctcca gatggggccc tgactacaac ctgaccatca gcaacctgga aagcggcgac 240
ttcggcgtgt actactgcca gcagtacgag ttcttcggcc agggcaccaa ggtgcaggtg 300
gacatcaagc gtacgggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630

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<210> 31

<211> 1833

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 31

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gaggtagac tgggtggagtc aggagggggg cttgtgaagc ccggtgggtc tctccgcctg 60
agctgttctg cctccggctt tgatttcgat aacgcctgga tgacctgggt caggcagcct 120
ccaggtaagg gactggagtg ggtgggaaga atcacaggct caggcgaggg ctggtccgtg 180
gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
acaggcaaat actacgactt ctggtggggc tatccccctg gcgaggaata ttttcaagac 360
tggggtcagg gaacccttgt tatcgtgtcc tccgacaaaa cccataacca ggtgcacctg 420
acacagagcg gacccgaagt gcggaagcct ggcacctctg tgaagggtgc ctgcaaggcc 480
cctggcaaca ccctgaaaac ctacgacctg cactgggtgc gcagcgtgcc aggacaggga 540
ctgcagtgga tgggctggat cagccacgag ggcgacaaga aagtgatcgt ggaacggttc 600
aaggccaaag tgaccatcga ctgggacaga agcaccaaca ccgcctacct gcagctgagc 660
ggcctgacct ctggcgatac cgccgtgtac tactgcgcca agggcagcaa gcaccggctg 720
agagactacg ccctgtacga cgatgacggc gccctgaact gggccgtgga tgtggactac 780
ctgagcaacc tgggaattctg gggccagggc acagccgtga ccgtgtcatc tgataagacc 840
cacaccgctt ccaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc 900
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 960
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgtcctacag 1020
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 1080
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtgga caagaaagtt 1140
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 1200
gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 1260
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 1320
aactggtatg ttgacggcgt ggagggtgat aatgccaaga caaagccgcg ggaggagcag 1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1500
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatgccgg 1560
gatgagctga ccaagaatca agtcagcctg tgggtgcctgg taaaaggctt ctatcccagc 1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680
cccgtgctgg actccgacgg ctcttcttc ctctactcaa aactcaccgt ggacaagagc 1740
aggtggcagc aggggaacgt cttctcatgc tccgtgtgtc atgaggctct gcacagccac 1800
tacacgcaga agagcctctc cctgtctccg ggt 1833

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<210> 32

4.__183952027041SEQLIST.TXT

<211> 1014

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 32

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gacttcgtgc tgacccagag ccctcacagc ctgagcgtga cacctggcga gagcgccagc 60
atcagctgca agagcagcca ctccctgatc cacggcgacc ggaacaacta cctggccttg 120
tacgtgcaga agcccggcag atccccccag ctgctgatct acctggccag cagcagagcc 180
agcggcgtgc ccgatagatt ttctggcagc ggcagcgaca aggacttcac cctgaagatc 240
agccgggttg aaaccgagga cgtgggcacc tactactgta tgcagggcag agagagcccc 300
tggacctttg gccagggcac caaggtggac atcaaggaca aaaccatac cgcacccgaa 360
ctgactcagg accctgccgt ctctgtggca ctgaagcaga ctgtgactat tacttgccga 420
ggcgactcac tgcggagcca ctacgcttcc tggatatcaga agaaaccgg ccaggcacct 480
gtgctgtgtg tctacggaaa gaacaatagg ccatctggca tccccgaccg cttttctggc 540
agtgcacag ggaaccgagc cagtctgacc attaccggcg cccaggctga ggacgaagcc 600
gattactatt gcagctcccg ggataagagc ggctccagac tgagcgtgtt cggaggagga 660
actaaactga ccgtcctcga taagacccat acccgtagcg tggccgctcc cagcgtgttc 720
atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 780
aacaacttct acccccgcga ggccaaagtg cagtgggaagg tggacaacgc cctgcagagc 840
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 900
agcacctga cactgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 960
accaccagg gcctgtctag ccccgtagc aagagcttca accggggcga gtgt 1014

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<210> 33

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 33

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

```

4. __183952027041SEQLIST.TXT

130		135		140	
Ala	Leu	Gly	Cys	Leu	Val
145		150		155	160
Ser	Trp	Asn	Ser	Gly	Ala
		165		170	175
Val	Leu	Gln	Ser	Gly	Leu
		180		185	190
Pro	Ser	Ser	Ser	Leu	Gly
		195		200	205
Lys	Pro	Ser	Asn	Thr	Lys
		210		215	220
Asp	Lys	Thr	His	Thr	Cys
225				230	235
Gly	Pro	Ser	Val	Phe	Leu
				245	250
Ile	Ser	Arg	Thr	Pro	Glu
				260	265
Glu	Asp	Pro	Glu	Val	Lys
				275	280
His	Asn	Ala	Lys	Thr	Lys
				290	295
Arg	Val	Val	Ser	Val	Leu
305				310	315
Lys	Glu	Tyr	Lys	Cys	Lys
				325	330
Glu	Lys	Thr	Ile	Ser	Lys
				340	345
Cys	Thr	Leu	Pro	Pro	Ser
				355	360
Leu	Ser	Cys	Ala	Val	Lys
				370	375
Trp	Glu	Ser	Asn	Gly	Gln
385				390	395
Val	Leu	Asp	Ser	Asp	Gly
				405	410
Asp	Lys	Ser	Arg	Trp	Gln
				420	425
His	Glu	Ala	Leu	His	Asn
				435	440
Pro	Gly				
					445
					450

<210> 34

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 34

4.__183952027041SEQLIST.TXT

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

<210> 35

<211> 602

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 35

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

4. 183952027041SEQLIST.TXT

			100					105				110			
Pro	Gly	Glu	Tyr	Phe	Gln	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Ile	
		115				120					125				
Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Gln	Met	Gln	Leu	Gln	Glu	Ser	Gly
		130				135					140				
Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ser	Val
145					150					155					160
Ser	Gly	Ala	Ser	Ile	Ser	Asp	Ser	Tyr	Trp	Ser	Trp	Ile	Arg	Arg	Ser
				165						170					
Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Val	His	Lys	Ser	Gly	Asp
			180					185					190		
Thr	Asn	Tyr	Ser	Pro	Ser	Leu	Lys	Ser	Arg	Val	Asn	Leu	Ser	Leu	Asp
		195					200					205			
Thr	Ser	Lys	Asn	Gln	Val	Ser	Leu	Ser	Leu	Val	Ala	Ala	Thr	Ala	Ala
		210				215					220				
Asp	Ser	Gly	Lys	Tyr	Tyr	Cys	Ala	Arg	Thr	Leu	His	Gly	Arg	Arg	Ile
225				230						235					240
Tyr	Gly	Ile	Val	Ala	Phe	Asn	Glu	Trp	Phe	Thr	Tyr	Phe	Tyr	Met	Asp
				245					250					255	
Val	Trp	Gly	Asn	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His
			260					265					270		
Thr	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser
			275				280					285			
Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp
		290				295					300				
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr
305				310						315					320
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr
				325					330					335	
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln
			340					345					350		
Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp
		355					360					365			
Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro
						375					380				
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
385				390						395					400
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
				405					410					415	
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn
			420					425					430		
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
		435					440					445			
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
				450		455									

4._183952027041SEQLIST.TXT

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      515              520              525
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
      530              535              540
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
545              550              555              560
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
      565              570              575
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
      580              585              590
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
      595              600

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<210> 36

<211> 331

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 36

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

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4._183952027041SEQLIST.TXT

Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe
				245					250					255	
Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln
			260					265					270		
Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
		275					280					285			
Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
	290					295					300				
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser
305					310					315					320
Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys					
				325					330						

<210> 37

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 37

caggtgcagc	tggtgcagtc	tggcggccag	atgaagaaac	ccggcgagag	catgcggatc	60
agctgcagag	ccagcggcta	cgagttcatc	gactgcaccc	tgaactggat	cagactggcc	120
cctggcaagc	ggcctgagtg	gatgggatgg	ctgaagccta	gaggcggagc	cgtgaactac	180
gccagacctc	tgcagggcag	agtgaccatg	accgaggacg	tgtacagcga	taccgccttc	240
ctggaactgc	ggagcctgac	cgtggatgat	accgccgtgt	acttctgcac	ccggggcaag	300
aactgcgact	acaactggga	cttcgagcac	tggggcagag	gcacccctgt	gatcgtgtca	360
agcgcgtcga	ccaaggcccc	cagcgtgttc	cctctggccc	ctagcagcaa	gagcacatct	420
ggcggaacag	ccgccctggg	ctgcctcgtg	aaggactact	ttcccgagcc	cgtgaccgtg	480
tcctggaatt	ctggcgccct	gaccagcggc	gtgcacacct	ttccagctgt	gctgcagtcc	540
agcggcctgt	acagcctgag	cagcgtcgtg	acagtgccca	gcagctctct	gggcacccag	600
acctacatct	gcaacgtgaa	ccacaagccc	agcaacacca	aggtggacaa	gaaggtggaa	660
cccaagagct	gcgacaagac	ccacacctgt	cccccttgct	ctgccccga	actgctggga	720
ggcccttccg	tgttcctgtt	ccccccaaag	cccaaggaca	ccctgatgat	cagccggacc	780
cccgaagtga	cctgcgtggt	ggtggatgtg	tcccacgagg	accctgaagt	gaagttcaat	840
tggtacgtgg	acggcgtgga	agtgcacaac	gccaaagacca	agccaagaga	ggaacagtac	900
aacagcacct	accgggtggt	gtccgtgctg	accgtgctgc	accaggactg	gctgaacggc	960
aaagagtaca	agtgcagggt	gtccaacaag	gccctgcctg	cccccatcga	gaaaaccatc	1020
agcaaggcca	agggccagcc	ccgcgaaccc	caggtgtgca	cactgcccc	aagcagggac	1080
gagctgacca	agaaccaggt	gtccctgagc	tgtgccgtga	aaggcttcta	cccctccgat	1140
atcgccgtgg	aatgggagag	caacggccag	cccgagaaca	actacaagac	cacccccct	1200
gtgctggaca	gcgacggctc	attcttcctg	gtgtccaagc	tgacagtgga	caagtcccgg	1260
tggcagcagg	gcaacgtgtt	cagctgctcc	gtgatgcacg	aggccctgca	caaccactac	1320
accagaagt	ccctgagcct	gagccccggc				1350

<210> 38

<211> 630

<212> DNA

<213> Artificial Sequence

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<220>

<223> Synthetic Construct

<400> 38

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atcagctgcc ggacaagcca gtacggcagc ctggcctggt atcagcagag gcctggacag 120
gccccagac tcgtgatcta cagcggcagc acaagagccg ccggaatccc cgatagattc 180
agcggctcca gatggggccc tgactacaac ctgaccatca gcaacctgga aagcggcgac 240
ttcggcgtgt actactgcca gcagtacgag ttcttcggcc agggcaccaa ggtgcagggtg 300
gacatcaagc gtacggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630
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<210> 39

<211> 1806

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 39

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agctgttctg cctccggctt tgatttcgat aacgcctgga tgacctgggt caggcagcct 120
ccaggtaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctggtccgtg 180
gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
acaggcaaat actacgactt ctggtggggc tatccccctg gcgaggaata ttttcaagac 360
tggggtcagg gaacccttgt tatcgtgtcc tccgacaaaa cccataccca gatgcagctg 420
caggagagcg gccctggact cgtgaagccc agcgagacct tgagcctgac atgcagcgtg 480
agcggcgcca gcatcagcga cagctactgg agctggatca ggaggagccc tggcaagggc 540
ctggagtgga tcggctacgt gcacaagagc ggcgacacca actacagccc ctccctgaag 600
tccagggtga acctgtccct ggacaccagc aagaaccagg tgagcctgtc cctggtggct 660
gccacagctg ctgacagcgg caagtactac tgtgccagga ccctgcacgg caggaggatc 720
tacggcatcg tggccttcaa cgagtggttc acctattctt acatggacgt gtggggcaac 780
ggcaccacag tgaccgtgag ctccgataag acccacaccg cttccaccaa gggcccatcg 840
gtcttcccc tggcaccctc ctccaagagc acctctgggg gcacagcggc cctgggctgc 900
ctggtcaagg actacttccc cgaaccgggtg acggtgtcgt ggaactcagg cgccctgacc 960
agcggcgtgc acaccttccc ggctgtccta cagtcctcag gactctactc cctcagcagc 1020
gtggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 1080
aagcccagca acaccaaggt ggacaagaaa gttgagccca aatcttgtga caaaactcac 1140
acatgcccac cgtgcccagc acctgaactc ctgggggggac cgtcagtctt cctcttcccc 1200
ccaaaacca aggacaccct catgatctcc cggacccttg aggtcacatg cgtggtgggtg 1260
gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt atgttgacgg cgtggagggtg 1320
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1380
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1440
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1500
gaaccacagg tgtacaccct gccccatgc cgggatgagc tgaccaagaa tcaagtcagc 1560
ctgtggtgcc tggtaaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1620
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gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1680
ttcctctact caaaactcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1740
tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1800
ccgggt 1806
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<210> 40

<211> 993

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 40

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ggaagcaggg ctgtgcagtg gtaccaacac agggccggac aggctcccag cctgatcatc 120
tacaacaacc aggacaggcc cagcggcatc cctgagaggt tcagcgggaag ccccgacagc 180
cccttcggaa ccacagccac cctgaccatc acaagcgtgg aagccggcga cgaggccgac 240
tactactgcc acatctggga cagcagggtg cccaccaagt ggggtgtttgg cggcggcacc 300
accctgaccg tgctggacaa aaccataacc gcatccgaac tgactcagga ccctgccgtc 360
tctgtggcac tgaagcagac tgtgactatt acttgccgag gcgactcact gcggagccac 420
tacgcttcct ggtatcagaa gaaacccggc caggcacctg tgctgctgtt ctacggaaag 480
aacaataggc catctggcat ccccgaccgc ttttctggca gtgcatcagg gaaccgagcc 540
agtctgacca ttaccggcgc ccaggctgag gacgaagccg attactattg cagctcccgg 600
gataagagcg gctccagact gagcgtgttc ggaggaggaa ctaaactgac cgtcctcgat 660
aagaccata cccgtacggg ggccgctccc agcgtgttca tcttcccacc tagcgacgag 720
cagctgaagt cggcacagc ctctgtctgtg tgcctgtga acaatttcta ccccgcgag 780
gccaaagtgc agtggaagggt ggacaacgcc ctgcagagcg gcaacagcca ggaaagcgtg 840
accgagcagg acagcaagga ctccacctac agcctgagca gcaccctgac actgagcaag 900
gccgactacg agaagcaca ggtgtacgcc tgcgaagtga cccaccaggg cctgtctagc 960
cccgtgacca agagcttcaa ccggggcgag tgt 993
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<210> 41

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 41

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Ser Met Arg Ile Ser Cys Arg Ala Ser Gly Tyr Glu Phe Ile Asp Cys
 20           25           30
Thr Leu Asn Trp Ile Arg Leu Ala Pro Gly Lys Arg Pro Glu Trp Met
 35           40           45
Gly Trp Leu Lys Pro Arg Gly Gly Ala Val Asn Tyr Ala Arg Pro Leu
 50           55           60
Gln Gly Arg Val Thr Met Thr Arg Asp Val Tyr Ser Asp Thr Ala Phe
 65           70           75           80
Leu Glu Leu Arg Ser Leu Thr Val Asp Asp Thr Ala Val Tyr Phe Cys
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														85															90															95
Thr	Arg	Gly	Lys		Asn	Cys	Asp	Tyr	Asn		Trp	Asp	Phe	Glu	His	Trp		Gly																										
														100															105															110
Arg	Gly	Thr	Pro	Val	Ile	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser																													
														115															120															125
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala																													
														130															135															140
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val																													
														145															150															155
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala																													
														165															170															175
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val																													
														180															185															190
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His																													
														195															200															205
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys																													
														210															215															220
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly																													
														225															230															235
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met																													
														245															250															255
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His																													
														260															265															270
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val																													
														275															280															285
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr																													
														290															295															300
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly																													
														305															310															315
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile																													
														325															330															335
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val																													
														340															345															350
Cys	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser																													
														355															360															365
Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu																													
														370															375															380
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro																													
														385															390															395
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr	Val																													
														405															410															415
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met																													
														420															425															430
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser																													
														435															440															445
Pro	Gly																																											450

<210>	42
<211>	210
<212>	PRT

4.___183952027041SEQLIST.TXT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 42

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

<210> 43

<211> 611

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 43

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

60

Lys 65	Ala	Lys	Val	Thr	Ile 70	Asp	Trp	Asp	Arg	Ser 75	Thr	Asn	Thr	Ala	Tyr 80
Leu	Gln	Leu	Ser	Gly 85	Leu	Thr	Ser	Gly	Asp 90	Thr	Ala	Val	Tyr	Tyr 95	Cys
Ala	Lys	Gly	Ser 100	Lys	His	Arg	Leu	Arg 105	Asp	Tyr	Ala	Leu	Tyr 110	Asp	Asp
Asp	Gly	Ala 115	Leu	Asn	Trp	Ala 120	Val	Asp	Val	Asp	Tyr	Leu	Ser	Asn	Leu
Glu	Phe 130	Trp	Gly	Gln	Gly 135	Thr	Ala	Val	Thr	Val	Ser 140	Ser	Asp	Lys	Thr
His 145	Thr	Glu	Val	Arg	Leu 150	Val	Glu	Ser	Gly	Gly 155	Gly	Leu	Val	Lys	Pro 160
Gly	Gly	Ser	Leu	Arg 165	Leu	Ser	Cys	Ser	Ala 170	Ser	Gly	Phe	Asp	Phe 175	Asp
Asn	Ala	Trp	Met 180	Thr	Trp	Val	Arg	Gln 185	Pro	Pro	Gly	Lys	Gly 190	Leu	Glu
Trp	Val	Gly 195	Arg	Ile	Thr	Gly 200	Pro	Gly	Glu	Gly	Trp	Ser 205	Val	Asp	Tyr
Ala	Glu 210	Ser	Val	Lys	Gly 215	Arg	Phe	Thr	Ile	Ser	Arg 220	Asp	Asn	Thr	Lys
Asn 225	Thr	Leu	Tyr	Leu	Glu 230	Met	Asn	Asn	Val	Arg 235	Thr	Glu	Asp	Thr	Gly 240
Tyr	Tyr	Phe	Cys	Ala 245	Arg	Thr	Gly	Lys	Tyr 250	Tyr	Asp	Phe	Trp	Trp 255	Gly
Tyr	Pro	Pro	Gly 260	Glu	Glu	Tyr	Phe	Gln 265	Asp	Trp	Gly	Gln	Gly 270	Thr	Leu
Val	Ile	Val 275	Ser	Ser	Asp	Lys	Thr	His 280	Thr	Ala	Ser	Thr 285	Lys	Gly	Pro
Ser	Val	Phe 290	Pro	Leu	Ala 295	Pro	Ser	Ser	Lys	Ser	Thr 300	Ser	Gly	Gly	Thr
Ala 305	Ala	Leu	Gly	Cys	Leu 310	Val	Lys	Asp	Tyr	Phe 315	Pro	Glu	Pro	Val	Thr
Val	Ser	Trp	Asn	Ser 325	Gly	Ala	Leu	Thr	Ser 330	Gly	Val	His	Thr	Phe 335	Pro
Ala	Val	Leu	Gln 340	Ser	Ser	Gly	Leu	Tyr 345	Ser	Leu	Ser	Ser	Val	Val	Thr
Val	Pro	Ser 355	Ser	Ser	Leu	Gly	Thr	Gln 360	Thr	Tyr	Ile	Cys 365	Asn	Val	Asn
His	Lys 370	Pro	Ser	Asn	Thr	Lys 375	Val	Asp	Lys	Lys	Val 380	Glu	Pro	Lys	Ser
Cys 385	Asp	Lys	Thr	His	Thr 390	Cys	Pro	Pro	Cys	Pro 395	Ala	Pro	Glu	Leu	Leu
Gly	Gly	Pro	Ser	Val 405	Phe	Leu	Phe	Pro	Pro 410	Lys	Pro	Lys	Asp	Thr	Leu
Met	Ile	Ser	Arg 420	Thr	Pro	Glu	Val	Thr 425	Cys	Val	Val	Val	Asp	Val	Ser
His	Glu	Asp 435	Pro	Glu	Val	Lys	Phe 440	Asn	Trp	Tyr	Val	Asp 445	Gly	Val	Glu
Val	His 450	Asn	Ala	Lys	Thr	Lys 455	Pro	Arg	Glu	Glu	Gln 460	Tyr	Asn	Ser	Thr
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn

4.__183952027041SEQLIST.TXT

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465          470          475          480
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
          485          490          495
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
          500          505          510
Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
          515          520          525
Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
          530          535          540
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545          550          555          560
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
          565          570          575
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
          580          585          590
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
          595          600          605
Ser Pro Gly
          610

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<210> 44

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 44

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

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4. __183952027041SEQLIST.TXT

Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Asp	Lys	Asp	Phe	Thr	Leu
			180					185					190		
Lys	Ile	Ser	Arg	Val	Glu	Thr	Glu	Asp	Val	Gly	Thr	Tyr	Tyr	Cys	Met
		195					200					205			
Gln	Gly	Arg	Glu	Ser	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Asp
	210					215					220				
Ile	Lys	Asp	Lys	Thr	His	Thr	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe
225					230					235					240
Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val
				245					250					255	
Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp
			260					265					270		
Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr
		275					280					285			
Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr
	290					295					300				
Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val
305					310					315					320
Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly
				325					330					335	

Glu Cys

<210> 45

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 45

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agctgcagag	ccagcggcta	cgagttcatc	gactgcaccc	tgaactggat	cagactggcc	120
cctggcaagc	ggcctgagtg	gatgggatgg	ctgaagccta	gaggcggagc	cgtgaactac	180
gccagacctc	tgcagggcag	agtgaccatg	accggggacg	tgtacagcga	taccgccttc	240
ctggaactgc	ggagcctgac	cgtggatgat	accgccgtgt	acttctgcac	ccggggcaag	300
aactgcgact	acaactggga	cttcgagcac	tggggcgagag	gcacccctgt	gatcgtgtca	360
agcgcgtcga	ccaaggggccc	cagcgtgttc	cctctggccc	ctagcagcaa	gagcacatct	420
ggcgggaacag	ccgccctggg	ctgcctcgtg	aaggactact	ttcccagagcc	cgtgaccgtg	480
tcctggaatt	ctggcgccct	gaccagcggc	gtgcacacct	ttccagctgt	gctgcagtcc	540
agcggcctgt	acagcctgag	cagcgtcgtg	acagtgccca	gcagctctct	gggcacccag	600
acctacatct	gcaacgtgaa	ccacaagccc	agcaacacca	aggtggacaa	gaaggtggaa	660
cccaagagct	gcgacaagac	ccacacctgt	cccccttgct	ctgccccga	actgctggga	720
ggcccttccg	tgttcctgtt	ccccccaaag	cccaaggaca	ccctgatgat	cagccggacc	780
cccgaagtga	cctgcgtggt	ggtggatgtg	tcccacgagg	accctgaagt	gaagttcaat	840
tggtacgtgg	acggcgtgga	agtgacacaac	gccaaagacca	agccaagaga	ggaacagtac	900
aacagcacct	accgggtggt	gtccgtgctg	accgtgctgc	accaggactg	gctgaacggc	960
aaagagtaca	agtgaaggt	gtccaacaag	gccctgcctg	cccccatcga	gaaaaccatc	1020
agcaaggcca	agggccagcc	ccgcgaaccc	caggtgtgca	cactgcccc	aagcagggac	1080
gagctgacca	agaaccaggt	gtccctgagc	tgtgccgtga	aaggcttcta	cccctccgat	1140

4. __183952027041SEQLIST.TXT

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atcgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cccccccct 1200
gtgctggaca gcgacggctc attcttcctg gtgtccaagc tgacagtgga caagtcccg 1260
tggcagcagg gcaacgtgtt cagctgctcc gtgatgcacg aggccctgca caaccactac 1320
accagaagt ccctgagcct gagccccggc                                     1350
```

<210> 46

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 46

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atcagctgcc ggacaagcca gtacggcagc ctggcctggg atcagcagag gcctggacag 120
gccccagac tcgtgatcta cagcggcagc acaagagccg ccggaatccc cgatagattc 180
agcggctcca gatggggccc tgactacaac ctgaccatca gcaacctgga aagcggcgac 240
ttcggcgtgt actactgcca gcagtacgag ttcttcggcc agggcaccaa ggtgcagggtg 300
gacatcaagc gtacgggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt                                     630
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<210> 47

<211> 1833

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 47

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tcctgcaagg cccctggcaa caccctgaaa acctacgacc tgcactgggt gcgcagcgtg 120
ccaggacagg gactgcagtg gatgggctgg atcagccacg agggcgacaa gaaagtgatc 180
gtggaacggg tcaaggccaa agtgaccatc gactgggaca gaagcaccaa caccgcctac 240
ctgcagctga gcggcctgac ctctggcgat accgccgtgt actactgcgc caagggcagc 300
aagcaccggc tgagagacta cgccctgtac gacgatgacg gcgccctgaa ctgggcccgtg 360
gatgtggact acctgagcaa cctggaattc tggggccagg gcacagccgt gaccgtgtca 420
tctgacaaaa cccataccga ggttagactg gtggagtcag gaggggggct tgtgaagccc 480
gggtgggtctc tccgcctgag ctgttctgcc tccggctttg atttcgataa cgcctggatg 540
acctgggtca ggcagcctcc aggtaaggga ctggagtggg tgggaagaat cacagggtcca 600
ggcgaggggc ggtccgtgga ctacgcggaa tctgttaaag ggcggtttac aatctcaagg 660
gacaatacca agaatacctt gtatttggag atgaacaacg tgagaactga agacaccgga 720
tattacttct gtgccagaac aggcaaatac tacgacttct ggtggggcta tccccctggc 780
gaggaatatt ttcaagactg gggtcaggga acccttggtt tcgtgtcctc cgataagacc 840
cacaccgctt ccaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 900
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 960
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgtcctacag 1020
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4. __183952027041SEQLIST.TXT

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tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 1080
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 1140
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 1200
gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg 1260
acccttgagg tcacatgcgt ggtgggtggac gtgagccacg aagaccctga ggtcaagttc 1320
aactggtatg ttgacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1500
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatgccgg 1560
gatgagctga ccaagaatca agtcagcctg tgggtgcctgg taaaaggctt ctatcccagc 1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactaaa gaccacgcct 1680
cccgtgctgg actccgacgg ctcttcttct ctctactcaa aactcaccgt ggacaagagc 1740
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800
tacacgcaga agagcctctc cctgtctccg ggt 1833

```

<210> 48

<211> 1014

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 48

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acttgccgag gcgactcact gcggagccac tacgcttcct ggtatcagaa gaaacccggc 120
caggcacctg tgctgctgtt ctacggaaag aacaataggc catctggcat ccccgaccgc 180
ttttctggca gtgcatcagg gaaccgagcc agtctgacca ttaccggcgc ccaggctgag 240
gacgaagccg attactattg cagctcccgg gataagagcg gctccagact gagcgtgttc 300
ggaggaggaa ctaaactgac cgtcctcgac aaaaccata ccgacttcgt gctgaccag 360
agccctcaca gcctgagcgt gacacctggc gagagcgcca gcatcagctg caagagcagc 420
cactccctga tccacggcga ccggaacaac tacctggctt ggtacgtgca gaagcccggc 480
agatccccc agctgctgat ctacctggcc agcagcagag ccagcggcgt gccgataga 540
ttttctggca gcggcagcga caaggacttc accctgaaga tcagccgggt ggaaaccgag 600
gacgtgggca cctactactg tatgcagggc agagagagcc cctggacctt tggccagggc 660
accaaggtgg acatcaagga taagacccat acccgtagcg tggccgctcc cagcgtgttc 720
atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 780
aacaacttct acccccgcca ggccaaagtg cagtgggaagg tggacaacgc cctgcagagc 840
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccacctc cagcctgagc 900
agcaccctga cactgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 960
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```

<210> 49

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 49

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

4.__183952027041SEQLIST.TXT

1	5	10	15
Ser Met Arg Ile Ser Cys Arg Ala Ser Gly Tyr Glu Phe Ile Asp Cys			
20	25	30	
Thr Leu Asn Trp Ile Arg Leu Ala Pro Gly Lys Arg Pro Glu Trp Met			
35	40	45	
Gly Trp Leu Lys Pro Arg Gly Gly Ala Val Asn Tyr Ala Arg Pro Leu			
50	55	60	
Gln Gly Arg Val Thr Met Thr Arg Asp Val Tyr Ser Asp Thr Ala Phe			
65	70	75	80
Leu Glu Leu Arg Ser Leu Thr Val Asp Asp Thr Ala Val Tyr Phe Cys			
85	90	95	
Thr Arg Gly Lys Asn Cys Asp Tyr Asn Trp Asp Phe Glu His Trp Gly			
100	105	110	
Arg Gly Thr Pro Val Ile Val Ser Ser Ala Ser Thr Lys Gly Pro Ser			
115	120	125	
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala			
130	135	140	
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val			
145	150	155	160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala			
165	170	175	
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val			
180	185	190	
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His			
195	200	205	
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys			
210	215	220	
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly			
225	230	235	240
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met			
245	250	255	
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His			
260	265	270	
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val			
275	280	285	
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr			
290	295	300	
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly			
305	310	315	320
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile			
325	330	335	
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val			
340	345	350	
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser			
355	360	365	
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu			
370	375	380	
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro			
385	390	395	400
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val			
405	410	415	
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met			

4. 183952027041SEQLIST.TXT

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
420 425 430
435 440 445
Pro Gly
450

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<210> 50
<211> 210
<212> PRT
<213> Artificial Sequence
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<220>
<223> Synthetic Construct

[illegible]

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<210> 51
<211> 612
<212> PRT
<213> Artificial Sequence
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 $\langle 220 \rangle$

4.___183952027041SEQLIST.TXT

<223> Synthetic Construct

<400> 51

Gln	Met	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
1				5					10					15	
Thr	Leu	Ser	Leu	Thr	Cys	Ser	Val	Ser	Gly	Ala	Ser	Ile	Ser	Asp	Ser
			20					25					30		
Tyr	Trp	Ser	Trp	Ile	Arg	Arg	Ser	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile
		35					40					45			
Gly	Tyr	Val	His	Lys	Ser	Gly	Asp	Thr	Asn	Tyr	Ser	Pro	Ser	Leu	Lys
	50					55					60				
Ser	Arg	Val	Asn	Leu	Ser	Leu	Asp	Thr	Ser	Lys	Asn	Gln	Val	Ser	Leu
65				70						75					80
Ser	Leu	Val	Ala	Ala	Thr	Ala	Ala	Asp	Ser	Gly	Lys	Tyr	Tyr	Cys	Ala
				85					90					95	
Arg	Thr	Leu	His	Gly	Arg	Arg	Ile	Tyr	Gly	Ile	Val	Ala	Phe	Asn	Glu
			100					105					110		
Trp	Phe	Thr	Tyr	Phe	Tyr	Met	Asp	Val	Trp	Gly	Asn	Gly	Thr	Gln	Val
		115					120					125			
Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Gln	Val	His	Leu	Thr	Gln	Ser
	130					135					140				
Gly	Pro	Glu	Val	Arg	Lys	Pro	Gly	Thr	Ser	Val	Lys	Val	Ser	Cys	Lys
145					150					155					160
Ala	Pro	Gly	Asn	Thr	Leu	Lys	Thr	Tyr	Asp	Leu	His	Trp	Val	Arg	Ser
				165					170					175	
Val	Pro	Gly	Gln	Gly	Leu	Gln	Trp	Met	Gly	Trp	Ile	Ser	His	Glu	Gly
			180					185					190		
Asp	Lys	Lys	Val	Ile	Val	Glu	Arg	Phe	Lys	Ala	Lys	Val	Thr	Ile	Asp
	195						200					205			
Trp	Asp	Arg	Ser	Thr	Asn	Thr	Ala	Tyr	Leu	Gln	Leu	Ser	Gly	Leu	Thr
	210					215					220				
Ser	Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Gly	Ser	Lys	His	Arg
225					230					235					240
Leu	Arg	Asp	Tyr	Ala	Leu	Tyr	Asp	Asp	Asp	Gly	Ala	Leu	Asn	Trp	Ala
				245					250					255	
Val	Asp	Val	Asp	Tyr	Leu	Ser	Asn	Leu	Glu	Phe	Trp	Gly	Gln	Gly	Thr
		260					265					270			
Ala	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Ala	Ser	Thr	Lys	Gly
		275					280					285			
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly
	290					295					300				
Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val
305					310					315					320
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe
				325					330					335	
Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val
			340					345					350		
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val
		355					360					365			
Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys
	370					375					380				
Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu

4.__183952027041SEQLIST.TXT

```

385          390          395          400
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
          405          410          415
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
          420          425          430
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
          435          440          445
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
          450          455          460
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
465          470          475          480
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
          485          490          495
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
          500          505          510
Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln
          515          520          525
Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
          530          535          540
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
545          550          555          560
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
          565          570          575
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
          580          585          590
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
          595          600          605
Leu Ser Pro Gly
          610

```

<210> 52
 <211> 334
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 52
Asp Phe Val Leu Thr Gln Ser Pro His Ser Leu Ser Val Thr Pro Gly
  1          5          10          15
Glu Ser Ala Ser Ile Ser Cys Lys Ser Ser His Ser Leu Ile His Gly
          20          25          30
Asp Arg Asn Asn Tyr Leu Ala Trp Tyr Val Gln Lys Pro Gly Arg Ser
          35          40          45
Pro Gln Leu Leu Ile Tyr Leu Ala Ser Ser Arg Ala Ser Gly Val Pro
          50          55          60
Asp Arg Phe Ser Gly Ser Gly Ser Asp Lys Asp Phe Thr Leu Lys Ile
65          70          75          80
Ser Arg Val Glu Thr Glu Asp Val Gly Thr Tyr Tyr Cys Met Gln Gly
          85          90          95

```


4. __183952027041SEQLIST.TXT

```

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

```

<210> 53

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 53

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caggtgcagc tgggtgcagtc tggcggccag atgaagaaac ccggcgagag catgcggatc 60
agctgcagag ccagcggcta cgagttcatc gactgcaccc tgaactggat cagactggcc 120
cctggcaagc ggcctgagtg gatgggatgg ctgaagccta gaggcggagc cgtgaactac 180
gccagacctc tgcagggcag agtgaccatg acccgggacg tgtacagcga taccgccttc 240
ctggaactgc ggagcctgac cgtggatgat accgccgtgt acttctgcac ccggggcaag 300
aactgcgact acaactggga cttcgagcac tggggcgagag gcacccctgt gatcgtgtca 360
agcgcgtcga ccaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 420
ggcggaaacag ccgccctggg ctgcctcgtg aaggactact ttcccagacc cgtgaccgtg 480
tcctggaatt ctggcgcctt gaccagcggc gtgcacacct ttccagctgt gctgcagtcc 540
agcggcctgt acagcctgag cagcgtcgtg acagtgccca gcagctctct gggcacccag 600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 660

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4. __183952027041SEQLIST.TXT

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cccaagagct gcgacaagac ccacacctgt ccccttgtc ctgccccga actgctggga 720
ggcccttccg tgttcctgtt ccccccaaag cccaaggaca ccctgatgat cagccggacc 780
cccgaagtga cctgcgtggg ggtggatgtg tcccacgagg accctgaagt gaagttcaat 840
tggtacgtgg acggcgtgga agtgcacaac gccaaagaca agccaagaga ggaacagtac 900
aacagcacct accgggtggg gtccgtgctg accgtgctgc accaggactg gctgaacggc 960
aaagagtaca agtgcaagggt gtccaacaag gccctgcctg ccccatcga gaaaaccatc 1020
agcaaggcca agggccagcc ccgcgaaccc cagggtgtgca cactgcccc aagcagggac 1080
gagctgacca agaaccagggt gtccctgagc tgtgccgtga aaggcttcta cccctccgat 1140
atcgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cccccccct 1200
gtgctggaca gcgacggctc attcttctg gtgtccaagc tgacagtgga caagtcccgg 1260
tggcagcagg gcaacgtgtt cagctgctcc gtgatgcacg aggccctgca caaccactac 1320
accagaagt ccctgagcct gagccccggc 1350

```

<210> 54

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 54

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atcagctgcc ggacaagcca gtacggcagc ctggcctggt atcagcagag gcctggacag 120
gccccagac tcgtgatcta cagcggcagc acaagagccg ccggaatccc cgatagattc 180
agcggctcca gatggggccc tgactacaac ctgaccatca gcaacctgga aagcggcgac 240
ttcggcgtgt actactgcca gcagtacgag ttcttcggcc agggcaccaa ggtgcagggtg 300
gacatcaagc gtacggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaagggt gtacgcctgc gaagtgaccc accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630

```

<210> 55

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 55

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acatgcagcg tgagcggcgc cagcatcagc gacagctact ggagctggat caggaggagc 120
cctggcaagg gcctggagtg gatcggctac gtgcacaaga gcggcgacac caactacagc 180
ccctccctga agtccagggt gaacctgtcc ctggacacca gcaagaacca ggtgagcctg 240
tccctggtgg ctgccacagc tgtgacagc ggcaagtact actgtgccag gaccctgcac 300
ggcaggagga tctacggcat cgtggccttc aacgagtggg tcacctactt ctacatggac 360
gtgtggggca acggcaccca ggtgaccgtg agctccgaca aaaccatac ccaggtgcac 420
ctgacacaga gcggacccga agtgcggaag cctggcacct ctgtgaagggt gtcctgcaag 480
ggccctggca acaccctgaa aacctacgac ctgcactggg tgcgcagcgt gccaggacag 540

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4. __183952027041SEQLIST.TXT

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ggactgcagt ggatgggctg gatcagccac gagggcgaca agaaagtgat cgtggaacgg 600
ttcaaggcca aagtgaccat cgactgggac agaagcacca acaccgccta cctgcagctg 660
agcggcctga cctctggcga taccgccgtg tactactgcg ccaagggcag caagcaccgg 720
ctgagagact acgccctgta cgacgatgac ggcgccctga actgggccgt ggatgtggac 780
tacctgagca acctggaatt ctggggccag ggcacagccg tgaccgtgtc atctgataag 840
accacaccg cttccacca gggcccatcg gtcttcccc tggcacctc ctccaagagc 900
acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccgggtg 960
acgggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 1020
cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 1080
accagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 1140
gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 1200
ctgggggggac cgtcagtctt cctcttcccc caaaaaccca aggacaccct catgatctcc 1260
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagacc tgaggtcaag 1320
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cagtacaaca gcacgtaccg tgtggtcagc gtctctaccg tcctgcacca ggactggctg 1440
aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1500
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatgc 1560
cgggatgagc tgaccaagaa tcaagtcagc ctgtggtgcc tggtaaaagg cttctatccc 1620
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cctcccgtgc tggactccga cggctcctt ttctctact caaaactcac cgtggacaag 1740
agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1800
cactacacgc agaagagcct ctccctgtct ccgggt 1836

```

<210> 56

<211> 1002

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 56

```

gacttcgtgc tgaccagag ccctcacagc ctgagcgtga cacctggcga gagcgccagc 60
atcagctgca agagcagcca ctccctgata cacggcgacc ggaacaacta cctggcttgg 120
tacgtgcaga agcccggcag atccccccag ctgctgatct acctggccag cagcagagcc 180
agcggcgtgc ccgatagatt ttctggcagc ggcagcgaca aggacttcac cctgaagatc 240
agccgggtgg aaaccgagga cgtgggcacc tactactgta tgcagggcag agagagcccc 300
tggaaccttg gccagggcac caaggtggac atcaaggaca aaaccatac ctccgacatc 360
agcgtggccc ccggagagac agccaggatc tcctgcggcg agaagagcct gggaagcagg 420
gctgtgcagt ggtaccaaca cagggccgga caggctccca gcctgatcat ctacaacaac 480
caggacaggc ccagcggcat ccctgagagg ttacgcggaa gcccgcagag ccccttcgga 540
accacagcca ccctgaccat cacaagcgtg gaagccggcg acgaggccga ctactactgc 600
cacatctggg acagcagggt gccaccaag tgggtgtttg gcggcggcac caccctgacc 660
gtgctggata agaccatac ccgtacgggt gccgtccca gcgtgttcat cttccacct 720
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 780
ccccgcgagg ccaaagtgca gtggaagggt gacaacgccc tgcagagcgg caacagccag 840
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgaca 900
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgc ccaccagggc 960
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```

<210> 57

<211> 451

4.__183952027041SEQLIST.TXT

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 57

Arg	Ala	His	Leu	Val	Gln	Ser	Gly	Thr	Ala	Met	Lys	Lys	Pro	Gly	Ala	1	5	10	15
Ser	Val	Arg	Val	Ser	Cys	Gln	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Ala	His	20	25	30	
Ile	Leu	Phe	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Val	35	40	45	
Gly	Trp	Ile	Lys	Pro	Gln	Tyr	Gly	Ala	Val	Asn	Phe	Gly	Gly	Gly	Phe	50	55	60	
Arg	Asp	Arg	Val	Thr	Leu	Thr	Arg	Asp	Val	Tyr	Arg	Glu	Ile	Ala	Tyr	65	70	75	80
Met	Asp	Ile	Arg	Gly	Leu	Lys	Pro	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Ala	Arg	Asp	Arg	Ser	Tyr	Gly	Asp	Ser	Trp	Ala	Leu	Asp	Ala	Trp		100	105	110	
Gly	Gln	Gly	Thr	Thr	Val	Val	Val	Ser	Ala	Ala	Ser	Thr	Lys	Gly	Pro	115	120	125	
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	130	135	140	
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	145	150	155	160
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	165	170	175	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	180	185	190	
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	195	200	205	
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	210	215	220	
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	225	230	235	240
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	245	250	255	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	260	265	270	
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	275	280	285	
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	290	295	300	
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	305	310	315	320
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	325	330	335	
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	340	345	350	
Val	Cys	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val				

4._183952027041SEQLIST.TXT

```

          355          360          365
Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
          370          375          380
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385          390          395          400
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
          405          410          415
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
          420          425          430
Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu
          435          440          445
Ser Pro Gly
          450

```

<210> 58

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 58

```

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

```

4.__183952027041SEQLIST.TXT

<210> 59
 <211> 615
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 59
 Glu Val Arg Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Asp Asn Ala
 20 25 30
 Trp Met Thr Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Gly Arg Ile Thr Gly Pro Gly Glu Gly Trp Ser Val Asp Tyr Ala Glu
 50 55 60
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Asn Thr
 65 70 75 80
 Leu Tyr Leu Glu Met Asn Asn Val Arg Thr Glu Asp Thr Gly Tyr Tyr
 85 90 95
 Phe Cys Ala Arg Thr Gly Lys Tyr Tyr Asp Phe Trp Trp Gly Tyr Pro
 100 105 110
 Pro Gly Glu Glu Tyr Phe Gln Asp Trp Gly Gln Gly Thr Leu Val Ile
 115 120 125
 Val Ser Ser Asp Lys Thr His Thr Gln Val Gln Leu Val Glu Ser Gly
 130 135 140
 Gly Gly Val Val Gln Pro Gly Thr Ser Leu Arg Leu Ser Cys Ala Ala
 145 150 155 160
 Ser Gln Phe Arg Phe Asp Gly Tyr Gly Met His Trp Val Arg Gln Ala
 165 170 175
 Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile Ser His Asp Gly Ile
 180 185 190
 Lys Lys Tyr His Ala Glu Lys Val Trp Gly Arg Phe Thr Ile Ser Arg
 195 200 205
 Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro
 210 215 220
 Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Lys Asp Leu Arg Glu Asp Glu
 225 230 235 240
 Cys Glu Glu Trp Trp Ser Asp Tyr Tyr Asp Phe Gly Lys Gln Leu Pro
 245 250 255
 Cys Ala Lys Ser Arg Gly Gly Leu Val Gly Ile Ala Asp Asn Trp Gly
 260 265 270
 Gln Gly Thr Met Val Thr Val Ser Ser Asp Lys Thr His Thr Ala Ser
 275 280 285
 Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
 290 295 300
 Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
 305 310 315 320
 Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val

4.__183952027041SEQLIST.TXT

```

          325          330          335
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
          340          345          350
Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
          355          360          365
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
          370          375          380
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
385          390          395          400
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
          405          410          415
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
          420          425          430
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
          435          440          445
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
          450          455          460
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
465          470          475          480
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
          485          490          495
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
          500          505          510
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr
          515          520          525
Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
          530          535          540
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
545          550          555          560
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
          565          570          575
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
          580          585          590
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
          595          600          605
Ser Leu Ser Leu Ser Pro Gly
          610          615

```

<210> 60

<211> 337

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 60

```

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
1          5          10          15
Lys Val Thr Ile Ser Cys Ser Gly Asn Thr Ser Asn Ile Gly Asn Asn
          20          25          30

```

4.__183952027041SEQLIST.TXT

Phe Val Ser Trp Tyr Gln Gln Arg Pro Gly Arg Ala Pro Gln Leu Leu
 35 40 45
 Ile Tyr Glu Thr Asp Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
 50 55 60
 Ala Ser Lys Ser Gly Thr Ser Gly Thr Leu Ala Ile Thr Gly Leu Gln
 65 70 75 80
 Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Ala Ala Ser Leu
 85 90 95
 Ser Ser Ala Arg Val Phe Gly Thr Gly Thr Lys Val Ile Val Leu Asp
 100 105 110
 Lys Thr His Thr Ala Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val
 115 120 125
 Ala Leu Lys Gln Thr Val Thr Ile Thr Cys Arg Gly Asp Ser Leu Arg
 130 135 140
 Ser His Tyr Ala Ser Trp Tyr Gln Lys Lys Pro Gly Gln Ala Pro Val
 145 150 155 160
 Leu Leu Phe Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg
 165 170 175
 Phe Ser Gly Ser Ala Ser Gly Asn Arg Ala Ser Leu Thr Ile Thr Gly
 180 185 190
 Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Arg Asp Lys
 195 200 205
 Ser Gly Ser Arg Leu Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val
 210 215 220
 Leu Asp Lys Thr His Thr Arg Thr Val Ala Ala Pro Ser Val Phe Ile
 225 230 235 240
 Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
 245 250 255
 Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
 260 265 270
 Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
 275 280 285
 Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
 290 295 300
 Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
 305 310 315 320
 His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
 325 330 335
 Cys

<210> 61

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 61

agagcccacc tgggtgcagtc tggcaccgcc atgaagaaac caggcgctc tgtgcgggtg 60

4. __183952027041SEQLIST.TXT

```

tcctgtcaga caagcggcta caccttcacc gccacatcc tgttctggtt ccggcaggcc 120
cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
ggcggaggct tccgggatag agtgaccctg acccgggacg tgtaccgca gatcgctac 240
atggacatcc ggggcctgaa gcccgatgac accgccgtgt actactgcgc cagagacaga 300
agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtggtggtg 360
tctgccgcct ctacaaaggg cccagcgtg ttccctctgg cccctagcag caagagcaca 420
tctggcggaa cagccgccct gggctgcctc gtgaaggact actttcccga gcccgtagcc 480
gtgtcctgga attctggcgc cctgaccagc ggcgtagcaca cctttccagc tgtgctgcag 540
tccagcggcc tgtacagcct gagcagcgtc gtgacagtgc ccagcagctc tctgggcacc 600
cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagaagggtg 660
gaacccaaga gctgcgacaa gaccacacc tgtccccctt gtcctgcccc cgaactgctg 720
ggaggccctt ccgtgttcct gttccccca aagcccaagg acaccctgat gatcagccgg 780
acccccgaag tgacctgcgt ggtggtggat gtgtcccacg aggaccctga agtgaagttc 840
aattggtacg tggacggcgt ggaagtgcac aacgccaaga ccaagccaag agaggaacag 900
tacaacagca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ctggctgaac 960
ggcaaagagt acaagtgcaa ggtgtccaac aaggccctgc ctgcccccat cgagaaaacc 1020
atcagcaagg ccaagggcc accccgcgaa cccaggtgt gcacactgcc cccaagcagg 1080
gacgagctga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccctcc 1140
gatatcgccg tggaatggga gagcaacggc cagcccgaga acaactaaa gaccaccccc 1200
cctgtgctgg acagcgacgg ctcatcttc ctggtgtcca agctgacagt ggacaagtcc 1260
cgggtggcagc agggcaacgt gttcagctgc tccgtgatgc acgaggccct gcacaaccac 1320
tacaccaga agtccctgag cctgagcccc ggcaag 1356

```

<210> 62

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 62

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atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgcccagc 180
agattttccg gcagcggctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctacct ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630

```

<210> 63

<211> 1845

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

4. __183952027041SEQLIST.TXT

<400> 63

```

gaggttagac tgggtggagtc aggagggggg cttgtgaagc ccggtgggtc tctccgcctg 60
agctgttctg cctccggctt tgatttcgat aacgcctgga tgacctgggt caggcagcct 120
ccaggttaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctggtccgtg 180
gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
acaggcaaat actacgactt ctggtggggc tatccccctg gcgaggaata ttttcaagac 360
tggggtcagg gaacccttgt tatcgtgtcc tccgacaaaa cccataacca ggtgcagttg 420
gtggagtctg ggggaggcgt ggtccagcct gggacgtccc tgagactctc ctgtgcagcc 480
tctcaattca ggtttgatgg ttatggcatg cactgggtcc gccaggcccc aggcaagggg 540
ctggagtggg tggcatctat atcacatgat ggaattaaaa agtatcacgc agaaaaagtg 600
tggggccgct tcacatctc cagagacaat tccaagaaca cactgtatct acaaatgaac 660
agcctgcgac ctgaggacac ggctctctac tactgtgcga aagatttgcg agaagacgaa 720
tgtgaagagt ggtggtcgga ttattacgat tttgggaaac aactcccttg cgcaaagtca 780
cgcggcggct tggttggaat tgctgataac tggggccaag ggacaatggt caccgtctct 840
tcagataaga cccacaccgc ttccaccaag ggcccacggt tcttccccct ggcaccctcc 900
tccaagagca cctctggggg cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc 960
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agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 1140
gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 1200
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc 1260
atgatctccc ggaccctga ggtcacatgc gtgggtgggtg acgtgagcca cgaagaccct 1320
gaggtcaagt tcaactggta tgttgacggc gtggaggtgc ataatgccaa gacaaaagccg 1380
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 1440
gactggctga atggcaagga gtacaagtgc aaggctctca acaaagccct cccagcccc 1500
atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1560
ccccatgcc gggatgagct gaccaagaat caagtcagcc tgtgggtgct ggtaaaaggc 1620
ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 1680
aagaccacgc ctcccggtg ggactccgac ggctccttct tcctctactc aaaactcacc 1740
gtggacaaga gcagggtggca gcagggggaac gtcttctcat gctccgtgat gcatgaggct 1800
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggt 1845

```

<210> 64

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 64

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cagtctgtgc tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc 60
tcctgtcttg gaaacacctc caacattggc aataattttg tgtcctggta tcaacagcgc 120
cccggcagag ccccccact cctcatttat gaaactgaca agcgaccctc agggattcct 180
gaccgattct ctgcttccaa gtctggtacg tcaggcacc cggccatcac cgggctgcag 240
actggggacg aggccgatta ttactgcgcc acatgggctg ccagcctgag ttccgcgcgt 300
gtcttcggaa ctgggaccaa ggtcatcgtc ctggacaaaa cccataccgc atccgaactg 360
actcaggacc ctgccgtctc tgtggcactg aagcagactg tgactattac ttgccagggc 420
gactactgc ggagccacta cgcttcttgg tatcagaaga aaccggcca ggcacctgtg 480
ctgctgttct acggaaagaa caataggcca tctggcatcc ccgaccgctt ttctggcagt 540
gcatcaggga accgagccag tctgaccatt accggcgccc aggctgagga cgaagccgat 600

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4. __183952027041SEQLIST.TXT

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tactattgca gctcccggga taagagcggc tccagactga gcgtgttcgg aggaggaact 660
aaactgaccg tcctcgataa gacccatacc cgtacggtgg ccgctcccag cgtgttcac 720
ttccaccta gcgacgagca gctgaagtcc ggcacagcct ctgtcgtgtg cctgctgaac 780
aacttctacc cccgcgaggc caaagtgcag tggaagggtgg acaacgccct gcagagcggc 840
aacagccagg aaagcgtgac cgagcaggac agcaaggact ccacctacag cctgagcagc 900
accctgacac tgagcaaggc cgactacgag aagcacaagg tgtacgcctg cgaagtgacc 960
caccagggcc tgtctagccc cgtgaccaag agcttcaacc ggggcgagtg t 1011
```

<210> 65

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 65

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Gln Val Gln Leu Val Gln Ser Gly Gly Gln Met Lys Lys Pro Gly Glu
 1          5          10          15
Ser Met Arg Ile Ser Cys Arg Ala Ser Gly Tyr Glu Phe Ile Asp Cys
 20        25        30
Thr Leu Asn Trp Ile Arg Leu Ala Pro Gly Lys Arg Pro Glu Trp Met
 35        40        45
Gly Trp Leu Lys Pro Arg Gly Gly Ala Val Asn Tyr Ala Arg Pro Leu
 50        55        60
Gln Gly Arg Val Thr Met Thr Arg Asp Val Tyr Ser Asp Thr Ala Phe
 65        70        75        80
Leu Glu Leu Arg Ser Leu Thr Val Asp Asp Thr Ala Val Tyr Phe Cys
 85        90        95
Thr Arg Gly Lys Asn Cys Asp Tyr Asn Trp Asp Phe Glu His Trp Gly
100       105       110
Arg Gly Thr Pro Val Ile Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115       120       125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130       135       140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145       150       155       160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165       170       175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180       185       190
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195       200       205
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210       215       220
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225       230       235       240
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245       250       255
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260       265       270
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
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4._183952027041SEQLIST.TXT

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

<210> 66

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 66

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

4._183952027041SEQLIST.TXT

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
 145 150 155 160
 Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
 165 170 175
 Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
 180 185 190
 Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
 195 200 205
 Glu Cys
 210

<210> 67

<211> 615

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 67

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

4. 183952027041SEQLIST.TXT

															245																250																255
Cys	Ala	Lys	Ser			Arg	Gly	Gly	Leu	Val	Gly	Ile	Ala	Asp	Asn	Trp	Gly																														
															260	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Ala	Ser																				
Gln	Gly	Thr	Met	Pro			Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Thr																														
															275	Phe			295	300																											
Thr	Lys	Gly	Pro	Ser	Val	295			Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr																														
															290	310			315																												
Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro																																
															305	320																															
Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val																																
															325	330			335																												
His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser																																
															340	345			350																												
Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile																																
															355	360			365																												
Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val																																
															370	375			380																												
Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala																																
															385	390			395																												
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro																																
															405	410			415																												
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val																																
															420	425			430																												
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val																																
															435	440			445																												
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln																																
															450	455			460																												
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln																																
															465	470			475																												
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala																																
															485	490			495																												
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro																																
															500	505			510																												
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Cys	Arg	Asp	Glu	Leu	Thr																																
															515	520			525																												
Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser																																
															530	535			540																												
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr																																
															545	550			555																												
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr																																
															565	570			575																												
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe																																
															580	585			590																												
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys																																
															595	600			605																												
Ser	Leu	Ser	Leu	Ser	Pro	Gly																																									
															610	615																															

<210>	68
<211>	337
<212>	PRT

4.__183952027041SEQLIST.TXT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 68

Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Ala	Ala	Pro	Gly	Gln	1	5	10	15
Lys	Val	Thr	Ile	Ser	Cys	Ser	Gly	Asn	Thr	Ser	Asn	Ile	Gly	Asn	Asn	20	25	30	
Phe	Val	Ser	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Arg	Ala	Pro	Gln	Leu	Leu	35	40	45	
Ile	Tyr	Glu	Thr	Asp	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	50	55	60	
Ala	Ser	Lys	Ser	Gly	Thr	Ser	Gly	Thr	Leu	Ala	Ile	Thr	Gly	Leu	Gln	65	70	75	80
Thr	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ala	Thr	Trp	Ala	Ala	Ser	Leu	85	90	95	
Ser	Ser	Ala	Arg	Val	Phe	Gly	Thr	Gly	Thr	Lys	Val	Ile	Val	Leu	Asp	100	105	110	
Lys	Thr	His	Thr	Ala	Ser	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	115	120	125	
Ala	Leu	Lys	Gln	Thr	Val	Thr	Ile	Thr	Cys	Arg	Gly	Asp	Ser	Leu	Arg	130	135	140	
Ser	His	Tyr	Ala	Ser	Trp	Tyr	Gln	Lys	Lys	Pro	Gly	Gln	Ala	Pro	Val	145	150	155	160
Leu	Leu	Phe	Tyr	Gly	Lys	Asn	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	165	170	175	
Phe	Ser	Gly	Ser	Ala	Ser	Gly	Asn	Arg	Ala	Ser	Leu	Thr	Ile	Thr	Gly	180	185	190	
Ala	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ser	Ser	Arg	Asp	Lys	195	200	205	
Ser	Gly	Ser	Arg	Leu	Ser	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	210	215	220	
Leu	Asp	Lys	Thr	His	Thr	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	225	230	235	240
Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	245	250	255	
Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	260	265	270	
Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	275	280	285	
Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	290	295	300	
Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	305	310	315	320
His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	325	330	335	
Cys																			

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<210> 69
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 69
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 agctgcagag ccagcggcta cgagttcatc gactgcaccc tgaactggat cagactggcc 120
 cctggcaagc ggcctgagtg gatgggatgg ctgaagccta gaggcggagc cgtgaactac 180
 gccagacctc tgcagggcag agtgaccatg acccgggacg tgtacagcga taccgccttc 240
 ctggaactgc ggagcctgac cgtggatgat accgccgtgt acttctgcac ccggggcaag 300
 aactgcgact acaactggga cttcgagcac tggggcagag gcacccctgt gatcgtgtca 360
 agcgcgtcga ccaagggtccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 420
 ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccgagcc cgtgaccgtg 480
 tcctggaatt ctggcgccct gaccagcggc gtgcacacct ttccagctgt gctgcagtcc 540
 agcggcctgt acagcctgag cagcgtcgtg acagtgccca gcagctctct gggcacccag 600
 acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 660
 cccaagagct gcgacaagac ccacacctgt ccccttctgc ctgccccga actgctggga 720
 ggcccttccg tgttcctgtt ccccccaaag cccaaggaca ccctgatgat cagccggacc 780
 cccgaagtga cctgcgtggg ggtggatgtg tcccacgagg accctgaagt gaagttcaat 840
 tgggtacgtg acggcgtgga agtgacacac gccaaagacca agccaagaga ggaacagtac 900
 aacagcacct accgggtggg gtccgtgctg accgtgctgc accaggactg gctgaacggc 960
 aaagagtaca agtgcaagggt gtccaacaag gccctgcctg ccccatcga gaaaaccatc 1020
 agcaaggcca agggccagcc ccgcgaaccc caggtgtgca cactgcccc aagcaggagc 1080
 gagctgacca agaaccagggt gtccctgagc tgtgccgtga aaggcttcta cccctccgat 1140
 atcgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cccccccct 1200
 gtgctggaca gcgacggctc attcttctct gtgtccaagc tgacagtgga caagtcccg 1260
 tggcagcagg gcaacgtgtt cagctgctcc gtgatgcacg aggcctgca caaccactac 1320
 acccagaagt ccctgagcct gagccccggc 1350

<210> 70
 <211> 630
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 70
 gagatcgtgc tgacacagag ccctggcacc ctgagcctgt ctccaggcga gacagccatc 60
 atcagctgcc ggacaagcca gtacggcagc ctggcctggg atcagcagag gcctggacag 120
 gccccagac tcgtgatcta cagcggcagc acaagagccg ccggaatccc cgatagattc 180
 agcggctcca gatggggccc tgactacaac ctgaccatca gcaacctgga aagcggcgac 240
 ttcggcgtgt actactgcca gcagtacgag ttcttcggcc agggcaccaa ggtgcagggtg 300
 gacatcaagc gtacgggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
 ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
 aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
 gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
 gactacgaga agcacaagggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600

gtgaccaaga gcttcaaccg gggcgagtgt

630

<210> 71

<211> 1845

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 71

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agctgttctg cctccggctt tgatttcgat aacgcctgga tgacctgggt caggcagcct 120
ccaggtaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctggtccgtg 180
gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
acaggcaaat actacgactt ctggtggggc tatccccctg gcgaggaata ttttcaagac 360
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gtggagtctg ggggaggcgt ggtccagcct gggacgtccc tgagactctc ctgtgcagcc 480
tctcaattca ggtttgatgg ttatggcatg cactgggtcc gccaggcccc aggcaagggg 540
ctggagtggg tggcatctat atcacatgat ggaattaaaa agtatcacgc agaaaaagt 600
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gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 1200
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc 1260
atgatctccc ggacccctga ggtcacatgc gtggtgggtg acgtgagcca cgaagaccct 1320
gagggtcaagt tcaactggta tgttgacggc gtggaggtgc ataatgcaa gacaaagccg 1380
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 1440
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aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctactc aaaactcacc 1740
gtggacaaga gcagggtggc gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1800
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<210> 72

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 72

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cccggcagag ccccccaact cctcatttat gaaactgaca agcgaccctc agggattcct 180
gaccgattct ctgcttccaa gtctggtacg tcaggcacc cgggctgcag 240
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gtcttcggaa ctgggaccaa ggtcatcgtc ctggacaaaa cccataccgc atccgaactg 360
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gcatcaggga accgagccag tctgaccatt accggcgccc aggctgagga cgaagccgat 600
tactattgca gctcccggga taagagcggc tccagactga gcgtgttcgg aggaggaact 660
aaactgaccg tcctcgataa gaccataacc cgtacggtgg ccgctcccag cgtgttcac 720
ttcccaccta gcgacgagca gctgaagtcc ggcacagcct ctgtcgtgtg cctgctgaac 780
aacttctacc cccgcgaggc caaagtgcag tggaagggtg acaacgccct gcagagcggc 840
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accctgacac tgagcaaggc cgactacgag aagcacaagg tgtacgcctg cgaagtgacc 960
caccagggcc tgtctagccc cgtgaccaag agcttcaacc ggggcgagtg t 1011

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<210> 73

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 73

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

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4._183952027041SEQLIST.TXT

195	200	205													
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys
210	215	220													
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
225	230	235													240
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
	245	250													255
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
	260	265													270
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
	275	280													285
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
	290	295													300
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
305	310	315													320
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
	325	330													335
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
	340	345													350
Cys	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
	355	360													365
Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
	370	375													380
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
385	390	395													400
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr	Val
	405	410													415
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
	420	425													430
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
	435	440													445
Pro	Gly														
450															

<210> 74

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 74

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1	5	10	15												
Glu	Thr	Ala	Ile	Ile	Ser	Cys	Arg	Thr	Ser	Gln	Tyr	Gly	Ser	Leu	Ala
	20	25	30												
Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Val	Ile	Tyr	Ser
	35	40	45												
Gly	Ser	Thr	Arg	Ala	Ala	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Arg
	50	55	60												

4. __183952027041SEQLIST.TXT

Trp Gly Pro Asp Tyr Asn Leu Thr Ile Ser Asn Leu Glu Ser Gly Asp
65 70 75 80
Phe Gly Val Tyr Tyr Cys Gln Gln Tyr Glu Phe Phe Gly Gln Gly Thr
85 90 95
Lys Val Gln Val Asp Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
100 105 110
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
115 120 125
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
130 135 140
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
145 150 155 160
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
165 170 175
Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
180 185 190
Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
195 200 205
Glu Cys
210

<210> 75

<211> 615

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 75

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

4. 183952027041SEQLIST.TXT

														165				170				175	
Phe	Asp	Phe	Asp	Asn	Ala	Trp	Met	Thr	Trp	Val	Arg	Gln	Pro	Pro	Gly								
														180				185				190	
Lys	Gly	Leu	Glu	Trp	Val	Gly	Arg	Ile	Thr	Gly	Pro	Gly	Glu	Gly	Trp								
														195				200				205	
Ser	Val	Asp	Tyr	Ala	Glu	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg								
														210				215				220	
Asp	Asn	Thr	Lys	Asn	Thr	Leu	Tyr	Leu	Glu	Met	Asn	Asn	Val	Arg	Thr								
														225				230				235	
Glu	Asp	Thr	Gly	Tyr	Tyr	Phe	Cys	Ala	Arg	Thr	Gly	Lys	Tyr	Tyr	Asp								
														240				245				250	
Phe	Trp	Trp	Gly	Tyr	Pro	Pro	Gly	Glu	Glu	Tyr	Phe	Gln	Asp	Trp	Gly								
														255				260				265	
Gln	Gly	Thr	Leu	Val	Ile	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Ala	Ser								
														270				275				280	
Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr								
														285				290				295	
Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro								
														300				305				310	
Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val								
														315				320				325	
His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser								
														330				335				340	
Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile								
														345				350				355	
Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val								
														360				365				370	
Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala								
														375				380				385	
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro								
														390				395				400	
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val								
														405				410				415	
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val								
														420				425				430	
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln								
														435				440				445	
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln								
														450				455				460	
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala								
														465				470				475	
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro								
														480				485				490	
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Cys	Arg	Asp	Glu	Leu	Thr								
														495				500				505	
Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser								
														510				515				520	
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr								
														525									

4. 183952027041SEQLIST.TXT

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 580 585 590
 595 600 605
 Ser Leu Ser Leu Ser Pro Gly
 610 615

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<210> 76
<211> 337
<212> PRT
<213> Artificial Sequence
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<220>
<223> Synthetic Construct

<400> 76															
Ala 1	Ser	Glu	Leu	Thr 5	Gln	Asp	Pro	Ala	Val 10	Ser	Val	Ala	Leu 15	Lys	Gln
Thr	Val	Thr	Ile 20	Thr	Cys	Arg	Gly	Asp 25	Ser	Leu	Arg	Ser	His 30	Tyr	Ala
Ser	Trp	Tyr 35	Gln	Lys	Lys	Pro	Gly 40	Gln	Ala	Pro	Val	Leu 45	Leu	Phe	Tyr
Gly	Lys 50	Asn	Asn	Arg	Pro	Ser 55	Gly	Ile	Pro	Asp	Arg 60	Phe	Ser	Gly	Ser
Ala 65	Ser	Gly	Asn	Arg	Ala 70	Ser	Leu	Thr	Ile	Thr 75	Gly	Ala	Gln	Ala	Glu 80
Asp	Glu	Ala	Asp	Tyr 85	Tyr	Cys	Ser	Ser	Arg 90	Asp	Lys	Ser	Gly	Ser 95	Arg
Leu	Ser	Val	Phe 100	Gly	Gly	Gly	Thr	Lys 105	Leu	Thr	Val	Leu	Asp 110	Lys	Thr
His	Thr	Gln 115	Ser	Val	Leu	Thr	Gln 120	Pro	Pro	Ser	Val	Ser	Ala 125	Ala	Pro
Gly	Gln 130	Lys	Val	Thr	Ile	Ser 135	Cys	Ser	Gly	Asn	Thr 140	Ser	Asn	Ile	Gly
Asn 145	Asn	Phe	Val	Ser	Trp 150	Tyr	Gln	Gln	Arg	Pro 155	Gly	Arg	Ala	Pro	Gln 160
Leu	Leu	Ile	Tyr 165	Glu	Thr	Asp	Lys	Arg	Pro 170	Ser	Gly	Ile	Pro	Asp 175	Arg
Phe	Ser	Ala	Ser 180	Lys	Ser	Gly	Thr	Ser 185	Gly	Thr	Leu	Ala	Ile 190	Thr	Gly
Leu	Gln	Thr 195	Gly	Asp	Glu	Ala	Asp 200	Tyr	Tyr	Cys	Ala	Thr 205	Trp	Ala	Ala
Ser	Leu 210	Ser	Ser	Ala	Arg	Val 215	Phe	Gly	Thr	Gly	Thr 220	Lys	Val	Ile	Val
Leu 225	Asp	Lys	Thr	His	Thr 230	Arg	Thr	Val	Ala	Ala 235	Pro	Ser	Val	Phe	Ile 240
Phe	Pro	Pro	Ser	Asp 245	Glu	Gln	Leu	Lys	Ser 250	Gly	Thr	Ala	Ser	Val 255	Val
Cys	Leu	Leu	Asn 260	Asn	Phe	Tyr	Pro	Arg 265	Glu	Ala	Lys	Val	Gln 270	Trp	Lys
Val	Asp	Asn 275	Ala	Leu	Gln	Ser	Gly 280	Asn	Ser	Gln	Glu	Ser	Val 285	Thr	Glu

4. __183952027041SEQLIST.TXT

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
 290 295 300
 Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
 305 310 315 320
 His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
 325 330 335
 Cys

<210> 77
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 77
 caggtgcagc tgggtgcagtc tggcggccag atgaagaaac ccggcgagag catgcggatc 60
 agctgcagag ccagcggcta cgagttcatc gactgcaccc tgaactggat cagactggcc 120
 cctggcaagc ggcctgagtg gatgggatgg ctgaagccta gaggcggagc cgtgaactac 180
 gccagacctc tgcagggcag agtgaccatg acccgggacg tgtacagcga taccgccttc 240
 ctggaactgc ggagcctgac cgtgggatgat accgccgtgt acttctgcac ccggggcaag 300
 aactgcgact acaactggga cttcgagcac tggggcgagag gcacccctgt gatcgtgtca 360
 agcgcgtcga ccaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 420
 ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccagagc cgtgaccgtg 480
 tcctggaatt ctggcgccct gaccagcggc gtgcacacct ttccagctgt gctgcagtcc 540
 agcggcctgt acagcctgag cagcgtcgtg acagtgccca gcagctctct gggcacccag 600
 acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 660
 cccaagagct gcgacaagac ccacacctgt ccccttctgc ctgccccga actgctggga 720
 ggcccttccg tgttcctgtt cccccaaaag cccaaggaca ccctgatgat cagccggacc 780
 cccgaagtga cctgcgtggg ggtggatgtg tcccacgagg accctgaagt gaagttcaat 840
 tgggtacgtg acggcgtgga agtgcacaac gccaaagaca agccaagaga ggaacagtac 900
 aacagcacct accgggtggg gtccgtgctg accgtgctgc accaggactg gctgaacggc 960
 aaagagtaca agtgcaaggt gtccaacaag gccctgcctg ccccatcga gaaaaccatc 1020
 agcaaggcca agggccagcc ccgcgaacc caggtgtgca cactgcccc aagcagggac 1080
 gagctgacca agaaccaggt gtccctgagc tgtgccgtga aaggcttcta cccctccgat 1140
 atcgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cccccccct 1200
 gtgctggaca gcgacggctc attcttcctg gtgtccaagc tgacagtgga caagtcccgg 1260
 tggcagcagg gcaacgtgtt cagctgctcc gtgatgcacg aggcctgca caaccactac 1320
 acccagaagt ccctgagcct gagccccggc 1350

<210> 78
 <211> 630
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 78

4. __183952027041SEQLIST.TXT

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gagatcgtgc tgacacagag ccctggcacc ctgagcctgt ctccaggcga gacagccatc 60
atcagctgcc ggacaagcca gtacggcagc ctggcctggg atcagcagag gcctggacag 120
gccccagac tcgtgatcta cagcggcagc acaagagccg ccggaatccc cgatagattc 180
agcggctcca gatggggccc tgactacaac ctgaccatca gcaacctgga aagcggcgac 240
ttcggcgtgt actactgcca gcagtacgag ttcttcggcc agggcaccaa ggtgcagggtg 300
gacatcaagc gtacgggtggc cgctcccagc gtgttcattt tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt                                     630

```

<210> 79

<211> 1845

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 79

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caggtgcagt tgggtggagtc tgggggaggc gtggtccagc ctgggacgtc cctgagactc 60
tcctgtgcag cctctcaatt caggtttgat gggtatggca tgcactgggt ccgccaggcc 120
ccaggcaagg ggctggagtg ggtggcatct atatcacatg atggaattaa aaagtatcac 180
gcagaaaaag tgtggggccg cttcaccatc tccagagaca attccaagaa cacactgtat 240
ctacaaatga acagcctgcg acctgaggac acggctctct actactgtgc gaaagatttg 300
cgagaagacg aatgtgaaga gtggtggctc gattattacg attttgggaa acaactccct 360
tgcgcaaagt cacgcggcgg cttggttgga attgctgata actggggcca agggacaatg 420
gtcaccgtct cttcagacaa aaccataacc gaggttagac tgggtggagtc aggagggggg 480
cttgtgaagc ccggtgggtc tctccgcctg agctgttctg cctccggctt tgatttcgat 540
aacgcctgga tgacctgggt caggcagcct ccaggtaagg gactggagtg ggtgggaaga 600
atcacaggtc caggcgaggg ctggtccgtg gactacgcgg aatctgttaa agggcggttt 660
acaatctcaa gggacaatac caagaatacc ttgtatttgg agatgaacaa cgtgagaact 720
gaagacaccg gatattactt ctgtgccaga acaggcaaat actacgactt ctggtccggc 780
tatccccctg gcgaggaata ttttcaagac tggggtcagg gaacccttgt tatcgtgtcc 840
tccgataaga cccacaccgc ttccaccaag ggcccatcgg tcttccccct ggcaccctcc 900
tccaagagca cctctggggg cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc 960
gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccc 1020
gctgtcctac agtcctcagg actctactcc ctacgagcgc tgggtgaccgt gccctccagc 1080
agcttgggca cccagacctc catctgcaac gtgaatcaca agcccagcaa caccaagggtg 1140
gacaagaaag ttgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 1200
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaaccaa ggacaccctc 1260
atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 1320
gaggtcaagt tcaactggta tgttgacggc gtggaggtgc ataatgccaa gacaaagccg 1380
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 1440
gactggctga atggcaagga gtacaagtgc aaggctctca acaaagccct cccagcccc 1500
atcgagaaaa ccatctcaa agccaaaggc cagccccgag aaccacaggt gtacaccctg 1560
ccccatgcc gggatgagct gaccaagaat caagtcagcc tgtggtgcct ggtaaaaggc 1620
ttctatccca gcgacatgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 1680
aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctactc aaaactcacc 1740
gtggacaaga gcagggtggc gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1800
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggt                                     1845

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4.___183952027041SEQLIST.TXT

<210> 80
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 80
 gcatccgaac tgactcagga ccctgccgtc tctgtggcac tgaagcagac tgtgactatt 60
 acttgccgag gcgactcact gcggagccac tacgcttcct ggtatcagaa gaaacccggc 120
 caggcacctg tgctgctgtt ctacggaaag aacaataggc catctggcat ccccgaccgc 180
 ttttctggca gtgcatcagg gaaccgagcc agtctgacca ttaccggcgc ccaggctgag 240
 gacgaagccg attactattg cagctcccgg gataagagcg gctccagact gagcgtgttc 300
 ggaggaggaa ctaaactgac cgtcctcgac aaaaccata cccagtctgt gctgacgcag 360
 ccgccctcag tgtctgcggc cccaggacag aaggtcacca tctcctgctc tggaaacacc 420
 tccaacattg gcaataatit tgtgtcctgg tatcaacagc gccccggcag agcccccaa 480
 ctctctattt atgaaactga caagcgacc tcagggattc ctgaccgatt ctctgcttcc 540
 aagtctggta cgtcaggcac cctggccatc accgggctgc agactgggga cgaggccgat 600
 tattactgcg ccacatgggc tgccagcctg agttccgcgc gtgtcttcgg aactgggacc 660
 aaggtcatcg tcctggataa gaccataacc cgtacggtgg ccgctcccag cgtgttcatc 720
 ttcccaccta gcgacgagca gctgaagtcc ggcacagcct ctgtcgtgtg cctgctgaac 780
 aacttctacc cccgcgaggc caaagtgcag tggaaggtgg acaacgccct gcagagcggc 840
 aacagccagg aaagcgtgac cgagcaggac agcaaggact ccacctacag cctgagcagc 900
 accctgacac tgagcaaggc cgactacgag aagcacaagg tgtacgcctg cgaagtgacc 960
 caccagggcc tgtctagccc cgtgaccaag agcttcaacc ggggcgagtg t 1011

<210> 81
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 81
 Arg Ala His Leu Val Gln Ser Gly Thr Ala Met Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Arg Val Ser Cys Gln Thr Ser Gly Tyr Thr Phe Thr Ala His
 20 25 30
 Ile Leu Phe Trp Phe Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
 35 40 45
 Gly Trp Ile Lys Pro Gln Tyr Gly Ala Val Asn Phe Gly Gly Gly Phe
 50 55 60
 Arg Asp Arg Val Thr Leu Thr Arg Asp Val Tyr Arg Glu Ile Ala Tyr
 65 70 75 80
 Met Asp Ile Arg Gly Leu Lys Pro Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Arg Ser Tyr Gly Asp Ser Ser Trp Ala Leu Asp Ala Trp
 100 105 110
 Gly Gln Gly Thr Thr Val Val Val Ser Ala Ala Ser Thr Lys Gly Pro

[illegible]

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<210> 82
<211> 210
<212> PRT
<213> Artificial Sequence
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<220>
<223> Synthetic Construct

4.__183952027041SEQLIST.TXT

<400> 82

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

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<210> 83

<211> 611

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 83

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

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4. 183952027041SEQLIST.TXT

															85																90																95
Phe	Cys	Ala	Arg	Thr	Gly	Lys	Tyr	Tyr	Asp	Phe	Trp	Trp	Gly	Tyr	Pro																																
															100																105																110
Pro	Gly	Glu	Glu	Tyr	Phe	Gln	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Ile																																
															115																120																125
Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Gln	Val	His	Leu	Thr	Gln	Ser	Gly																																
															130																135																140
Pro	Glu	Val	Arg	Lys	Pro	Gly	Thr	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala																																
															145																150																155
Pro	Gly	Asn	Thr	Leu	Lys	Thr	Tyr	Asp	Leu	His	Trp	Val	Arg	Ser	Val																																
															165																170																175
Pro	Gly	Gln	Gly	Leu	Gln	Trp	Met	Gly	Trp	Ile	Ser	His	Glu	Gly	Asp																																
															180																185																190
Lys	Lys	Val	Ile	Val	Glu	Arg	Phe	Lys	Ala	Lys	Val	Thr	Ile	Asp	Trp																																
															195																200																205
Asp	Arg	Ser	Thr	Asn	Thr	Ala	Tyr	Leu	Gln	Leu	Ser	Gly	Leu	Thr	Ser																																
															210																215																220
Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Gly	Ser	Lys	His	Arg	Leu																																
															225																230																235
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Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Ala	Ser	Thr	Lys	Gly	Pro																																
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Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr																																
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Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr																																
															305																310																315
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro																																
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Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr																																
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Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn																																
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His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser																																
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Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu																																
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Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu																																
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Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser																																
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His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu																																
															435																440																445
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr																																
															450																455																460
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn																																
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Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro																																

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[illegible]

<210> 84

<211> 338

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 84

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

4. __183952027041SEQLIST.TXT

Lys	Ser	Gly	Ser	Arg	Leu	Ser	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr
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Val	Leu	Asp	Lys	Thr	His	Thr	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe
225					230					235					240
Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val
				245					250					255	
Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp
		260						265					270		
Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr
		275					280					285			
Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr
		290				295					300				
Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val
305					310					315					320
Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly
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Glu Cys

<210> 85

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 85

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cctgtgctgg acagcgacgg ctattcttc ctggtgtcca agctgacagt ggacaagtcc 1260
cgggtggcagc agggcaacgt gttcagctgc tccgtgatgc acgaggccct gcacaaccac 1320
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4.__183952027041SEQLIST.TXT

<210> 86
 <211> 630
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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 ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgccccagc 180
 agatttttccg gcagcggcctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
 gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
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 aaagtgcagt ggaaggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
 gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
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<210> 87
 <211> 1833
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 87
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 ccaggttaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctggtccgtg 180
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 aaggccaaag tgaccatcga ctgggacaga agcaccaaca ccgcctacct gcagctgagc 660
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4. __183952027041SEQLIST.TXT

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<210> 88

<211> 1014

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 88

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<210> 89

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 89

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20          25          30
Ile Leu Phe Trp Phe Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val

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Arg 65	Asp	Arg	Val	Thr	Leu	Thr	Arg	Asp	Val	Tyr	Arg	Glu	Ile	Ala	Tyr			
Met	Asp	Ile	Arg	Gly	Leu	Lys	Pro	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys			
				85					90					95				
Ala	Arg	Asp	Arg	Ser	Tyr	Gly	Asp	Ser	Ser	Trp	Ala	Leu	Asp	Ala	Trp			
				100					105					110				
Gly	Gln	Gly	Thr	Thr	Val	Val	Val	Ser	Ala	Ala	Ser	Thr	Lys	Gly	Pro			
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr			
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr			
145					150					155					160			
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro			
				165						170				175				
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr			
				180						185				190				
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser			
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu			
225					230					235					240			
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu			
				245						250				255				
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser			
				260					265					270				
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr			
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn			
305					310					315					320			
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro			
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Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln			
				340						345				350				
Val	Cys	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val			
Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val			
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro			
385					390					395					400			
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr			
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450

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

<220>
 <223> Synthetic Construct

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

<210> 91
 <211> 602
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 91
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Gly	Arg	Ile	Thr	Gly	Pro	Gly	Glu	Gly	Trp	Ser	Val	Asp	Tyr	Ala	Glu
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Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Thr	Lys	Asn	Thr
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Leu	Tyr	Leu	Glu	Met	Asn	Asn	Val	Arg	Thr	Glu	Asp	Thr	Gly	Tyr	Tyr
				85					90					95	
Phe	Cys	Ala	Arg	Thr	Gly	Lys	Tyr	Tyr	Asp	Phe	Trp	Trp	Gly	Tyr	Pro
		100						105					110		
Pro	Gly	Glu	Glu	Tyr	Phe	Gln	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Ile
	115						120					125			
Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Gln	Met	Gln	Leu	Gln	Glu	Ser	Gly
	130					135					140				
Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ser	Val
145					150					155					160
Ser	Gly	Ala	Ser	Ile	Ser	Asp	Ser	Tyr	Trp	Ser	Trp	Ile	Arg	Arg	Ser
			165						170					175	
Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Val	His	Lys	Ser	Gly	Asp
		180						185					190		
Thr	Asn	Tyr	Ser	Pro	Ser	Leu	Lys	Ser	Arg	Val	Asn	Leu	Ser	Leu	Asp
	195						200					205			
Thr	Ser	Lys	Asn	Gln	Val	Ser	Leu	Ser	Leu	Val	Ala	Ala	Thr	Ala	Ala
	210					215					220				
Asp	Ser	Gly	Lys	Tyr	Tyr	Cys	Ala	Arg	Thr	Leu	His	Gly	Arg	Arg	Ile
225					230					235					240
Tyr	Gly	Ile	Val	Ala	Phe	Asn	Glu	Trp	Phe	Thr	Tyr	Phe	Tyr	Met	Asp
			245						250					255	
Val	Trp	Gly	Asn	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His
		260						265					270		
Thr	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser
	275						280					285			
Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp
	290					295					300				
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr
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		340						345					350		
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	355						360					365			
Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro
	370					375					380				
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
385				390						395					400
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
			405						410					415	
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn

4. __183952027041SEQLIST.TXT

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      420      425      430
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
      435      440      445
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
      450      455      460
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
465      470      475      480
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
      485      490      495
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
      500      505      510
Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
      515      520      525
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
      530      535      540
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
545      550      555      560
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
      565      570      575
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
      580      585      590
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
      595      600

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<210> 92

<211> 331

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 92

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

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4. __183952027041SEQLIST.TXT

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

<210> 93

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 93

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tcctgtcaga	caagcggcta	caccttcacc	gccacatcc	tgttcttggtt	ccggcaggcc	120
cctggcagag	gactggaatg	ggtgggatgg	atcaagcccc	agtatggcgc	cgtgaacttc	180
ggcggaggct	tccgggatag	agtgaccctg	accggggacg	tgtaccgcga	gatcgacctac	240
atggacatcc	ggggcctgaa	gcccgatgac	accgccgtgt	actactgcgc	cagagacaga	300
agctacggcg	acagcagctg	ggctctggat	gcttggggcc	agggcacaac	cgtggtggtg	360
tctgccgcct	ctacaaaggg	ccccagcgtg	ttccctctgg	cccctagcag	caagagcaca	420
tctggcggaa	cagccgccct	gggctgcctc	gtgaaggact	actttcccga	gcccgtgacc	480
gtgtcctgga	attctggcgc	cctgaccagc	ggcgtgcaca	cctttccagc	tgtgctgcag	540
tccagcggcc	tgtacagcct	gagcagcgtc	gtgacagtgc	ccagcagctc	tctgggcacc	600
cagacctaca	tctgcaacgt	gaaccacaag	cccagcaaca	ccaaggtgga	caagaaggtg	660
gaaccacaaga	gctgcgacaa	gaccacacac	tgtccccctt	gtcctgcccc	cgaactgctg	720
ggaggccctt	ccgtgttcct	gttcccccca	aagcccaagg	acaccctgat	gatcagccgg	780
acccccgaag	tgacctgcgt	ggtggtggat	gtgtcccacg	aggaccctga	agtgaagtcc	840
aattggtacg	tggacggcgt	ggaagtgcac	aacgccaaga	ccaagccaag	agaggaacag	900
tacaacagca	cctaccgggt	ggtgtccgtg	ctgaccgtgc	tgcaccagga	ctggctgaac	960
ggcaaagagt	acaagtgcaa	ggtgtccaac	aaggccctgc	ctgcccccat	cgagaaaacc	1020

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atcagcaagg ccaagggcca gccccgcgaa cccaggtgt gcacactgcc cccaagcagg 1080
gacgagctga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccctcc 1140
gatatcgccg tggaatggga gagcaacggc cagcccgaga acaactacaa gaccaccccc 1200
cctgtgctgg acagcgacgg ctcatcttc ctggtgtcca agctgacagt ggacaagtc 1260
cggtggcagc agggcaacgt gttcagctgc tccgtgatgc acgaggccct gcacaaccac 1320
tacaccaga agtccctgag cctgagcccc ggcaag 1356

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<210> 94

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 94

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tacatccacg tgacccagag cccagcagc ctgtccgtgt ccatcggcga cagagtgacc 60
atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgccagc 180
agattttccg gcagcggtt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctacct ccgcgaggcc 420
aaagtgcagt ggaaggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630

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<210> 95

<211> 1806

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 95

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agctgttctg cctccggctt tgatttcgat aacgcctgga tgacctgggt caggcagcct 120
ccaggttaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctggtccgtg 180
gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
acaggcaaat actacgactt ctggtggggc tatccccctg gcgaggaata ttttcaagac 360
tggggtcagg gaacccttgt tatcgtgtcc tccgacaaaa cccataccca gatgcagctg 420
caggagagcg gccctggact cgtgaagccc agcgagacc tgagcctgac atgcagcgtg 480
agcggcgcca gcatcagcga cagctactgg agctggatca ggaggagccc tggcaagggc 540
ctggagtgga tcggctacgt gcacaagagc ggcgacacca actacagccc ctccctgaag 600
tccagggtga acctgtccct ggacaccagc aagaaccagg tgagcctgtc cctggtggct 660
gccacagctg ctgacagcgg caagtactac tgtgccagga ccctgcacgg caggaggatc 720
tacggcatcg tggccttcaa cgagtggttc acctacttct acatggacgt gtggggcaac 780
ggcaccacag tgaccgtgag ctccgataag acccacaccg cttccaccaa gggcccatcg 840
gtcttcccc tggcaccctc ctccaagagc acctctgggg gcacagcggc cctgggctgc 900

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4. __183952027041SEQLIST.TXT

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ctgggtcaagg actacttccc cgaaccgggtg acgggtgtcgt ggaactcagg cgccctgacc 960
agcggcggtgc acaccttccc ggctgtccta cagtcctcag gactctactc cctcagcagc 1020
gtgggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 1080
aagcccagca acaccaaggt ggacaagaaa gttgagccca aatcttgtga caaaactcac 1140
acatgcccac cgtgcccagc acctgaactc ctgggggggac cgtcagtcctt cctcttcccc 1200
ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtgggtggtg 1260
gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt atgttgacgg cgtggagggtg 1320
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1380
gtcctcacccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1440
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1500
gaaccacagg tgtacaccct gccccatgc cgggatgagc tgaccaagaa tcaagtcagc 1560
ctgtgggtgcc tggtaaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1620
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1680
ttcctctact caaaactcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1740
tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1800
ccgggt 1806

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<210> 96

<211> 993

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 96

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ggaagcaggg ctgtgcagtg gtaccaacac agggccggac aggctcccag cctgatcatc 120
tacaacaacc aggacaggcc cagcggcatc cctgagaggt tcagcggaag ccccgacagc 180
cccttcggaa ccacagccac cctgaccatc acaagcgtgg aagccggcga cgaggccgac 240
tactactgcc acatctggga cagcagggtg cccaccaagt ggggtgtttg cggcggcacc 300
accctgaccg tgctggacaa aaccataacc gcatccgaac tgactcagga ccctgccgtc 360
tctgtggcac tgaagcagac tgtgactatt acttgccgag gcgactcact gcggagccac 420
tacgcttcct ggtatcagaa gaaacccggc caggcacctg tgctgctgtt ctacggaaag 480
aacaataggc catctggcat ccccgaccgc ttttctggca gtgcatcagg gaaccgagcc 540
agtctgacca ttaccggcgc ccaggctgag gacgaagccg attactattg cagctcccgg 600
gataagagcg gctccagact gagcgtgttc ggaggaggaa ctaaaactgac cgtcctcgat 660
aagacccata cccgtacggg ggccgctccc agcgtgttca tcttcccacc tagcgacgag 720
cagctgaagt ccggcacagc ctctgtcgtg tgcctgctga acaacttcta ccccgcgag 780
gccaaagtgc agtggaaggt ggacaacgcc ctgcagagcg gcaacagcca ggaaagcgtg 840
accgagcagg acagcaagga ctccacctac agcctgagca gcaccctgac actgagcaag 900
gccgactacg agaagcaciaa ggtgtacgcc tgcgaagtga cccaccaggg cctgtctagc 960
cccgtgacca agagcttcaa ccggggcgag tgt 993

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<210> 97

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

4.__183952027041SEQLIST.TXT

<400> 97

Gln	Val	His	Leu	Thr	Gln	Ser	Gly	Pro	Glu	Val	Arg	Lys	Pro	Gly	Thr
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Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Pro	Gly	Asn	Thr	Leu	Lys	Thr	Tyr
			20					25					30		
Asp	Leu	His	Trp	Val	Arg	Ser	Val	Pro	Gly	Gln	Gly	Leu	Gln	Trp	Met
		35					40					45			
Gly	Trp	Ile	Ser	His	Glu	Gly	Asp	Lys	Lys	Val	Ile	Val	Glu	Arg	Phe
	50					55					60				
Lys	Ala	Lys	Val	Thr	Ile	Asp	Trp	Asp	Arg	Ser	Thr	Asn	Thr	Ala	Tyr
65					70				75						80
Leu	Gln	Leu	Ser	Gly	Leu	Thr	Ser	Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Lys	Gly	Ser	Lys	His	Arg	Leu	Arg	Asp	Tyr	Ala	Leu	Tyr	Asp	Asp
			100					105					110		
Asp	Gly	Ala	Leu	Asn	Trp	Ala	Val	Asp	Val	Asp	Tyr	Leu	Ser	Asn	Leu
		115					120					125			
Glu	Phe	Trp	Gly	Gln	Gly	Thr	Ala	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr
	130					135						140			
Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser
145					150					155					160
Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu
			165					170						175	
Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His
			180					185					190		
Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser
		195					200						205		
Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys
	210					215					220				
Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu
225					230					235					240
Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro
			245						250					255	
Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys
		260						265					270		
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val
	275						280					285			
Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp
	290					295					300				
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr
305					310					315					320
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp
				325					330					335	
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu
		340						345					350		
Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg
		355					360						365		
Glu	Pro	Gln	Val	Cys	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys
	370					375					380				
Asn	Gln	Val	Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp
385					390					395					400
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys

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				405					410				415		
Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser
				420					425				430		
Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser
			435				440					445			
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
	450					455					460				
Leu	Ser	Leu	Ser	Pro	Gly										
465					470										

<210> 98
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 98															
Asp	Phe	Val	Leu	Thr	Gln	Ser	Pro	His	Ser	Leu	Ser	Val	Thr	Pro	Gly
1				5					10					15	
Glu	Ser	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	His	Ser	Leu	Ile	His	Gly
			20					25					30		
Asp	Arg	Asn	Asn	Tyr	Leu	Ala	Trp	Tyr	Val	Gln	Lys	Pro	Gly	Arg	Ser
		35					40					45			
Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Ala	Ser	Ser	Arg	Ala	Ser	Gly	Val	Pro
	50					55					60				
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Asp	Lys	Asp	Phe	Thr	Leu	Lys	Ile
65				70					75					80	
Ser	Arg	Val	Glu	Thr	Glu	Asp	Val	Gly	Thr	Tyr	Tyr	Cys	Met	Gln	Gly
			85					90						95	
Arg	Glu	Ser	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Asp	Ile	Lys
			100					105					110		
Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu
	115						120					125			
Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe
	130					135					140				
Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln
145					150				155					160	
Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
			165					170					175		
Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
			180				185						190		
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser
	195					200						205			
Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys					
	210					215									

<210> 99
 <211> 602

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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 99

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Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Asp Asn Ala
 20           25           30
Trp Met Thr Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Val
 35           40           45
Gly Arg Ile Thr Gly Pro Gly Glu Gly Trp Ser Val Asp Tyr Ala Glu
 50           55           60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Asn Thr
 65           70           75           80
Leu Tyr Leu Glu Met Asn Asn Val Arg Thr Glu Asp Thr Gly Tyr Tyr
 85           90           95
Phe Cys Ala Arg Thr Gly Lys Tyr Tyr Asp Phe Trp Trp Gly Tyr Pro
100          105          110
Pro Gly Glu Glu Tyr Phe Gln Asp Trp Gly Gln Gly Thr Leu Val Ile
115          120          125
Val Ser Ser Asp Lys Thr His Thr Gln Met Gln Leu Gln Glu Ser Gly
130          135          140
Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val
145          150          155          160
Ser Gly Ala Ser Ile Ser Asp Ser Tyr Trp Ser Trp Ile Arg Arg Ser
165          170          175
Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Val His Lys Ser Gly Asp
180          185          190
Thr Asn Tyr Ser Pro Ser Leu Lys Ser Arg Val Asn Leu Ser Leu Asp
195          200          205
Thr Ser Lys Asn Gln Val Ser Leu Ser Leu Val Ala Ala Thr Ala Ala
210          215          220
Asp Ser Gly Lys Tyr Tyr Cys Ala Arg Thr Leu His Gly Arg Arg Ile
225          230          235          240
Tyr Gly Ile Val Ala Phe Asn Glu Trp Phe Thr Tyr Phe Tyr Met Asp
245          250          255
Val Trp Gly Asn Gly Thr Gln Val Thr Val Ser Ser Asp Lys Thr His
260          265          270
Thr Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
275          280          285
Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
290          295          300
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
305          310          315          320
Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
325          330          335
Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
340          345          350
Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp

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355	360	365																	
Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro				
370	375	380																	
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro				
385	390	395	400																
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr				
	405	410	415																
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn				
	420	425	430																
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg				
	435	440	445																
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val				
	450	455	460																
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser				
465	470	475	480																
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys				
	485	490	495																
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Cys	Arg	Asp				
	500	505	510																
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu	Val	Lys	Gly	Phe				
	515	520	525																
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu				
	530	535	540																
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe				
545	550	555	560																
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly				
	565	570	575																
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr				
	580	585	590																
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly										
	595	600																	

<210> 100

<211> 331

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 100

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

4. __183952027041SEQLIST.TXT

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

<210> 101

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 101

caggtgcacc tgacacagag cggacccgaa gtgcggaagc ctggcacctc tgtgaaggtg 60
 tcctgcaagg cccctggcaa caccctgaaa acctacgacc tgcactgggt gcgcagcgtg 120
 ccaggacagg gactgcagtg gatgggctgg atcagccacg agggcgacaa gaaagtgatc 180
 gtggaacggt tcaaggccaa agtgaccatc gactgggaca gaagcaccaa caccgcctac 240
 ctgcagctga gcggcctgac ctctggcgat accgccgtgt actactgcgc caagggcagc 300
 aagcaccggc tgagagacta cgccctgtac gacgatgacg gcgccctgaa ctgggccgtg 360
 gatgtggact acctgagcaa cctggaattc tggggccagg gcacagccgt gaccgtgtca 420
 tctgcttcga ccaagggccc cagcgtgttc cctctggccc ctacgagcaa gagcacatct 480
 ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccagacc cgtgaccgtg 540

4. __183952027041SEQLIST.TXT

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tcctggaatt ctggcgccct gaccagcggc gtgcacacct ttccagctgt gctgcagtcc 600
agcggcctgt acagcctgag cagcgtcgtg acagtgccca gcagctctct gggcacccag 660
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 720
cccaagagct gcgacaagac ccacacctgt ccccttgctc ctgccccga actgctggga 780
ggcccttccg tgttcctgtt cccccaaag cccaaggaca ccctgatgat cagccggacc 840
cccgaagtga cctgcgtggt ggtggatgtg tcccacgagg accctgaagt gaagttcaat 900
tggtacgtgg acggcgtgga agtgcacaac gccaaagacca agccaagaga ggaacagtac 960
aacagcacct accgggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc 1020
aaagagtaca agtgcaaggt gtccaacaag gccctgcctg ccccatcga gaaaaccatc 1080
agcaaggcca agggccagcc ccggaaccc caggtgtgca cactgcccc aagcagggac 1140
gagctgacca agaaccaggt gtccctgagc tgtgccgtga aaggcttcta cccctccgat 1200
atcgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cccccccct 1260
gtgctggaca gcgacggctc attcttcctg gtgtccaagc tgacagtgga caagtccgg 1320
tggcagcagg gcaacgtgtt cagctgctcc gtgatgcacg aggccttgca caaccactac 1380
accagaagt ccctgagcct gagccccggc aag                                     1413

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<210> 102

<211> 657

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 102

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gacttcgtgc tgacccagag ccctcacagc ctgagcgtga cacctggcga gagcgccagc 60
atcagctgca agagcagcca ctccctgatc cacggcgacc ggaacaacta cctggcttgg 120
tacgtgcaga agcccggcag atccccccag ctgctgatct acctggccag cagcagagcc 180
agcggcgtgc ccgatagatt ttctggcagc ggacgagaca aggacttcac cctgaagatc 240
agccgggtgg aaaccgagga cgtgggcacc tactactgta tgcagggcag agagagcccc 300
tggaaccttg gccagggcac caaggtggac atcaagcgta cgggtggccgc tcccagcgtg 360
ttcatcttcc cacctagcga cgagcagctg aagtccggca cagcctctgt cgtgtgcctg 420
ctgaacaact tctacccccg cgaggccaaa gtgcagtgga aggtggacaa cgccctgcag 480
agcggcaaca gccaggaaag cgtgaccgag caggacagca aggactccac ctacagcctg 540
agcagcacc tgacactgag caaggccgac tacgagaagc acaaggtgta cgcctgcgaa 600
gtgacccacc agggcctgtc tagccccgtg accaagagct tcaaccgggg cgagtgt 657

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<210> 103

<211> 1806

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 103

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gaggttagac tgggtggagtc aggagggggg cttgtgaagc ccggtgggtc tctccgcctg 60
agctgttctg cctccggctt tgatttcgat aacgcctgga tgacctgggt caggcagcct 120
ccaggttaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctggtccgtg 180
gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
acaggcaaat actacgactt ctggtggggc tatccccctg gcgaggaata ttttcaagac 360

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4. __183952027041SEQLIST.TXT

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tgggggtcagg gaacccttgt tatcgtgtcc tccgacaaaa cccataccca gatgcagctg 420
caggagagcg gccctggact cgtgaagccc agcgagaccc tgagcctgac atgcagcgtg 480
agcggcgcca gcatcagcga cagctactgg agctggatca ggaggagccc tggcaagggc 540
ctggagtgga tcggctacgt gcacaagagc ggcgacacca actacagccc ctccctgaag 600
tccagggtga acctgtccct ggacaccagc aagaaccagg tgagcctgtc cctggtggct 660
gccacagctg ctgacagcgg caagtactac tgtgccagga ccctgcacgg caggaggatc 720
tacggcatcg tggccttcaa cgagtggttc acctacttct acatggacgt gtggggcaac 780
ggcaccacagg tgaccgtgag ctccgataag acccacaccg cttccaccaa gggcccatcg 840
gtcttccccc tggcaccctc ctccaagagc acctctgggg gcacagcggc cctgggctgc 900
ctgggtcaagg actacttccc cgaaccgggtg acgggtgtcgt ggaactcagg cgccctgacc 960
agcggcgctgc acaccttccc ggctgtccta cagtcctcag gactctactc cctcagcagc 1020
gtgggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 1080
aagcccagca acaccaaggt ggacaagaaa gttgagccca aatcttgtga caaaactcac 1140
acatgcccac cgtgcccagc acctgaactc ctgggggggac cgtcagtcct cctcttcccc 1200
ccaaaaccca aggacaccct catgatctcc cggacccttg aggtcacatg cgtggtgggtg 1260
gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt atgttgacgg cgtggagggtg 1320
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1380
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1440
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1500
gaaccacagg tgtacaccct gccccatgc cgggatgagc tgaccaagaa tcaagtcagc 1560
ctgtgggtgcc tggtaaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1620
gggcagccgg agaacaacta caagaccag cctcccgtgc tggactccga cggctccttc 1680
ttcctctact caaaactcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1740
tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1800
ccgggt 1806

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<210> 104

<211> 993

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 104

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tccgacatca gcgtggcccc cggagagaca gccaggatct cctgcggcga gaagagcctg 60
ggaagcaggg ctgtgcagtg gtaccaacac agggccggac aggctcccag cctgatcatc 120
tacaacaacc aggacaggcc cagcggcatc cctgagaggt tcagcgggaag ccccgacagc 180
cccttcggaa ccacagccac cctgaccatc acaagcgtgg aagccggcga cgaggccgac 240
tactactgcc acatctggga cagcagggtg cccaccaagt ggggtgtttg cggcggcacc 300
accctgaccg tgctggacaa aaccataacc gcatccgaac tgactcagga ccctgccgtc 360
tctgtggcac tgaagcagac tgtgactatt acttgccgag gcgactcact gcggagccac 420
tacgcttcct ggtatcagaa gaaacccggc caggcacctg tgctgctgtt ctacggaaag 480
aacaataggc catctggcat ccccgaccgc ttttctggca gtgcatcagg gaaccgagcc 540
agtctgacca ttaccggcgc ccaggctgag gacgaagccg attactattg cagctcccgg 600
gataagagcg gctccagact gagcgtgttc ggaggaggaa ctaaactgac cgtcctcgat 660
aagaccata cccgtacggt ggccgctccc agcgtgttca tcttcccacc tagcgacgag 720
cagctgaagt ccggcacagc ctctgtcgtg tgcctgctga acaacttcta ccccgcgag 780
gccaaagtgc agtggaaagg ggacaacgcc ctgcagagcg gcaacagcca ggaaagcgtg 840
accgagcagg acagcaagga ctccacctac agcctgagca gcaccctgac actgagcaag 900
gccgactacg agaagcaca ggtgtacgcc tgcgaagtga cccaccaggg cctgtctagc 960
cccgtgacca agagcttcaa ccggggcgag tgt 993

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4.__183952027041SEQLIST.TXT

<210> 105
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 105
 Arg Ala His Leu Val Gln Ser Gly Thr Ala Met Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Arg Val Ser Cys Gln Thr Ser Gly Tyr Thr Phe Thr Ala His
 20 25 30
 Ile Leu Phe Trp Phe Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
 35 40 45
 Gly Trp Ile Lys Pro Gln Tyr Gly Ala Val Asn Phe Gly Gly Gly Phe
 50 55 60
 Arg Asp Arg Val Thr Leu Thr Arg Asp Val Tyr Arg Glu Ile Ala Tyr
 65 70 75 80
 Met Asp Ile Arg Gly Leu Lys Pro Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Arg Ser Tyr Gly Asp Ser Ser Trp Ala Leu Asp Ala Trp
 100 105 110
 Gly Gln Gly Thr Thr Val Val Val Ser Ala Ala Ser Thr Lys Gly Pro
 115 120 125
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
 210 215 220
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 225 230 235 240
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 325 330 335

4._183952027041SEQLIST.TXT

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
340 345 350
Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
355 360 365
Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
370 375 380
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385 390 395 400
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
405 410 415
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445
Ser Pro Gly
450

<210> 106

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 106

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

4._183952027041SEQLIST.TXT

195
Glu Cys
210

200

205

<210> 107
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 107
Gln Val His Leu Thr Gln Ser Gly Pro Glu Val Arg Lys Pro Gly Thr
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Pro Gly Asn Thr Leu Lys Thr Tyr
20 25 30
Asp Leu His Trp Val Arg Ser Val Pro Gly Gln Gly Leu Gln Trp Met
35 40 45
Gly Trp Ile Ser His Glu Gly Asp Lys Lys Val Ile Val Glu Arg Phe
50 55 60
Lys Ala Lys Val Thr Ile Asp Trp Asp Arg Ser Thr Asn Thr Ala Tyr
65 70 75 80
Leu Gln Leu Ser Gly Leu Thr Ser Gly Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Gly Ser Lys His Arg Leu Arg Asp Tyr Ala Leu Tyr Asp Asp
100 105 110
Asp Gly Ala Leu Asn Trp Ala Val Asp Val Asp Tyr Leu Ser Asn Leu
115 120 125
Glu Phe Trp Gly Gln Gly Thr Ala Val Thr Val Ser Ser Asp Lys Thr
130 135 140
His Thr Glu Val Arg Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro
145 150 155 160
Gly Gly Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Asp
165 170 175
Asn Ala Trp Met Thr Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu
180 185 190
Trp Val Gly Arg Ile Thr Gly Pro Gly Glu Gly Trp Ser Val Asp Tyr
195 200 205
Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys
210 215 220
Asn Thr Leu Tyr Leu Glu Met Asn Asn Val Arg Thr Glu Asp Thr Gly
225 230 235 240
Tyr Tyr Phe Cys Ala Arg Thr Gly Lys Tyr Tyr Asp Phe Trp Trp Gly
245 250 255
Tyr Pro Pro Gly Glu Glu Tyr Phe Gln Asp Trp Gly Gln Gly Thr Leu
260 265 270
Val Ile Val Ser Ser Asp Lys Thr His Thr Ala Ser Thr Lys Gly Pro
275 280 285
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
290 295 300

4. __183952027041SEQLIST.TXT

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
305 310 315 320
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
325 330 335
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
340 345 350
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
355 360 365
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
370 375 380
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
435 440 445
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
450 455 460
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
485 490 495
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510
Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
515 520 525
Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
565 570 575
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605
Ser Pro Gly
610

<210> 108

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 108

Ala Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Lys Gln

4.__183952027041SEQLIST.TXT

1				5				10					15				
Thr	Val	Thr	Ile	Thr	Cys	Arg	Gly	Asp	Ser	Leu	Arg	Ser	His	Tyr	Ala		
			20					25					30				
Ser	Trp	Tyr	Gln	Lys	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Leu	Phe	Tyr		
		35					40					45					
Gly	Lys	Asn	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser		
	50					55				60							
Ala	Ser	Gly	Asn	Arg	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu		
65					70					75					80		
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ser	Ser	Arg	Asp	Lys	Ser	Gly	Ser	Arg		
			85						90					95			
Leu	Ser	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Asp	Lys	Thr		
			100					105					110				
His	Thr	Asp	Phe	Val	Leu	Thr	Gln	Ser	Pro	His	Ser	Leu	Ser	Val	Thr		
		115					120					125					
Pro	Gly	Glu	Ser	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	His	Ser	Leu	Ile		
	130					135					140						
His	Gly	Asp	Arg	Asn	Asn	Tyr	Leu	Ala	Trp	Tyr	Val	Gln	Lys	Pro	Gly		
145					150					155					160		
Arg	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Ala	Ser	Ser	Arg	Ala	Ser	Gly		
			165					170						175			
Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Asp	Lys	Asp	Phe	Thr	Leu		
			180					185					190				
Lys	Ile	Ser	Arg	Val	Glu	Thr	Glu	Asp	Val	Gly	Thr	Tyr	Tyr	Cys	Met		
		195					200					205					
Gln	Gly	Arg	Glu	Ser	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Asp		
	210					215					220						
Ile	Lys	Asp	Lys	Thr	His	Thr	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe		
225					230					235					240		
Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val		
			245					250						255			
Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp		
			260					265						270			
Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr		
		275					280					285					
Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr		
	290					295					300						
Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val		
305					310					315					320		
Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly		
				325					330					335			

Glu Cys

<210> 109

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

4.__183952027041SEQLIST.TXT

<400> 109

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cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
ggcggaggct tccgggatat agtgaccctg acccgggacg tgtaccgca gatcgccctac 240
atggacatcc ggggcctgaa gcccgatgac accgccgtgt actactgcgc cagagacaga 300
agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtggtgggtg 360
tctgccgcct ctacaaaggg cccagcgtg ttccctctgg cccctagcag caagagcaca 420
tctggcggaa cagccgccct gggctgcctc gtgaaggact actttcccga gcccgtagacc 480
gtgtcctgga attctggcgc cctgaccagc ggcgtgcaca cttttccagc tgtgctgcag 540
tccagcggcc tgtacagcct gagcagcgtc gtgacagtgc ccagcagctc tctgggcacc 600
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gaaccaaga gctgcgacaa gaccacacc tgtccccctt gtcctgcccc cgaactgctg 720
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aattggtacg tggacggcgt ggaagtgcac aacgccaaga ccaagccaag agaggaacag 900
tacaacagca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ctggctgaac 960
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gacgagctga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccctcc 1140
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cctgtgctgg acagcgacgg ctcatcttc ctggtgtcca agctgacagt ggacaagttc 1260
cgggtggcagc agggcaacgt gttcagctgc tccgtgatgc acgaggccct gcacaaccac 1320
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<210> 110

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 110

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ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgcccagc 180
agattttccg gcagcggctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630

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<210> 111

<211> 1833

<212> DNA

<213> Artificial Sequence

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<220>

<223> Synthetic Construct

<400> 111

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tcctgcaagg cccctggcaa caccctgaaa acctacgacc tgcactgggt gcgcagcgtg 120
ccaggacagg gactgcagtg gatgggctgg atcagccacg agggcgacaa gaaagtgatc 180
gtggaacggg tcaaggccaa agtgaccatc gactgggaca gaagcaccaa caccgcctac 240
ctgcagctga gcggcctgac ctctggcgat accgccgtgt actactgcgc caagggcagc 300
aagcaccggc tgagagacta cgccctgtac gacgatgacg gcgccctgaa ctgggcccgtg 360
gatgtggact acctgagcaa cctggaattc tggggccagg gcacagccgt gaccgtgtca 420
tctgacaaaa ccataccga ggttagactg gtggagtcag gaggggggct tgtgaagccc 480
ggtgggtctc tccgcctgag ctgttctgcc tccggctttg atttcgataa cgcctggatg 540
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ggcgaggggc ggtccgtgga ctacgcggaa tctgttaaag ggcggtttac aatctcaagg 660
gacaatacca agaatacctt gtatttggag atgaacaacg tgagaactga agacaccgga 720
tattacttct gtgccagaac aggcaaatac tacgacttct ggtggggcta tccccctggc 780
gaggaatatt ttcaagactg gggtcaggga acccttgtaa tcgtgtcctc cgataagacc 840
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tctgggggca cagcggccct gggctgcctg gtcaaggact acttcccga accggtgacg 960
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cccgtgctgg actccgacgg ctcttcttc ctctactcaa aactcaccgt ggacaagagc 1740
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tacacgcaga agagcctctc cctgtctccg ggt 1833

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<210> 112

<211> 1014

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 112

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acttgccgag gcgactcact gcggagccac tacgcttcct ggtatcagaa gaaaccggc 120
caggcacctg tgctgctgtt ctacggaaag aacaataggc catctggcat ccccgaccgc 180
ttttctggca gtgcatcagg gaaccgagcc agtctgacca ttaccggcgc ccaggctgag 240
gacgaagccg attactattg cagctcccgg gataagagcg gctccagact gagcgtgttc 300
ggaggaggaa ctaaactgac cgtcctcgac aaaaccata ccgacttcgt gctgaccagc 360
agccctcaca gcctgagcgt gacacctggc gagagcgcca gcatcagctg caagagcagc 420

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cactccctga tccacggcga ccggaacaac tacctggctt ggtacgtgca gaagcccggc 480
agatcccccc agctgctgat ctacctggcc agcagcagag ccagcggcgt gcccgataga 540
ttttctggca gcggcagcga caaggacttc accctgaaga tcagccgggt ggaaaccgag 600
gacgtgggca cctactactg tatgcagggc agagagagcc cctggacctt tggccagggc 660
accaaggtgg acatcaagga taagacccat acccgtagcg tggccgctcc cagcgtgttc 720
atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 780
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ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 900
agcaccctga cactgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 960
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<210> 113

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 113

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

4. __183952027041SEQLIST.TXT

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

<210> 114

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 114

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

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[illegible]

<210> 115

 $\langle 211 \rangle$ 602

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 115

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

4._183952027041SEQLIST.TXT

Thr	Ser	Lys	Asn	Gln	Val	Ser	Leu	Ser	Leu	Val	Ala	Ala	Thr	Ala	Ala
210						215					220				
Asp	Ser	Gly	Lys	Tyr	Tyr	Cys	Ala	Arg	Thr	Leu	His	Gly	Arg	Arg	Ile
225					230					235					240
Tyr	Gly	Ile	Val	Ala	Phe	Asn	Glu	Trp	Phe	Thr	Tyr	Phe	Tyr	Met	Asp
				245					250					255	
Val	Trp	Gly	Asn	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His
			260					265					270		
Thr	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser
		275					280					285			
Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp
		290				295					300				
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr
305					310					315					320
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr
				325					330					335	
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln
			340					345					350		
Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp
		355					360					365			
Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro
	370					375					380				
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
385					390					395					400
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
				405					410					415	
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn
			420					425					430		
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
		435					440						445		
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
		450					455					460			
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
465					470					475					480
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
				485					490					495	
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Cys	Arg	Asp
			500					505					510		
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu	Val	Lys	Gly	Phe
		515					520					525			
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
		530				535					540				
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
545					550					555					560
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
				565					570					575	
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
			580					585					590		
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly						
		595					600								

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<210> 116

<211> 331

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 116

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Glu	Lys	Ser	Leu	Gly	Ser	Arg	Ala	Val	Gln	Trp	Tyr	Gln	His	Arg	Ala
			20					25					30		
Gly	Gln	Ala	Pro	Ser	Leu	Ile	Ile	Tyr	Asn	Asn	Gln	Asp	Arg	Pro	Ser
		35					40					45			
Gly	Ile	Pro	Glu	Arg	Phe	Ser	Gly	Ser	Pro	Asp	Ser	Pro	Phe	Gly	Thr
	50					55				60					
Thr	Ala	Thr	Leu	Thr	Ile	Thr	Ser	Val	Glu	Ala	Gly	Asp	Glu	Ala	Asp
65					70				75						80
Tyr	Tyr	Cys	His	Ile	Trp	Asp	Ser	Arg	Val	Pro	Thr	Lys	Trp	Val	Phe
			85					90						95	
Gly	Gly	Gly	Thr	Thr	Leu	Thr	Val	Leu	Asp	Lys	Thr	His	Thr	Ala	Ser
			100					105					110		
Glu	Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Lys	Gln	Thr	Val
		115					120					125			
Thr	Ile	Thr	Cys	Arg	Gly	Asp	Ser	Leu	Arg	Ser	His	Tyr	Ala	Ser	Trp
	130					135					140				
Tyr	Gln	Lys	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Leu	Phe	Tyr	Gly	Lys
145					150					155					160
Asn	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ala	Ser
				165				170						175	
Gly	Asn	Arg	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu	Asp	Glu
			180					185					190		
Ala	Asp	Tyr	Tyr	Cys	Ser	Ser	Arg	Asp	Lys	Ser	Gly	Ser	Arg	Leu	Ser
		195					200					205			
Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Asp	Lys	Thr	His	Thr
	210					215					220				
Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu
225					230					235					240
Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe
				245					250					255	
Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln
			260					265					270		
Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
		275					280					285			
Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
	290					295						300			
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser
305					310					315					320
Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys					
				325					330						

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<210> 117
 <211> 1413
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 117
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 tcctgcaagg cccctggcaa caccctgaaa acctacgacc tgcactgggt gcgcagcgtg 120
 ccaggacagg gactgcagtg gatgggctgg atcagccacg agggcgacaa gaaagtgatc 180
 gtggaacggg tcaaggccaa agtgaccatc gactgggaca gaagcaccaa caccgcctac 240
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 aagcacccggc tgagagacta cgccctgtac gacgatgacg gcgccctgaa ctggggccgtg 360
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 tctgcttcga ccaaggggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 480
 ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccagacc cgtgaccgtg 540
 tcctggaatt ctggcgccct gaccagcggc gtgcacacct ttccagctgt gctgcagtcc 600
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 aacagcacct accgggtggg gtccgtgctg accgtgctgc accaggactg gctgaacggc 1020
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 agcaaggcca agggccagcc ccgcaaccc caggtgtgca cactgcccc aagcaggggac 1140
 gagctgacca agaaccaggt gtccctgagc tgtgccgtga aaggcttcta cccctccgat 1200
 atcgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cccccccct 1260
 gtgctggaca gcgacggctc attcttctg gtgtccaagc tgacagtgga caagtcccg 1320
 tggcagcagg gcaacgtgtt cagctgtctc gtgatgcacg aggcctgca caaccactac 1380
 acccagaagt ccctgagcct gagccccggc aag 1413

<210> 118
 <211> 657
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 118
 gacttcgtgc tgacccagag ccctcacagc ctgagcgtga cacctggcga gagcgccagc 60
 atcagctgca agagcagcca ctccctgatc caggcgacc ggaacaacta cctggcttgg 120
 tacgtgcaga agcccgagc atccccccag ctgctgatct acctggccag cagcagagcc 180
 agcggcgtgc ccgatagatt ttctggcagc ggcagcgaca aggacttcac cctgaagatc 240
 agccgggtgg aaaccgagga cgtgggcacc tactactgta tgcagggcag agagagcccc 300
 tggacctttg gccagggcac caaggtggac atcaagcgta cgggtggccgc tcccagcgtg 360
 ttcatcttcc cacctagcga cgagcagctg aagtccggca cagcctctgt cgtgtgcctg 420
 ctgaacaact tctacccccg cgaggccaaa gtgcagtgga aggtggacaa cgccctgcag 480

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agcggcaaca gccaggaaag cgtgaccgag caggacagca aggactccac ctacagcctg 540
agcagcacc tgacactgag caaggccgac tacgagaagc acaagggtgta cgcctgcgaa 600
gtgaccacc agggcctgtc tagccccgtg accaagagct tcaaccgggg cgagtgt 657
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<210> 119

<211> 1806

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 119

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agctgttctg cctccggctt tgatttcgat aacgcctgga tgacctgggt caggcagcct 120
ccaggtaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctgggtccgtg 180
gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
acaggcaaat actacgactt ctggtccggc tatccccctg gcgaggaata ttttcaagac 360
tggggtcagg gaacccttgt tatcgtgtcc tccgacaaaa cccataccca gatgcagctg 420
caggagagcg gccctggact cgtgaagccc agcgagacc tgagcctgac atgcagcgtg 480
agcggcgcca gcatcagcga cagctactgg agctggatca ggaggagccc tggcaagggc 540
ctggagtggg tgggtacgt gcacaagagc ggcgacacca actacagccc ctccctgaag 600
tccagggtga acctgtccct ggacaccagc aagaaccagg tgagcctgtc cctggtggct 660
gccacagctg ctgacagcgg caagtactac tgtgccagga ccctgcacgg caggaggatc 720
tacggcatcg tggccttcaa cgagtgggtc acctacttct acatggacgt gtggggcaac 780
ggcaccaggg tgaccgtgag ctccgataag acccacaccg cttccacca gggcccatcg 840
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ctgggtcaagg actacttccc cgaaccgggtg acgggtgtcgt ggaactcagg cgccctgacc 960
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aagcccagca acaccaaggt ggacaagaaa gttgagccca aatcttgtga caaaactcac 1140
acatgcccac cgtgcccagc acctgaactc ctgggggggac cgtcagtcct cctcttcccc 1200
ccaaaaccca aggacaccct catgatctcc cggaccctg aggtcacatg cgtggtggtg 1260
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cataatgcc aagacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1380
gtcctcacg tcctgcacca ggactggctg aatggcaagg agtacaagt caaggtctcc 1440
aacaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1500
gaaccacagg tgtacaccct gccccatgc cgggatgagc tgaccaagaa tcaagtacgc 1560
ctgtggtgcc tggtaaaagg cttctatccc agcgacatc ccgtggagt ggagagcaat 1620
gggcagccgg agaacaacta caagaccag cctcccgtgc tggactccga cggctccttc 1680
ttcctctact caaaactcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1740
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ccgggt 1806
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<210> 120

<211> 993

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

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<400> 120

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ggaagcaggg ctgtgcagtg gtaccaacac agggccggac aggctcccag cctgatcatc 120
tacaacaacc aggacaggcc cagcggcatc cctgagaggt tcagcgggaag ccccgacagc 180
cccttcggaa ccacagccac cctgaccatc acaagcgtgg aagccggcga cgaggccgac 240
tactactgcc acatctggga cagcagggtg cccaccaagt ggggtgtttgg cggcggcacc 300
accctgaccg tgctggacaa aaccataacc gcatccgaac tgactcagga ccctgccgtc 360
tctgtggcac tgaagcagac tgtgactatt acttgccgag gcgactcact gcggagccac 420
tacgcttcct ggtatcagaa gaaaccggc caggcacctg tgctgctgtt ctacggaaag 480
aacaataggc catctggcat ccccgaccgc ttttctggca gtgcatcagg gaaccgagcc 540
agtctgacca ttaccggcgc ccaggctgag gacgaagccg attactattg cagctcccgg 600
gataagagcg gctccagact gagcgtgttc ggaggaggaa ctaaactgac cgtcctcgat 660
aagaccata cccgtacggg ggccgctccc agcgtgttca tcttcccacc tagcgacgag 720
cagctgaagt ccggcacagc ctctgtcgtg tgctgtctga acaacttcta ccccgcgag 780
gccaaagtgc agtggaaggt ggacaacgcc ctgcagagcg gcaacagcca ggaaagcgtg 840
accgagcagg acagcaagga ctccacctac agcctgagca gcaccctgac actgagcaag 900
gccgactacg agaagcaca ggtgtacgcc tgcgaagtga cccaccaggg cctgtctagc 960
cccgtagcca agagcttcaa ccggggcgag tgt 993
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<210> 121

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 121

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

<210> 122

$\langle 211 \rangle$ 210

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 122

Tyr 1	Ile	His	Val	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Val	Ser	Ile	Gly
Asp	Arg	Val	Thr 20	Ile	Asn	Cys	Gln	Thr 25	Ser	Gln	Gly	Val	Gly 30	Ser	Asp
Leu	His	Trp 35	Tyr	Gln	His	Lys	Pro 40	Gly	Arg	Ala	Pro	Lys 45	Leu	Leu	Ile

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

<210> 123

<211> 602

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 123

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

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145					150					155				160
Ser	Gly	Ala	Ser	Ile	Ser	Asp	Ser	Tyr	Trp	Ser	Trp	Ile	Arg	Arg Ser
				165					170					175
Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Val	His	Lys	Ser	Gly Asp
			180					185					190	
Thr	Asn	Tyr	Ser	Pro	Ser	Leu	Lys	Ser	Arg	Val	Asn	Leu	Ser	Leu Asp
		195					200					205		
Thr	Ser	Lys	Asn	Gln	Val	Ser	Leu	Ser	Leu	Val	Ala	Ala	Thr	Ala Ala
	210					215				220				
Asp	Ser	Gly	Lys	Tyr	Tyr	Cys	Ala	Arg	Thr	Leu	His	Gly	Arg	Arg Ile
225					230					235				240
Tyr	Gly	Ile	Val	Ala	Phe	Asn	Glu	Trp	Phe	Thr	Tyr	Phe	Tyr	Met Asp
				245					250					255
Val	Trp	Gly	Asn	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr His
			260					265					270	
Thr	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser Ser
		275					280					285		
Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys Asp
	290					295					300			
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu Thr
305					310					315				320
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu Tyr
				325					330					335
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr Gln
		340					345					350		
Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val Asp
		355				360					365			
Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro Pro
	370				375					380				
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe Pro
385				390					395					400
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val Thr
				405					410					415
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe Asn
			420					425					430	
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro Arg
	435					440					445			
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr Val
	450					455				460				
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val Ser
465					470				475					480
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala Lys
				485				490						495
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Cys	Arg Asp
			500					505					510	
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu	Val	Lys	Gly Phe
		515					520					525		
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro Glu
	530					535				540				
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser Phe
545					550				555					560
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln Gly

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				565					570				575				
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr		
			580					585					590				
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly								
		595					600										

<210> 124

<211> 331

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 124

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

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Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
290						295					300				
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser
305					310					315					320
Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys					
				325					330						

<210> 125
 <211> 1356
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 125
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 cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
 ggcggaggct tccgggatag agtgaccctg acccgggacg tgtaccgcga gatcgccctac 240
 atggacatcc ggggcctgaa gcccgatgac accgccgtgt actactgcgc cagagacaga 300
 agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtgggtggg 360
 tctgccgcct ctacaaaggg cccagcgtg ttccctctgg ccctagcag caagagcaca 420
 tctggcggaa cagccgccct gggctgcctc gtgaaggact actttcccga gcccgtagacc 480
 gtgtcctgga attctggcgc cctgaccagc ggcgtgcaca cctttccagc tgtgctgcag 540
 tccagcggcc tgtacagcct gagcagcgtc gtgacagtgc ccagcagctc tctgggcacc 600
 cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagaagggtg 660
 gaaccaaga gctgcgacaa gaccacacc tgtccccctt gtcctgcccc cgaactgctg 720
 ggaggccctt ccgtgttcct gttcccccca aagcccaagg acaccctgat gatcagccgg 780
 acccccgaag tgacctgctg ggtgggtggat gtgtcccacg aggaccctga agtgaagttc 840
 aattggtacg tggacggcgt ggaagtgcac aacgccaaga ccaagccaag agaggaacag 900
 tacaacagca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ctggctgaac 960
 ggcaaagagt acaagtcaa ggtgtccaac aaggccctgc ctgccccat cgagaaaacc 1020
 atcagcaagg ccaaggcca gccccgcgaa cccaggtgt gcacactgcc cccaagcagg 1080
 gacgagctga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccctcc 1140
 gatatgccg tggaatggga gagcaacggc cagcccgaga acaactaca gaccacccc 1200
 cctgtgctgg acagcgacgg ctcatcttc ctggtgtcca agctgacagt ggacaagtcc 1260
 cgggtggcagc agggcaacgt gttcagctgc tccgtgatgc acgaggccct gcacaaccac 1320
 tacaccaga agtccctgag cctgagcccc ggcaag 1356

<210> 126
 <211> 630
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 126
 tacatccacg tgacccagag ccccgacgac ctgtccgtgt ccatcggcga cagagtgacc 60
 atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120

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ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgcccagc 180
agatttttccg gcagcggtct ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcagggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacgggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630

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<210> 127

<211> 1806

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 127

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agctgttctg cctccggctt tgatttcgat aacgcctgga tgacctgggt caggcagcct 120
ccaggtaagg gactggagtg ggtgggaaga atcacaggct caggcgaggg ctgggtccgtg 180
gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
acaggcaaat actacgactt ctgggtccggc tatccccctg gcgaggaata ttttcaagac 360
tggggtcagg gaacccttgt tatcgtgtcc tccgacaaaa ccataacca gatgcagctg 420
caggagagcg gccctggact cgtgaagccc agcgagacct tgagcctgac atgcagcgtg 480
agcggcgcca gcatcagcga cagctactgg agctggatca ggaggagccc tggcaagggc 540
ctggagtgga tcggctacgt gcacaagagc ggcgacacca actacagccc ctccctgaag 600
tccagggtga acctgtccct ggacaccagc aagaaccagg tgagcctgtc cctggtggct 660
gccacagctg ctgacagcgg caagtactac tgtgccagga ccctgcacgg caggaggatc 720
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ggcaccacagg tgaccgtgag ctccgataag acccacaccg cttccaccaa gggcccatcg 840
gtcttcccc tggcaccctc ctccaagagc acctctgggg gcacagcggc cctgggctgc 900
ctgggtcaagg actacttccc cgaaccggtg acggtgtcgt ggaactcagg cgccctgacc 960
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tgctccgtga tgcagaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1800
ccgggt 1806

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<210> 128

4.__183952027041SEQLIST.TXT

<211> 993

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 128

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ggaagcaggg ctgtgcagtg gtaccaacac agggccggac aggctcccag cctgatcatc 120
tacaacaacc aggacaggcc cagcggcatc cctgagaggt tcagcgggaag ccccgacagc 180
cccttcggaa ccacagccac cctgaccatc acaagcgtgg aagccggcga cgaggccgac 240
tactactgcc acatctggga cagcaggggtg cccaccaagt gggtgttttg cggcggcacc 300
accctgaccg tgctggacaa aaccataacc gcatccgaac tgactcagga ccctgccgtc 360
tctgtggcac tgaagcagac tgtgactatt acttgccgag gcgactcact gcggagccac 420
tacgcttcct ggtatcagaa gaaacccggc caggcacctg tgctgctgtt ctacggaaag 480
aacaataggc catctggcat ccccgaccgc ttttctggca gtgcatcagg gaaccgagcc 540
agtctgacca ttaccggcgc ccaggctgag gacgaagccg attactattg cagctcccgg 600
gataagagcg gctccagact gagcgtgttc ggaggaggaa ctaaactgac cgtcctcgat 660
aagacccata cccgtacggg ggccgctccc agcgtgttca tcttcccacc tagcgacgag 720
cagctgaagt cgggcacagc ctctgtcgtg tgcctgctga acaatttcta ccccgcgag 780
gccaaagtgc agtgggaagg ggacaacgcc ctgcagagcg gcaacagcca ggaaagcgtg 840
accgagcagg acagcaagga ctccacctac agcctgagca gcaccctgac actgagcaag 900
gccgactacg agaagcaca ggtgtacgcc tgcgaagtga cccaccaggg cctgtctagc 960
cccgtagacca agagcttcaa ccggggcgag tgt 993
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<210> 129

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 129

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

4. 183952027041SEQLIST.TXT

130					135					140						
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	
145					150					155						
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	
				165					170					175		
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	
				180					185					190		
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	
				195					200					205		
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	
				210					215					220		
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	
225					230					235					240	
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	
				245					250					255		
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	
				260					265					270		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	
				275					280					285		
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	
				290					295					300		
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	
305					310					315					320	
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	
				325					330					335		
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	
				340					345					350		
Val	Cys	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	
				355					360					365		
Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	
				370					375					380		
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	
385					390					395					400	
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr	
				405					410					415		
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	
				420					425					430		
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	
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Ser	Pro	Gly														
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<210> 130
<211> 210
<212> PRT
<213> Artificial Sequence
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<220>
<223> Synthetic Construct

<400> 130

4.__183952027041SEQLIST.TXT

```

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

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<210> 131
 <211> 612
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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<400> 131
Gln Val His Leu Thr Gln Ser Gly Pro Glu Val Arg Lys Pro Gly Thr
 1           5           10           15
Ser Val Lys Val Ser Cys Lys Ala Pro Gly Asn Thr Leu Lys Thr Tyr
          20           25           30
Asp Leu His Trp Val Arg Ser Val Pro Gly Gln Gly Leu Gln Trp Met
          35           40           45
Gly Trp Ile Ser His Glu Gly Asp Lys Lys Val Ile Val Glu Arg Phe
          50           55           60
Lys Ala Lys Val Thr Ile Asp Trp Asp Arg Ser Thr Asn Thr Ala Tyr
65          70          75          80
Leu Gln Leu Ser Gly Leu Thr Ser Gly Asp Thr Ala Val Tyr Tyr Cys
          85          90          95
Ala Lys Gly Ser Lys His Arg Leu Arg Asp Tyr Ala Leu Tyr Asp Asp

```

4. 183952027041SEQLIST.TXT

Protein 1															
Protein 2															
Protein 3															
Protein 4															
Protein 5															
Protein 6															
Protein 7															
Protein 8															
Protein 9															
Protein 10															
Protein 11															
Protein 12															
Protein 13															
Protein 14															
Protein 15															
Protein 16															
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Protein 92															
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Protein 94															
Protein 95															
Protein 96															
Protein 97															
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Protein 99															
Protein 100															

4._183952027041SEQLIST.TXT

515		520		525	
Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala					
530		535		540	
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr					
545		550		555	560
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu					
	565		570		575
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser					
	580		585		590
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser					
	595	600		605	
Leu Ser Pro Gly					
610					

<210> 132

<211> 334

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 132

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

4. __183952027041SEQLIST.TXT

Thr	His	Thr	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro
225					230					235					240
Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu
				245					250					255	
Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn
			260					265					270		
Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser
		275					280					285			
Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala
	290					295					300				
Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly
305					310					315					320
Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys		
				325						330					

<210> 133

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 133

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tcctgtcaga	caagcggcta	caccttcacc	gccacatcc	tggtcttggt	ccggcaggcc	120
cctggcagag	gactggaatg	ggtgggatgg	atcaagcccc	agtatggcgc	cgtgaacttc	180
ggcggaggct	tccgggatag	agtgaccctg	accggggacg	tgtaccgcga	gatcgcttac	240
atggacatcc	ggggcctgaa	gcccgatgac	accgccgtgt	actactgcgc	cagagacaga	300
agctacggcg	acagcagctg	ggctctggat	gcttggggcc	agggcacaac	cgtggtggtg	360
tctgccgcct	ctacaaaggg	ccccagcgtg	ttccctctgg	cccctagcag	caagagcaca	420
tctggcggaa	cagccgccct	gggctgcctc	gtgaaggact	actttcccga	gcccgtagacc	480
gtgtcctgga	attctggcgc	cctgaccagc	ggcgtgcaca	cctttccagc	tgtgctgcag	540
tccagcggcc	tgtacagcct	gagcagcgtc	gtgacagtgc	ccagcagctc	tctgggcacc	600
cagacctaca	tctgcaacgt	gaaccacaag	cccagcaaca	ccaaggtgga	caagaagggtg	660
gaaccaaga	gctgcgacaa	gaccacacc	tgtccccctt	gtcctgcccc	cgaactgctg	720
ggaggccctt	ccgtgttcct	gttcccccca	aagcccaagg	acaccctgat	gatcagccgg	780
acccccgaag	tgacctgcgt	ggtggtggat	gtgtcccacg	aggaccctga	agtgaagtcc	840
aattggtacg	tggaacggcg	ggaagtgcac	aacgccaaga	ccaagccaag	agaggaacag	900
tacaacagca	cctaccgggt	ggtgtccgtg	ctgaccgtgc	tgcaccagga	ctggctgaac	960
ggcaaagagt	acaagtgcaa	ggtgtccaac	aaggccctgc	ctgcccccat	cgagaaaacc	1020
atcagcaagg	ccaagggcca	gccccgcgaa	ccccagggtg	gcacactgcc	ccaagcagg	1080
gacgagctga	ccaagaacca	ggtgtcccctg	agctgtgccg	tgaaaggctt	ctaccctcc	1140
gatatcgccg	tggaatggga	gagcaacggc	cagcccgaga	acaactacaa	gaccaccccc	1200
cctgtgtctg	acagcgacgg	ctcattcttc	ctggtgtcca	agctgacagt	ggacaagtcc	1260
cggtggcagc	agggcaacgt	gttcagctgc	tccgtgatgc	acgaggccct	gcacaaccac	1320
tacaccaga	agtcctgag	cctgagcccc	ggcaag			1356

<210> 134

<211> 630

<212> DNA

4.__183952027041SEQLIST.TXT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 134

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atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgcccagc 180
agattttccg gcagcggctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630
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<210> 135

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 135

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tcctgcaagg cccctggcaa caccctgaaa acctacgacc tgcactgggt gcgcagcgtg 120
ccaggacagg gactgcagtg gatgggctgg atcagccacg agggcgacaa gaaagtgatc 180
gtggaacggg tcaaggccaa agtgaccatc gactgggaca gaagcaccaa caccgcctac 240
ctgcagctga gcggcctgac ctctggcgat accgccgtgt actactgcgc caagggcagc 300
aagcaccggc tgagagacta cgccctgtac gacgatgacg gcgccctgaa ctgggcccgtg 360
gatgtggact acctgagcaa cctggaattc tggggccagg gcacagccgt gaccgtgtca 420
tctgacaaaa cccataccca gatgcagctg caggagagcg gccctggact cgtgaagccc 480
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agctggatca ggaggagccc tggcaagggc ctggagtgga tcggctacgt gcacaagagc 600
ggcgacacca actacagccc ctccctgaag tccagggtga acctgtccct ggacaccagc 660
aagaaccagg tgagcctgtc cctggtgggt gccacagctg ctgacagcgg caagtactac 720
tgtgccagga ccctgcacgg caggaggatc tacggcatcg tggccttcaa cgagtgtgtc 780
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accacaccg cttccaccaa gggcccatcg gtcttcccc tggcaccctc ctccaagagc 900
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ttcaactggt atgttgacgg cgtggaggtg cataatgcc aagacaaagcc gcgggaggag 1380
cagtacaaca gcacgtaccg tgtggtcagc gtcttcaccg tcctgcacca ggactggctg 1440
aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1500
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4. __183952027041SEQLIST.TXT

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accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatgc 1560
cgggatgagc tgaccaagaa tcaagtcagc ctgtgggtgcc tggtaaaagg cttctatccc 1620
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1680
cctcccgtgc tggactccga cggctccttc ttcctctact caaaactcac cgtggacaag 1740
agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac 1800
cactacacgc agaagagcct ctccctgtct ccgggt 1836
```

<210> 136

<211> 1002

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 136

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tccgacatca gcgtggcccc cggagagaca gccaggatct cctgcggcga gaagagcctg 60
ggaagcaggg ctgtgcagtg gtaccaacac agggccggac aggctcccag cctgatcatc 120
tacaacaacc aggacaggcc cagcggcatc cctgagaggt tcagcgggaag ccccgacagc 180
cccttcggaa ccacagccac cctgaccatc acaagcgtgg aagccggcga cgaggccgac 240
tactactgcc acatctggga cagcagggtg cccaccaagt gggtgtttgg cggcggcacc 300
accctgaccg tgctggacaa aaccataacc gacttcgtgc tgaccagag ccctcacagc 360
ctgagcgtga cacctggcga gagcgccagc atcagctgca agagcagcca ctccctgatc 420
cacggcgacc ggaacaacta cctggcttgg tacgtgcaga agcccggcag atccccccag 480
ctgctgatct acctggccag cagcagagcc agcggcgtgc ccgatagatt ttctggcagc 540
ggcagcgaca aggacttcac cctgaagatc agccgggtgg aaaccgagga cgtgggcacc 600
tactactgta tgcagggcag agagagcccc tggacctttg gccagggcac caaggtggac 660
atcaaggata agaccatac ccgtacggtg gccgtccca gcgtgttcat cttccacct 720
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 780
ccccgcgagg ccaaagtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag 840
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgaca 900
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 960
ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 1002
```

<210> 137

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 137

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

4.___183952027041SEQLIST.TXT

65					70					75				80
Met	Asp	Ile	Arg	Gly	Leu	Lys	Pro	Asp	Asp	Thr	Ala	Val	Tyr	Tyr Cys
				85					90					95
Ala	Arg	Asp	Arg	Ser	Tyr	Gly	Asp	Ser	Ser	Trp	Ala	Leu	Asp	Ala Trp
			100					105					110	
Gly	Gln	Gly	Thr	Thr	Val	Val	Val	Ser	Ala	Ala	Ser	Thr	Lys	Gly Pro
		115					120					125		
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly Thr
	130					135				140				
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val Thr
145					150				155					160
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe Pro
			165					170						175
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val Thr
		180					185					190		
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val Asn
	195					200						205		
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys Ser
	210				215						220			
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu Leu
225					230				235					240
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr Leu
			245					250					255	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val Ser
		260						265					270	
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val Glu
	275						280					285		
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser Thr
	290					295					300			
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu Asn
305					310				315					320
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala Pro
				325					330					335
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro Gln
	340						345						350	
Val	Cys	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln Val
	355					360						365		
Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala Val
	370					375				380				
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr Pro
385					390				395					400
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu Thr
			405					410						415
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser Val
		420					425					430		
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser Leu
	435					440						445		
Ser	Pro	Gly												
	450													

<210> 138

4.__183952027041SEQLIST.TXT

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 138

```

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

```

<210> 139

<211> 602

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 139

```

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

```

4. 183952027041SEQLIST.TXT

		35					40				45				
Gly 50	Tyr 50	Val	His	Lys	Ser	Gly 55	Asp	Thr	Asn	Tyr	Ser 60	Pro	Ser	Leu	Lys
Ser 65	Arg	Val	Asn	Leu	Ser 70	Leu	Asp	Thr	Ser	Lys 75	Asn	Gln	Val	Ser	Leu 80
Ser	Leu	Val	Ala	Ala 85	Thr	Ala	Ala	Asp	Ser 90	Gly	Lys	Tyr	Tyr	Cys 95	Ala
Arg	Thr	Leu	His 100	Gly	Arg	Arg	Ile	Tyr 105	Gly	Ile	Val	Ala	Phe	Asn	Glu
Trp	Phe	Thr	Tyr	Phe	Tyr	Met	Asp	Val	Trp	Gly	Asn	Gly	Thr	Gln	Val
		115					120					125			
Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Glu	Val	Arg	Leu	Val	Glu	Ser
		130					135					140			
Gly 145	Gly	Gly	Leu	Val	Lys 150	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ser 160
Ala	Ser	Gly	Phe	Asp	Phe 165	Asp	Asn	Ala	Trp	Met	Thr	Trp	Val	Arg	Gln
									170					175	
Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Gly	Arg	Ile	Thr	Gly	Pro	Gly
			180					185					190		
Glu	Gly	Trp	Ser	Val	Asp	Tyr	Ala	Glu	Ser	Val	Lys	Gly	Arg	Phe	Thr
		195					200					205			
Ile	Ser	Arg	Asp	Asn	Thr	Lys	Asn	Thr	Leu	Tyr	Leu	Glu	Met	Asn	Asn
		210				215						220			
Val	Arg	Thr	Glu	Asp	Thr	Gly	Tyr	Tyr	Phe	Cys	Ala	Arg	Thr	Gly	Lys
225					230					235					240
Tyr	Tyr	Asp	Phe	Trp	Ser	Gly	Tyr	Pro	Pro	Gly	Glu	Glu	Tyr	Phe	Gln
				245					250					255	
Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Ile	Val	Ser	Ser	Asp	Lys	Thr	His
			260					265					270		
Thr	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser
		275					280					285			
Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp
		290				295					300				
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr
305					310					315					320
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr
			325						330					335	
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln
			340					345					350		
Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp
		355					360					365			
Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro
		370				375					380				
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
385					390					395					400
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
				405					410					415	
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn
			420												

4.__183952027041SEQLIST.TXT

```

      450      455      460
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
465      470      475      480
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
      485      490      495
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
      500      505      510
Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe
      515      520      525
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
      530      535      540
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
545      550      555      560
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
      565      570      575
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
      580      585      590
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
      595      600

```

<210> 140

<211> 331

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 140

```

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

```

4.__183952027041SEQLIST.TXT

Gly	Thr	Thr	Ala	Thr	Leu	Thr	Ile	Thr	Ser	Val	Glu	Ala	Gly	Asp	Glu
			180					185					190		
Ala	Asp	Tyr	Tyr	Cys	His	Ile	Trp	Asp	Ser	Arg	Val	Pro	Thr	Lys	Trp
		195					200					205			
Val	Phe	Gly	Gly	Gly	Thr	Thr	Leu	Thr	Val	Leu	Asp	Lys	Thr	His	Thr
	210					215					220				
Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu
225					230					235					240
Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe
			245						250					255	
Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln
		260						265					270		
Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
	275						280					285			
Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
	290					295					300				
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser
305					310					315					320
Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys					
			325						330						

<210> 141

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 141

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agagcccacc tgggtgcagtc tggcaccgcc atgaagaaac caggcgcctc tgtgcgggtg 60
tcctgtcaga caagcggcta caccttcacc gccacatcc tgttctgggt ccggcaggcc 120
cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
ggcggaggct tccgggatag agtgaccctg acccgggacg tgtaccgcga gatcgacctac 240
atggacatcc ggggcctgaa gcccgatgac accgccgtgt actactgcgc cagagacaga 300
agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtggtggtg 360
tctgccgcct ctacaaaggg cccagcgtg ttccctctgg cccctagcag caagagcaca 420
tctggcggaa cagccgccct gggctgcctc gtgaaggact actttcccga gcccgtagacc 480
gtgtcctgga attctggcgc cctgaccagc ggcgtgcaca cctttccagc tgtgctgcag 540
tccagcggcc tgtacagcct gagcagcgtc gtgacagtgc ccagcagctc tctgggcacc 600
cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagaaggtg 660
gaacccaaga gctgcgacaa gaccacacc tgtccccctt gtcctgcccc cgaactgctg 720
ggaggccctt ccgtgttcct gttcccccca aagcccaagg acaccctgat gatcagccgg 780
acccccgaag tgacctgcgt ggtggtggat gtgtccacg aggaccctga agtgaagttc 840
aattggtacg tggacggcgt ggaagtgcac aacgccaaga ccaagccaag agaggaacag 900
tacaacagca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ctggctgaac 960
ggcaaagagt acaagtgcaa ggtgtccaac aaggccctgc ctgcccccat cgagaaaacc 1020
atcagcaagg ccaagggcca gccccgcgaa cccaggtgt gcacactgcc cccaagcagg 1080
gacgagctga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccctcc 1140
gatatcgccg tggaatggga gagcaacggc cagcccgaga acaactacaa gaccaccccc 1200
cctgtgctgg acagcgacgg ctcatcttc ctggtgtcca agctgacagt ggacaagtcc 1260

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4. __183952027041SEQLIST.TXT

cggtggcagc agggcaacgt gttcagctgc tccgtgatgc acgaggccct gcacaaccac 1320
tacaccaga agtccctgag cctgagcccc ggcaag 1356

<210> 142

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 142

tacatccacg tgacccagag ccccagcagc ctgtccgtgt ccatcggcga cagagtgacc 60
atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgcccagc 180
agattttccg gcagcggctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacgggtggc cgtctccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcagtggt 630

<210> 143

<211> 1806

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 143

cagatgcagc tgcaggagag cggccctgga ctctgtgaagc ccagcgagac cctgagcctg 60
acatgcagcg tgagcggcgc cagcatcagc gacagctact ggagctggat caggaggagc 120
cctggcaagg gcctggagtg gatcggctac gtgcacaaga gcggcgacac caactacagc 180
ccctccctga agtccagggt gaacctgtcc ctggacacca gcaagaacca ggtgagcctg 240
tccctggtgg ctgccacagc tgctgacagc ggcaagtact actgtgccag gaccctgcac 300
ggcaggagga tctacggcat cgtggccttc aacgagtgggt tcacctactt ctacatggac 360
gtgtggggca acggcaccca ggtgaccgtg agctccgaca aaaccatac cgagggttaga 420
ctggtggagt caggaggggg gcttgtgaag cccggtgggt ctctccgcct gagctgttct 480
gcctccggct ttgatttcga taacgcctgg atgacctggg tcaggcagcc tccaggtaag 540
ggactggagt ggggtgggaag aatcacaggt ccaggcgagg gctggtccgt ggactacgcg 600
gaatctgtta aaggcggtt tacaatctca agggacaata ccaagaatac cttgtatttg 660
gagatgaaca acgtgagaac tgaagacacc ggatattact tctgtgccag aacaggcaaa 720
tactacgact tctggtccgg ctatccccct ggcgaggaat attttcaaga ctggggctcag 780
ggaacccttg ttatcgtgtc ctccgataag acccacaccg cttccaccaaa gggcccatcg 840
gtcttcccc tggcacccctc ctccaagagc acctctgggg gcacagcggc cctgggctgc 900
ctggtcaagg actacttccc cgaaccgggt acggtgtcgt ggaactcagg cgccctgacc 960
agcggcgtgc acaccttccc ggctgtccta cagtctctag gactctactc cctcagcagc 1020
gtggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 1080
aagcccagca acaccaaggt ggacaagaaa gttgagccca aatcttgtga caaaactcac 1140

4. __183952027041SEQLIST.TXT

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acatgcccac cgtgcccagc acctgaactc ctgggggggac cgtcagtcctt cctctttcccc 1200
ccaaaaccca aggcacacct catgatctcc cggacccttg aggtcacatg cgtgggtggg 1260
gacgtgagcc acgaagaccc tgaggtcaag ttcaactggg atgttgacgg cgtggaggtg 1320
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1380
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1440
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1500
gaaccacagg tgtacaccct gcccccatgc cgggatgagc tgaccaagaa tcaagtcagc 1560
ctgtgggtgcc tggtaaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1620
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1680
ttcctctact caaaactcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1740
tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1800
ccgggt 1806

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<210> 144

<211> 993

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 144

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acttgccgag gcgactcact gcggagccac tacgcttctt ggtatcagaa gaaacccggc 120
caggcacctg tgctgtgtt ctacggaaag aacaataggc catctggcat ccccgaccgc 180
ttttctggca gtgcatcagg gaaccgagcc agtctgacca ttaccggcgc ccaggctgag 240
gacgaagccg attactattg cagctcccgg gataagagcg gctccagact gagcgtgttc 300
ggaggaggaa ctaaactgac cgtcctcgac aaaaccata cctccgacat cagcgtggcc 360
cccgagagaga cagccaggat ctctgcggc gagaagagcc tgggaagcag ggctgtgcag 420
tggtaccaac acagggccgg acaggctccc agcctgatca tctacaacaa ccaggacagg 480
cccagcggca tccctgagag gttcagcggg agccccgaca gccccttcgg aaccacagcc 540
accctgacca tcacaagcgt ggaagccggc gacgaggccg actactactg ccacatctgg 600
gacagcaggg tgcacaccaa gtgggtgtt ggcgccggca ccaccctgac cgtgctggat 660
aagaccata cccgtacggg ggccgctccc agcgtgttca tcttccacc tagcgacgag 720
cagctgaagt ccggcacagc ctctgtcgtg tgcctgctga acaacttcta ccccgcgag 780
gccaaagtgc agtgggaagg ggacaacgcc ctgcagagcg gcaacagcca ggaaagcgtg 840
accgagcagg acagcaagga ctccacctac agcctgagca gcaccctgac actgagcaag 900
gccgactacg agaagcaca ggtgtacgcc tgcgaagtga cccaccaggg cctgtctagc 960
ccggtgacca agagcttcaa ccggggcgag tgt 993

```

<210> 145

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 145

```

Glu Val Arg Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1           5           10          15
Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Asp Asn Ala

```

4. 183952027041SEQLIST.TXT

[illegible]

4._183952027041SEQLIST.TXT

	435		440		445
His	Tyr	Thr	Gln	Lys	Ser
	450		455		460

<210> 146
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 146

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

<210> 147
 <211> 612
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

4.__183952027041SEQLIST.TXT

<400> 147

Gln	Met	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
1				5					10					15	
Thr	Leu	Ser	Leu	Thr	Cys	Ser	Val	Ser	Gly	Ala	Ser	Ile	Ser	Asp	Ser
			20					25					30		
Tyr	Trp	Ser	Trp	Ile	Arg	Arg	Ser	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile
	35						40					45			
Gly	Tyr	Val	His	Lys	Ser	Gly	Asp	Thr	Asn	Tyr	Ser	Pro	Ser	Leu	Lys
	50					55					60				
Ser	Arg	Val	Asn	Leu	Ser	Leu	Asp	Thr	Ser	Lys	Asn	Gln	Val	Ser	Leu
65					70					75					80
Ser	Leu	Val	Ala	Ala	Thr	Ala	Ala	Asp	Ser	Gly	Lys	Tyr	Tyr	Cys	Ala
			85					90						95	
Arg	Thr	Leu	His	Gly	Arg	Arg	Ile	Tyr	Gly	Ile	Val	Ala	Phe	Asn	Glu
			100					105						110	
Trp	Phe	Thr	Tyr	Phe	Tyr	Met	Asp	Val	Trp	Gly	Asn	Gly	Thr	Gln	Val
	115						120					125			
Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Gln	Val	His	Leu	Thr	Gln	Ser
	130					135					140				
Gly	Pro	Glu	Val	Arg	Lys	Pro	Gly	Thr	Ser	Val	Lys	Val	Ser	Cys	Lys
145					150					155					160
Ala	Pro	Gly	Asn	Thr	Leu	Lys	Thr	Tyr	Asp	Leu	His	Trp	Val	Arg	Ser
			165					170						175	
Val	Pro	Gly	Gln	Gly	Leu	Gln	Trp	Met	Gly	Trp	Ile	Ser	His	Glu	Gly
			180					185					190		
Asp	Lys	Lys	Val	Ile	Val	Glu	Arg	Phe	Lys	Ala	Lys	Val	Thr	Ile	Asp
	195						200					205			
Trp	Asp	Arg	Ser	Thr	Asn	Thr	Ala	Tyr	Leu	Gln	Leu	Ser	Gly	Leu	Thr
	210					215					220				
Ser	Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Gly	Ser	Lys	His	Arg
225					230					235					240
Leu	Arg	Asp	Tyr	Ala	Leu	Tyr	Asp	Asp	Asp	Gly	Ala	Leu	Asn	Trp	Ala
				245				250						255	
Val	Asp	Val	Asp	Tyr	Leu	Ser	Asn	Leu	Glu	Phe	Trp	Gly	Gln	Gly	Thr
			260					265					270		
Ala	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Ala	Ser	Thr	Lys	Gly
		275				280					285				
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly
	290					295				300					
Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val
305					310					315					320
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe
				325					330					335	
Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val
			340					345					350		
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val
		355					360					365			
Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys
	370					375					380				
Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu
385					390					395					400
Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr

4.__183952027041SEQLIST.TXT

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          405          410          415
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
          420          425          430
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
          435          440          445
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
          450          455          460
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
465          470          475          480
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
          485          490          495
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
          500          505          510
Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln
          515          520          525
Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
          530          535          540
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
545          550          555          560
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
          565          570          575
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
          580          585          590
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
          595          600          605
Leu Ser Pro Gly
          610

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<210> 148

<211> 334

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 148

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

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4. 183952027041SEQLIST.TXT

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

<210> 149

<211> 1383

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 149

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ccaggttaagg	gactggagtg	ggtgggaaga	atcacaggtc	caggcgagggt	ctggtccgtg	180
gactacgcgg	aatctgttaa	agggcggttt	acaatctcaa	gggacaatac	caagaatacc	240
ttgtatattgg	agatgaacaa	cgtgagaact	gaagacaccg	gatattactt	ctgtgccaga	300
acaggcaaat	actacgactt	ctgggtccggc	tatccccctg	gcgaggaata	ttttcaagac	360
tgggggtcagg	gaacccttgt	tatcgtgtcc	tccgcgtcga	ccaagggccc	cagcgtgttc	420
cctctggccc	ctagcagcaa	gagcacatct	ggcggaacag	ccgccctggg	ctgcctcgtg	480
aaggactact	ttcccagacc	cgtgaccgtg	tcctggaatt	ctggcgccct	gaccagcggc	540
gtgcacacct	ttccagctgt	gctgcagtcc	agcggcctgt	acagcctgag	cagcgtcgtg	600
acagtgccca	gcagctctct	gggcaccag	acctacatct	gcaacgtgaa	ccacaagccc	660
agcaaacacca	aggtggacaa	gaaggtggaa	ccaagagct	gcgacaagac	ccacacctgt	720
cccccttgtc	ctgccccga	actgctggga	ggcccttccg	tgttcctgtt	ccccccaaag	780

4. __183952027041SEQLIST.TXT

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cccaaggaca ccctgatgat cagccggacc cccgaagtga cctgcgtggt ggtggatgtg 840
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gccaaagacca agccaagaga ggaacagtac aacagcacct accgggtggt gtccgtgctg 960
accgtgctgc accaggactg gctgaacggc aaagagtaca agtgcaaggt gtccaacaag 1020
gccctgcctg ccccatcga gaaaaccatc agcaaggcca agggccagcc ccgcgaaccc 1080
caggtgtgca cactgcccc aagcaggga gactgacca agaaccaggt gtccctgagc 1140
tgtgccgtga aaggcttcta cccctccgat atcgccgtgg aatgggagag caacggccag 1200
cccgagaaca actacaagac cccccccct gtgctggaca gcgacggctc attcttcctg 1260
gtgtccaagc tgacagtgga caagtcccgg tggcagcagg gcaacgtgtt cagctgctcc 1320
gtgatgcacg aggcctgca caaccactac acccagaagt ccctgagcct gagccccggc 1380
aag
1383

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<210> 150

<211> 645

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 150

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acttgccgag gcgactcact gcggagccac tacgcttcct ggtatcagaa gaaacccggc 120
caggcacctg tgctgctgtt ctacggaaag aacaataggc catctggcat ccccgaccgc 180
ttttctggca gtgcatcagg gaaccgagcc agtctgacca ttaccggcgc ccaggctgag 240
gacgaagccg attactattg cagctcccgg gataagagcg gctccagact gagcgtgttc 300
ggaggaggaa ctaaactgac cgtcctcagt cagcccaagg ctgccccctc ggtcactctg 360
ttcccgcct cagtgaggga gcttcaagcc aacaaggcca cactggtgtg tctcataagt 420
gacttctacc cgggagccgt gacagtggcc tggaaggcag atagcagccc cgtcaaggcg 480
ggagtggaga ccaccacacc ctccaacaa agcaacaaca agtacgcggc cagcagctac 540
ctgagcctga cgcctgagca gtggaagtcc cacagaagct acagctgcca ggtcacgcat 600
gaaggagca ccgtggagaa gacagtggcc cctacagaat gttca
645

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<210> 151

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 151

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acatgcagcg tgagcggcgc cagcatcagc gacagctact ggagctggat caggaggagc 120
cctggcaagg gcctggagtg gatcggctac gtgcacaaga gcggcgacac caactacagc 180
ccctccctga agtccagggt gaacctgtcc ctggacacca gcaagaacca ggtgagcctg 240
tccctggtgg ctgccacagc tgctgacagc ggcaagtact actgtgccag gaccctgcac 300
ggcaggagga tctacggcat cgtggccttc aacgagtggg tcacctactt ctacatggac 360
gtgtggggca acggcaccca ggtgaccgtg agctccgaca aaaccatac ccaggctcac 420
ctgacacaga gcggacccga agtgcggaag cctggcacct ctgtgaaggt gtcctgcaag 480
gccctggca acaccctgaa aacctacgac ctgcactggg tgcgcagcgt gccaggacag 540
ggactgcagt ggatgggctg gatcagccac gagggcgaca agaaagtgat cgtggaacgg 600

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4. __183952027041SEQLIST.TXT

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ttcaaggcca aagtgaccat cgactgggac agaagcacca acaccgccta cctgcagctg 660
agcggcctga cctctggcga taccgccgtg tactactgcg ccaagggcag caagcaccgg 720
ctgagagact acgccctgta cgacgatgac ggcgccctga actgggccgt ggatgtggac 780
tacctgagca acctggaatt ctggggccag ggcacagccg tgaccgtgtc atctgataag 840
acccacaccg cttccaccaaa gggcccatcg gtcttcccc tggcaccctc ctccaagagc 900
acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 960
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cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 1080
accagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 1140
gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 1200
ctgggggggac cgtcagtctt cctcttcccc caaaaaccca aggacaccct catgatctcc 1260
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagacc tgaggtcaag 1320
ttcaactggt atgttgacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1380
cagtacaaca gcacgtaccg tgtggtcagc gtcttcaccg tcctgcacca ggactggctg 1440
aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1500
accatctcca aagccaaaagg gcagccccga gaaccacagg tgtacaccct gccccatgc 1560
cgggatgagc tgaccaagaa tcaagtcagc ctgtggtgcc tggtaaaagg cttctatccc 1620
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1680
cctcccgtgc tggactccga cggctcctt ttcctctact caaaactcac cgtggacaag 1740
agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcagaggc tctgcacaac 1800
cactacacgc agaagagcct ctccctgtct ccgggt 1836

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<210> 152

<211> 1002

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 152

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atcagctgca agagcagcca ctccctgac caggcgacc ggaacaacta cctggcttgg 120
tacgtgcaga agcccggcag atccccagc ctgctgatct acctggccag cagcagagcc 180
agcggcgtgc ccgatagatt ttctggcagc ggcagcgaca aggacttcac cctgaagatc 240
agccgggtgg aaaccgagga cgtgggcacc tactactgta tgcagggcag agagagcccc 300
tggaaccttg gccagggcac caaggtggac atcaaggaca aaaccatac ctccgacatc 360
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gctgtgcagt ggtaccaaca cagggccgga caggctccca gcctgatcat ctacaacaac 480
caggacaggc ccagcggcat ccctgagagg ttcagcggaa gccccgacag ccccttcgga 540
accacagcca ccctgaccat cacaagcgtg gaagccggcg acgaggccga ctactactgc 600
cacatctggg acagcagggt gccaccaag tgggtgtttg gcggcggcac caccctgacc 660
gtgctggata agaccatac ccgtacggtg gccgtccca gcgtgttcat cttccacct 720
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 780
ccccgcgagg ccaaagtgca gtggaaggtg gacaacgcc tgcagagcgg caacagccag 840
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgaca 900
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 960
ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 1002

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<210> 153

<211> 451

<212> PRT

4.__183952027041SEQLIST.TXT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 153

Arg	Ala	His	Leu	Val	Gln	Ser	Gly	Thr	Ala	Met	Lys	Lys	Pro	Gly	Ala	1	5	10	15
Ser	Val	Arg	Val	Ser	Cys	Gln	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Ala	His	20	25	30	
Ile	Leu	Phe	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Val	35	40	45	
Gly	Trp	Ile	Lys	Pro	Gln	Tyr	Gly	Ala	Val	Asn	Phe	Gly	Gly	Gly	Phe	50	55	60	
Arg	Asp	Arg	Val	Thr	Leu	Thr	Arg	Asp	Val	Tyr	Arg	Glu	Ile	Ala	Tyr	65	70	75	80
Met	Asp	Ile	Arg	Gly	Leu	Lys	Pro	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Ala	Arg	Asp	Arg	Ser	Tyr	Gly	Asp	Ser	Ser	Trp	Ala	Leu	Asp	Ala	Trp	100	105	110	
Gly	Gln	Gly	Thr	Thr	Val	Val	Val	Ser	Ala	Ala	Ser	Thr	Lys	Gly	Pro	115	120	125	
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	130	135	140	
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	145	150	155	160
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	165	170	175	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	180	185	190	
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	195	200	205	
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	210	215	220	
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	225	230	235	240
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	245	250	255	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	260	265	270	
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	275	280	285	
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	290	295	300	
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	305	310	315	320
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	325	330	335	
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	340	345	350	
Val	Cys	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	355	360	365	

4._183952027041SEQLIST.TXT

Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
 405 410 415
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445
 Ser Pro Gly
 450

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

<220>
 <223> Synthetic Construct

<400> 154
 Tyr Ile His Val Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ile Gly
 1 5 10 15
 Asp Arg Val Thr Ile Asn Cys Gln Thr Ser Gln Gly Val Gly Ser Asp
 20 25 30
 Leu His Trp Tyr Gln His Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
 35 40 45
 His His Thr Ser Ser Val Glu Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Phe His Thr Ser Phe Asn Leu Thr Ile Ser Asp Leu Gln Ala
 65 70 75 80
 Asp Asp Ile Ala Thr Tyr Tyr Cys Gln Val Leu Gln Phe Phe Gly Arg
 85 90 95
 Gly Ser Arg Leu His Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
 100 105 110
 Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
 115 120 125
 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
 130 135 140
 Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
 145 150 155 160
 Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
 165 170 175
 Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
 180 185 190
 Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
 195 200 205
 Glu Cys
 210

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<210> 155
 <211> 612
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 155
 Gln Met Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Ala Ser Ile Ser Asp Ser
 20 25 30
 Tyr Trp Ser Trp Ile Arg Arg Ser Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Val His Lys Ser Gly Asp Thr Asn Tyr Ser Pro Ser Leu Lys
 50 55 60
 Ser Arg Val Asn Leu Ser Leu Asp Thr Ser Lys Asn Gln Val Ser Leu
 65 70 75 80
 Ser Leu Val Ala Ala Thr Ala Ala Asp Ser Gly Lys Tyr Tyr Cys Ala
 85 90 95
 Arg Thr Leu His Gly Arg Arg Ile Tyr Gly Ile Val Ala Phe Asn Glu
 100 105 110
 Trp Phe Thr Tyr Phe Tyr Met Asp Val Trp Gly Asn Gly Thr Gln Val
 115 120 125
 Thr Val Ser Ser Asp Lys Thr His Thr Gln Val His Leu Thr Gln Ser
 130 135 140
 Gly Pro Glu Val Arg Lys Pro Gly Thr Ser Val Lys Val Ser Cys Lys
 145 150 155 160
 Ala Pro Gly Asn Thr Leu Lys Thr Tyr Asp Leu His Trp Val Arg Ser
 165 170 175
 Val Pro Gly Gln Gly Leu Gln Trp Met Gly Trp Ile Ser His Glu Gly
 180 185 190
 Asp Lys Lys Val Ile Val Glu Arg Phe Lys Ala Lys Val Thr Ile Asp
 195 200 205
 Trp Asp Arg Ser Thr Asn Thr Ala Tyr Leu Gln Leu Ser Gly Leu Thr
 210 215 220
 Ser Gly Asp Thr Ala Val Tyr Tyr Cys Ala Lys Gly Ser Lys His Arg
 225 230 235 240
 Leu Arg Asp Tyr Ala Leu Tyr Asp Asp Asp Gly Ala Leu Asn Trp Ala
 245 250 255
 Val Asp Val Asp Tyr Leu Ser Asn Leu Glu Phe Trp Gly Gln Gly Thr
 260 265 270
 Ala Val Thr Val Ser Ser Asp Lys Thr His Thr Ala Ser Thr Lys Gly
 275 280 285
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 290 295 300
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 305 310 315 320
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 325 330 335

4.__183952027041SEQLIST.TXT

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Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
    340                      345                      350
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
    355                      360                      365
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    370                      375                      380
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
    385                      390                      395                      400
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
    405                      410                      415
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
    420                      425                      430
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
    435                      440                      445
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    450                      455                      460
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
    465                      470                      475                      480
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
    485                      490                      495
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
    500                      505                      510
Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln
    515                      520                      525
Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    530                      535                      540
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    545                      550                      555                      560
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
    565                      570                      575
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
    580                      585                      590
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
    595                      600                      605
Leu Ser Pro Gly
    610

```

<210> 156

<211> 334

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 156

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

```

4._183952027041SEQLIST.TXT

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      35      40      45
Pro Gln Leu Leu Ile Tyr Leu Ala Ser Ser Arg Ala Ser Gly Val Pro
  50      55      60
Asp Arg Phe Ser Gly Ser Gly Ser Asp Lys Asp Phe Thr Leu Lys Ile
  65      70      75      80
Ser Arg Val Glu Thr Glu Asp Val Gly Thr Tyr Tyr Cys Met Gln Gly
      85      90      95
Arg Glu Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
  100      105      110
Asp Lys Thr His Thr Ser Asp Ile Ser Val Ala Pro Gly Glu Thr Ala
  115      120      125
Arg Ile Ser Cys Gly Glu Lys Ser Leu Gly Ser Arg Ala Val Gln Trp
  130      135      140
Tyr Gln His Arg Ala Gly Gln Ala Pro Ser Leu Ile Ile Tyr Asn Asn
  145      150      155      160
Gln Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Pro Asp
      165      170      175
Ser Pro Phe Gly Thr Thr Ala Thr Leu Thr Ile Thr Ser Val Glu Ala
      180      185      190
Gly Asp Glu Ala Asp Tyr Tyr Cys His Ile Trp Asp Ser Arg Val Pro
  195      200      205
Thr Lys Trp Val Phe Gly Gly Gly Thr Thr Leu Thr Val Leu Asp Lys
  210      215      220
Thr His Thr Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
  225      230      235      240
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
      245      250      255
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
  260      265      270
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
  275      280      285
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
  290      295      300
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
  305      310      315      320
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
      325      330

```

<210> 157

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 157

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agagcccacc tgggtgcagtc tggcaccgcc atgaagaaac caggcgccctc tgtgcgggtg 60
tcctgtcaga caagcggcta caccttcacc gccacatcc tgttctgggtt ccggcaggcc 120
cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
ggcggaggct tccgggatag agtgaccctg acccgggacg tgtaccgcga gatgcctac 240

```

4. __183952027041SEQLIST.TXT

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atggacatcc ggggcctgaa gcccgatgac accgccgtgt actactgcgc cagagacaga 300
agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtggtggtg 360
tctgccgcct ctacaaaggg cccagcgtg ttccctctgg cccttagcag caagagcaca 420
tctggcggaa cagccgccct gggctgcctc gtgaaggact actttcccga gcccgtagacc 480
gtgtcctgga attctggcgc cctgaccagc ggcgtgcaca cttttccagc tgtgtctgcag 540
tccagcggcc tgtacagcct gagcagcgtc gtgacagtgc ccagcagctc tctgggcacc 600
cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagaagggtg 660
gaaccaaga gctgcgacaa gaccacacc tgtccccctt gtcctgcccc cgaactgctg 720
ggaggccctt ccgtgttcct gttcccccca aagcccaagg acaccctgat gatcagccgg 780
acccccgaag tgacctgcgt ggtggtggat gtgtcccacg aggaccctga agtgaagtgc 840
aattggtacg tggacggcgt ggaagtgcac aacgccaaga ccaagccaag agaggaacag 900
tacaacagca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ctggctgaac 960
ggcaaagagt acaagtgcaa ggtgtccaac aaggccctgc ctgcccccat cgagaaaacc 1020
atcagcaagg ccaagggcca gccccgcgaa cccaggtgtg gcacactgcc cccaagcagg 1080
gacgagctga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccctcc 1140
gatatcgccg tggaatggga gagcaacggc cagcccgaga acaactacaa gaccaccccc 1200
cctgtgtctg acagcgacgg ctattcttc ctggtgtcca agctgacagt ggacaagtcc 1260
cggtggcagc agggcaacgt gttcagctgc tccgtgatgc acgaggccct gcacaaccac 1320
tacaccaga agtccctgag cctgagcccc ggcaag 1356

```

<210> 158

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 158

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tacatccacg tgaccagag cccagcagc ctgtccgtgt ccatcggcga cagagtgacc 60
atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgcccagc 180
agattttccg gcagcggctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630

```

<210> 159

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 159

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cagatgcagc tgcaggagag cggccctgga ctctgaagc ccagcgagac cctgagcctg 60
acatgcagcg tgagcggcgc cagcatcagc gacagctact ggagctggat caggaggagc 120

```

4. __183952027041SEQLIST.TXT

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cctggcaagg gcctggagtg gatcggctac gtgcacaaga gcggcgacac caactacagc 180
ccctccctga agtccagggt gaacctgtcc ctggacacca gcaagaacca ggtgagcctg 240
tccctggtgg ctgccacagc tgctgacagc ggcaagtact actgtgccag gaccctgcac 300
ggcaggagga tctacggcat cgtggccttc aacgagtggg tcacctactt ctacatggac 360
gtgtggggca acggcaccca ggtgaccgtg agctccgaca aaaccatac ccaggtgcac 420
ctgacacaga gcggacccga agtgcggaag cctggcacct ctgtgaaggt gtcctgcaag 480
gcccctggca acaccctgaa aacctacgac ctgcactggg tgcgcagcgt gccaggacag 540
ggactgcagt ggatgggctg gatcagccac gagggcgaca agaaagtgat cgtggaacgg 600
ttcaaggcca aagtgaccat cgactgggac agaagcacca acaccgcta cctgcagctg 660
agcggcctga cctctggcga taccgccgtg tactactgcg ccaagggcag caagcaccgg 720
ctgagagact acgccctgta cgacgatgac ggcgccctga actgggccgt ggatgtggac 780
tacctgagca acctggaatt ctggggccag ggcacagccg tgaccgtgtc atctgataag 840
acccacaccg cttccaccaaa gggcccatcg gtcttcccc tggcacctc ctccaagagc 900
acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 960
acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 1020
cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 1080
accagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 1140
gttgagccca aatcttgtga caaaactcac acatgccac cgtgcccagc acctgaactc 1200
ctgggggggac cgtcagtctt cctcttcccc caaaaaccca aggacacct catgatctcc 1260
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagacc tgaggtcaag 1320
ttcaactggt atgttgacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1380
cagtacaaca gcacgtaccg tgtggtcagc gtcttcaccg tcctgcacca ggactggctg 1440
aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1500
accatctcca aagccaaagg gcagccccga gaaccacagg tgtaaccct gcccccatgc 1560
cgggatgagc tgaccaagaa tcaagtcagc ctgtggtgcc tggtaaaagg cttctatccc 1620
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1680
cctcccgtgc tggactccga cggctcctt ttcctctact caaaactcac cgtggacaag 1740
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1800
cactacacgc agaagagcct ctccctgtct ccgggt 1836

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<210> 160

<211> 1002

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 160

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gacttcgtgc tgacccagag ccctcacagc ctgagcgtga cacctggcga gagcgccagc 60
atcagctgca agagcagcca ctccctgatc cacggcgacc ggaacaacta cctggcttgg 120
tacgtgcaga agcccggcag atccccccag ctgctgatct acctggccag cagcagagcc 180
agcggcgtgc ccgatagatt ttctggcagc ggcagcgaca aggacttcac cctgaagatc 240
agccgggtgg aaaccgagga cgtgggcacc tactactgta tgcagggcag agagagcccc 300
tggaaccttg gccagggcac caaggtggac atcaaggaca aaaccatac ctccgacatc 360
agcgtggccc ccggagagac agccaggatc tcctgcggcg agaagagcct gggaagcagg 420
gctgtgcagt ggtaccaaca cagggccgga caggctccca gcctgatcat ctacaacaac 480
caggacaggc ccagcggcat ccctgagagg ttcagcggaa gccccgacag ccccttcgga 540
accacagcca ccctgaccat cacaagcgtg gaagccggcg acgaggccga ctactactgc 600
cacatctggg acagcagggt gccaccaag tgggtgtttg gcggcggcac caccctgacc 660
gtgctggata agaccatac ccgtacggtg gccgtccca gcgtgttcat cttcccacct 720
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caatttctac 780

```


ccccgcgagg	ccaaagtgca	gtggaaggtg	gacaacgcc	tgcagagcgg	caacagccag	840
gaaagcgtga	ccgagcagga	cagcaaggac	tccacctaca	gcctgagcag	caccctgaca	900
ctgagcaagg	ccgactacga	gaagcacaa	gtgtacgcct	gcgaagtga	ccaccagggc	960
ctgtctagcc	ccgtgaccaa	gagcttcaac	cggggcgagt	gt		1002

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<210> 161
<211> 470
<212> PRT
<213> Artificial Sequence
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<220>
<223> Synthetic Construct

<400> 161															
Gln 1	Val	His	Leu	Thr 5	Gln	Ser	Gly	Pro	Glu 10	Val	Arg	Lys	Pro	Gly 15	Thr
Ser	Val	Lys	Val 20	Ser	Cys	Lys	Ala	Pro 25	Gly	Asn	Thr	Leu	Lys 30	Thr	Tyr
Asp	Leu	His 35	Trp	Val	Arg	Ser	Val 40	Pro	Gly	Gln	Gly	Leu	Gln 45	Trp	Met
Gly	Trp	Ile	Ser	His	Glu	Gly 55	Asp	Lys	Lys	Val	Ile 60	Val	Glu	Arg	Phe
Lys 65	Ala	Lys	Val	Thr	Ile 70	Asp	Trp	Asp	Arg	Ser	Thr	Asn	Thr	Ala	Tyr 80
Leu	Gln	Leu	Ser	Gly 85	Leu	Thr	Ser	Gly	Asp	Thr	Ala	Val	Tyr	Tyr 95	Cys
Ala	Lys	Gly	Ser 100	Lys	His	Arg	Leu	Arg 105	Asp	Tyr	Ala	Leu	Tyr 110	Asp	Asp
Asp	Gly	Ala 115	Leu	Asn	Trp	Ala	Val 120	Asp	Val	Asp	Tyr	Leu	Ser 125	Asn	Leu
Glu	Phe	Trp	Gly	Gln	Gly	Thr 135	Ala	Val	Thr	Val	Ser 140	Ser	Ala	Ser	Thr
Lys 145	Gly	Pro	Ser	Val	Phe 150	Pro	Leu	Ala	Pro	Ser	Ser 155	Lys	Ser	Thr	Ser 160
Gly	Gly	Thr	Ala	Ala 165	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro 175	Glu
Pro	Val	Thr	Val 180	Ser	Trp	Asn	Ser	Gly 185	Ala	Leu	Thr	Ser	Gly 190	Val	His
Thr	Phe	Pro	Ala 195	Val	Leu	Gln	Ser	Ser 200	Gly	Leu	Tyr	Ser	Leu	Ser	Ser
Val	Val	Thr	Val 210	Pro	Ser	Ser	Ser 215	Leu	Gly	Thr	Gln 220	Thr	Tyr	Ile	Cys
Asn 225	Val	Asn	His	Lys	Pro 230	Ser	Asn	Thr	Lys	Val	Asp 235	Lys	Lys	Val	Glu 240
Pro	Lys	Ser	Cys	Asp 245	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala 255	Pro
Glu	Leu	Leu	Gly 260	Gly	Pro	Ser	Val	Phe 265	Leu	Phe	Pro	Pro	Lys	Pro 270	Lys
Asp	Thr	Leu	Met 275	Ile	Ser	Arg	Thr	Pro 280	Glu	Val	Thr	Cys	Val	Val	Val
Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp
290 295 300															

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

<210> 162

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 162

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

4.__183952027041SEQLIST.TXT

145					150					155					160
Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
				165					170					175	
Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
			180					185					190		
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser
		195					200					205			
Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys					
	210					215									

<210> 163
 <211> 592
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 163

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

4._183952027041SEQLIST.TXT

```

Ser Ala Asp Lys Thr His Thr Ala Ser Thr Lys Gly Pro Ser Val Phe
    260                265                270
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    275                280                285
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
    290                295                300
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
    305                310                315                320
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
    325                330                335
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
    340                345                350
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
    355                360                365
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
    370                375                380
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
    385                390                395                400
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
    405                410                415
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
    420                425                430
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    435                440                445
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
    450                455                460
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
    465                470                475                480
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
    485                490                495
Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp
    500                505                510
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    515                520                525
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
    530                535                540
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
    545                550                555                560
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
    565                570                575
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
    580                585                590

```

<210> 164

<211> 329

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

4.__183952027041SEQLIST.TXT

<400> 164

```

Tyr Ile His Val Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ile Gly
 1           5           10           15
Asp Arg Val Thr Ile Asn Cys Gln Thr Ser Gln Gly Val Gly Ser Asp
 20           25           30
Leu His Trp Tyr Gln His Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
 35           40           45
His His Thr Ser Ser Val Glu Asp Gly Val Pro Ser Arg Phe Ser Gly
 50           55           60
Ser Gly Phe His Thr Ser Phe Asn Leu Thr Ile Ser Asp Leu Gln Ala
 65           70           75           80
Asp Asp Ile Ala Thr Tyr Tyr Cys Gln Val Leu Gln Phe Phe Gly Arg
 85           90           95
Gly Ser Arg Leu His Ile Lys Asp Lys Thr His Thr Ala Ser Glu Leu
100          105          110
Thr Gln Asp Pro Ala Val Ser Val Ala Leu Lys Gln Thr Val Thr Ile
115          120          125
Thr Cys Arg Gly Asp Ser Leu Arg Ser His Tyr Ala Ser Trp Tyr Gln
130          135          140
Lys Lys Pro Gly Gln Ala Pro Val Leu Leu Phe Tyr Gly Lys Asn Asn
145          150          155          160
Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ala Ser Gly Asn
165          170          175
Arg Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp
180          185          190
Tyr Tyr Cys Ser Ser Arg Asp Lys Ser Gly Ser Arg Leu Ser Val Phe
195          200          205
Gly Gly Gly Thr Lys Leu Thr Val Leu Asp Lys Thr His Thr Arg Thr
210          215          220
Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
225          230          235          240
Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
245          250          255
Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
260          265          270
Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
275          280          285
Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
290          295          300
Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
305          310          315          320
Thr Lys Ser Phe Asn Arg Gly Glu Cys
325

```

<210> 165

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

4.__183952027041SEQLIST.TXT

<400> 165

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caggtgcacc tgacacagag cggacccgaa gtgcggaagc ctggcacctc tgtgaaggtg 60
tcctgcaagg cccctggcaa caccctgaaa acctacgacc tgcactgggt gcgcagcgtg 120
ccaggacagg gactgcagtg gatgggctgg atcagccacg agggcgacaa gaaagtgatc 180
gtggaacggt tcaaggccaa agtgaccatc gactgggaca gaagcaccaa caccgcctac 240
ctgcagctga gcggcctgac ctctggcgat accgccgtgt actactgcgc caagggcagc 300
aagcacgggc tgagagacta cgccctgtac gacgatgacg gcgccctgaa ctgggccgtg 360
gatgtggact acctgagcaa cctggaattc tggggccagg gcacagccgt gaccgtgtca 420
tctgcttcga ccaaggggcc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 480
ggcggaaacag ccgccctggg ctgcctcgtg aaggactact ttcccagacc cgtgaccgtg 540
tcctggaatt ctggcgccct gaccagcggc gtgcacacct ttccagctgt gctgcagtcc 600
agcggcctgt acagcctgag cagcgtcgtg acagtgccca gcagctctct gggcacccag 660
acctacatct gcaacgtgaa ccacaagccc agcaaacca aggtggacaa gaaggtggaa 720
cccaagagct gcgacaagac ccacacctgt ccccttgtc ctgccccga actgctggga 780
ggcccttccg tgttcctgtt cccccaaaag cccaaggaca ccctgatgat cagccggacc 840
cccgaagtga cctgcgtggt ggtggatgtg tcccacgagg accctgaagt gaagttcaat 900
tggtacgtgg acggcgtgga agtgcacaac gccaaagaca agccaagaga ggaacagtac 960
aacagcacct accgggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc 1020
aaagagtaca agtgcaaggt gtccaacaag gccctgcctg ccccatcga gaaaaccatc 1080
agcaaggcca agggccagcc ccgcaaccc caggtgtgca cactgcccc aagcagggac 1140
gagctgacca agaaccaggt gtccctgagc tgtgccgtga aaggcttcta cccctccgat 1200
atcgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cccccccct 1260
gtgctggaca gcgacggctc attcttctg gtgtccaagc tgacagtgga caagtcccgg 1320
tggcagcagg gcaacgtgtt cagctgtctc gtgatgcacg aggccctgca caaccactac 1380
accagaagt ccctgagcct gagccccggc aag 1413
```

<210> 166

<211> 657

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 166

```
gacttcgtgc tgaccagag ccctcacagc ctgagcgtga cacctggcga gagcgccagc 60
atcagctgca agagcagcca ctccctgatc caggcgacc ggaacaacta cctggcttgg 120
tacgtgcaga agcccggcag atccccccag ctgctgatct acctggccag cagcagagcc 180
agcggcgtgc ccgatagatt ttctggcagc ggcagcgaca aggacttcac cctgaagatc 240
agccgggtgg aaaccgagga cgtgggcacc tactactgta tgcagggcag agagagcccc 300
tggaaccttg gccagggcac caaggtggac atcaagcgtg cggtggccgc tcccagcgtg 360
ttcatcttcc cacctagcga cgagcagctg aagtccggca cagcctctgt cgtgtgcctg 420
ctgaacaact tctacccccg cgaggccaaa gtgcagtgga aggtggacaa cgccctgcag 480
agcggcaaca gccaggaaa cgtgaccgag caggacagca aggactccac ctacagcctg 540
agcagcacc tgacactgag caaggccgac tacgagaagc acaaggtgta cgcctgcgaa 600
gtgaccacc agggcctgtc tagccccgtg accaagagct tcaaccgggg cgagtgt 657
```

<210> 167

<211> 1776

<212> DNA

<213> Artificial Sequence

4.__183952027041SEQLIST.TXT

<220>

<223> Synthetic Construct

<400> 167

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gaggtttagac tgggtggagtc aggagggggg cttgtgaagc ccggtgggtc tctccgcctg 60
agctgttctg cctccggctt tgatttcgat aacgcctgga tgacctgggt caggcagcct 120
ccaggtaagg gactggagtg ggtgggaaga atcacaggct caggcgaggg ctgggtccgtg 180
gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
acaggcaaat actacgactt ctgggtccggc tatccccctg gcgaggaata ttttcaagac 360
tggggtcagg gaacccttgt tatcgtgtcc tccgacaaaa cccataccag agcccacctg 420
gtgcagtctg gcaccgccat gaagaaacca ggcgcctctg tgcgggtgtc ctgtcagaca 480
agcggctaca ccttcaccgc ccacatcctg ttctggttcc ggcaggcccc tggcagagga 540
ctggaatggg tgggatggat caagccccag tatggcgccg tgaacttcgg cggaggcttc 600
cgggatagag tgacctgac ccgggacgtg taccgcgaga tcgcctacat ggacatccgg 660
ggcctgaagc ccgatgacac cgccgtgtac tactgcgcca gagacagaag ctacggcgac 720
agcagctggg ctctggatgc ttggggccag ggcacaaccg tgggtggtgtc tgccgataag 780
accacaccg cttccacca gggcccatcg gtcttcccc tggcaccctc ctccaagagc 840
acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 900
acgggtgtcg ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 960
cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 1020
accagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 1080
gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 1140
ctgggggggac cgtcagtctt cctcttcccc caaaaaccca aggacaccct catgatctcc 1200
cggacccctg aggtcacatg cgtggtgggtg gacgtgagcc acgaagacc tgagggtcaag 1260
ttcaactggt atgttgacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1320
cagtacaaca gcacgtaccg tgtggtcagc gtcttcaccg tcctgcacca ggactggctg 1380
aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1440
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatgc 1500
cgggatgagc tgaccaagaa tcaagtcagc ctgtggtgcc tggtaaaagg cttctatccc 1560
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1620
cctcccgtgc tggactccga cggctcctt ttctctact caaaactcac cgtggacaag 1680
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1740
cactacacgc agaagagcct ctccctgtct ccgggt 1776

```

<210> 168

<211> 987

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 168

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tacatccacg tgacccagag ccccagcagc ctgtccgtgt ccatcggcga cagagtgacc 60
atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggagatgg cgtgccagc 180
agattttccg gcagcggtt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagg acaaaaccca taccgcatcc gaactgactc aggaccctgc cgtctctgtg 360
gcactgaagc agactgtgac tattacttgc cgaggcgact cactgcggag ccactacgct 420

```

4. __183952027041SEQLIST.TXT

```

tcctgggtatc agaagaaacc cggccaggca cctgtgctgc tgttctacgg aaagaacaat 480
aggccatctg gcatccccga ccgcttttct ggcagtgcac cagggaaccg agccagtctg 540
accattaccg gcgcccaggc tgaggacgaa gccgattact attgcagctc ccgggataag 600
agcggctcca gactgagcgt gttcggagga ggaactaaac tgaccgtcct cgataagacc 660
catacccgta cgggtggccgc tcccagcgtg ttcattcttc cacctagcga cgagcagctg 720
aagtccggca cagcctctgt cgtgtgcctg ctgaacaact tctacccccg cgaggccaaa 780
gtgcagtgga aggtggacaa cgccctgcag agcggcaaca gccaggaaaag cgtgaccgag 840
caggacagca aggactccac ctacagcctg agcagcacc tgacactgag caaggccgac 900
tacgagaagc acaaggtgta cgcctgcgaa gtgaccacc agggcctgtc tagccccgtg 960
accaagagct tcaaccgggg cgagtgt 987

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<210> 169

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 169

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

4. __183952027041SEQLIST.TXT

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

<210> 170

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 170

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

4. 183952027041SEQLIST.TXT

			100					105				110			
Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu
		115					120					125			
Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe
		130				135					140				
Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln
145					150					155				160	
Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser
				165					170					175	
Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu
			180					185				190			
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser
		195					200					205			
Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys					
		210				215									

<210> 171

$\langle 211 \rangle$ 550

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 171

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

4.__183952027041SEQLIST.TXT

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Tyr Leu Glu Met Asn Asn Val Arg Thr Glu Asp Thr Gly Tyr Tyr Phe
210                215                220
Cys Ala Arg Thr Gly Lys Tyr Tyr Asp Phe Trp Ser Gly Tyr Pro Pro
225                230                235                240
Gly Glu Glu Tyr Phe Gln Asp Trp Gly Gln Gly Thr Leu Val Ile Val
245                250                255
Ser Ser Asp Lys Thr His Thr Ala Ser Thr Lys Gly Pro Ser Val Phe
260                265                270
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
275                280                285
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
290                295                300
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
305                310                315                320
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
325                330                335
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
340                345                350
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
355                360                365
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
370                375                380
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
385                390                395                400
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
405                410                415
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
420                425                430
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
435                440                445
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
450                455                460
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
465                470                475                480
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
485                490                495
Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp
500                505                510
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
515                520                525
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
530                535                540
Asp Ser Asp Gly Ser Phe
545                550

```

<210> 172

<211> 329

<212> PRT

<213> Artificial Sequence

<220>

4.___183952027041SEQLIST.TXT

<223> Synthetic Construct

<400> 172

Ala	Ser	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Lys	Gln
1				5					10					15	
Thr	Val	Thr	Ile	Thr	Cys	Arg	Gly	Asp	Ser	Leu	Arg	Ser	His	Tyr	Ala
			20				25						30		
Ser	Trp	Tyr	Gln	Lys	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Leu	Phe	Tyr
		35					40					45			
Gly	Lys	Asn	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser
	50					55				60					
Ala	Ser	Gly	Asn	Arg	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu
65					70				75						80
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ser	Ser	Arg	Asp	Lys	Ser	Gly	Ser	Arg
			85						90					95	
Leu	Ser	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Asp	Lys	Thr
			100					105					110		
His	Thr	Tyr	Ile	His	Val	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Val	Ser
		115					120					125			
Ile	Gly	Asp	Arg	Val	Thr	Ile	Asn	Cys	Gln	Thr	Ser	Gln	Gly	Val	Gly
	130					135					140				
Ser	Asp	Leu	His	Trp	Tyr	Gln	His	Lys	Pro	Gly	Arg	Ala	Pro	Lys	Leu
145					150				155						160
Leu	Ile	His	His	Thr	Ser	Ser	Val	Glu	Asp	Gly	Val	Pro	Ser	Arg	Phe
			165					170						175	
Ser	Gly	Ser	Gly	Phe	His	Thr	Ser	Phe	Asn	Leu	Thr	Ile	Ser	Asp	Leu
			180					185					190		
Gln	Ala	Asp	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Val	Leu	Gln	Phe	Phe
		195					200					205			
Gly	Arg	Gly	Ser	Arg	Leu	His	Ile	Lys	Asp	Lys	Thr	His	Thr	Arg	Thr
	210					215					220				
Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu
225					230					235					240
Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro
			245						250					255	
Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly
		260					265						270		
Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr
		275					280					285			
Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His
	290					295					300				
Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val
305				310						315					320
Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys							
				325											

<210> 173

<211> 1413

<212> DNA

<213> Artificial Sequence

4.__183952027041SEQLIST.TXT

<220>

<223> Synthetic Construct

<400> 173

```
caggtgcacc tgacacagag cggacccgaa gtgcggaagc ctggcacctc tgtgaaggtg 60
tcctgcaagg cccctggcaa caccctgaaa acctacgacc tgcactgggt gcgcagcgtg 120
ccaggacagg gactgcagtg gatgggctgg atcagccacg agggcgacaa gaaagtgatc 180
gtggaacggg tcaaggccaa agtgaccatc gactgggaca gaagcaccaa caccgcctac 240
ctgcagctga gcggcctgac ctctggcgat accgccgtgt actactgcgc caagggcagc 300
aagcaccggc tgagagacta cgccctgtac gacgatgacg gcgccctgaa ctgggcccgtg 360
gatgtggact acctgagcaa cctggaattc tggggccagg gcacagccgt gaccgtgtca 420
tctgcttcga ccaaggggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 480
ggcggaaacag ccgccctggg ctgcctcgtg aaggactact ttcccagacc cgtgaccgtg 540
tcctggaatt ctggcgccct gaccagcggc gtgcacacct ttccagctgt gctgcagtcc 600
agcggcctgt acagcctgag cagcgtcgtg acagtgccca gcagctctct gggcacccag 660
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 720
cccaagagct gcgacaagac ccacacctgt ccccttgtc ctgccccga actgctggga 780
ggcccttccg tgttcctgtt cccccc aaag cccaaggaca ccctgatgat cagccggacc 840
cccgaagtga cctgcgtggg ggtggatgtg tcccacgagg accctgaagt gaagttcaat 900
tggtacgtgg acggcgtgga agtgcacaac gccaaagaca agccaagaga ggaacagtac 960
aacagcacct accgggtggg gtccgtgctg accgtgctgc accaggactg gctgaacggc 1020
aaagagtaca agtgcaaggt gtccaacaag gccctgcctg ccccatcga gaaaaccatc 1080
agcaaggcca agggccagcc ccgcgaacc caggtgtgca cactgcccc aagcaggggac 1140
gagctgacca agaaccaggt gtccctgagc tgtgccgtga aaggcttcta cccctccgat 1200
atcgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cccccccct 1260
gtgctggaca gcgacggctc attcttcctg gtgtccaagc tgacagtgga caagtcccgg 1320
tggcagcagg gcaacgtgtt cagctgctcc gtgatgcacg aggccttgca caaccactac 1380
accagaagt ccctgagcct gagccccggc aag 1413
```

<210> 174

<211> 657

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 174

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gacttcgtgc tgacccagag ccctcacagc ctgagcgtga cacctggcga gagcgccagc 60
atcagctgca agagcagcca ctccctgatc cacggcgacc ggaacaacta cctggcttgg 120
tacgtgcaga agcccggcag atccccccag ctgctgatct acctggccag cagcagagcc 180
agcggcgtgc ccgatagatt ttctggcagc ggcagcgaca aggacttcac cctgaagatc 240
agccgggtgg aaaccgagga cgtgggcacc tactactgta tgcagggcag agagagcccc 300
tggaaccttg gccagggcac caaggtggac atcaagcgta cgggtggccgc tcccagcgtg 360
ttcatcttcc cacctagcga cgagcagctg aagtccggca cagcctctgt cgtgtgcctg 420
ctgaacaact tctacccccg cgaggccaaa gtgcagtgga aggtggacaa cgccctgcag 480
agcggcaaca gccaggaaaag cgtgaccgag caggacagca aggactccac ctacagcctg 540
agcagcacc tgacactgag caaggccgac tacgagaagc acaaggtgta cgcctgcgaa 600
gtgacccacc agggcctgtc tagccccgtg accaagagct tcaaccgggg cgagtgt 657
```

<210> 175

<211> 1776

4.__183952027041SEQLIST.TXT

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 175

```

agagcccacc tgggtgcagtc tggcaccgcc atgaagaaac caggcgcctc tgtgcgggtg 60
tcctgtcaga caagcggcta caccttcacc gccacatcc tgttctgggt ccggcaggcc 120
cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
ggcggaggct tccgggatag agtgaccctg acccgggacg tgtaccgcga gatcgctac 240
atggacatcc ggggcctgaa gccgatgac accgccgtgt actactgcgc cagagacaga 300
agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtggtggtg 360
tctgccgaca aaaccatac cgaggtaga ctggtggagt caggaggggg gcttgtgaag 420
cccgtgggt ctctccgct gagctgttct gcctccggct ttgatttcga taacgcctgg 480
atgacctggg tcaggcagcc tccaggtaag ggactggagt ggggtgggaag aatcacaggt 540
ccaggcgagg gctggtccgt ggactacgcg gaatctgtta aagggcggtt tacaatctca 600
agggacaata ccaagaatac cttgtatttg gagatgaaca acgtgagaac tgaagacacc 660
ggatattact tctgtgccag aacaggcaaa tactacgact tctggtccgg ctatccccct 720
ggcgaggaat attttcaaga ctgggggtcag ggaacccttg ttatcgtgtc ctccgataag 780
accacaccg cttccacca gggcccatcg gtcttcccc tggcaccctc ctccaagagc 840
acctctgggg gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 900
acgggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 960
cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 1020
accagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa 1080
gttgagccca aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc 1140
ctggggggac cgtcagtcct cctcttcccc caaaaacca aggacaccct catgatctcc 1200
cggaccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagacc tgaggtcaag 1260
ttcaactggt atgttgacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 1320
cagtacaaca gcacgtaccg tgtggtcagc gtctcaccg tcctgcacca ggactggctg 1380
aatggcaagg agtacaagt caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1440
accatctcca aagccaaagg gcagccccga gaaccacagg tgtacaccct gccccatgc 1500
cgggatgagc tgaccaagaa tcaagtcagc ctgtggtgcc tggtaaaagg cttctatccc 1560
agcgacatcg ccgtggagt ggagagcaat gggcagccgg agaacaacta caagaccacg 1620
ctcccgtgc tggactccga cggctcctt ttctctact caaaactcac cgtggacaag 1680
agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1740
cactacacgc agaagagcct ctccctgtct ccgggt 1776

```

<210> 176

<211> 987

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 176

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gcatccgaac tgactcagga ccctgccgtc tctgtggcac tgaagcagac tgtgactatt 60
acttgccgag gcgactcact gcggagccac tacgcttcct ggtatcagaa gaaacccggc 120
caggcacctg tgctgtgtt ctacggaaaag aacaataggc catctggcat ccccgaccgc 180
ttttctggca gtgcatcagg gaaccgagcc agtctgacca ttaccggcgc ccaggctgag 240
gacgaagccg attactattg cagctcccgg gataagagcg gctccagact gagcgtgttc 300

```

4. __183952027041SEQLIST.TXT

```

ggaggaggaa ctaaactgac cgtcctcgac aaaacccata cctacatcca cgtgacccag 360
agccccagca gcctgtccgt gtccatcggc gacagagtga ccatcaactg ccagacctct 420
cagggcggtgg gcagcgacct gactgggtat cagcacaagc ctggcagagc cccaagctg 480
ctgatccacc acacaagcag cgtggaagat ggcgtgcccc gcagattttc cggcagcggc 540
ttccacacca gcttcaacct gaccatcagc gatctgcagg ccgacgacat tgccacctac 600
tattgtcagg tgctgcagtt cttcggcaga ggcagcagac tgcacatcaa ggataagacc 660
catacccgtg cgggtggccgc tcccagcgtg ttcattcttc cacctagcga cgagcagctg 720
aagtccggca cagcctctgt cgtgtgcctg ctgaacaact tctacccccg cgaggccaaa 780
gtgcagtggg aggtggacaa cgccctgcag agcgggcaaca gccaggaaaag cgtgaccgag 840
caggacagca aggactccac ctacagcctg agcagcaccc tgacactgag caaggccgac 900
tacgagaagc acaaggtgta cgcctgcgaa gtgaccacc agggcctgtc tagccccgtg 960
accaagagct tcaaccgggg cgagtgt 987

```

<210> 177

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 177

```

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

```

4. __183952027041SEQLIST.TXT

```

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
      245                      250                      255
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
      260                      265                      270
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
      275                      280                      285
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
      290                      295                      300
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
      305                      310                      315                      320
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
      325                      330                      335
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
      340                      345                      350
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser
      355                      360                      365
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys
      370                      375                      380
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
      385                      390                      395                      400
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
      405                      410                      415
Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
      420                      425                      430
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
      435                      440                      445
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
      450                      455                      460

```

<210> 178

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 178

```

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

```


4. 183952027041SEQLIST.TXT

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

<210> 179

 $\langle 211 \rangle$ 602

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 179

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

4. __183952027041SEQLIST.TXT

Gln	Leu	Ser	Gly	Leu	Thr	Ser	Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
210						215					220				
Lys	Gly	Ser	Lys	His	Arg	Leu	Arg	Asp	Tyr	Ala	Leu	Tyr	Asp	Asp	Asp
225					230					235					240
Gly	Ala	Leu	Asn	Trp	Ala	Val	Asp	Val	Asp	Tyr	Leu	Ser	Asn	Leu	Glu
			245						250					255	
Phe	Trp	Gly	Gln	Gly	Thr	Ala	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His
		260						265					270		
Thr	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser
		275					280					285			
Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp
	290					295					300				
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr
305					310					315					320
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr
				325					330					335	
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln
			340					345					350		
Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp
		355					360					365			
Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro
	370					375					380				
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
385					390					395					400
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
				405					410					415	
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn
			420					425					430		
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
		435					440						445		
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
	450					455					460				
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
465					470					475					480
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
				485					490					495	
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Cys	Arg	Asp
			500					505					510		
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu	Val	Lys	Gly	Phe
		515					520					525			
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
	530					535					540				
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
545					550					555					560
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
				565					570					575	
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
			580					585					590		
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly						
		595					600								

4.__183952027041SEQLIST.TXT

<210> 180

<211> 332

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 180

```

Asp Phe Val Leu Thr Gln Ser Pro His Ser Leu Ser Val Thr Pro Gly
 1          5          10          15
Glu Ser Ala Ser Ile Ser Cys Lys Ser Ser His Ser Leu Ile His Gly
 20          25          30
Asp Arg Asn Asn Tyr Leu Ala Trp Tyr Val Gln Lys Pro Gly Arg Ser
 35          40          45
Pro Gln Leu Leu Ile Tyr Leu Ala Ser Ser Arg Ala Ser Gly Val Pro
 50          55          60
Asp Arg Phe Ser Gly Ser Gly Ser Asp Lys Asp Phe Thr Leu Lys Ile
 65          70          75          80
Ser Arg Val Glu Thr Glu Asp Val Gly Thr Tyr Tyr Cys Met Gln Gly
 85          90          95
Arg Glu Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
100          105          110
Asp Lys Thr His Thr Tyr Ile His Val Thr Gln Ser Pro Ser Ser Leu
115          120          125
Ser Val Ser Ile Gly Asp Arg Val Thr Ile Asn Cys Gln Thr Ser Gln
130          135          140
Gly Val Gly Ser Asp Leu His Trp Tyr Gln His Lys Pro Gly Arg Ala
145          150          155          160
Pro Lys Leu Leu Ile His His Thr Ser Ser Val Glu Asp Gly Val Pro
165          170          175
Ser Arg Phe Ser Gly Ser Gly Phe His Thr Ser Phe Asn Leu Thr Ile
180          185          190
Ser Asp Leu Gln Ala Asp Asp Ile Ala Thr Tyr Tyr Cys Gln Val Leu
195          200          205
Gln Phe Phe Gly Arg Gly Ser Arg Leu His Ile Lys Asp Lys Thr His
210          215          220
Thr Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
225          230          235          240
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
245          250          255
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
260          265          270
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
275          280          285
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
290          295          300
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
305          310          315          320
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
325          330

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4.__183952027041SEQLIST.TXT

<210> 181
 <211> 1383
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 181
 gaggttagac tgggtggagtc aggagggggg cttgtgaagc ccggtgggtc tctccgcctg 60
 agctgttctg cctccggctt tgatttcgat aacgcctgga tgacctgggt caggcagcct 120
 ccaggtaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctggtccgtg 180
 gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
 ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
 acaggcaaat actacgactt ctggtccggc tatccccctg gcgaggaata ttttcaagac 360
 tggggtcagg gaacccttgt tatcgtgtcc tccgcgtcga ccaagggcc cagcgtgttc 420
 cctctggccc ctagcagcaa gagcacatct ggcggaacag ccgccctggg ctgcctcgtg 480
 aaggactact ttcccagacc cgtgaccgtg tcctggaatt ctggcgccct gaccagcggc 540
 gtgcacacct ttccagctgt gctgcagtcc agcggcctgt acagcctgag cagcgtcgtg 600
 acagtgccca gcagctctct gggcacccag acctacatct gcaacgtgaa ccacaagccc 660
 agcaacacca aggtggacaa gaaggtggaa cccaagagct gcgacaagac ccacacctgt 720
 ccccttgtc ctgccccga actgctggga ggcccttccg tgttcctgtt cccccaaag 780
 cccaaggaca ccctgatgat cagccggacc cccgaagtga cctgcgtggg ggtggatgtg 840
 tcccacgagg accctgaagt gaagttcaat tggtagctgg acggcgtgga agtgcacaac 900
 gccaaagaca agccaagaga ggaacagtac aacagcacct accgggtggg gtccgtgctg 960
 accgtgctgc accaggactg gctgaacggc aaagagtaca agtgcaaggt gtccaacaag 1020
 gccctgcctg ccccatcga gaaaaccatc agcaaggcca agggccagcc ccgcgaacc 1080
 cagggtgtgca cactgcccc aagcaggac gagctgacca agaaccaggt gtccctgagc 1140
 tgtgccgtga aaggcttcta cccctccgat atcgccgtgg aatgggagag caacggccag 1200
 ccgagaaca actacaagac cccccccct gtgctggaca gcgacggctc attcttcctg 1260
 gtgtccaagc tgacagtgga caagtcccgg tggcagcagg gcaacgtgtt cagctgtctc 1320
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 aag 1383

<210> 182
 <211> 645
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 182
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 caggcacctg tgctgtgtt ctacggaaag aacaataggc catctggcat ccccgaccgc 180
 ttttctggca gtgcatcagg gaaccgagcc agtctgacca ttaccggcgc ccaggctgag 240
 gacgaagccg attactattg cagctcccgg gataagagcg gctccagact gagcgtgttc 300
 ggaggaggaa ctaaactgac cgtcctcagt cagcccaagg ctgccccctc ggtcactctg 360
 ttcccgcctt cgagtgagga gcttcaagcc aacaaggcca cactggtgtg tctcataagt 420
 gacttctacc cgggagccgt gacagtggcc tggaaggcag atagcagccc cgtcaaggcg 480

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ggagtggaga ccaccacacc ctccaaacaa agcaacaaca agtacgcggc cagcagctac 540
ctgagcctga cgctgagca gtggaagtcc cacagaagct acagctgcca ggtcacgcat 600
gaagggagca ccgtggagaa gacagtggcc cctacagaat gttca 645
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<210> 183

<211> 1806

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 183

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cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
ggcggaggct tccgggatag agtgaccctg acccgggacg tgtaccgca gatcgctac 240
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agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtggtggtg 360
tctgccgaca aaaccatac ccagggtcac ctgacacaga gcggaccga agtgcggaag 420
cctggcacct ctgtgaaggt gtcctgcaag gccctggca acacctgaa aacctacgac 480
ctgcactggg tgcgcagcgt gccaggacag ggactgcagt ggatgggctg gatcagccac 540
gagggcgaca agaaagtgat cgtggaacgg ttcaaggcca aagtgaccat cgactgggac 600
agaagcacca acaccgcta cctgcagctg agcggcctga cctctggcga taccgccgtg 660
tactactgca ccaaggcag caagcaccgg ctgagagact acgccctgta cgacgatgac 720
ggcgccctga actgggccgt ggatgtggac tacctgagca acctggaatt ctggggccag 780
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ccaaaaccca aggacaccct catgatctcc cggaccctg aggtcacatg cgtggtggtg 1260
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gaaccacagg tgtacaccct gccccatgc cgggatgagc tgaccaagaa tcaagtacg 1560
ctgtggtgcc tggtaaaagg cttctatccc agcgacatc ccgtggagt ggagagcaat 1620
gggcagccgg agaacaacta caagaccag cctcccgtgc tggactccga cggctccttc 1680
ttcctctact caaaactcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1740
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ccgggt 1806
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<210> 184

<211> 996

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

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<400> 184

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tacgtgcaga agcccggcag atccccccag ctgctgatct acctggccag cagcagagcc 180
agcggcgtgc ccgatatagatt ttctggcagc ggcagcgaca aggacttcac cctgaagatc 240
agccgggttg aaaccgagga cgtgggcacc tactactgta tgcagggcag agagagcccc 300
tggaaccttg gccagggcac caaggtggac atcaaggaca aaaccatac ctacatccac 360
gtgacccaga gccccagcag cctgtccgtg tccatcggcg acagagtgc catcaactgc 420
cagacctctc agggcggtggg cagcgacctg cactggtatc agcacaagcc tggcagagcc 480
cccaagctgc tgatccacca cacaagcagc gtggaagatg gcgtgcccag cagattttcc 540
ggcagcggct tccacaccag cttcaacctg accatcagcg atctgcaggc cgacgacatt 600
gccacctact attgtcaggt gctgcagttc ttcggcagag gcagcagact gcacatcaag 660
gataagaccc ataccgtac ggtggccgct cccagcgtgt tcattttccc acctagcgac 720
gagcagctga agtccggcac agcctctgtc gtgtgcctgc tgaacaactt ctacccccgc 780
gaggccaaag tgcagtggaa ggtggacaac gccctgcaga gcggcaacag ccaggaaagc 840
gtgaccgagc aggacagcaa ggactccacc tacagcctga gcagcacct gacactgagc 900
aaggccgact acgagaagca caaggtgtac gcctgcgaag tgaccacca gggcctgtct 960
agccccgtga ccaagagctt caaccggggc gactgt 996

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<210> 185

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 185

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

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180														185														190																											
Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Leu	Gly																																									
195														200														205																											
Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys																																								
210														215														220																											
Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys																																								
225														230														235														240													
Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu																																								
245														250														255																											
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu																																								
260														265														270																											
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys																																								
275														280														285																											
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys																																								
290														295														300																											
Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu																																								
305														310														315														320													
Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys																																								
325														330														335																											
Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys																																								
340														345														350																											
Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Cys	Thr	Leu	Pro	Pro	Ser																																								
355														360														365																											
Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Ser	Cys	Ala	Val	Lys																																								
370														375														380																											
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln																																								
385														390														400																											
Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly																																								
405														410														415																											
Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln																																								
420														425														430																											
Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn																																								
435														440														445																											
His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly																																												
450														455														460																											

<210> 186

<211> 215

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 186

Ala	Ser	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Lys	Gln
1				5					10					15	
Thr	Val	Thr	Ile	Thr	Cys	Arg	Gly	Asp	Ser	Leu	Arg	Ser	His	Tyr	Ala
			20					25					30		
Ser	Trp	Tyr	Gln	Lys	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Leu	Phe	Tyr
		35					40					45			

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

<210> 187

<211> 602

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 187

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

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145		150		155		160
Gly	Ala	Ser	Val	Arg	Val	Ser
				165		170
Ala	His	Ile	Leu	Phe	Trp	Phe
				180		185
Trp	Val	Gly	Trp	Ile	Lys	Pro
				195		200
Gly	Phe	Arg	Asp	Arg	Val	Thr
				210		215
Ala	Tyr	Met	Asp	Ile	Arg	Gly
225				230		235
Tyr	Cys	Ala	Arg	Asp	Arg	Ser
				245		250
Ala	Trp	Gly	Gln	Gly	Thr	Thr
				260		265
Thr	Ala	Ser	Thr	Lys	Gly	Pro
				275		280
Lys	Ser	Thr	Ser	Gly	Gly	Thr
				290		295
Tyr	Phe	Pro	Glu	Pro	Val	Thr
305				310		315
Ser	Gly	Val	His	Thr	Phe	Pro
				325		330
Ser	Leu	Ser	Ser	Val	Val	Thr
				340		345
Thr	Tyr	Ile	Cys	Asn	Val	Asn
				355		360
Lys	Lys	Val	Glu	Pro	Lys	Ser
				370		375
Cys	Pro	Ala	Pro	Glu	Leu	Leu
385				390		395
Pro	Lys	Pro	Lys	Asp	Thr	Leu
				405		410
Cys	Val	Val	Val	Asp	Val	Ser
				420		425
Trp	Tyr	Val	Asp	Gly	Val	Glu
				435		440
Glu	Glu	Gln	Tyr	Asn	Ser	Thr
				450		455
Leu	His	Gln	Asp	Trp	Leu	Asn
465				470		475
Asn	Lys	Ala	Leu	Pro	Ala	Pro
				485		490
Gly	Gln	Pro	Arg	Glu	Pro	Gln
				500		505
Glu	Leu	Thr	Lys	Asn	Gln	Val
				515		520
Tyr	Pro	Ser	Asp	Ile	Ala	Val
				530		535
Asn	Asn	Tyr	Lys	Thr	Thr	Pro
545				550		555
Phe	Leu	Tyr	Ser	Lys	Leu	Thr

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				565					570				575				
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr		
			580					585					590				
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly								
		595					600										

<210> 188

<211> 332

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 188

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

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Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 290 295 300
 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 305 310 315 320
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 325 330

<210> 189
 <211> 1383
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 189
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 ccaggtaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctggtccgtg 180
 gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
 ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
 acaggcaaat actacgactt ctggtccggc tatccccctg gcgaggaata ttttcaagac 360
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 aaggactact ttcccagacc cgtgaccgtg tcctggaatt ctggcgccct gaccagcggc 540
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 cagggtgtgca cactgcccc aagcagggac gagctgacca agaaccaggt gtccctgagc 1140
 tgtgccgtga aaggcttcta cccctccgat atcgccgtgg aatgggagag caacggccag 1200
 ccgagaaca actacaagac cccccccct gtgctggaca gcgacggctc attcttcctg 1260
 gtgtccaagc tgacagtgga caagtcccgg tggcagcagg gcaacgtgtt cagctgctcc 1320
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 aag 1383

<210> 190
 <211> 645
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 190
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acttgccgag gcgactcact gcggagccac tacgcttcct ggtatcagaa gaaacccggc 120
caggcacctg tgctgctgtt ctacggaaag aacaataggc catctggcat ccccgaccgc 180
ttttctggca gtgcatcagg gaaccgagcc agtctgacca ttaccggcgc ccaggctgag 240
gacgaagccg attactattg cagctcccgg gataagagcg gctccagact gagcgtgttc 300
ggaggaggaa ctaaactgac cgtcctcagt cagcccaagg ctgccccctc ggctactctg 360
ttcccgccct cgagtgagga gcttcaagcc aacaaggcca cactggtgtg tctcataagt 420
gacttctacc cgggagccgt gacagtggcc tggaaggcag atagcagccc cgtcaaggcg 480
ggagtggaga ccaccacacc ctccaaacaa agcaacaaca agtacgcggc cagcagctac 540
ctgagcctga cgcctgagca gtggaagtcc cacagaagct acagctgcca ggtcacgcat 600
gaaggggagca ccgtggagaa gacagtggcc cctacagaat gttca 645

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<210> 191

<211> 996

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 191

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ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgcccagc 180
agattttccg gcagcggctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagg acaaaaccca taccgacttc gtgctgacct agagccctca cagcctgagc 360
gtgacacctg gcgagagcgc cagcatcagc tgcaagagca gccactccct gatccacggc 420
gaccggaaca actacctggc ttggtacgtg cagaagcccg gcagatcccc ccagctgctg 480
atctacctgg ccagcagcag agccagcggc gtgcccagata gattttcttg cagcggcagc 540
gacaaggact tcacctgaa gatcagccgg gtggaaaccg aggacgtggg cacctactac 600
tgtatgcagg gcagagagag cccctggacc tttggccagg gcaccaaggt ggacatcaag 660
gataagaccc ataccctgac ggtggccgct cccagcgtgt tcatcttccc acctagcgac 720
gagcagctga agtccggcac agcctctgtc gtgtgcctgc tgaacaactt ctacccccgc 780
gaggccaaag tgcatgtgaa ggtggacaac gccctgcaga gcggcaacag ccaggaaagc 840
gtgaccgagc aggacagcaa ggactccacc tacagcctga gcagcaccct gacactgagc 900
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agccccgtga ccaagagctt caaccggggc gagtgt 996

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<210> 192

<211> 996

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 192

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atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgcccagc 180
agattttccg gcagcggctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300

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4. __183952027041SEQLIST.TXT

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gaccggaaca actacctggc ttggtacgtg cagaagcccg gcagatcccc ccagctgctg 480
atctacctgg ccagcagcag agccagcggc gtgcccgata gattttctgg cagcggcagc 540
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tgtatgcagg gcagagagag cccctggacc tttggccagg gcaccaaggt ggacatcaag 660
gataagaccc ataccgtac ggtggccgct cccagcgtgt tcattttccc acctagcgac 720
gagcagctga agtccggcac agcctctgtc gtgtgcctgc tgaacaactt ctacccccgc 780
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gtgaccgagc aggacagcaa ggactccacc tacagcctga gcagcacct gacactgagc 900
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agccccgtga ccaagagctt caaccggggc gagtgt 996

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<210> 193

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 193

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

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4.__183952027041SEQLIST.TXT

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
325 330 335
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350
Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365
Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
405 410 415
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Leu
420 425 430
His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445
Pro Gly
450

<210> 194

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 194

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

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[illegible]

<210> 195

<211> 615

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 195

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

4.__183952027041SEQLIST.TXT

Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro
210						215					220				
Glu	Asp	Thr	Ala	Leu	Tyr	Tyr	Cys	Ala	Lys	Asp	Leu	Arg	Glu	Asp	Glu
225					230					235					240
Cys	Glu	Glu	Trp	Trp	Ser	Asp	Tyr	Tyr	Asp	Phe	Gly	Lys	Gln	Leu	Pro
				245					250					255	
Cys	Ala	Lys	Ser	Arg	Gly	Gly	Leu	Val	Gly	Ile	Ala	Asp	Asn	Trp	Gly
			260				265						270		
Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Ala	Ser
		275					280					285			
Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr
	290					295					300				
Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro
305				310						315					320
Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val
				325					330					335	
His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser
			340					345						350	
Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile
		355					360					365			
Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val
370						375					380				
Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala
385					390					395					400
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
				405					410					415	
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
			420					425					430		
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
		435					440					445			
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
	450					455					460				
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
465					470					475					480
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
				485					490					495	
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
			500					505					510		
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Cys	Arg	Asp	Glu	Leu	Thr
		515					520					525			
Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
		530				535					540				
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
545					550					555					560
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
				565					570					575	
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
			580					585					590		
Ser	Cys	Ser	Val	Leu	His	Glu	Ala	Leu	His	Ser	His	Tyr	Thr	Gln	Lys
		595					600					605			
Ser	Leu	Ser	Leu	Ser	Pro	Gly									
610						615									

4.___183952027041SEQLIST.TXT

<210> 196
 <211> 337
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 196
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 Lys Val Thr Ile Ser Cys Ser Gly Asn Thr Ser Asn Ile Gly Asn Asn
 20 25 30
 Phe Val Ser Trp Tyr Gln Gln Arg Pro Gly Arg Ala Pro Gln Leu Leu
 35 40 45
 Ile Tyr Glu Thr Asp Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
 50 55 60
 Ala Ser Lys Ser Gly Thr Ser Gly Thr Leu Ala Ile Thr Gly Leu Gln
 65 70 75 80
 Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Ala Ala Ser Leu
 85 90 95
 Ser Ser Ala Arg Val Phe Gly Thr Gly Thr Lys Val Ile Val Leu Asp
 100 105 110
 Lys Thr His Thr Ala Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val
 115 120 125
 Ala Leu Lys Gln Thr Val Thr Ile Thr Cys Arg Gly Asp Ser Leu Arg
 130 135 140
 Ser His Tyr Ala Ser Trp Tyr Gln Lys Lys Pro Gly Gln Ala Pro Val
 145 150 155 160
 Leu Leu Phe Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg
 165 170 175
 Phe Ser Gly Ser Ala Ser Gly Asn Arg Ala Ser Leu Thr Ile Thr Gly
 180 185 190
 Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Arg Asp Lys
 195 200 205
 Ser Gly Ser Arg Leu Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val
 210 215 220
 Leu Asp Lys Thr His Thr Arg Thr Val Ala Ala Pro Ser Val Phe Ile
 225 230 235 240
 Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
 245 250 255
 Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
 260 265 270
 Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
 275 280 285
 Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
 290 295 300
 Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
 305 310 315 320
 His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu

Cys

<210> 197
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 197
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 agctgcagag ccagcggcta cgagttcatc gactgcaccc tgaactggat cagactggcc 120
 cctggcaagc ggccctgagtg gatgggatgg ctgaagccta gaggcggagc cgtgaactac 180
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 aactgcgact acaactggga cttcgagcac tggggcagag gcacccctgt gatcgtgtca 360
 agcgcgtcga ccaagggccc cagcgtgttc cctctggccc ctacgagcaa gagcacatct 420
 ggcggaacag ccgccctggg ctgcctcgtg aaggactact ttcccagacc cgtgaccgtg 480
 tcctggaatt ctggcgccct gaccagcggc gtgcacacct ttccagctgt gctgcagtc 540
 agcggcctgt acagcctgag cagcgtcgtg acagtgccca gcagctctct gggcacccag 600
 acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 660
 cccaagagct gcgacaagac ccacacctgt ccccttgtc ctgccccga actgctggga 720
 ggcccttccg tgttcctgtt cccccaaaag cccaaggaca ccctgatgat cagccggacc 780
 cccgaagtga cctgcgtggg ggtggatgtg tcccacgagg accctgaagt gaagttcaat 840
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 agcaaggcca agggccagcc ccgcgaaccc cagggtgtgca cactgcccc aagcagggac 1080
 gagctgacca agaaccaggt gtccctgagc tgtgccgtga aaggcttcta cccctccgat 1140
 atcgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cccccccct 1200
 gtgctggaca gcgacggctc attcttcctg gtgtccaagc tgacagtgga caagtcgccg 1260
 tggcagcagg gcaacgtgtt cagctgtccc gtgctgcatg aggctctgca cagccactac 1320
 acgcagaaga gcctctccct gtctccgggt 1350

<210> 198
 <211> 630
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 198
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 atcagctgcc ggacaagcca gtacggcagc ctggcctggg atcagcagag gcctggacag 120
 gccccagac tcgtgatcta cagcggcagc acaagagccg ccggaatccc cgatagattc 180
 agcggctcca gatggggccc tgactacaac ctgaccatca gcaacctgga aagcggcgac 240
 ttggcgtgt actactgcca gcagtacgag ttcttcggcc agggcaccaa ggtgcagggt 300

4. __183952027041SEQLIST.TXT

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ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgaccc accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630

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<210> 199

<211> 1845

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 199

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ccaggttaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctggtccgtg 180
gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
acaggcaaat actacgactt ctggtccggc tatccccctg gcgaggaata ttttcaagac 360
tggggtcagg gaacccttgt tatcgtgtcc tccgacaaaa ccataacca ggtgcagttg 420
gtggagtctg ggggaggcgt ggtccagcct gggacgtccc tgagactctc ctgtgcagcc 480
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tccaagagca cctctggggg cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc 960
gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccc 1020
gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 1080
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ccccatgcc gggatgagct gaccaagaat caagtcagcc tgtgggtgcct ggtaaaaggc 1620
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aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctactc aaaactcacc 1740
gtggacaaga gcagggtggc gcaggggaac gtcttctcat gctccgtgct gcatgaggct 1800
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<210> 200

<211> 1011

<212> DNA

<213> Artificial Sequence

4.__183952027041SEQLIST.TXT

<220>

<223> Synthetic Construct

<400> 200

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cccggcagag ccccccaact cctcatttat gaaactgaca agcgaccctc agggattcct 180
gaccgattct ctgcttccaa gtctggtacg tcaggcacc tggccatcac cgggctgcag 240
actggggacg aggccgatta ttactgcgcc acatgggctg ccagcctgag ttccgcgcgt 300
gtcttcggaa ctgggaccaa ggtcatcgtc ctggacaaaa ccataccgc atccgaactg 360
actcaggacc ctgccgtctc tgtggcactg aagcagactg tgactattac ttgccgaggc 420
gactcactgc ggagccacta cgcttcctgg tatcagaaga aacccgcca ggcacctgtg 480
ctgctgttct acggaaagaa caataggcca tctggcatcc ccgaccgctt ttctggcagt 540
gcatcaggga accgagccag tctgaccatt accggcgccc aggctgagga cgaagccgat 600
tactattgca gctcccggga taagagcggc tccagactga gcgtgttcgg aggaggaact 660
aaactgaccg tcctcgataa gaccataacc cgtacggtgg ccgctcccag cgtgttcac 720
ttcccaccta gcgacgagca gctgaagtcc ggcacagcct ctgtcgtgtg cctgctgaac 780
aacttctacc ccgcgaggc caaagtgcag tggaagggtg acaacgccct gcagagcggc 840
aacagccagg aaagcgtgac cgagcaggac agcaaggact ccacctacag cctgagcagc 900
accctgacac tgagcaaggc cgactacgag aagcacaagg tgtacgcctg cgaagtgacc 960
caccagggcc tgtctagccc cgtgaccaag agcttcaacc ggggcgagtg t 1011

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<210> 201

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 201

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

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4.__183952027041SEQLIST.TXT

Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
				165					170					175	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
			180					185					190		
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
		195					200					205			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser
	210					215					220				
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
225					230					235					240
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
				245					250					255	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
			260					265					270		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
		275					280					285			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
		290				295					300				
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
305					310					315					320
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro
				325					330					335	
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
			340					345					350		
Val	Cys	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val
		355					360					365			
Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val
	370					375					380				
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro
385					390					395					400
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr
				405					410					415	
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val
			420					425					430		
Leu	His	Glu	Ala	Leu	His	Ser	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu
		435					440					445			
Ser	Pro	Gly													
		450													

<210> 202

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 202

Tyr	Ile	His	Val	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Val	Ser	Ile	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Asn	Cys	Gln	Thr	Ser	Gln	Gly	Val	Gly	Ser	Asp

4. __183952027041SEQLIST.TXT

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

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<210> 203

<211> 615

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 203

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

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4. __183952027041SEQLIST.TXT

Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly
130						135					140				
Gly	Gly	Val	Val	Gln	Pro	Gly	Thr	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala
145					150					155					160
Ser	Gln	Phe	Arg	Phe	Asp	Gly	Tyr	Gly	Met	His	Trp	Val	Arg	Gln	Ala
				165					170					175	
Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Ser	Ile	Ser	His	Asp	Gly	Ile
			180					185					190		
Lys	Lys	Tyr	His	Ala	Glu	Lys	Val	Trp	Gly	Arg	Phe	Thr	Ile	Ser	Arg
		195					200					205			
Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro
		210				215					220				
Glu	Asp	Thr	Ala	Leu	Tyr	Tyr	Cys	Ala	Lys	Asp	Leu	Arg	Glu	Asp	Glu
225					230					235					240
Cys	Glu	Glu	Trp	Trp	Ser	Asp	Tyr	Tyr	Asp	Phe	Gly	Lys	Gln	Leu	Pro
				245					250					255	
Cys	Ala	Lys	Ser	Arg	Gly	Gly	Leu	Val	Gly	Ile	Ala	Asp	Asn	Trp	Gly
			260					265						270	
Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Ala	Ser
		275					280					285			
Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr
	290					295					300				
Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro
305					310					315					320
Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val
				325					330					335	
His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser
			340					345					350		
Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile
		355					360					365			
Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val
	370					375					380				
Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala
385					390					395					400
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
				405					410					415	
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
			420					425					430		
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
		435					440					445			
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
	450					455					460				
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
465					470					475					480
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
				485					490					495	
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
			500					505					510		
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Cys	Arg	Asp	Glu	Leu	Thr
		515					520					525			
Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
	530					535					540				

4.__183952027041SEQLIST.TXT

Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
545					550					555					560
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
				565					570						575
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
			580				585						590		
Ser	Cys	Ser	Val	Leu	His	Glu	Ala	Leu	His	Ser	His	Tyr	Thr	Gln	Lys
	595						600					605			
Ser	Leu	Ser	Leu	Ser	Pro	Gly									
	610					615									

<210> 204

<211> 337

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 204

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

4. 183952027041SEQLIST.TXT

[illegible]

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<210> 205
<211> 1353
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic Construct

<400> 205						
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tcctgtcaga	caagcggcta	caccttcacc	gcccacatcc	tgttcttggt	ccggcaggcc	120
cctggcagag	gactggaatg	ggtgggatgg	atcaagcccc	agtatggcgc	cgtgaacttc	180
ggcggaggct	tccgggatag	agtgaccctg	acccgggacg	tgtaccgcga	gatcgcctac	240
atggacatcc	ggggcctgaa	gcccgatgac	accgccgtgt	actactgcgc	cagagacaga	300
agctacggcg	acagcagctg	ggctctggat	gcttggggcc	agggcacaac	cgtggtggtg	360
tctgccgcct	ctacaaaagg	ccccagcgtg	ttccctctgg	cccctagcag	caagagcaca	420
tctggcggaa	cagccgcctt	gggctgcctc	gtgaaggact	actttcccga	gcccgtgacc	480
gtgtcctgga	attctggcgc	cctgaccagc	ggcgtgcaca	cctttccagc	tgtgctgcag	540
tccagcggcc	tgtacagcct	gagcagcgtc	gtgacagtgc	ccagcagctc	tctgggcacc	600
cagacctaca	tctgcaacgt	gaaccacaag	cccagcaaca	ccaaggtgga	caagaaggtg	660
gaaccceaaga	gctgcgacaa	gaccacaccc	tgtccccctt	gtcctgcccc	cgaactgctg	720
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acccccgaag	tgacctgcgt	ggtggtggat	gtgtcccacg	aggaccctga	agtgaagttc	840
aatttggtacg	tggacggcgt	ggaagtgcac	aacgccaaga	ccaagccaag	agaggaacag	900
tacaacagca	cctaccgggt	ggtgtccgtg	ctgaccgtgc	tgcaccagga	ctggctgaac	960
ggcaaagagt	acaagtgcaa	ggtgtccaac	aaggccctgc	ctgcccccat	cgagaaaacc	1020
atcagcaagg	ccaagggccca	gccccgcgaa	cccaggtgt	gcacactgcc	cccaagcagg	1080
gacgagctga	ccaagaacca	ggtgtccctg	agctgtgccg	tgaaaggctt	ctacccttc	1140
gatatcgccg	tggaatggga	gagcaacggc	cagcccgaga	acaactacaa	gaccaccccc	1200
cctgtgtctgg	acagcgacgg	ctcattcttc	ctggtgtcca	agctgacagt	ggacaagtcc	1260
cgggtggcagc	agggcaacgt	gttcagctgc	tccgtgctgc	atgaggctct	gcacagccac	1320
tacacgcaga	agagcctctc	cctgtctccg	ggt			1353

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<210> 206
<211> 630
<212> DNA
<213> Artificial Sequence
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4.__183952027041SEQLIST.TXT

<220>

<223> Synthetic Construct

<400> 206

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atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgcccagc 180
agattttccg gcagcggctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacgggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630
```

<210> 207

<211> 1845

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 207

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ccaggtaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctggtccgtg 180
gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
acaggcaaat actacgactt ctggtccggc tatccccctg gcgaggaata ttttcaagac 360
tgggggtcagg gaacccttgt tatcgtgtcc tccgacaaaa cccataccca ggtgcagttg 420
gtggagtctg ggggaggcgt ggtccagcct gggacgtccc tgagactctc ctgtgcagcc 480
tctcaattca ggtttgatgg ttatggcatg cactgggtcc gccaggcccc aggcaagggg 540
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tgtgaagagt ggtggtcgga ttattacgat tttgggaaac aactcccttg cgcaaagtca 780
cgcggcggct tggttggaat tgctgataac tggggccaag ggacaatggt caccgtctct 840
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tccaagagca cctctggggg cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc 960
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cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc 1260
atgatctccc ggacccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 1320
gaggtcaagt tcaactggta tgttgacggc gtggaggtgc ataatgcaa gacaaagccg 1380
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 1440
gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagcccc 1500
atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1560
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4.__183952027041SEQLIST.TXT

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ccccatgcc gggatgagct gaccaagaat caagtcagcc tgtggtgcct ggtaaaaggc 1620
ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 1680
aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctactc aaaactcacc 1740
gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgct gcatgaggct 1800
ctgcacagcc actacacgca gaagagcctc tccctgtctc cgggt 1845

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<210> 208

<211> 1011

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 208

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tcctgctctg gaaacacctc caacattggc aataattttg tgtcctggta tcaacagcgc 120
cccggcagag ccccccaact cctcatttat gaaactgaca agcgaccctc agggattcct 180
gaccgattct ctgcttccaa gtctggtacg tcaggcacc cgggctgcag 240
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gtcttcggaa ctgggaccaa ggtcatcgtc ctggacaaaa cccataccgc atccgaactg 360
actcaggacc ctgccgtctc tgtggcactg aagcagactg tgactattac ttgccgaggc 420
gactcactgc ggagccacta cgcttcctgg tatcagaaga aaccggcca ggcacctgtg 480
ctgctgttct acggaaagaa caataggcca tctggcatcc ccgaccgctt ttctggcagt 540
gcatcaggga accgagccag tctgaccatt accggcgccc aggctgagga cgaagccgat 600
tactattgca gctcccggga taagagcggc tccagactga gcgtgttcgg aggaggaact 660
aaactgaccg tcctcgataa gaccatacc cgtacggtgg ccgctccag cgtgttcatc 720
ttcccaccta gcgacgagca gctgaagtcc ggcacagcct ctgtcgtgtg cctgctgaac 780
aacttctacc ccgcgaggc caaagtgcag tggaaggtgg acaacgccct gcagagcggc 840
aacagccagg aaagcgtgac cgagcaggac agcaaggact ccacctacag cctgagcagc 900
accctgacac tgagcaaggc cgactacgag aagcacaagg tgtacgcctg cgaagtgacc 960
caccagggcc tgtctagccc cgtgaccaag agcttcaacc ggggcgagtg t 1011

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<210> 209

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 209

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

```

4.__183952027041SEQLIST.TXT

```

Met Asp Ile Arg Gly Leu Lys Pro Asp Asp Thr Ala Val Tyr Tyr Cys
      85                      90                      95
Ala Arg Asp Arg Ser Tyr Gly Asp Ser Ser Trp Ala Leu Asp Ala Trp
      100                    105                    110
Gly Gln Gly Thr Thr Val Val Val Ser Ala Ala Ser Thr Lys Gly Pro
      115                    120                    125
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
      130                    135                    140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
      145                    150                    155                    160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
      165                    170                    175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
      180                    185                    190
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
      195                    200                    205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
      210                    215                    220
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
      225                    230                    235                    240
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
      245                    250                    255
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
      260                    265                    270
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
      275                    280                    285
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
      290                    295                    300
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
      305                    310                    315                    320
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
      325                    330                    335
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
      340                    345                    350
Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
      355                    360                    365
Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
      370                    375                    380
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
      385                    390                    395                    400
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
      405                    410                    415
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
      420                    425                    430
Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu
      435                    440                    445
Ser Pro Gly
      450

```

<210> 210

<211> 210

4.___183952027041SEQLIST.TXT

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 210

```

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

```

<210> 211

<211> 611

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 211

```

Glu Val Arg Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1           5           10          15
Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Asp Asn Ala
          20          25          30
Trp Met Thr Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Val
          35          40          45

```

4.__183952027041SEQLIST.TXT

Gly	Arg	Ile	Thr	Gly	Pro	Gly	Glu	Gly	Trp	Ser	Val	Asp	Tyr	Ala	Glu
50						55					60				
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Thr	Lys	Asn	Thr
65					70					75					80
Leu	Tyr	Leu	Glu	Met	Asn	Asn	Val	Arg	Thr	Glu	Asp	Thr	Gly	Tyr	Tyr
				85					90					95	
Phe	Cys	Ala	Arg	Thr	Gly	Lys	Tyr	Tyr	Asp	Phe	Trp	Ser	Gly	Tyr	Pro
			100					105					110		
Pro	Gly	Glu	Glu	Tyr	Phe	Gln	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Ile
		115					120					125			
Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Gln	Val	His	Leu	Thr	Gln	Ser	Gly
	130					135					140				
Pro	Glu	Val	Arg	Lys	Pro	Gly	Thr	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala
145					150					155					160
Pro	Gly	Asn	Thr	Leu	Lys	Thr	Tyr	Asp	Leu	His	Trp	Val	Arg	Ser	Val
				165					170					175	
Pro	Gly	Gln	Gly	Leu	Gln	Trp	Met	Gly	Trp	Ile	Ser	His	Glu	Gly	Asp
			180					185					190		
Lys	Lys	Val	Ile	Val	Glu	Arg	Phe	Lys	Ala	Lys	Val	Thr	Ile	Asp	Trp
		195					200					205			
Asp	Arg	Ser	Thr	Asn	Thr	Ala	Tyr	Leu	Gln	Leu	Ser	Gly	Leu	Thr	Ser
	210					215				220					
Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Gly	Ser	Lys	His	Arg	Leu
225					230					235					240
Arg	Asp	Tyr	Ala	Leu	Tyr	Asp	Asp	Asp	Gly	Ala	Leu	Asn	Trp	Ala	Val
				245					250					255	
Asp	Val	Asp	Tyr	Leu	Ser	Asn	Leu	Glu	Phe	Trp	Gly	Gln	Gly	Thr	Ala
			260					265					270		
Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Ala	Ser	Thr	Lys	Gly	Pro
		275				280						285			
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
	290					295					300				
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
305					310					315					320
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
				325					330					335	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
			340					345					350		
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
		355				360						365			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser
	370					375					380				
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
385					390				395						400
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
				405					410					415	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
			420					425					430		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
		435					440					445			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
	450					455					460				

4._183952027041SEQLIST.TXT

```

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465                               470               475                   480
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                               485               490                   495
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
                               500               505                   510
Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
                               515               520               525
Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
                               530               535               540
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545                               550               555                   560
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                               565               570                   575
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
                               580               585               590
Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu
                               595               600               605
Ser Pro Gly
                               610

```

<210> 212

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 212

```

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

```

[illegible]

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

<220>
<223> Synthetic Construct

<400>	213					
agagcccacc	tggtgcagtc	tggcaccgcc	atgaagaaac	caggcgcctc	tgtgcgggtg	60
tcctgtcaga	caagcggcta	caccttcacc	gcccacatcc	tgttctgggt	ccggcaggcc	120
cctggcagag	gactggaatg	ggtgggatgg	atcaagcccc	agtatggcgc	cgtgaacttc	180
ggcggaggct	tccgggatag	agtgacctg	acccgggacg	tgtaccgcga	gatcgcctac	240
atggacatcc	ggggcctgaa	gcccgatgac	accgccgtgt	actactgcgc	cagagacaga	300
agctacggcg	acagcagctg	ggctctggat	gcttggggcc	agggcacaac	cgtggtggtg	360
tctgccgcct	ctacaaaagg	ccccagcgtg	ttccctctgg	cccctagcag	caagagcaca	420
tctggcggaa	cagccgcctt	gggctgcctc	gtgaaggact	actttcccga	gcccgtgacc	480
gtgtcctgga	attctggcgc	cctgaccagc	ggcgtgcaca	cctttccagc	tgtgctgcag	540
tccagcggcc	tgtacagcct	gagcagcgtc	gtgacagtgc	ccagcagctc	tctgggcacc	600
cagacctaca	tctgcaacgt	gaaccacaag	cccagcaaca	ccaaggtgga	caagaaggtg	660
gaacccaaga	gctgcgacaa	gaccacacac	tgtccccctt	gtcctgcccc	cgaactgctg	720
ggaggccctt	ccgtgttctt	gttcccccca	aagcccaagg	acaccctgat	gatcagccgg	780
acccccgaag	tgacctgcgt	ggtggtggat	gtgtcccacg	aggaccctga	agtgaagttc	840
aatttggtacg	tggacggcgt	ggaagtgcac	aacgccaaga	ccaagccaag	agaggaacag	900
tacaacagca	cctaccgggt	ggtgtccgtg	ctgaccgtgc	tgcaccagga	ctggctgaac	960
ggcaaagagt	acaagtgcaa	ggtgtccaac	aaggccctgc	ctgcccccat	cgagaaaacc	1020
atcagcaagg	ccaagggcca	gccccgcgaa	ccccaggtgt	gcacactgcc	ccaagcagg	1080

4. __183952027041SEQLIST.TXT

```

gacgagctga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccctcc 1140
gatatcgccg tggaatggga gagcaacggc cagcccgaga acaactacaa gaccaccccc 1200
cctgtgctgg acagcgacgg ctcatcttc ctggtgtcca agctgacagt ggacaagtcc 1260
cgggtggcagc agggcaacgt gttcagctgc tccgtgctgc acgaggccct gcacagccac 1320
tacaccaga agtcctgag cctgagcccc ggc 1353

```

<210> 214

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 214

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tacatccacg tgaccagag cccagcagc ctgtccgtgt ccatcggcga cagagtgacc 60
atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgccagc 180
agattttccg gcagcggctt ccacaccagc ttccagctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacgggtggc cgctcccagc gtgttcattt tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctacct ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630

```

<210> 215

<211> 1833

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 215

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gaggtagac tgggtggagtc aggagggggg cttgtgaagc ccggtgggtc tctccgcctg 60
agctgttctg cctccggctt tgatttcgat aacgcctgga tgacctgggt caggcagcct 120
ccaggtaagg gactggagtg ggtgggaaga atcacaggct caggcgaggg ctggtccgtg 180
gactacgcgg aatctgttaa agggcgggtt acaatctcaa gggacaatac caagaatacc 240
ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
acaggcaaat actacgactt ctggtccggc tatccccctg gcgaggaata ttttcaagac 360
tggggtcagg gaacccttgt tatcgtgtcc tccgacaaaa cccataccca ggtgcacctg 420
acacagagcg gaccggaagt gcggaagcct ggcacctctg tgaagggtgc ctgcaaggcc 480
cctggcaaca ccctgaaaac ctacgacctg cactgggtgc gcagcgtgcc aggacaggga 540
ctgcagtgga tgggctggat cagccacgag ggcgacaaga aagtgatcgt ggaacggttc 600
aaggccaaag tgaccatcga ctgggacaga agcaccaaca ccgcctacct gcagctgagc 660
ggcctgacct ctggcgatac cgccgtgtac tactgcgcca agggcagcaa gcaccggctg 720
agagactacg ccctgtacga cgatgacggc gccctgaact gggccgtgga tgtggactac 780
ctgagcaacc tggaattctg gggccagggc acagccgtga ccgtgtcatc tgataagacc 840
cacaccgctt ccaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc 900
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 960

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4. __183952027041SEQLIST.TXT

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gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgtcctacag 1020
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 1080
cagacctaca tctgcaacgt gaatcacaa cccagcaaca ccaaggtgga caagaaagtt 1140
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 1200
gggggaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctcccgg 1260
acccctgagg tcacatgctg ggtggtggac gtgagccacg aagaccctga ggtcaagtcc 1320
aactggtatg ttgacggcgt ggaggtgcat aatgccaaga caaagccgag ggaggagcag 1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1500
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatgccgg 1560
gatgagctga ccaagaatca agtcagcctg tggtgcctgg taaaaggctt ctatcccagc 1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680
cccgtgctgg actccgacgg ctccttcttc ctctactcaa aactcaccgt ggacaagagc 1740
aggtggcagc aggggaacgt cttctcatgc tccgtgctgc atgaggctct gcacagccac 1800
tacacgcaga agagcctctc cctgtctccg ggt 1833
```

<210> 216

<211> 1014

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 216

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gacttcgtgc tgacccagag ccctcacagc ctgagcgtga cacctggcga gagcgccagc 60
atcagctgca agagcagcca ctccctgatc cacggcgacc ggaacaacta cctggcttgg 120
tacgtgcaga agcccggcag atccccccag ctgctgatct acctggccag cagcagagcc 180
agcggcgtgc ccgatagatt ttctggcagc ggcagcgaca aggacttcac cctgaagatc 240
agccgggtgg aaaccgagga cgtgggcacc tactactgta tgcagggcag agagagcccc 300
tggaaccttg gccagggcac caaggtggac atcaaggaca aaaccatac cgcattccgaa 360
ctgactcagg accctgccgt ctctgtggca ctgaagcaga ctgtgactat tacttgccga 420
ggcgactcac tgcggagcca ctacgcttcc tggtatcaga agaaaccgg ccaggcacct 480
gtgctgctgt tctacggaaa gaacaatagg ccatctggca tccccgaccg ctttcttggc 540
agtgcacagc ggaaccgagc cagtctgacc attaccggcg cccaggctga ggacgaagcc 600
gattactatt gcagctcccg ggataagagc ggctccagac tgagcgtgtt cggaggagga 660
actaaactga ccgtcctcga taagacccat accgtacgg tggccgctcc cagcgtgttc 720
atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 780
aacaacttct acccccgcga ggccaaagtg cagtgggaagg tggacaacgc cctgcagagc 840
ggcaacagcc aggaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 900
agcaccctga cactgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 960
accaccagg gcctgtctag ccccgtagc aagagcttca accggggcga gtgt 1014
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<210> 217

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 217

4. __183952027041SEQLIST.TXT

Arg	Ala	His	Leu	Val	Gln	Ser	Gly	Thr	Ala	Met	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Arg	Val	Ser	Cys	Gln	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Ala	His
			20					25					30		
Ile	Leu	Phe	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Val
		35					40					45			
Gly	Trp	Ile	Lys	Pro	Gln	Tyr	Gly	Ala	Val	Asn	Phe	Gly	Gly	Gly	Phe
	50					55				60					
Arg	Asp	Arg	Val	Thr	Leu	Thr	Arg	Asp	Val	Tyr	Arg	Glu	Ile	Ala	Tyr
65					70				75					80	
Met	Asp	Ile	Arg	Gly	Leu	Lys	Pro	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85				90						95	
Ala	Arg	Asp	Arg	Ser	Tyr	Gly	Asp	Ser	Ser	Trp	Ala	Leu	Asp	Ala	Trp
			100					105					110		
Gly	Gln	Gly	Thr	Thr	Val	Val	Val	Ser	Ala	Ala	Ser	Thr	Lys	Gly	Pro
		115					120					125			
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
	130					135					140				
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
145					150					155					160
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
			165					170						175	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
			180					185					190		
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
		195					200					205			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser
	210					215					220				
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
225					230					235					240
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
			245					250						255	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
			260					265					270		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
		275					280					285			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
	290					295					300				
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
305					310					315					320
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro
				325				330						335	
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
			340					345					350		
Val	Cys	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val
		355					360					365			
Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val
	370					375					380				
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro
385					390					395					400
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr
				405					410					415	

4._183952027041SEQLIST.TXT

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430
 Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445
 Ser Pro Gly
 450

<210> 218
 <211> 210
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 218
 Tyr Ile His Val Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ile Gly
 1 5 10 15
 Asp Arg Val Thr Ile Asn Cys Gln Thr Ser Gln Gly Val Gly Ser Asp
 20 25 30
 Leu His Trp Tyr Gln His Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
 35 40 45
 His His Thr Ser Ser Val Glu Glu Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Phe His Thr Ser Phe Asn Leu Thr Ile Ser Asp Leu Gln Ala
 65 70 75 80
 Asp Asp Ile Ala Thr Tyr Tyr Cys Gln Val Leu Gln Phe Phe Gly Arg
 85 90 95
 Gly Ser Arg Leu His Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
 100 105 110
 Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
 115 120 125
 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
 130 135 140
 Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
 145 150 155 160
 Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
 165 170 175
 Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
 180 185 190
 Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
 195 200 205
 Glu Cys
 210

<210> 219
 <211> 611
 <212> PRT
 <213> Artificial Sequence

4.__183952027041SEQLIST.TXT

<220>

<223> Synthetic Construct

<400> 219

Glu	Val	Arg	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	Pro	Gly	Gly	1	5	10	15
Ser	Leu	Arg	Leu	Ser	Cys	Ser	Ala	Ser	Gly	Phe	Asp	Phe	Asp	Asn	Ala	20	25	30	
Trp	Met	Thr	Trp	Val	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	35	40	45	
Gly	Arg	Ile	Thr	Gly	Pro	Gly	Glu	Gly	Trp	Ser	Val	Asp	Tyr	Ala	Glu	50	55	60	
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Thr	Lys	Asn	Thr	65	70	75	80
Leu	Tyr	Leu	Glu	Met	Asn	Asn	Val	Arg	Thr	Glu	Asp	Thr	Gly	Tyr	Tyr	85	90	95	
Phe	Cys	Ala	Arg	Thr	Gly	Lys	Tyr	Tyr	Asp	Phe	Trp	Ser	Gly	Tyr	Pro	100	105	110	
Pro	Gly	Glu	Glu	Tyr	Phe	Gln	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Ile	115	120	125	
Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Gln	Val	His	Leu	Thr	Gln	Ser	Gly	130	135	140	
Pro	Glu	Val	Arg	Lys	Pro	Gly	Thr	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	145	150	155	160
Pro	Gly	Asn	Thr	Leu	Lys	Thr	Tyr	Asp	Leu	His	Trp	Val	Arg	Ser	Val	165	170	175	
Pro	Gly	Gln	Gly	Leu	Gln	Trp	Met	Gly	Trp	Ile	Ser	His	Glu	Gly	Asp	180	185	190	
Lys	Lys	Val	Ile	Val	Glu	Arg	Phe	Lys	Ala	Lys	Val	Thr	Ile	Asp	Trp	195	200	205	
Asp	Arg	Ser	Thr	Asn	Thr	Ala	Tyr	Leu	Gln	Leu	Ser	Gly	Leu	Thr	Ser	210	215	220	
Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Gly	Ser	Lys	His	Arg	Leu	225	230	235	240
Arg	Asp	Tyr	Ala	Leu	Tyr	Asp	Asp	Asp	Gly	Ala	Leu	Asn	Trp	Ala	Val	245	250	255	
Asp	Val	Asp	Tyr	Leu	Ser	Asn	Leu	Glu	Phe	Trp	Gly	Gln	Gly	Thr	Ala	260	265	270	
Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Ala	Ser	Thr	Lys	Gly	Pro	275	280	285	
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	290	295	300	
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	305	310	315	320
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	325	330	335	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	340	345	350	
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	355	360	365	
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	370	375	380	

4.__183952027041SEQLIST.TXT

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
435 440 445
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
450 455 460
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
485 490 495
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510
Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
515 520 525
Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
565 570 575
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590
Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605
Ser Pro Gly
610

<210> 220

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 220

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

4. 183952027041SEQLIST.TXT

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

$\langle 210 \rangle$ 221

<211> 1353

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 221

agagcccacc	tggtgcagtc	tggcaccgcc	atgaagaaac	caggcgcctc	tgtgcgggtg	60
tcctgtcaga	caagcggcta	caccttcacc	gccacatcc	tgttctggtt	ccggcaggcc	120
cctggcagag	gactggaatg	ggtgggatgg	atcaagcccc	agtatggcgc	cgtgaacttc	180
ggcggaggct	tccgggatag	agtgaccctg	acccgggacg	tgtaccgcga	gatcgcctac	240
atggacatcc	ggggcctgaa	gcccgatgac	accgccgtgt	actactgcgc	cagagacaga	300
agctacggcg	acagcagctg	ggctctggat	gcttggggcc	agggcacaac	cgtggtggtg	360
tctgccgcct	ctacaaaggg	ccccagcgtg	ttccctctgg	cccctagcag	caagagcaca	420
tctggcggaa	cagccgccct	gggctgcctc	gtgaaggact	actttccga	gcccgtgacc	480

4. __183952027041SEQLIST.TXT

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gtgtcctgga attctggcgc cctgaccagc ggcgtgcaca cttttccagc tgtgctgcag 540
tccagcggcc tgtacagcct gagcagcgtc gtgacagtgc ccagcagctc tctgggcacc 600
cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagaagggtg 660
gaacccaaga gctgcgacaa gaccacacc tgtccccctt gtcctgcccc cgaactgctg 720
ggaggccctt ccgtgttcct gttcccccca aagcccaagg acaccctgat gatcagccgg 780
acccccgaag tgacctgcgt ggtggtggat gtgtccacg aggacctga agtgaagttc 840
aattggtacg tggacggcgt ggaagtgcac aacgccaaga ccaagccaag agaggaacag 900
tacaacagca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ctggctgaac 960
ggcaaagagt acaagtgcaa ggtgtccaac aaggccctgc ctgcccccat cgagaaaacc 1020
atcagcaagg ccaagggcca gccccgcgaa cccaggtgt gcacactgcc cccaagcagg 1080
gacgagctga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccctcc 1140
gatatcgccg tggaatggga gagcaacggc cagcccgaga acaactaaa gaccaccccc 1200
cctgtgctgg acagcgacgg ctcatcttc ctggtgtcca agctgacagt ggacaagtcc 1260
cgggtggcagc agggcaacgt gttcagctgc tccgtgctgc acgaggccct gcacagccac 1320
tacaccaga agtccctgag cctgagcccc ggc 1353
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<210> 222

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 222

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tacatccacg tgacccagag ccccagcagc ctgtccgtgt ccatcggcga cagagtgacc 60
atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagaagg cgtgcccagc 180
agatthttccg gcagcggtt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctacct ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630
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<210> 223

<211> 1833

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 223

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gaggttagac tgggtggagtc aggagggggg cttgtgaagc ccggtgggtc tctccgcctg 60
agctgttctg cctccggctt tgatttcgat aacgcctgga tgacctgggt caggcagcct 120
ccaggttaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctggtccgtg 180
gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
acaggcaaat actacgactt ctggtccggc tatccccctg gcgaggaata ttttcaagac 360
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4. __183952027041SEQLIST.TXT

tgggggtcagg	gaacccttgt	tatcgtgtcc	tccgacaaaa	cccataccca	ggtgcacctg	420
acacagagcg	gacccgaagt	gcggaagcct	ggcacctctg	tgaaggtgtc	ctgcaaggcc	480
cctggcaaca	ccctgaaaac	ctacgacctg	cactgggtgc	gcagcgtgcc	aggacagggg	540
ctgcagtgga	tgggctggat	cagccacgag	ggcgacaaga	aagtgatcgt	ggaacgggtc	600
aaggccaaag	tgaccatcga	ctgggacaga	agcaccaaca	ccgcctacct	gcagctgagc	660
ggcctgacct	ctggcgatac	cgccgtgtac	tactgcgcca	agggcagcaa	gcaccggctg	720
agagactacg	ccctgtacga	cgatgacggc	gccctgaact	gggcccgtgga	tgtggactac	780
ctgagcaacc	tgggaattctg	gggccagggc	acagccgtga	ccgtgtcatc	tgataagacc	840
cacaccgctt	ccaccaaggg	cccacgtgtc	ttccccctgg	caccctcctc	caagagcacc	900
tctgggggca	cagcggccct	gggctgcctg	gtcaaggact	acttccccga	accggtgacg	960
gtgtcgtgga	actcaggcgc	cctgaccagc	ggcgtgcaca	ccttcccggc	tgtcctacag	1020
tcctcaggac	tctactccct	cagcagcgtg	gtgaccgtgc	cctccagcag	cttgggcacc	1080
cagacctaca	tctgcaacgt	gaatcacaag	cccagcaaca	ccaaggtgga	caagaaagt	1140
gagcccaaat	cttgtgacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaactcctg	1200
gggggaccgt	cagtcttcct	cttcccccca	aaacccaagg	acaccctcat	gatctcccgg	1260
acccttgagg	tcacatgcgt	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	1320
aactggtatg	ttgacggcgt	ggaggtgcat	aatgccaaaga	caaagccgcg	ggaggagcag	1380
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	1440
ggcaaggagt	acaagtgcaa	ggtctccaac	aaagccctcc	cagcccccat	cgagaaaacc	1500
atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatgccgg	1560
gatgagctga	ccaagaatca	agtcagcctg	tggtgcctgg	taaaaggctt	ctatcccagc	1620
gacatcgccg	tggagtgagg	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	1680
ccggtgctgg	actccgacgg	ctccttcttc	ctctactcaa	aactcaccgt	ggacaagagc	1740
aggtggcagc	aggggaacgt	cttctcatgc	tccgtgctgc	atgaggctct	gcacagccac	1800
tacacgcaga	agagcctctc	cctgtctccg	ggt			1833

<210> 224

<211> 1014

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 224

gacttcgtgc	tgacccagag	ccctcacagc	ctgagcgtga	cacctggcga	gagcgccagc	60
atcagctgca	agagcagcca	ctccctgatc	cacggcgacc	ggaacaacta	cctggcttgg	120
tacgtgcaga	agcccggcag	atccccccag	ctgctgatct	acctggccag	cagcagagcc	180
agcggcgctg	ccgatagatt	ttctggcagc	ggcagcgaca	aggacttcac	cctgaagatc	240
agccgggttg	aaaccgagga	cgtgggcacc	tactactgta	tgcagggcag	agagagcccc	300
tggacctttg	gccagggcac	caaggtggac	atcaaggaca	aaaccatac	cgcatccgaa	360
ctgactcagg	accctgccgt	ctctgtggca	ctgaagcaga	ctgtgactat	tacttgccga	420
ggcgactcac	tgcggagcca	ctacgcttcc	tggtatcaga	agaaaccggg	ccaggcacct	480
gtgctgctgt	tctacggaaa	gaacaatagg	ccatctggca	tccccgaccg	cttttctggc	540
agtgcatcag	ggaaccgagc	cagtctgacc	attaccggcg	cccaggctga	ggacgaagcc	600
gattactatt	gcagctcccc	ggataagagc	ggctccagac	tgagcgtgtt	cggaggagga	660
actaaactga	ccgtcctcga	taagacccat	accctgacgg	tggccgctcc	cagcgtgttc	720
atcttccac	ctagcgacga	gcagctgaag	tccggcacag	cctctgtcgt	gtgcctgctg	780
aacaacttct	acccccgcga	ggccaaagt	cagtgggaagg	tggacaacgc	cctgcagagc	840
ggcaacagcc	aggaaagcgt	gaccgagcag	gacagcaagg	actccaccta	cagcctgagc	900
agcaccctga	cactgagcaa	ggccgactac	gagaagcaca	aggtgtacgc	ctgcgaagtg	960
accaccaggg	gcctgtctag	ccccgtgacc	aagagcttca	accggggcga	gtgt	1014

4.__183952027041SEQLIST.TXT

<210> 225
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 225
 Arg Ala His Leu Val Gln Ser Gly Thr Ala Met Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Arg Val Ser Cys Gln Thr Ser Gly Tyr Thr Phe Thr Ala His
 20 25 30
 Ile Leu Phe Trp Phe Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
 35 40 45
 Gly Trp Ile Lys Pro Gln Tyr Gly Ala Val Asn Phe Gly Gly Gly Phe
 50 55 60
 Arg Asp Arg Val Thr Leu Thr Arg Asp Val Tyr Arg Glu Ile Ala Tyr
 65 70 75 80
 Met Asp Ile Arg Gly Leu Lys Pro Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Arg Ser Tyr Gly Asp Ser Ser Trp Ala Leu Asp Ala Trp
 100 105 110
 Gly Gln Gly Thr Thr Val Val Val Ser Ala Ala Ser Thr Lys Gly Pro
 115 120 125
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
 210 215 220
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 225 230 235 240
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 275 280 285
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 290 295 300
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 305 310 315 320
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 325 330 335

4._183952027041SEQLIST.TXT

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
340 345 350
Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
355 360 365
Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
370 375 380
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385 390 395 400
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
405 410 415
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430
Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445
Ser Pro Gly
450

<210> 226

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 226

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

195
 Glu Cys
 210

200
 205

<210> 227
 <211> 611
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 227

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

4. __183952027041SEQLIST.TXT

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
305 310 315 320
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
325 330 335
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
340 345 350
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
355 360 365
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
370 375 380
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
405 410 415
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
435 440 445
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
450 455 460
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
485 490 495
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510
Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
515 520 525
Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
565 570 575
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590
Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605
Ser Pro Gly
610

<210> 228

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 228

Asp Phe Val Leu Thr Gln Ser Pro His Ser Leu Ser Val Thr Pro Gly

4.__183952027041SEQLIST.TXT

1	5	10	15
Glu Ser Ala Ser Ile Ser Cys Lys Ser Ser His Ser Leu Ile His Gly			
20	25	30	
Asp Arg Asn Asn Tyr Leu Ala Trp Tyr Val Gln Lys Pro Gly Arg Ser			
35	40	45	
Pro Gln Leu Leu Ile Tyr Leu Ala Ser Ser Arg Ala Ser Gly Val Pro			
50	55	60	
Asp Arg Phe Ser Gly Ser Gly Ser Asp Lys Asp Phe Thr Leu Lys Ile			
65	70	75	80
Ser Arg Val Glu Thr Glu Asp Val Gly Thr Tyr Tyr Cys Met Gln Gly			
85	90	95	
Arg Glu Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys			
100	105	110	
Asp Lys Thr His Thr Ala Ser Glu Leu Thr Gln Asp Pro Ala Val Ser			
115	120	125	
Val Ala Leu Lys Gln Thr Val Thr Ile Thr Cys Arg Gly Asp Ser Leu			
130	135	140	
Arg Ser His Tyr Ala Ser Trp Tyr Gln Lys Lys Pro Gly Gln Ala Pro			
145	150	155	160
Val Leu Leu Phe Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp			
165	170	175	
Arg Phe Ser Gly Ser Ala Ser Gly Asn Arg Ala Ser Leu Thr Ile Thr			
180	185	190	
Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Arg Asp			
195	200	205	
Lys Ser Gly Ser Arg Leu Ser Val Phe Gly Gly Gly Thr Lys Leu Thr			
210	215	220	
Val Leu Asp Lys Thr His Thr Arg Thr Val Ala Ala Pro Ser Val Phe			
225	230	235	240
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val			
245	250	255	
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp			
260	265	270	
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr			
275	280	285	
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr			
290	295	300	
Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val			
305	310	315	320
Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly			
325	330	335	

Glu Cys

<210> 229

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

4. __183952027041SEQLIST.TXT

<400> 229

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agagcccacc tgggtgcagtc tggcaccgcc atgaagaaac caggcgccctc tgtgcgggtg 60
tcctgtcaga caagcggcta caccttcacc gccacatcc tgttctgggt ccggcaggcc 120
cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
ggcggaggct tccgggatat agtgaccctg acccgggacg tgtaccgca gatcgccctac 240
atggacatcc ggggcctgaa gcccgatgac accgccgtgt actactgcgc cagagacaga 300
agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtgggtggg 360
tctgccgcct ctacaaaggg cccagcgtg ttccctctgg cccttagcag caagagcaca 420
tctggcggaa cagccgccct gggctgcctc gtgaaggact actttcccga gcccgtagacc 480
gtgtcctgga attctggcgc cctgaccagc ggcgtgcaca cttttccagc tgtgctgcag 540
tccagcggcc tgtacagcct gagcagcgtc gtgacagtgc ccagcagctc tctgggcacc 600
cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagaagggtg 660
gaacccaaga gctgcgacaa gaccacacc tgtccccctt gtcctgcccc cgaactgctg 720
ggaggccctt ccgtgttcct gttcccccca aagcccaagg acaccctgat gatcagccgg 780
acccccgaag tgacctgcgt ggtggtggat gtgtcccacg aggaccctga agtgaagttc 840
aattgggtacg tggacggcgt ggaagtgcac aacgccaaga ccaagccaag agaggaacag 900
tacaacagca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ctggctgaac 960
ggcaaagagt acaagtgcaa ggtgtccaac aaggccctgc ctgcccccat cgagaaaacc 1020
atcagcaagg ccaagggcc accccgcgaa cccaggtgt gcacactgcc cccaagcagg 1080
gacgagctga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccctcc 1140
gatatcgccg tggaatggga gagcaacggc cagcccgaga acaactacaa gaccaccccc 1200
cctgtgctgg acagcgacgg ctcatcttc ctggtgtcca agctgacagt ggacaagttc 1260
cgggtggcagc agggcaacgt gttcagctgc tccgtgctgc acgaggccct gcacagccac 1320
tacaccaga agtccctgag cctgagcccc ggc 1353

```

<210> 230

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 230

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tacatccacg tgacccagag cccagcagc ctgtccgtgt ccatcggcga cagagtgacc 60
atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgc cgtgcccagc 180
agattttccg gcagcggctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630

```

<210> 231

<211> 1833

<212> DNA

<213> Artificial Sequence

4.__183952027041SEQLIST.TXT

<220>

<223> Synthetic Construct

<400> 231

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gaggtttagac tgggtggagtc aggagggggg cttgtgaagc ccggtgggtc tctccgcctg 60
agctgttctg cctccggctt tgatttcgat aacgcctgga tgacctgggt caggcagcct 120
ccaggtaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctggtccgtg 180
gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
ttgtattttg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
acaggcaaat actacgactt ctggtccggc tatccccctg gcgaggaata ttttcaagac 360
tggggtcagg gaacccttgt tatcgtgtcc tccgacaaaa cccataccca ggtgcacctg 420
acacagagcg gacccgaagt gcggaagcct ggcacctctg tgaaggtgtc ctgcaaggcc 480
cctggcaaca ccctgaaaac ctacgacctg cactgggtgc gcagcgtgcc aggacaggga 540
ctgcagtgga tgggctggat cagccacgag ggcgacaaga aagtgatcgt ggaacggttc 600
aaggccaaag tgaccatcga ctgggacaga agcaccaaca ccgcctacct gcagctgagc 660
ggcctgacct ctggcgatac cgccgtgtac tactgcgcca agggcagcaa gcaccggctg 720
agagactacg ccctgtacga cgatgacggc gccctgaact gggccgtgga tgtggactac 780
ctgagcaacc tggaattctg gggccagggc acagccgtga ccgtgtcatc tgataagacc 840
cacaccgctt ccaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc 900
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 960
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag 1020
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 1080
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagt 1140
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 1200
gggggaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctcccgg 1260
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagt 1320
aactggtatg ttgacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1500
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatgccgg 1560
gatgagctga ccaagaatca agtcagcctg tgggtgcctgg taaaaggctt ctatcccagc 1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1680
cccgtgctgg actccgacgg ctcttcttc ctctactcaa aactcaccgt ggacaagagc 1740
aggtggcagc aggggaacgt cttctcatgc tccgtgctgc atgaggctct gcacagccac 1800
tacacgcaga agagcctctc cctgtctccg ggt 1833

```

<210> 232

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 232

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Arg Ala His Leu Val Gln Ser Gly Thr Ala Met Lys Lys Pro Gly Ala
 1           5           10          15
Ser Val Arg Val Ser Cys Gln Thr Ser Gly Tyr Thr Phe Thr Ala His
          20          25          30
Ile Leu Phe Trp Phe Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
          35          40          45
Gly Trp Ile Lys Pro Gln Tyr Gly Ala Val Asn Phe Gly Gly Gly Phe

```


60

[illegible]

4.___183952027041SEQLIST.TXT

<210> 233
 <211> 210
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 233
 Tyr Ile His Val Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ile Gly
 1 5 10 15
 Asp Arg Val Thr Ile Asn Cys Gln Thr Ser Gln Gly Val Gly Ser Asp
 20 25 30
 Leu His Trp Tyr Gln His Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
 35 40 45
 His His Thr Ser Ser Val Glu Glu Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Phe His Thr Ser Phe Gln Leu Thr Ile Ser Asp Leu Gln Ala
 65 70 75 80
 Asp Asp Ile Ala Thr Tyr Tyr Cys Gln Val Leu Gln Phe Phe Gly Arg
 85 90 95
 Gly Ser Arg Leu His Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
 100 105 110
 Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
 115 120 125
 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
 130 135 140
 Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
 145 150 155 160
 Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
 165 170 175
 Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
 180 185 190
 Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
 195 200 205
 Glu Cys
 210

<210> 234
 <211> 611
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 234
 Glu Val Arg Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Asp Asn Ala

4. 183952027041SEQLIST.TXT

				20				25					30		
Trp	Met	Thr	Trp	Val	Arg	Gln	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40				45				
Gly	Arg	Ile	Thr	Gly	Pro	Gly	Glu	Gly	Trp	Ser	Val	Asp	Tyr	Ala	Glu
	50					55					60				
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Thr	Lys	Asn	Thr
65					70					75				80	
Leu	Tyr	Leu	Glu	Met	Asn	Asn	Val	Arg	Thr	Glu	Asp	Thr	Gly	Tyr	Tyr
				85						90				95	
Phe	Cys	Ala	Arg	Thr	Gly	Lys	Tyr	Tyr	Asp	Phe	Trp	Ser	Gly	Tyr	Pro
			100						105				110		
Pro	Gly	Glu	Glu	Tyr	Phe	Gln	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Ile
		115					120					125			
Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Gln	Val	His	Leu	Thr	Gln	Ser	Gly
	130					135					140				
Pro	Glu	Val	Arg	Lys	Pro	Gly	Thr	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala
145					150					155					160
Pro	Gly	Asn	Thr	Leu	Lys	Thr	Tyr	Asp	Leu	His	Trp	Val	Arg	Ser	Val
				165					170				175		
Pro	Gly	Gln	Gly	Leu	Gln	Trp	Met	Gly	Trp	Ile	Ser	His	Glu	Gly	Asp
			180					185					190		
Lys	Lys	Val	Ile	Val	Glu	Arg	Phe	Lys	Ala	Lys	Val	Thr	Ile	Asp	Trp
		195					200					205			
Asp	Arg	Ser	Thr	Asn	Thr	Ala	Tyr	Leu	Gln	Leu	Ser	Gly	Leu	Thr	Ser
	210					215					220				
Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Gly	Ser	Lys	His	Arg	Leu
225					230					235					240
Arg	Asp	Tyr	Ala	Leu	Tyr	Asp	Asp	Asp	Gly	Ala	Leu	Asn	Trp	Ala	Val
				245					250				255		
Asp	Val	Asp	Tyr	Leu	Ser	Asn	Leu	Glu	Phe	Trp	Gly	Gln	Gly	Thr	Ala
			260					265					270		
Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Ala	Ser	Thr	Lys	Gly	Pro
		275					280					285			
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
	290					295					300				
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
305					310					315					320
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
				325					330					335	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
			340					345					350		
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
		355					360					365			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser
	370					375									

4._183952027041SEQLIST.TXT

```

      435              440              445
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
      450              455              460
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465              470              475              480
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
      485              490              495
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
      500              505              510
Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
      515              520              525
Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
      530              535              540
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545              550              555              560
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
      565              570              575
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
      580              585              590
Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu
      595              600              605
Ser Pro Gly
      610

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<210> 235

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 235

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

```

4._183952027041SEQLIST.TXT

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

<210> 236
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 236
agagcccacc tgggtgcagtc tggcaccgcc atgaagaaac caggcgcctc tgtgcgggtg 60
tcctgtcaga caagcggcta caccctcacc gccacatcc tgttcttggt ccggcaggcc 120
cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
ggcggaggct tccgggatag agtgaccctg acccgggacg tgtaccgca gatcgctac 240
atggacatcc ggggcctgaa gcccgatgac accgccgtgt actactgcgc cagagacaga 300
agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtggtggtg 360
tctgccgcct ctacaaaggg cccagcgtg ttccctctgg ccctagcag caagagcaca 420
tctggcggaa cagccgccct gggctgcctc gtgaaggact actttcccga gcccgtagacc 480
gtgtcctgga attctggcgc cctgaccagc ggcgtgcaca cttttccagc tgtgctgcag 540
tccagcggcc tgtacagcct gagcagcgtc gtgacagtgc ccagcagctc tctgggcacc 600
cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagaagggtg 660
gaacccaaga gctgcgacaa gaccacacc tgtccccctt gtcctgcccc cgaactgctg 720
ggaggccctt ccgtgttcct gttccccca aagcccaagg acaccctgat gatcagccgg 780
acccccgaag tgacctgcgt ggtggtggat gtgtccacg aggaccctga agtgaagttc 840
aattggtacg tggacggcgt ggaagtgcac aacgccaaga ccaagccaag agaggaacag 900

4. __183952027041SEQLIST.TXT

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tacaacagca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ctggctgaac 960
ggcaaagagt acaagtgcaa ggtgtccaac aaggccctgc ctgcccccat cgagaaaacc 1020
atcagcaagg ccaagggccca gccccgcgaa cccaggtgtg gcacactgcc cccaagcagg 1080
gacgagctga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccctcc 1140
gatatcgccg tggaatggga gagcaacggc cagcccagaga acaactacaa gaccaccccc 1200
cctgtgctgg acagcgacgg ctcatcttc ctggtgtcca agctgacagt ggacaagtcc 1260
cgggtggcagc agggcaacgt gttcagctgc tccgtgctgc acgaggccct gcacagccac 1320
tacaccaga agtccctgag cctgagcccc ggc 1353
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<210> 237

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 237

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tacatccacg tgacccagag ccccagcagc ctgtccgtgt ccatcggcga cagagtgacc 60
atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagaagg cgtgcccagc 180
agatthttccg gcagcggtt ccacaccagc ttccagctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630
```

<210> 238

<211> 1833

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 238

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gaggttagac tggtggagtc aggagggggg cttgtgaagc ccggtgggtc tctccgcctg 60
agctgttctg cctccggctt tgatttcgat aacgcctgga tgacctgggt caggcagcct 120
ccaggtaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctggtccgtg 180
gactacgcgg aatctgttaa agggcggttt acaatctcaa gggacaatac caagaatacc 240
ttgtatttgg agatgaacaa cgtgagaact gaagacaccg gatattactt ctgtgccaga 300
acaggcaaat actacgactt ctggtccggc tatccccctg gcgaggaata ttttcaagac 360
tggggtcagg gaaccttgt tatcgtgtcc tccgacaaaa cccataccca ggtgcacctg 420
acacagagcg gacccgaagt gcggaagcct ggcacctctg tgaagggtgc ctgcaaggcc 480
cctggcaaca ccctgaaaac ctacgacctg cactgggtgc gcagcgtgcc aggacaggga 540
ctgcagtgga tgggctggat cagccacgag ggcgacaaga aagtgatcgt ggaacggttc 600
aaggccaaag tgaccatcga ctgggacaga agcaccaaca ccgcctacct gcagctgagc 660
ggcctgacct ctggcgatac cgccgtgtac tactgcgcca agggcagcaa gcaccggctg 720
agagactacg ccctgtacga cgatgacggc gccctgaact gggccgtgga tgtggactac 780
```

4. __183952027041SEQLIST.TXT

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ctgagcaacc  tggaattctg  gggccagggc  acagccgtga  ccgtgtcatc  tgataagacc  840
cacaccgctt  ccaccaaggg  cccatcggtc  ttccccctgg  caccctcctc  caagagcacc  900
tctggggggc  cagcggccct  gggctgcctg  gtcaaggact  acttccccga  accggtgacg  960
gtgtcgtgga  actcaggcgc  cctgaccagc  ggcgtgcaca  ccttcccggc  tgtcctacag  1020
tcctcaggac  tctactccct  cagcagcgtg  gtgaccgtgc  cctccagcag  cttgggcacc  1080
cagacctaca  tctgcaacgt  gaatcacaag  cccagcaaca  ccaaggtgga  caagaaagtt  1140
gagcccaaatt  cttgtgacaa  aactcacaca  tgcccaccgt  gccagcacc  tgaactcctg  1200
gggggaccgt  cagtcttcct  cttcccccca  aaaccaagg  acaccctcat  gatctcccgg  1260
acccttgagg  tcacatgcgt  ggtggtggac  gtgagccacg  aagaccctga  ggtcaagttc  1320
aactggtatg  ttgacggcgt  ggaggtgcat  aatgccaaaga  caaagccgcg  ggaggagcag  1380
tacaacagca  cgtaccgtgt  ggtcagcgtc  ctcaccgtcc  tgcaccagga  ctggctgaat  1440
ggcaaggagt  acaagtgcaa  ggtctccaac  aaagccctcc  cagcccccat  cgagaaaacc  1500
atctccaaag  ccaaagggca  gccccgagaa  ccacaggtgt  acaccctgcc  cccatgccgg  1560
gatgagctga  ccaagaatca  agtcagcctg  tggcgcctgg  taaaaggctt  ctatcccagc  1620
gacatcgccg  tggagtggga  gagcaatggg  cagccggaga  acaactacaa  gaccacgcct  1680
cccgtgctgg  actccgacgg  ctcttcttct  ctctactcaa  aactcaccgt  ggacaagagc  1740
aggtggcagc  aggggaacgt  cttctcatgc  tccgtgctgc  atgaggctct  gcacagccac  1800
tacacgcaga  agagcctctc  cctgtctccg  ggt  1833

```

<210> 239

<211> 1014

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 239

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gacttcgtgc  tgaccagag  ccctcacagc  ctgagcgtga  cacctggcga  gagcgccagc  60
atcagctgca  agagcagcca  ctccctgatc  cagggcgacc  ggaacaacta  cctggcttgg  120
tacgtgcaga  agcccggcag  atccccccag  ctgctgatct  acctggccag  cagcagagcc  180
agcggcgtgc  ccgatagatt  ttctggcagc  ggcagcgaca  aggacttcac  cctgaagatc  240
agccgggtgg  aaaccgagga  cgtgggcacc  tactactgta  tgcagggcag  agagagcccc  300
tggacctttg  gccagggcac  caaggtggac  atcaaggaca  aaaccatac  cgcattccgaa  360
ctgactcagg  accctgccgt  ctctgtggca  ctgaagcaga  ctgtgactat  tacttgccga  420
ggcgactcac  tgcggagcca  ctacgcttcc  tggatatcaga  agaaaccgg  ccaggcacct  480
gtgctgctgt  tctacggaaa  gaacaatagg  ccatctggca  tccccgaccg  cttttctggc  540
agtgcacag  ggaaccgagc  cagtctgacc  attaccggcg  cccaggctga  ggacgaagcc  600
gattactatt  gcagctcccg  ggataagagc  ggctccagac  tgagcgtgtt  cggaggagga  660
actaaactga  ccgtcctcga  taagacccat  acccgtagcg  tggccgctcc  cagcgtgttc  720
atcttccac  ctacgacga  gcagctgaag  tccggcacag  cctctgtcgt  gtgcctgctg  780
aacaacttct  accccgcga  ggccaaagt  cagtgggaag  tggacaacgc  cctgcagagc  840
ggcaacagcc  aggaaagcgt  gaccgagcag  gacagcaagg  actccaccta  cagcctgagc  900
agcaccctga  cactgagcaa  ggccgactac  gagaagcaca  aggtgtacgc  ctgcgaagt  960
accaccagg  gcctgtctag  ccccgtagc  aagagcttca  accggggcga  gtgt  1014

```

<210> 240

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

4.__183952027041SEQLIST.TXT

<223> Synthetic Construct

<400> 240

Arg	Ala	His	Leu	Val	Gln	Ser	Gly	Thr	Ala	Met	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Arg	Val	Ser	Cys	Gln	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Ala	His
			20					25					30		
Ile	Leu	Phe	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Val
		35					40					45			
Gly	Trp	Ile	Lys	Pro	Gln	Tyr	Gly	Ala	Val	Asn	Phe	Gly	Gly	Gly	Phe
	50					55				60					
Arg	Asp	Arg	Val	Thr	Leu	Thr	Arg	Asp	Val	Tyr	Arg	Glu	Ile	Ala	Tyr
65					70				75						80
Met	Asp	Ile	Arg	Gly	Leu	Lys	Pro	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Asp	Arg	Ser	Tyr	Gly	Asp	Ser	Ser	Trp	Ala	Leu	Asp	Ala	Trp
			100					105					110		
Gly	Gln	Gly	Thr	Thr	Val	Val	Val	Ser	Ala	Ala	Ser	Thr	Lys	Gly	Pro
		115					120					125			
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
	130					135					140				
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
145					150				155						160
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
			165						170					175	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
			180					185					190		
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
	195						200					205			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser
	210					215					220				
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
225					230				235						240
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
			245						250					255	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
		260						265					270		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
		275					280					285			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
	290					295					300				
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
305					310					315					320
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro
			325						330					335	
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
			340					345					350		
Val	Cys	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val
		355					360					365			
Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val
	370					375					380				
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro

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```

385          390          395          400
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr
          405          410          415
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
          420          425          430
Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu
          435          440          445
Ser Pro Gly
          450

```

<210> 241
 <211> 210
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

```

<400> 241
Tyr Ile His Val Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ile Gly
 1          5          10          15
Asp Arg Val Thr Ile Asn Cys Gln Thr Ser Gln Gly Val Gly Ser Asp
          20          25          30
Leu His Trp Tyr Gln His Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
          35          40          45
His His Thr Ser Ser Val Glu Asp Ala Val Pro Ser Arg Phe Ser Gly
          50          55          60
Ser Gly Phe His Thr Ser Phe Gln Leu Thr Ile Ser Asp Leu Gln Ala
65          70          75          80
Asp Asp Ile Ala Thr Tyr Tyr Cys Gln Val Leu Gln Phe Phe Gly Arg
          85          90          95
Gly Ser Arg Leu His Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
          100          105          110
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
          115          120          125
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
          130          135          140
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
145          150          155          160
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
          165          170          175
Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
          180          185          190
Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
          195          200          205
Glu Cys
          210

```

<210> 242
 <211> 611

4.__183952027041SEQLIST.TXT

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 242

Glu	Val	Arg	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	Pro	Gly	Gly	1	5	10	15
Ser	Leu	Arg	Leu	Ser	Cys	Ser	Ala	Ser	Gly	Phe	Asp	Phe	Asp	Asn	Ala	20	25	30	
Trp	Met	Thr	Trp	Val	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	35	40	45	
Gly	Arg	Ile	Thr	Gly	Pro	Gly	Glu	Gly	Trp	Ser	Val	Asp	Tyr	Ala	Glu	50	55	60	
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Thr	Lys	Asn	Thr	65	70	75	80
Leu	Tyr	Leu	Glu	Met	Asn	Asn	Val	Arg	Thr	Glu	Asp	Thr	Gly	Tyr	Tyr	85	90	95	
Phe	Cys	Ala	Arg	Thr	Gly	Lys	Tyr	Tyr	Asp	Phe	Trp	Ser	Gly	Tyr	Pro	100	105	110	
Pro	Gly	Glu	Glu	Tyr	Phe	Gln	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val	Ile	115	120	125	
Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Gln	Val	His	Leu	Thr	Gln	Ser	Gly	130	135	140	
Pro	Glu	Val	Arg	Lys	Pro	Gly	Thr	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	145	150	155	160
Pro	Gly	Asn	Thr	Leu	Lys	Thr	Tyr	Asp	Leu	His	Trp	Val	Arg	Ser	Val	165	170	175	
Pro	Gly	Gln	Gly	Leu	Gln	Trp	Met	Gly	Trp	Ile	Ser	His	Glu	Gly	Asp	180	185	190	
Lys	Lys	Val	Ile	Val	Glu	Arg	Phe	Lys	Ala	Lys	Val	Thr	Ile	Asp	Trp	195	200	205	
Asp	Arg	Ser	Thr	Asn	Thr	Ala	Tyr	Leu	Gln	Leu	Ser	Gly	Leu	Thr	Ser	210	215	220	
Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Gly	Ser	Lys	His	Arg	Leu	225	230	235	240
Arg	Asp	Tyr	Ala	Leu	Tyr	Asp	Asp	Asp	Gly	Ala	Leu	Asn	Trp	Ala	Val	245	250	255	
Asp	Val	Asp	Tyr	Leu	Ser	Asn	Leu	Glu	Phe	Trp	Gly	Gln	Gly	Thr	Ala	260	265	270	
Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Ala	Ser	Thr	Lys	Gly	Pro	275	280	285	
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	290	295	300	
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	305	310	315	320
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	325	330	335	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	340	345	350	
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn				

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```

      355      360      365
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
      370      375      380
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385      390      395      400
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
      405      410      415
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
      420      425      430
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
      435      440      445
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
      450      455      460
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465      470      475      480
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
      485      490      495
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
      500      505      510
Val Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val
      515      520      525
Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
      530      535      540
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545      550      555      560
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
      565      570      575
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
      580      585      590
Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu
      595      600      605
Ser Pro Gly
      610

```

<210> 243

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 243

```

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

```

4. __183952027041SEQLIST.TXT

```

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

```

<210> 244

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 244

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agagcccacc tgggtgcagtc tggcaccgcc atgaagaaac caggcgcctc tgtgcgggtg 60
tcctgtcaga caagcggcta caccttcacc gccacatcc tgttctgggt cgcgcaggcc 120
cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
ggcggaggct tccgggatag agtgaccctg acccgggacg tgtaccgcga gatcgacctac 240
atggacatcc ggggcctgaa gcccgatgac accgccgtgt actactgcgc cagagacaga 300

```

4. __183952027041SEQLIST.TXT

```

agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtgggtgggtg 360
tctgccgcct ctacaaaggg ccccagcgtg ttccctctgg cccctagcag caagagcaca 420
tctggcggaa cagccgccct gggctgcctc gtgaaggact actttcccga gcccgtagacc 480
gtgtcctgga attctggcgc cctgaccagc ggcgtgcaca cttttccagc tgtgctgcag 540
tccagcggcc tgtacagcct gagcagcgtc gtgacagtgc ccagcagctc tctgggcacc 600
cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagaagggtg 660
gaacccaaga gctgcgacaa gaccacacc tgtccccctt gtcctgcccc cgaactgctg 720
ggaggccctt ccgtgttcct gttcccccca aagcccaagg acaccctgat gatcagccgg 780
acccccgaag tgacctgcgt ggtgggtggat gtgtcccacg aggaccctga agtgaagtgc 840
aattggtacg tggacggcgt ggaagtgcac aacgccaaga ccaagccaag agaggaacag 900
tacaacagca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ctggctgaac 960
ggcaaagagt acaagtgcaa ggtgtccaac aaggccctgc ctgcccccat cgagaaaacc 1020
atcagcaagg ccaaggcca gccccgcgaa cccaggtgt gcacactgcc cccaagcagg 1080
gacgagctga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccctcc 1140
gatatcgccg tggaatggga gagcaacggc cagcccgaga acaactaaa gaccaccccc 1200
cctgtgctgg acagcgacgg ctcatcttc ctggtgtcca agctgacagt ggacaagtcc 1260
cggtggcagc agggcaacgt gttcagctgc tccgtgctgc acgaggccct gcacagccac 1320
tacaccaga agtccctgag cctgagcccc ggc 1353

```

<210> 245

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 245

```

tacatccacg tgaccagag ccccagcagc ctgtccgtgt ccatcggcga cagagtgacc 60
atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgc cgtgcccagc 180
agattttccg gcagcggctt ccacaccagc ttccagctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcagggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacgggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtgt 630

```

<210> 246

<211> 1833

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 246

```

gaggttagac tgggtggagtc aggagggggg cttgtgaagc ccggtgggtc tctccgcctg 60
agctgttctg cctccggctt tgatttcgat aacgcctgga tgacctgggt caggcagcct 120
ccaggtaagg gactggagtg ggtgggaaga atcacaggtc caggcgaggg ctggtccgtg 180

```

4. __183952027041SEQLIST.TXT

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<211> 17

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

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Gly Lys Asn Cys Asp Tyr Asn Trp Asp Phe Glu His

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Gly Tyr Thr Phe Thr Ala His Ile

1 5

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Ile Lys Pro Gln Tyr Gly Ala Val

1 5

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Asp Arg Ser Tyr Gly Asp Ser Ser Trp Ala Leu Asp Ala

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Gly Phe Asp Phe Asp Asn Ala Trp

1 5

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Ile Thr Gly Pro Gly Glu Gly Trp Ser Val
1 5 10

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Thr Gly Lys Tyr Tyr Asp Phe Trp Ser Gly Tyr Pro Pro Gly Glu Glu
1 5 10 15
Tyr Phe Gln Asp
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Gly Asn Thr Leu Lys Thr Tyr Asp
1 5

<210> 258

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<400> 258

Ile Ser His Glu Gly Asp Lys Lys
1 5

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Cys	Ala	Lys	Gly	Ser	Lys	His	Arg	Leu	Arg	Asp	Tyr	Ala	Leu	Tyr	Asp
1				5				10					15		
Asp	Asp	Gly	Ala	Leu	Asn	Trp	Ala	Val	Asp	Val	Asp	Tyr	Leu	Ser	Asn
		20						25					30		
Leu	Glu	Phe	Trp												
		35													

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<400> 260

Ser	Gly	Ala	Ser	Ile	Ser	Asp	Ser	Tyr
1				5				

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Val	His	Lys	Ser	Gly	Asp	Thr
1				5		

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<400> 262

Ala	Arg	Thr	Leu	His	Gly	Arg	Arg	Ile	Tyr	Gly	Ile	Val	Ala	Phe	Asn
1				5				10						15	
Glu	Trp	Phe	Thr	Tyr	Phe	Tyr	Met	Asp	Val						
			20					25							

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 Gln Phe Arg Phe Asp Gly Tyr Gly
 1 5

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<400> 264
 Ile Ser His Asp Gly Ile Lys Lys
 1 5

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<220>
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<400> 265
 Cys Ala Lys Asp Leu Arg Glu Asp Glu Cys Glu Glu Trp Trp Ser Asp
 1 5 10 15
 Tyr Tyr Asp Phe Gly Lys Gln Leu Pro Cys Ala Lys Ser Arg Gly Gly
 20 25 30
 Leu Val Gly Ile Ala Asp Asn Trp
 35 40

<210> 266
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Arg Thr Ser Gln Tyr Gly Ser Leu Ala
1 5

<210> 267

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Ser Gly Ser Thr Arg Ala Ala
1 5

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<400> 268

Gln Gln Tyr Glu Phe
1 5

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<400> 269

Gln Gly Val Gly Ser Asp
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His Thr Ser
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Gln Val Leu Gln Phe
1 5

<210> 272
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<400> 272
Arg Gly Asp Ser Leu Arg Ser His Tyr Ala Ser
1 5 10

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<400> 273
Gly Lys Asn Asn Arg Pro Ser
1 5

<210> 274
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Ser Ser Arg Asp Lys Ser Gly Ser Arg Leu Ser Val
1 5 10

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<400> 275

His Ser Leu Ile His Gly Asp Arg Asn Asn Tyr
1 5 10

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Leu Ala Ser
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Cys Met Gln Gly Arg Glu Ser Pro Trp Thr Phe
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Ser Leu Gly Ser Arg Ala
1 5

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Asn Asn Gln
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His Ile Trp Asp Ser Arg Val Pro Thr Lys Trp Val
1 5 10

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<400> 281

Thr Ser Asn Ile Gly Asn Asn Phe
1 5

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Glu Thr Asp
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<400> 283
Ala Thr Trp Ala Ala Ser Leu Ser Ser Ala Arg Val
1 5 10

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<400> 284
Arg Arg Arg Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser
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Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu Trp Tyr Ile Arg Arg
20 25 30
Arg

<210> 285
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Gly Gly Gly Gly
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Gly Gly Gly Gly Gly
1 5

<210> 287

<211> 6

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Gly Gly Gly Gly Gly Gly
1 5

<210> 288

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<400> 288

Gly Gly Gly Gly Gly Gly Gly
1 5

<210> 289

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Gly Gly Gly Gly Gly Gly Gly Gly
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<210> 290

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Gly Gly Gly Gly Ser
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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
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Thr Lys Gly Pro Ser
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<400> 294

Thr Val Ala Ala Pro

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<210> 295

<211> 5

<212> PRT

<213> Artificial Sequence

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Gln Pro Lys Ala Ala

1 5

<210> 296

<211> 5

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<223> Synthetic Construct

<400> 296

Gln Arg Ile Glu Gly

1 5

<210> 297

<211> 7

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<400> 297

Ala Ser Thr Lys Gly Pro Ser

1 5

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<211> 7

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<220>

<223> Synthetic Construct

<400> 298

Arg Thr Val Ala Ala Pro Ser
1 5

<210> 299

<211> 7

<212> PRT

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<400> 299

Gly Gln Pro Lys Ala Ala Pro
1 5

<210> 300

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His Ile Asp Ser Pro Asn Lys
1 5

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<211> 449

<212> PRT

<213> Artificial Sequence

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<223> Synthetic Construct

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

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[illegible]

<210> 303

$\langle 211 \rangle$ 210

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 303

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

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Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
  130                135                140
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
145                150                155                160
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
                165                170                175
Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
                180                185                190
Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
                195                200                205
Glu Cys
  210

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<210> 304

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<212> PRT

<213> Artificial Sequence

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<400> 304

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

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4.___183952027041SEQLIST.TXT

225					230					235				240
Ser	Ser	Arg	Thr	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu
				245					250					255
Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys
			260					265					270	
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser
		275					280					285		
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser
	290					295					300			
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser
305					310					315				320
Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn
			325						330					335
Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro
		340						345					350	
Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
		355					360					365		
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
	370					375					380			
Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe
385				390					395					400
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
			405						410					415
Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
			420					425					430	
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
		435					440					445		
Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
	450				455						460			
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Cys	Thr	Leu	Pro	Pro	Ser	Gln
465				470						475				480
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly
			485						490					495
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
			500					505					510	
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
	515					520						525		
Phe	Leu	Val	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu
	530					535					540			
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
545				550					555					560
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys				
			565						570					

<210> 305

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

4.___183952027041SEQLIST.TXT

<400> 305

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Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1           5           10           15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Gln Ser Leu Val His Asn
 20           25           30
Asn Ala Asn Thr Tyr Leu Ser Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35           40           45
Pro Gln Ser Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50           55           60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65           70           75           80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gly Gln Gly
 85           90           95
Thr Gln Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys
 100          105          110
Gly Gln Pro Lys Ala Ala Pro Asp Ile Gln Met Thr Gln Ser Pro Ser
 115          120          125
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala
 130          135          140
Ser Gln Asn Ile Tyr Val Trp Leu Asn Trp Tyr Gln Gln Lys Pro Gly
 145          150          155          160
Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Asn Leu His Thr Gly
 165          170          175
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 180          185          190
Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln
 195          200          205
Gln Gly Gln Thr Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu
 210          215          220
Ile Lys Thr Lys Gly Pro Ser Arg Thr Val Ala Ala Pro Ser Val Phe
 225          230          235          240
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
 245          250          255
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
 260          265          270
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
 275          280          285
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
 290          295          300
Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
 305          310          315          320
Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
 325          330          335
Glu Cys

```

<210> 306

<211> 1347

<212> DNA

<213> Artificial Sequence

4.__183952027041SEQLIST.TXT

<220>

<223> Synthetic Construct

<400> 306

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agagcccacc tgggtgcagtc tggcaccgcc atgaagaaac caggcgcctc tgtgctgggtg 60
tcctgtcaga caagcggcta caccttcacc gccacatcc tgttcttggtt ccggcaggcc 120
cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
ggcggaggct tccgggatag agtgaccctg acccgggacg tgtaccgcga gatcgacctac 240
atggacatcc ggggcctgaa gcccgatgac accgccgtgt actactgcgc cagagacaga 300
agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtggtgggtg 360
tctgccgcct ctacaaaggg cccctcgggtg ttccctctgg ccccttgtag cagaagcacc 420
agcgaatcta cagccgccct gggctgcctc gtgaaggact actttcccga gcccgtagacc 480
gtgtcctgga actctggcgc tctgacaagc ggctgtgcaca cctttccagc cgtgctccag 540
agcagcggcc tgtactctct gagcagcgtc gtgacagtgc ccagcagcag cctgggcacc 600
aagacctaca cctgtaacgt ggaccacaag cccagcaaca ccaaggtgga caagcgggtg 660
gaatctaagt acggccctcc ctgccctcct tgcccagccc ctgaatttct gggcggaccc 720
tccgtgttcc tgttcccccc aaagcccaag gacaccctga tgatcagccg gacccccgaa 780
gtgacctgcg tgggtggtgga tgtgtcccag gaagatcccg aggtgcagtt caattggtac 840
gtggacggcg tggaagtgca caacgccaag accaagccca gagaggaaca gttcaacagc 900
acctaccggg tgggtgtccgt gctgaccgtg ctgcaccagg actggctgaa cggcaaagag 960
tacaagtgca aggtgtccaa caagggcctg cccagctcca tcgagaaaac catcagcaag 1020
gccaaaggcc agccccgcga gcctcaagtg tataccctgc ccccttgcca ggaagagatg 1080
accaagaacc aggtgtccct gtggtgtctc gtgaaaggct tctaccccag cgacattgcc 1140
gtggaatggg agagcaacgg ccagcccag aacaactaca agaccacccc ccctgtgctg 1200
gacagcgacg gctcattctt cctgtactcc aagctgaccg tggacaagag ccggtggcag 1260
gaaggcaacg tgttcagctg ctccgtgatg cacgaggccc tgcacaacca ctacaccag 1320
aagtccctgt ctctgtccct gggcaag 1347

```

<210> 307

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 307

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tacatccacg tgaccagag cccagcagc ctgtccgtgt ccatcggcga cagagtgacc 60
atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgccagc 180
agattttccg gcagcggctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaaggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacc accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcagtggt 630

```

<210> 308

<211> 1713

4.__183952027041SEQLIST.TXT

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 308

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caggtgcagc tgggtgcagtc tggcgccgag gtcgtgaaac ctggcgcctc tgtgaagggtg 60
tcctgcaagg ccagcggcta caccctttacc agctactaca tccactgggt gcgccaggcc 120
cctggacagg gactggaatg gatcggcagc atctaccccc gcaacgtgaa caccaactac 180
gcccagaagt tccagggcag agccaccctg accgtggaca ccagcatcag caccgcctac 240
atggaactga gccggctgag aagcgacgac accgccgtgt actactgcac ccggtccac 300
tacggcctgg attggaactt cgacgtgtgg ggcaagggca ccaccgtgac agtgtctagc 360
agccagggtgc agctgggtgga atctggcggc ggagtgggtgc agcctggcag aagcctgaga 420
ctgagctgtg ccgccagcgg cttcaccttc accaaggcct ggatgcactg ggtgcgccag 480
gcccctggaa agcagctgga atgggtggcc cagatcaagg acaagagcaa cagctacgcc 540
acctactacg ccgacagcgt gaaggggcgg ttcacatca gccgggacga cagcaagaac 600
accctgtacc tgcagatgaa cagcctgcgg gccgaggaca ccgccgtgta ctactgtcgg 660
ggcgtgtact atgccctgag ccccttcgat tactggggcc agggaaacct cgtgaccgtg 720
tctagtcgga ccgccagcac aaaggggcca tcggtgttcc ctctggcccc ttgcagcaga 780
agcaccagcg aatctacagc cgccctgggc tgcctcgtga aggactactt tcccagagcc 840
gtgaccgtgt cctggaactc tggcgctctg acaagcggcg tgcacacctt tccagccgtg 900
ctccagagca gcggcctgta ctctctgagc agcgtcgtga cagtgcacag cagcagcctg 960
ggcaccaaga cctacacctg taacgtggac cacaagccca gcaacaccaa ggtggacaag 1020
cgggtggaat ctaagtacgg ccctccctgc cctccttgcc cagcccctga atttctgggc 1080
ggaccctccg tgttcctgtt cccccc aaag cccaaggaca ccctgatgat cagccggacc 1140
cccgaagtga cctgcgtggg ggtggatgtg tcccaggaag atcccagagt gcagttcaat 1200
tggtacgtgg acggcgtgga agtgacaaac gccaaagaca agcccagaga ggaacagttc 1260
aacagcacct accgggtggg gtccgtgctg accgtgctgc accaggactg gctgaacggc 1320
aaagagtaca agtgcaagg gtccaacaag ggcctgcccc gctccatcga gaaaaccatc 1380
agcaaggcca agggccagcc ccgcgagcct caagtgtgta ccctgcccc tagccaggaa 1440
gagatgacca agaaccagg gtccctgagc tgtgccgtga aaggcttcta cccagcgac 1500
attgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cccccccct 1560
gtgctggaca gcgacggctc attcttcctg gtgtccaagc tgaccgtgga caagagccgg 1620
tggcaggaag gcaacgtgtt cagctgtctc gtgatgcacg aggcctgca caaccactac 1680
accagaagt ccctgtctct gtccctgggc aag 1713

```

<210> 309

<211> 1014

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 309

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gacatcgtga tgaccagac cccctgagc ctgagcgtga cacctggaca gcctgccagc 60
atcagctgca agagcagcca gagcctgggt cacaacaacg ccaacaccta cctgagctgg 120
tatctgcaga agcccggcca gagccccag tccctgatct acaagggtgc caacagattc 180
agcggcgtgc ccgacagatt ctccggcagc ggctctggca ccgacttcac cctgaagatc 240
agccgggtgg aagccgagga cgtgggcgtg tactattgtg gccagggcac ccagtacccc 300
ttcacctttg gcagcggcac caagtgga atcaagggcc agcccaaggc cgccccgcac 360

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4. __183952027041SEQLIST.TXT

```

atccagatga cccagagccc cagcagcctg tctgccagcg tgggcgacag agtgaccatc 420
acctgtcagg ccagccagaa catctacgtg tggctgaact ggtatcagca gaagcccggc 480
aaggcccccag agctgtctgat ctacaaggcc agcaacctgc acaccggcgt gccagcaga 540
ttttctggca gcggctccgg caccgacttc accctgacaa tcagctccct gcagcccagag 600
gacattgcca cctactactg ccagcagggc cagacctacc cctacacctt tggccagggc 660
accaagctgg aatcaagac caagggcccc agccgtacgg tggccgctcc cagcgtgttc 720
atctttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 780
aacaacttct acccccgcga ggccaaagtg cagtgggaagg tggacaacgc cctgcagagc 840
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 900
agcaccctga cactgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 960
accaccagg gcctgtctag ccccgtagacc aagagcttca accggggcga gtgt 1014

```

<210> 310

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 310

```

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

```

4.__183952027041SEQLIST.TXT

```

                245                250                255
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
                260                265                270
Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
                275                280                285
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
                290                295                300
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                310                315                320
Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
                325                330                335
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
                340                345                350
Leu Pro Pro Cys Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp
                355                360                365
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                370                375                380
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                390                395                400
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                410                415
Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
                420                425                430
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
                435                440                445
Lys

```

<210> 311

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 311

```

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

```

4.__183952027041SEQLIST.TXT

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

<210> 312

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 312

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

4.___183952027041SEQLIST.TXT

210	215	220
Ala Leu Ser Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val		
225	230	235
Ser Ser Arg Thr Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala		240
	245	250
Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu		255
	260	265
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly		270
	275	280
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser		285
	290	295
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu		300
305	310	315
Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr		320
	325	330
Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro		335
	340	345
Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro		350
	355	360
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr		365
	370	375
Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn		380
385	390	395
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg		400
	405	410
Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val		415
	420	425
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser		430
	435	440
Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys		445
	450	455
Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Gln Glu		460
465	470	475
Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe		480
	485	490
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu		495
	500	505
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe		510
	515	520
Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly		525
	530	535
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr		540
545	550	555
Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys		560
	565	570

<210> 313

<211> 342

<212> PRT

<213> Artificial Sequence

4.__183952027041SEQLIST.TXT

<220>

<223> Synthetic Construct

<400> 313

```

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1           5           10           15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Val His Asn
 20           25           30
Asn Ala Asn Thr Tyr Leu Ser Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35           40           45
Pro Gln Ser Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50           55           60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65           70           75           80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gly Gln Gly
 85           90           95
Thr Gln Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys
100          105          110
Gly Gln Pro Lys Ala Ala Pro Asp Ile Val Leu Thr Gln Ser Pro Ala
115          120          125
Ser Leu Ala Val Ser Pro Gly Gln Arg Ala Thr Ile Thr Cys Arg Ala
130          135          140
Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln
145          150          155          160
Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Phe Ala Ala Ser Asn
165          170          175
Val Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
180          185          190
Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asn Asp Val Ala Asn
195          200          205
Tyr Tyr Cys Gln Gln Ser Arg Lys Val Pro Tyr Thr Phe Gly Gln Gly
210          215          220
Thr Lys Leu Glu Ile Lys Thr Lys Gly Pro Ser Arg Thr Val Ala Ala
225          230          235          240
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
245          250          255
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
260          265          270
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
275          280          285
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
290          295          300
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
305          310          315          320
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
325          330          335
Phe Asn Arg Gly Glu Cys
340

```

<210> 314

<211> 1347

4.___183952027041SEQLIST.TXT

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 314

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agagcccacc tgggtgcagtc tggcaccgcc atgaagaaac caggcgcctc tgtgcgggtg 60
tcctgtcaga caagcggcta caccctcacc gccacatcc tgttctgggt ccggcaggcc 120
cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
ggcggaggct tccgggatag agtgaccctg acccgggacg tgtaccgcga gatcgctac 240
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aagacctaca cctgtaacgt ggaccacaag cccagcaaca ccaaggtgga caagcgggtg 660
gaatctaagt acggccctcc ctgccctcct tgcccagccc ctgaatttct gggcggaccc 720
tccgtgttcc tgttcccccc aaagcccaag gacaccctga tgatcagccg gacccccgaa 780
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gacagcgacg gctcattctt cctgtactcc aagctgaccg tggacaagag ccggtggcag 1260
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<210> 315

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 315

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ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaaagtgg cgtgcccagc 180
agattttccg gcagcggctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagc gtacggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcagatgt 630

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4.__183952027041SEQLIST.TXT

<210> 316
 <211> 1713
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 316
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 cctggaaaag gcctggaatg gctgggctg atctgggctg gcggaggcac caactacaac 180
 cccagcctga agtccagaaa gaccatcagc aaggacacca gcaagaacca ggtgtccctg 240
 aagctgagca gcgtgacagc cgccgatacc gccgtgtact actgcgccag agacaagggc 300
 tacagctact actacagcat ggactactgg ggccagggca ccaccgtgac cgtgtcatcc 360
 tctcaggtgc agctgggtgga atctggcggc ggagtgggtgc agcctggcag aagcctgaga 420
 ctgagctgtg ccgccagcgg cttcacctt accaaggcct ggatgcactg ggtgcgccag 480
 gcccttgga agcagctgga atgggtggcc cagatcaagg acaagagcaa cagctacgcc 540
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 gtgctggaca gcgacggctc attcttcctg gtgtccaagc tgaccgtgga caagagccgg 1620
 tggcaggaag gcaacgtgtt cagctgtctc gtgatgcacg aggcctgca caaccactac 1680
 acccagaagt ccctgtctct gtccctgggc aag 1713

<210> 317
 <211> 1026
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 317
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 tatctgcaga agcccgcca gagccccag tccctgatct acaaggtgtc caacagattc 180
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4. __183952027041SEQLIST.TXT

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atcgtgctga cacagagccc tgctagcctg gccgtgtctc ctggacagag ggccaccatc 420
acctgtagag ccagcgagag cgtggaatat tacgtgacca gcctgatgca gtggtatcag 480
cagaagcccc gccagcccc caagctgctg attttcgccg ccagcaacgt ggaaagcggc 540
gtgccagcca gattttccgg cagcggctct ggcaccgact tcaccctgac catcaacccc 600
gtggaagcca acgacgtggc caactactac tgccagcaga gccggaaggt gccctacacc 660
tttggccagg gcaccaagct ggaaatcaag accaagggcc ccagccgtac ggtggccgct 720
cccagcgtgt tcatcttccc acctagcgac gagcagctga agtccggcac agcctctgtc 780
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<210> 318

<211> 468

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 318

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

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4. __183952027041SEQLIST.TXT

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Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                230                235                240
Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu
                245                250                255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                260                265                270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
                275                280                285
Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
                290                295                300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
305                310                315                320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325                330                335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser
                340                345                350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
                355                360                365
Val Tyr Thr Leu Pro Pro Cys Gln Glu Glu Met Thr Lys Asn Gln Val
                370                375                380
Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                390                395                400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405                410                415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                420                425                430
Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val
                435                440                445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
                450                455                460
Ser Leu Gly Lys
465

```

<210> 319

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 319

```

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

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4.__183952027041SEQLIST.TXT

```

65          70          75          80
Ser Arg Val Glu Thr Glu Asp Val Gly Thr Tyr Tyr Cys Met Gln Gly
          85          90          95
Arg Glu Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
          100         105         110
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
          115         120         125
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
          130         135         140
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145          150         155         160
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
          165         170         175
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
          180         185         190
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
          195         200         205
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
          210         215

```

<210> 320

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 320

```

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

```

4._183952027041SEQLIST.TXT

```

Asn Ser Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
    180                      185                      190
Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser
    195                      200                      205
Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Arg Gly Val Tyr Tyr
    210                      215                      220
Ala Leu Ser Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
    225                      230                      235                      240
Ser Ser Arg Thr Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
    245                      250                      255
Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
    260                      265                      270
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
    275                      280                      285
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
    290                      295                      300
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
    305                      310                      315                      320
Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
    325                      330                      335
Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
    340                      345                      350
Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
    355                      360                      365
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    370                      375                      380
Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
    385                      390                      395                      400
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
    405                      410                      415
Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
    420                      425                      430
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
    435                      440                      445
Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
    450                      455                      460
Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Gln Glu
    465                      470                      475                      480
Glu Met Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe
    485                      490                      495
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    500                      505                      510
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    515                      520                      525
Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
    530                      535                      540
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    545                      550                      555                      560
Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
    565                      570

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4.__183952027041SEQLIST.TXT

<210> 321

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 321

Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Ser	Val	Thr	Pro	Gly
1				5				10					15		
Gln	Pro	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Val	His	Asn
			20				25					30			
Asn	Ala	Asn	Thr	Tyr	Leu	Ser	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser
		35					40					45			
Pro	Gln	Ser	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro
	50					55					60				
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65				70						75				80	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Gly	Gln	Gly
			85					90					95		
Thr	Gln	Tyr	Pro	Phe	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Val	Glu	Ile	Lys
			100					105					110		
Gly	Gln	Pro	Lys	Ala	Ala	Pro	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser
		115					120					125			
Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Gln	Ala
	130					135					140				
Ser	Gln	Asn	Ile	Tyr	Val	Trp	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly
145				150						155				160	
Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Ala	Ser	Asn	Leu	His	Thr	Gly
			165					170						175	
Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu
			180					185					190		
Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln
		195					200					205			
Gln	Gly	Gln	Thr	Tyr	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu
	210					215					220				
Ile	Lys	Thr	Lys	Gly	Pro	Ser	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe
225				230						235				240	
Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val
			245					250						255	
Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp
		260						265					270		
Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr
		275					280					285			
Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr
	290					295					300				
Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val
305				310						315				320	
Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly
			325						330					335	
Glu	Cys														

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<210> 322
 <211> 1404
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 322
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 ccaggacagg gactgcagtg gatgggctgg atcagccacg agggcgacaa gaaagtgatc 180
 gtggaacggg tcaaggccaa agtgaccatc gactgggaca gaagcaccaa caccgcctac 240
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 aagcacccggc tgagagacta cgccctgtac gacgatgacg gcgccctgaa ctgggccgtg 360
 gatgtggact acctgagcaa cctggaattc tggggccagg gcacagccgt gaccgtgtca 420
 tctgcttcga ccaaggggccc ctcggtgttc cctctggccc cttgcagcag aagcaccagc 480
 gaatctacag ccgccctggg ctgcctcgtg aaggactact ttcccagacc cgtgaccgtg 540
 tcctggaact ctggcgctct gacaagcggc gtgcacacct ttccagccgt gctccagagc 600
 agcggcctgt actctctgag cagcgtcgtg acagtgccca gcagcagcct gggcaccaag 660
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 tctaagtacg gccctccctg ccctccttgc ccagcccctg aatttctggg cggaccctcc 780
 gtgttcctgt tcccccaaaa gcccaaggac accctgatga tcagccggac cccgaagtg 840
 acctgcgtgg tgggtgatgt gtcccaggaa gatcccaggg tgcagttcaa ttggtacgtg 900
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 taccgggtgg tgtccgtgct gaccgtgctg caccaggact ggctgaacgg caaagagtac 1020
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 aaggggcagc cccgcgagcc tcaagtgtat accctgcccc cttgccagga agagatgacc 1140
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 gaatggggaga gcaacggcca gcccgagaac aactacaaga ccaccccccc tgtgctggac 1260
 agcgacggct cattcttcct gtactccaag ctgaccgtgg acaagagccg gtggcaggaa 1320
 ggcaacgtgt tcagctgctc cgtgatgcac gaggccctgc acaaccacta caccagaag 1380
 tccctgtctc tgtccctggg caag 1404

<210> 323
 <211> 657
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 323
 gacttcgtgc tgacccagag ccctcacagc ctgagcgtga cacctggcga gagcgccagc 60
 atcagctgca agagcagcca ctccctgata cacggcgacc ggaacaacta cctggccttg 120
 tacgtgcaga agcccggcag atccccccag ctgctgatct acctggccag cagcagagcc 180
 agcggcgtgc ccgatagatt ttctggcagc ggcagcgaca aggacttcac cctgaagatc 240
 agccgggtgg aaaccgagga cgtgggcacc tactactgta tgcagggcag agagagcccc 300
 tggacctttg gccagggcac caaggtggac atcaagcgta cggtggccgc tcccagcgtg 360

4._183952027041SEQLIST.TXT

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agcggcaaca gccaggaaag cgtgaccgag caggacagca aggactccac ctacagcctg 540
agcagcacc tgacactgag caaggccgac tacgagaagc acaagggtga cgccctgcga 600
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```

<210> 324

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 324

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caggtgcagc tgggtgcagtc tggcgccgag gtcgtgaaac ctggcgccctc tgtgaagggtg 60
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cctggacagg gactggaatg gatcggcagc atctaccccc gcaacgtgaa caccaactac 180
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<210> 325

<211> 1014

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

4.__183952027041SEQLIST.TXT

<400> 325

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<210> 326

<211> 468

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 326

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

```

4.__183952027041SEQLIST.TXT

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      180      185      190
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
      195      200      205
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys
      210      215      220
Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225      230      235      240
Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu
      245      250      255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
      260      265      270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
      275      280      285
Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
      290      295      300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
305      310      315      320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
      325      330      335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser
      340      345      350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
      355      360      365
Val Tyr Thr Leu Pro Pro Cys Gln Glu Glu Met Thr Lys Asn Gln Val
      370      375      380
Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385      390      395      400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
      405      410      415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
      420      425      430
Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val
      435      440      445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
      450      455      460
Ser Leu Gly Lys
465

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<210> 327

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 327

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

```

4.__183952027041SEQLIST.TXT

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

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<210> 328

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 328

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

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130					135					140				
Ser	Gly	Phe	Thr	Phe	Thr	Lys	Ala	Trp	Met	His	Trp	Val	Arg	Gln
				150					155					160
Pro	Gly	Lys	Gln	Leu	Glu	Trp	Val	Ala	Gln	Ile	Lys	Asp	Lys	Ser
			165					170					175	
Ser	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr
		180					185					190		
Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser
	195					200					205			
Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Arg	Gly	Val	Tyr	Tyr
210					215					220				
Leu	Ser	Pro	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
				230					235					240
Ser	Arg	Thr	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala
			245					250					255	
Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu
		260					265					270		
Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly
	275					280					285			
Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser
290					295					300				
Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu
				310					315					320
Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr
			325					330					335	
Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro
		340					345					350		
Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
	355					360					365			
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
370					375					380				
Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn
				390					395					400
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
			405					410					415	
Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
		420					425					430		
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
	435					440					445			
Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
450					455					460				
Gln	Pro	Arg	Glu	Pro	Gln	Val	Cys	Thr	Leu	Pro	Pro	Ser	Gln	Glu
				470					475					480
Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe
			485					490					495	
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
		500					505					510		
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp					

4.__183952027041SEQLIST.TXT

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 Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 565 570

<210> 329
 <211> 342
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 329
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Val His Asn
 20 25 30
 Asn Ala Asn Thr Tyr Leu Ser Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Ser Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gly Gln Gly
 85 90 95
 Thr Gln Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys
 100 105 110
 Gly Gln Pro Lys Ala Ala Pro Asp Ile Val Leu Thr Gln Ser Pro Ala
 115 120 125
 Ser Leu Ala Val Ser Pro Gly Gln Arg Ala Thr Ile Thr Cys Arg Ala
 130 135 140
 Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln
 145 150 155 160
 Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Phe Ala Ala Ser Asn
 165 170 175
 Val Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
 180 185 190
 Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asn Asp Val Ala Asn
 195 200 205
 Tyr Tyr Cys Gln Gln Ser Arg Lys Val Pro Tyr Thr Phe Gly Gln Gly
 210 215 220
 Thr Lys Leu Glu Ile Lys Thr Lys Gly Pro Ser Arg Thr Val Ala Ala
 225 230 235 240
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 245 250 255
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 260 265 270
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 275 280 285
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 290 295 300

4. __183952027041SEQLIST.TXT

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 305 310 315 320
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 325 330 335
 Phe Asn Arg Gly Glu Cys
 340

<210> 330
 <211> 1404
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 330
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 ccaggacagg gactgcagtg gatgggctgg atcagccacg agggcgacaa gaaagtgatc 180
 gtggaacggg tcaaggccaa agtgaccatc gactgggaca gaagcaccaa caccgcctac 240
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 aagcacgggc tgagagacta cgccctgtac gacgatgacg gcgccctgaa ctgggccgtg 360
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 tcctggaact ctggcgctct gacaagcggc gtgcacacct ttccagccgt gctccagagc 600
 agcggcctgt actctctgag cagcgtcgtg acagtgccca gcagcagcct gggcaccaaag 660
 acctacacct gtaacgtgga ccacaagccc agcaacacca aggtggacaa gcgggtggaa 720
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 aagaaccagg tgtccctgtg gtgtctcgtg aaaggcttct accccagcga cattgccgtg 1200
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 tcctgtctc tgtccctggg caag 1404

<210> 331
 <211> 657
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 331
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<210> 332

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 332

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cctggaaaag gcctggaatg gctgggcgtg atctgggctg gcggaggcac caactacaac 180
cccagcctga agtccagaaa gaccatcagc aaggacacca gcaagaacca ggtgtccctg 240
aagctgagca gcgtgacagc cgccgatacc gccgtgtact actgcgccag agacaagggc 300
tacagctact actacagcat ggactactgg ggccagggca ccaccgtgac cgtgtcatcc 360
tctcaggtgc agctggtgga atctggcggc ggagtgtgag agcctggcag aagcctgaga 420
ctgagctgtg ccgccagcgg cttcacctt accaaggcct ggatgactg ggtgcgccag 480
gcccctggaa agcagctgga atgggtggcc cagatcaagg acaagagcaa cagctacgcc 540
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<210> 333

<211> 1026

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 333

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tatctgcaga agcccggcca gagcccccag tccctgatct acaaggtgtc caacagattc 180
agcggcggtgc ccgacagatt ctccggcagc ggctctggca ccgacttcac cctgaagatc 240
agccgggtgg aagccgagga cgtgggcgtg tactattgtg gccagggcac ccagtacccc 300
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atcgtgctga cacagagccc tgctagcctg gccgtgtctc ctggacagag ggccaccatc 420
acctgtagag ccagcgagag cgtggaatat tacgtgacca gcctgatgca gtggtatcag 480
cagaagcccc gccagcccc caagctgctg attttcgccg ccagcaacgt ggaaagcggc 540
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gtggaagcca acgacgtggc caactactac tgccagcaga gccggaaggt gccctacacc 660
tttggccagg gcaccaagct ggaaatcaag accaagggcc ccagccgtac ggtggccgct 720
cccagcgtgt tcattttccc acctagcgac gagcagctga agtccggcac agcctctgtc 780
gtgtgcctgc tgaacaactt ctacccccgc gaggccaaag tgcagtggaa ggtggacaac 840
gccctgcaga gcggcaacag ccaggaaagc gtgaccgagc aggacagcaa ggactccacc 900
tacagcctga gcagaccct gacactgagc aaggccgact acgagaagca caaggtgtac 960
gcctgcgaag tgacccacca gggcctgtct agccccgtga ccaagagctt caaccggggc 1020
gagtgt 1026

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<210> 334

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 334

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

```

130					135					140					
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
150					155					160					
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
165					170					175					
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
180					185					190					
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	
195					200					205					
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	
210	215					220					225				
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	
230					235					240					
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	
245					250					255					
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	
260					265					270					
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	
275					280					285					
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	
290	295					300					305				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	
310					315					320					
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	
325					330					335					
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	
340					345					350					
Pro	Cys	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	
355					360					365					
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	
370	375					380					385				
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	
390					395					400					
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	
405					410					415					
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	
420					425					430					
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
435					440					445					

<213> Artificial Sequence

<223> Synthetic Construct

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

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

<210> 336

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 336

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

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		115					120				125				
Gly 130	Gly 130	Val	Val	Gln	Pro	Gly 135	Arg	Ser	Leu	Arg 140	Leu	Ser	Cys	Ala	
Ala 145	Ser	Gly	Phe	Thr	Phe 150	Thr	Lys	Ala	Trp	Met 155	His	Trp	Val	Arg	Gln 160
Ala	Pro	Gly	Lys	Gln	Leu	Glu	Trp	Val	Ala	Gln	Ile	Lys	Asp	Lys	Ser
				165					170					175	
Asn	Ser	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr
			180						185				190		
Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser
		195					200					205			
Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Arg	Gly	Val	Tyr	Tyr
	210					215				220					
Ala	Leu	Ser	Pro	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
225					230					235					240
Ser	Ser	Arg	Thr	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala
				245					250				255		
Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu
			260					265					270		
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly
		275					280					285			
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser
	290					295					300				
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu
305					310					315					320
Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr
				325					330					335	
Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro
		340						345					350		
Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
		355					360				365				
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
	370					375					380				
Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn
385					390					395					400
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
				405					410					415	
Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
			420					425					430		
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
		435					440					445			
Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
	450					455					460				
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Cys	Thr	Leu	Pro	Pro	Ser	Gln	Glu
465					470					475					480
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly</	

4.__183952027041SEQLIST.TXT

530		535		540	
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr					
545		550		555	560
Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys					
	565		570		

<210> 337

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 337

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

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Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
 290 295 300
 Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
 305 310 315 320
 Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
 325 330 335
 Glu Cys

<210> 338
 <211> 1344
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 338
 caggtgcagc tgggtgcagtc tggcggccag atgaagaaac ccggcgagag catgcggatc 60
 agctgcagag ccagcggcta cgagttcatc gactgcaccc tgaactggat cagactggcc 120
 cctggcaagc ggcctgagtg gatgggatgg ctgaagccta gaggcggagc cgtgaactac 180
 gccagacctc tgcagggcag agtgaccatg acccgggacg tgtacagcga taccgccttc 240
 ctggaactgc ggagcctgac cgtggatgat accgccgtgt acttctgcac ccggggcaag 300
 aactgacgact acaactggga cttcgagcac tggggcgagag gcacccctgt gatcgtgtca 360
 agcgcgtcga ccaagggccc ctcggtgttc cctctggccc cttgcagcag aagcaccagc 420
 gaatctacag ccgccctggg ctgcctcgtg aaggactact ttcccagagc cgtgaccgtg 480
 tcctggaact ctggcgctct gacaagcggc gtgcacacct ttccagccgt gctccagagc 540
 agcggcctgt actctctgag cagcgtcgtg acagtgccca gcagcagcct gggcaccaag 600
 acctacacct gtaacgtgga ccacaagccc agcaacacca aggtggacaa gcgggtggaa 660
 tctaagtacg gccctccctg ccctccttgc ccagcccctg aatttctggg cggaccctcc 720
 gtgttcctgt tcccccaaaa gcccaaggac accctgatga tcagccggac cccgaagtg 780
 acctgcgtgg tgggtggatgt gtcccaggaa gatcccagg tgcagttcaa ttggtacgtg 840
 gacggcgtgg aagtgcacaa cgccaagacc aagcccagag aggaacagtt caacagcacc 900
 taccgggtgg tgtccgtgct gaccgtgctg caccaggact ggctgaacgg caaagagtac 960
 aagtgaagg tgtccaacaa gggcctgccc agctccatcg agaaaaccat cagcaaggcc 1020
 aagggccagc ccgcgagcc tcaagtgtat accctgcccc cttgccagga agagatgacc 1080
 agaaccagg tgtccctgtg gtgtctcgtg aaaggcttct accccagcga cattgccgtg 1140
 gaatgggaga gcaacggcca gcccgagaac aactacaaga ccaccccccc tgtgtctggac 1200
 agcgacggct cattcttcct gtactccaag ctgaccgtgg acaagagccg gtggcaggaa 1260
 ggcaacgtgt tcagctgctc cgtgatgcac gaggccctgc acaaccacta caccagaag 1320
 tccctgtctc tgtccctggg caag 1344

<210> 339
 <211> 630
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 339

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gagatcgtgc tgacacagag ccctggcacc ctgagcctgt ctccaggcga gacagccatc 60
atcagctgcc ggacaagcca gtacggcagc ctggcctggg atcagcagag gcctggacag 120
gccccagac tcgtgatcta cagcggcagc acaagagccg ccggaatccc cgatagattc 180
agcggctcca gatggggccc tgactacaac ctgaccatca gcaacctgga aagcggcgac 240
ttcggcgtgt actactgcca gcagtacgag ttcttcggcc agggcaccaa ggtgcagggtg 300
gacatcaagc gtacgggtggc cgctcccagc gtgttcattt tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtg 630

```

<210> 340

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 340

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cagggtgcagc tgggtgcagtc tggcgccgag gtcgtgaaac ctggcgccctc tgtgaagggtg 60
tcctgcaagg ccagcggcta cacctttacc agctactaca tccactgggt gcgccaggcc 120
cctggacagg gactggaatg gatcggcagc atctacccc gcaacgtgaa caccaactac 180
gcccagaagt tccagggcag agccaccctg accgtggaca ccagcatcag caccgcctac 240
atggaactga gccggctgag aagcgacgac accgccgtgt actactgcac ccggtccac 300
tacggcctgg attggaactt cgacgtgtgg ggcaagggca ccaccgtgac agtgtctagc 360
agccagggtgc agctgggtgga atctggcggc ggagtgggtgc agcctggcag aagcctgaga 420
ctgagctgtg ccgccagcgg cttcaccttc accaaggcct ggatgactg ggtgcgccag 480
gcccctggaa agcagctgga atgggtggcc cagatcaagg acaagagcaa cagctacgcc 540
acctactacg ccgacagcgt gaagggccgg ttcaccatca gccgggacga cagcaagaac 600
accctgtacc tgcagatgaa cagcctgcgg gccgaggaca ccgccgtgta ctactgtcgg 660
ggcgtgtact atgccctgag ccccttcgat tactggggcc agggaaacct cgtgaccgtg 720
tctagtcgga ccgccagcac aaagggccca tcggtgttcc ctctggcccc ttgcagcaga 780
agcaccagcg aatctacagc cgccctgggc tgccctcgtga aggactactt tcccgagccc 840
gtgaccgtgt cctggaactc tggcgctctg acaagcggcg tgcacacctt tccagccgtg 900
ctccagagca gcggcctgta ctctctgagc agcgtcgtga cagtgccag cagcagcctg 960
ggcaccaaga cctacacctg taacgtggac cacaagccca gcaacaccaa ggtggacaag 1020
cgggtggaat ctaagtacgg ccctccctgc cctccttgcc cagcccctga atttctgggc 1080
ggaccctccg tgttcctgtt cccccaaaag cccaaggaca ccctgatgat cagccggacc 1140
cccgaagtga cctgcgtggg ggtggatgtg tcccaggaag atcccagggt gcagttcaat 1200
tggtacgtgg acggcgtgga agtgcacaac gccaaagaca agcccagaga ggaacagttc 1260
aacagcacct accgggtggg gtccgtgctg accgtgctgc accaggactg gctgaacggc 1320
aaagagtaca agtgcaagg gtccaacaag ggcctgccc gctccatcga gaaaaccatc 1380
agcaaggcca agggccagcc ccgcgagcct caagtgtgta ccctgcccc tagccaggaa 1440
gagatgacca agaaccagg gtcccctgagc tgtgccgtga aaggcttcta ccccgcgac 1500
attgccgtgg aatgggagag caacggccag ccgagaaca actacaagac cccccccct 1560
gtgctggaca gcgacggctc attcttcctg gtgtccaagc tgaccgtgga caagaccgg 1620
tggcaggaag gcaacgtgtt cagctgtctc gtgatgcagc aggcctgca caaccactac 1680
accagaagt ccctgtctct gtccctgggc aag 1713

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<210> 341

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<211> 1014

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 341

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atcagctgca agagcagcca gagcctggtg cacaacaacg ccaacaccta cctgagctgg 120
tatctgcaga agcccggcca gagccccag tccctgatct acaaggtgtc caacagattc 180
agcggcgtgc ccgacagatt ctccggcagc ggctctggca ccgacttcac cctgaagatc 240
agccgggtgg aagccgagga cgtgggcgtg tactattgtg gccagggcac ccagtacccc 300
ttcacctttg gcagcggcac caaggtggaa atcaagggcc agcccaaggc cgccccgcac 360
atccagatga cccagagccc cagcagcctg tctgccagcg tgggcgacag agtgaccatc 420
acctgtcagg ccagccagaa catctacgtg tggctgaact ggtatcagca gaagcccggc 480
aaggccccc aagctgctgat ctacaaggcc agcaacctgc acaccggcgt gccagcaga 540
ttttctggca gcggctccgg caccgacttc accctgacaa tcagctccct gcagcccgag 600
gacattgcca cctactactg ccagcagggc cagacctacc cctacacctt tggccagggc 660
accaagctgg aaatcaagac caagggcccc agccgtacgg tggccgctcc cagcgtgttc 720
atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 780
aacaacttct acccccgcga ggccaaagtg cagtgggaagg tggacaacgc cctgcagagc 840
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 900
agcaccctga cactgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 960
accaccagg gcctgtctag ccccgtagc aagagcttca accggggcga gtgt 1014

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<210> 342

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 342

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

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130	135	140																	
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val				
145				150						155					160				
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala				
				165					170						175				
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val				
			180					185						190					
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His				
			195				200					205							
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly				
	210					215					220								
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser				
225					230					235					240				
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg				
				245					250						255				
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro				
			260					265						270					
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala				
		275					280					285							
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val				
	290				295					300									
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr				
305					310				315						320				
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr				
			325						330						335				
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu				
			340					345						350					
Pro	Pro	Cys	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys				
		355					360					365							
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser				
	370					375					380								
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp				
385					390					395					400				
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser				
				405					410						415				
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala				
		420					425						430						
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys				
	435					440					445								

<210> 343

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 343

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

4._183952027041SEQLIST.TXT

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

<210> 344

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 344

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

4._183952027041SEQLIST.TXT

					115						120						125	
Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala			
					130						135						140	
Ala	Ser	Gly	Phe	Thr	Phe	Thr	Lys	Ala	Trp	Met	His	Trp	Val	Arg	Gln			
145						150						155						160
Ala	Pro	Gly	Lys	Gln	Leu	Glu	Trp	Val	Ala	Gln	Ile	Lys	Asp	Lys	Ser			
					165						170						175	
Asn	Ser	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr			
					180						185						190	
Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser			
					195						200						205	
Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Arg	Gly	Val	Tyr	Tyr			
					210						215						220	
Ala	Leu	Ser	Pro	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val			
225						230						235						240
Ser	Ser	Arg	Thr	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala			
					245						250						255	
Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu			
					260						265						270	
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly			
					275						280						285	
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser			
					290						295						300	
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu			
305						310						315						320
Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr			
					325						330						335	
Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro			
					340						345						350	
Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro			
					355						360						365	
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr			
					370						375						380	
Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn			
385						390						395						400
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg			
					405						410						415	
Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val			
					420						425						430	
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser			
					435						440						445	
Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys			
					450						455						460	
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Cys	Thr	Leu	Pro	Pro	Ser	Gln	Glu			
465						470						475						480
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe			
					485						490						495	
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu			
					500						505						510	
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe			
					515						520						525	
Phe	Leu	Val	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly			

4._183952027041SEQLIST.TXT

530		535		540	
Asn	Val	Phe	Ser	Cys	Ser
545		550		555	
Thr	Gln	Lys	Ser	Leu	Ser
		565		570	

<210> 345
 <211> 342
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 345

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

4._183952027041SEQLIST.TXT

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 290 295 300
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 305 310 315 320
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 325 330 335
 Phe Asn Arg Gly Glu Cys
 340

<210> 346
 <211> 1344
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 346
 caggtgcagc tgggtgcagtc tggcggccag atgaagaaac ccggcgagag catgcggatc 60
 agctgcagag ccagcggcta cgagttcatc gactgcaccc tgaactggat cagactggcc 120
 cctggcaagc ggcttgagtg gatgggatgg ctgaagccta gaggcggagc cgtgaactac 180
 gccagacctc tgcagggcag agtgaccatg acccgggacg tgtacagcga taccgccttc 240
 ctggaactgc ggagcctgac cgtggatgat accgccgtgt acttctgcac ccggggcaag 300
 aactgacgact acaactggga cttcgagcac tggggcgagag gcacccctgt gatcgtgtca 360
 agcgcgtcga ccaagggccc ctcggtgttc cctctggccc cttgcagcag aagcaccagc 420
 gaatctacag ccgccctggg ctgcctcgtg aaggactact ttcccagagc cgtgaccgtg 480
 tcctggaact ctggcgctct gacaagcggc gtgcacacct ttccagccgt gctccagagc 540
 agcggcctgt actctctgag cagcgtcgtg acagtgccca gcagcagcct gggcaccaag 600
 acctacacct gtaacgtgga ccacaagccc agcaacacca aggtggacaa gcgggtggaa 660
 tctaagtacg gccctccctg ccctccttgc ccagcccctg aatttctggg cggaccctcc 720
 gtgttcctgt tcccccaaaa gcccaaggac accctgatga tcagccggac cccgaagtg 780
 acctgcgtgg tgggtggatgt gtcccaggaa gatcccagg tgcagttcaa ttggtacgtg 840
 gacggcgtgg aagtgcacaa cgccaagacc aagcccagag aggaacagtt caacagcacc 900
 taccgggtgg tgtccgtgct gaccgtgctg caccaggact ggctgaacgg caaagagtac 960
 aagtgaagg tgtccaacaa gggcctgccc agctccatcg agaaaaccat cagcaaggcc 1020
 aagggccagc ccgcgagcc tcaagtgtat accctgcccc cttgccagga agagatgacc 1080
 aagaaccagg tgtccctgtg gtgtctcgtg aaaggcttct accccagcga cattgccgtg 1140
 gaatgggaga gcaacggcca gcccgagaac aactacaaga ccaccccccc tgtgctggac 1200
 agcgacggct cattcttcct gtactccaag ctgaccgtgg acaagagccg gtggcaggaa 1260
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 tccctgtctc tgtccctggg caag 1344

<210> 347
 <211> 630
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 347

4. __183952027041SEQLIST.TXT

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atcagctgcc ggacaagcca gtacggcagc ctggcctggt atcagcagag gcctggacag 120
gccccagac tcgtgatcta cagcggcagc acaagagccg ccggaatccc cgatagattc 180
agcggctcca gatggggccc tgactacaac ctgaccatca gcaacctgga aagcggcgac 240
ttcggcgtgt actactgcca gcagtacgag ttcttcggcc agggcaccaa ggtgcagggtg 300
gacatcaagc gtacgggtggc cgctcccagc gtgttcatct tcccacctag cgacgagcag 360
ctgaagtccg gcacagcctc tgtcgtgtgc ctgctgaaca acttctaccc ccgcgaggcc 420
aaagtgcagt ggaagggtgga caacgccctg cagagcggca acagccagga aagcgtgacc 480
gagcaggaca gcaaggactc cacctacagc ctgagcagca ccctgacact gagcaaggcc 540
gactacgaga agcacaaggt gtacgcctgc gaagtgacct accagggcct gtctagcccc 600
gtgaccaaga gcttcaaccg gggcgagtg 630

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<210> 348

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 348

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acctgtaccg tgtccggctt cagcctgagc gactacggcg tgcactgggt gcgccagcca 120
cctggaaaag gcctggaatg gctgggcgtg atctgggctg gcggaggcac caactacaac 180
cccagcctga agtccagaaa gaccatcagc aaggacacca gcaagaacca ggtgtccctg 240
aagctgagca gcgtgacagc cgccgatacc gccgtgtact actgcgccag agacaagggc 300
tacagctact actacagcat ggactactgg ggccagggca ccaccgtgac cgtgtcatcc 360
tctcaggtgc agctgggtgga atctggcggc ggagtggtgc agcctggcag aagcctgaga 420
ctgagctgtg ccgccagcgg cttcacctt accaaggcct ggatgactg ggtgcgccag 480
gcccctggaa agcagctgga atgggtggcc cagatcaagg acaagagcaa cagctacgcc 540
acctactacg ccgacagcgt gaagggccgg ttcaccatca gccgggacga cagcaagaac 600
accctgtacc tgcagatgaa cagcctgcgg gccgaggaca ccgccgtgta ctactgtcgg 660
ggcgtgtact atgccctgag ccccttcgat tactggggcc agggaaacct cgtgaccgtg 720
tctagtcgga ccgcttcgac caagggccca tcggtgttcc ctctggcccc ttgcagcaga 780
agcaccagcg aatctacagc cgccctgggc tgccctgtga aggactactt tcccagagcc 840
gtgaccgtgt cctggaactc tggcgctctg acaagcggcg tgcacacctt tccagccgtg 900
ctccagagca gcggcctgta ctctctgagc agcgtcgtga cagtgccag cagcagcctg 960
ggcaccaaga cctacacctg taacgtggac cacaagccca gcaacaccaa ggtggacaag 1020
cgggtggaat ctaagtacgg ccctccctgc cctccttgcc cagcccctga atttctgggc 1080
ggaccctccg tgttcctgtt cccccaaaag cccaaggaca ccctgatgat cagccggacc 1140
cccgaagtga cctgcgtggt ggtggatgtg tcccaggaag atcccagggt gcagttcaat 1200
tggtacgtgg acggcgtgga agtgcacaac gccaaagaca agcccagaga ggaacagttc 1260
aacagcacct accgggtggt gtccgtgtgc accgtgtgc accaggactg gctgaacggc 1320
aaagagtaca agtgcaaggt gtccaacaag ggcctgcca gctccatcga gaaaaccatc 1380
agcaaggcca agggccagcc ccgcgagcct caagtgtgta ccctgcccc tagccaggaa 1440
gagatgacca agaaccaggt gtccctgagc tgtgccgtga aaggcttcta cccagcgac 1500
attgccgtgg aatgggagag caacggccag ccgagaaca actacaagac cccccccct 1560
gtgctggaca gcgacggctc attcttcctg gtgtccaagc tgaccgtgga caagagccgg 1620
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<210> 349

4.__183952027041SEQLIST.TXT

<211> 1026

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 349

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atcagctgca agagcagcca gagcctgggtg cacaacaacg ccaacaccta cctgagctgg 120
tatctgcaga agcccggcca gagccccag tccctgatct acaaggtgtc caacagattc 180
agcggcgtgc ccgacagatt ctccggcagc ggctctggca ccgacttcac cctgaagatc 240
agccgggtgg aagccgagga cgtgggcgtg tactattgtg gccagggcac ccagtacccc 300
ttcacctttg gcagcggcac caaggtggaa atcaagggcc agcccaaggc cgccccgcac 360
atcgtgctga cacagagccc tgctagcctg gccgtgtctc ctggacagag ggccaccatc 420
acctgtagag ccagcgagag cgtggaatat tacgtgacca gcctgatgca gtggtatcag 480
cagaagcccg gccagcccc caagctgctg attttcgccg ccagcaacgt ggaaagcggc 540
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gtggaagcca acgacgtggc caactactac tgccagcaga gccggaaggt gccctacacc 660
tttgccagg gcaccaagct ggaaatcaag accaagggcc ccagccgtac ggtggccgct 720
cccagcgtgt tcatcttccc acctagcgac gagcagctga agtccggcac agcctctgtc 780
gtgtgcctgc tgaacaactt ctacccccgc gaggccaaag tgcagtggaa ggtggacaac 840
gccctgcaga gcggcaacag ccaggaaagc gtgaccgagc aggacagcaa ggactccacc 900
tacagcctga gcagcacct gacactgagc aaggccgact acgagaagca caaggtgtac 960
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gagtgt                                     1026

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<210> 350

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 350

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

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4.__183952027041SEQLIST.TXT

Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala
130						135					140				
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
			165						170					175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
		210				215					220				
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225					230					235					240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
			245						250					255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
			260					265					270		
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
		275					280					285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
	290					295					300				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305					310					315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
				325					330					335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
		340						345					350		
Pro	Cys	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu
		355					360					365			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	370					375					380				
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385					390					395					400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg
			405						410					415	
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
		420						425					430		
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
		435					440					445			

<210> 351

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 351

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

4.__183952027041SEQLIST.TXT

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

```

<210> 352

<211> 573

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 352

```

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

```

4. __183952027041SEQLIST.TXT

Gly	Gln	Gly	Thr	Thr	Val	Val	Val	Ser	Ala	Ser	Gln	Val	Gln	Leu	Val	115	120	125
Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	130	135	140
Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Thr	Lys	Ala	Trp	Met	His	Trp	Val	145	150	155
Arg	Gln	Ala	Pro	Gly	Lys	Gln	Leu	Glu	Trp	Val	Ala	Gln	Ile	Lys	Asp	165	170	175
Lys	Ser	Asn	Ser	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	180	185	190
Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	195	200	205
Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Arg	Gly	Val	210	215	220
Tyr	Tyr	Ala	Leu	Ser	Pro	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	225	230	235
Thr	Val	Ser	Ser	Arg	Thr	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	245	250	255
Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	260	265	270
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	275	280	285
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	290	295	300
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	305	310	315
Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	325	330	335
Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	340	345	350
Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	355	360	365
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	370	375	380
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	385	390	395
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	405	410	415
Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	420	425	430
Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	435	440	445
Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	450	455	460
Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Cys	Thr	Leu	Pro	Pro	Ser	465	470	475
Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Ser	Cys	Ala	Val	Lys	485	490	495
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	500	505	510
Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	515	520	525

4._183952027041SEQLIST.TXT

Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
530 535 540
Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
545 550 555 560
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
565 570

<210> 353
<211> 334
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 353
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Gln Ser Leu Val His Asn
20 25 30
Asn Ala Asn Thr Tyr Leu Ser Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Gln Ser Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gly Gln Gly
85 90 95
Thr Gln Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys
100 105 110
Gly Gln Pro Lys Ala Ala Pro Tyr Ile His Val Thr Gln Ser Pro Ser
115 120 125
Ser Leu Ser Val Ser Ile Gly Asp Arg Val Thr Ile Asn Cys Gln Thr
130 135 140
Ser Gln Gly Val Gly Ser Asp Leu His Trp Tyr Gln His Lys Pro Gly
145 150 155 160
Arg Ala Pro Lys Leu Leu Ile His His Thr Ser Ser Val Glu Asp Gly
165 170 175
Val Pro Ser Arg Phe Ser Gly Ser Gly Phe His Thr Ser Phe Asn Leu
180 185 190
Thr Ile Ser Asp Leu Gln Ala Asp Asp Ile Ala Thr Tyr Tyr Cys Gln
195 200 205
Val Leu Gln Phe Phe Gly Arg Gly Ser Arg Leu His Ile Lys Thr Lys
210 215 220
Gly Pro Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
225 230 235 240
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
245 250 255
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
260 265 270
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser

4._183952027041SEQLIST.TXT

275	280	285
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala		
290	295	300
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly		
305	310	315
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys		
325	330	

<210> 354
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 354

caggtgcagc	tggtgcagtc	tggcgccgag	gtcgtgaaac	ctggcgccctc	tgtgaagggtg	60
tcctgcaagg	ccagcggcta	cacctttacc	agctactaca	tccactgggt	gcgccaggcc	120
cctggacagg	gactggaatg	gatcggcagc	atctacccc	gcaacgtgaa	caccaactac	180
gcccagaagt	tccagggcag	agccaccctg	accgtggaca	ccagcatcag	caccgcctac	240
atggaactga	gccggctgag	aagcgacgac	accgccgtgt	actactgcac	ccgggtccac	300
tacggcctgg	attggaactt	cgacgtgtgg	ggcaagggca	ccaccgtgac	agtgtctagc	360
gcgtcgacca	agggccctc	ggtgttccct	ctggccctt	gcagcagaag	caccagcgaa	420
tctacagccg	ccctgggctg	cctcgtgaag	gactactttc	ccgagcccgt	gaccgtgtcc	480
tggaactctg	gcgctctgac	aagcggcgtg	cacacctttc	cagccgtgct	ccagagcagc	540
ggcctgtact	ctctgagcag	cgctcgtgaca	gtgcccagca	gcagcctggg	caccaagacc	600
tacacctgta	acgtggacca	caagcccagc	aacaccaagg	tggacaagcg	ggtggaatct	660
aagtacggcc	ctccctgccc	tccttgccc	gcccctgaat	ttctgggcgg	accctccgtg	720
ttcctgttcc	ccccaaagcc	caaggacacc	ctgatgatca	gccggacccc	cgaagtgacc	780
tgcgtggtgg	tggatgtgtc	ccaggaagat	cccagaggtg	agttcaattg	gtacgtggac	840
ggcgtggaag	tgcaacaacg	caagaccaag	cccagagagg	aacagttcaa	cagcacctac	900
cgggtggtgt	ccgtgctgac	cgtgctgcac	caggactggc	tgaacggcaa	agagtacaag	960
tgcaaggtgt	ccaacaaggg	cctgcccagc	tccatcgaga	aaaccatcag	caaggccaag	1020
ggccagcccc	gcgagcctca	agtgtatacc	ctgccccctt	gccaggaaga	gatgaccaag	1080
aaccaggtgt	ccctgtggtg	tctcgtgaaa	ggcttctacc	ccagcgacat	tgccgtggaa	1140
tgggagagca	acggccagcc	cgagaacaac	tacaagacca	ccccccctgt	gctggacagc	1200
gacggctcat	tcttctgtga	ctccaagctg	accgtggaca	agagccggtg	gcaggaaggc	1260
aacgtgttca	gctgctccgt	gatgcacgag	gccctgcaca	accactacac	ccagaagtcc	1320
ctgtctctgt	ccctgggcaa	g				1341

<210> 355
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 355

gacatccaga	tgacccagag	ccccagcagc	ctgtctgcca	gcgtgggcga	cagagtgacc	60
------------	------------	------------	------------	------------	------------	----

4. __183952027041SEQLIST.TXT

```

atcacctgtc aggccagcca gaacatctac gtgtggctga actggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacaag gccagcaacc tgcacaccgg cgtgcccagc 180
agattttctg gcagcggctc cggcaccgac ttcaccctga caatcagctc cctgcagccc 240
gaggacattg ccacctacta ctgccagcag ggccagacct acccctacac ctttggccag 300
ggcaccaagc tggaaatcaa gcgtacgggtg gccgctccca gcgtgttcat cttcccacct 360
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 420
ccccgcgagg ccaagggtgca gtggaagggtg gacaatgccc tgcaagcggg caacagccag 480
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600
ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 642

```

<210> 356

<211> 1719

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 356

```

agagcccacc tgggtgcagtc tggcaccgcc atgaagaaac caggcgcctc tgtgcgggtg 60
tcctgtcaga caagcggcta caccttcacc gccacatcc tgttcttggtt ccggcaggcc 120
cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
ggcggaggct tccgggatag agtgaccctg acccgggacg tgtaccgca gatcgacctac 240
atggacatcc ggggcctgaa gcccgatgac accgccgtgt actactgcgc cagagacaga 300
agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtggtggtg 360
tctgcctctc aggtgcagct ggtggaatct ggcgcgagg tggtgcagcc tggcagaagc 420
ctgagactga gctgtgccgc cagcggcttc accttcacca aggcctggat gactgggtg 480
cgccaggccc ctggaaagca gctggaatgg gtggcccaga tcaaggacaa gagcaacagc 540
tacgccacct actacgccga cagcgtgaag ggccggttca ccatcagccg ggacgacagc 600
aagaacaccc tgtacctgca gatgaacagc ctgcggggccg aggacaccgc cgtgtactac 660
tgtcggggcg tgtactatgc cctgagcccc ttcgattact ggggccaggg aaccctcgtg 720
accgtgtcta gtcggaccgc ttcgaccaag ggccatcgg tgttccctct ggccccttgc 780
agcagaagca ccagcgaatc tacagccgcc ctgggctgcc tcgtgaagga ctactttccc 840
gagcccgtga ccgtgtcctg gaactctggc gctctgacaa gcggcgtgca cacctttcca 900
gccgtgtccc agagcagcgg cctgtactct ctgagcagcg tcgtgacagt gcccagcagc 960
agcctgggca ccaagaccta cacctgtaac gtggaccaca agcccagcaa caccaagggtg 1020
gacaagcggg tggaaatctaa gtacggccct ccctgccctc cttgcccagc ccctgaattt 1080
ctgggcggac cctccgtgtt cctgttcccc ccaaagccca aggacaccct gatgatcagc 1140
cggacccccg aagtgcacctg cgtggtggtg gatgtgtccc aggaagatcc cgagggtgcag 1200
ttcaattggt acgtggacgg cgtggaagtg cacaacgcc agaccaagcc cagagaggaa 1260
cagttcaaca gcacctaccg ggtggtgtcc gtgctgaccg tgctgcacca ggactggctg 1320
aacggcaaag agtacaagtg caagggtgtcc aacaagggcc tgcccagctc catcgagaaa 1380
accatcagca aggccaaggg ccagccccgc gagcctcaag tgtgtaccct gccccctagc 1440
caggaagaga tgaccaagaa ccagggtgtcc ctgagctgtg ccgtgaaagg cttctacccc 1500
agcgacattg ccgtggaatg ggagagcaac ggccagcccg agaacaacta caagaccacc 1560
ccccctgtgc tggacagcga cggctcattc ttcctggtgt ccaagctgac cgtggacaag 1620
agccggtggc aggaaggcaa cgtgttcagc tgctccgtga tgcacagggc cctgcacaac 1680
cactacaccc agaagtcctt gtctctgtcc ctgggcaag 1719

```

<210> 357

<211> 1002

4.__183952027041SEQLIST.TXT

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 357

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gacatcgtga tgacccagac cccctgagc ctgagcgtga cacctggaca gcctgccagc 60
atcagctgca agagcagcca gagcctggtg cacaacaacg ccaacaccta cctgagctgg 120
tatctgcaga agcccggcca gagcccccag tccctgatct acaaggtgtc caacagattc 180
agcggcgtgc ccgacagatt ctccggcagc ggctctggca ccgacttcac cctgaagatc 240
agccgggtgg aagccgagga cgtgggcgtg tactattgtg gccagggcac ccagtacccc 300
ttcacctttg gcagcggcac caaggtggaa atcaagggcc agcccaaggc cgccccctac 360
atccacgtga cccagagccc cagcagcctg tccgtgtcca tcggcgacag agtgaccatc 420
aactgccaga cctctcaggg cgtgggcagc gacctgcact ggtatcagca caagcctggc 480
agagcccca agctgctgat ccaccacaca agcagcgtgg aagatggcgt gccagcaga 540
ttttccggca gcggcttcca caccagcttc aacctgacca tcagcgatct gcaggccgac 600
gacattgcca cctactattg tcaggtgctg cagttcttcg gcagaggcag cagactgcac 660
atcaagacca agggccccag ccgtacggtg gccgctccca gcgtgttcat cttcccacct 720
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 780
ccccgcgagg ccaaagtgc gtggaagggt gacaacgccc tgcagagcgg caacagccag 840
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgaca 900
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgc ccaccagggc 960
ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 1002

```

<210> 358

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 358

```

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

```

4.__183952027041SEQLIST.TXT

```

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                150                155                160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                170                175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
                180                185                190
Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
                195                200                205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
                210                215                220
Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
225                230                235                240
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                250                255
Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
                260                265                270
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                275                280                285
Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
                290                295                300
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                310                315                320
Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
                325                330                335
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
                340                345                350
Pro Cys Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
                355                360                365
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                370                375                380
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                390                395                400
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                410                415
Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
                420                425                430
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
                435                440                445

```

<210> 359

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 359

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1                5                10                15
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asn Ile Tyr Val Trp

```

4. __183952027041SEQLIST.TXT

```

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

```

<210> 360

<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 360

```

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

```


4.__183952027041SEQLIST.TXT

Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	130	135	140
Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Thr	Lys	Ala	Trp	145	150	155
Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gln	Leu	Glu	Trp	Val	Ala	165	170	175
Gln	Ile	Lys	Asp	Lys	Ser	Asn	Ser	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp	Ser	180	185	190
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Leu	195	200	205
Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	210	215	220
Cys	Arg	Gly	Val	Tyr	Tyr	Ala	Leu	Ser	Pro	Phe	Asp	Tyr	Trp	Gly	Gln	225	230	235
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Ala	Ser	Thr	245	250	255
Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	260	265	270
Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	275	280	285
Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	290	295	300
Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	305	310	315
Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	325	330	335
Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	340	345	350
Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	355	360	365
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	370	375	380
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	385	390	395
Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	405	410	415
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	420	425	430
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	435	440	445
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	450	455	460
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	465	470	475
Val	Cys	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	485	490	495
Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	500	505	510
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	515	520	525
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr	530	535	540

4._183952027041SEQLIST.TXT

Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val
 545 550 555 560
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 565 570 575
 Ser Leu Gly Lys
 580

<210> 361

<211> 332

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 361

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

4._183952027041SEQLIST.TXT

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

<210> 362
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 362

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tcctgcaagg	ccagcggcta	cacctttacc	agctactaca	tccactgggt	gcgccaggcc	120
cctggacagg	gactggaatg	gatcggcagc	atctaccccg	gcaacgtgaa	caccaactac	180
gcccagaagt	tccagggcag	agccaccctg	accgtggaca	ccagcatcag	caccgcctac	240
atggaactga	gccggctgag	aagcgacgac	accgccgtgt	actactgcac	ccgggtccac	300
tacggcctgg	attggaactt	cgacgtgtgg	ggcaagggca	ccaccgtgac	agtgtctagc	360
gcgtcgacca	agggccctc	ggtgttccct	ctggccctt	gcagcagaag	caccagcgaa	420
tctacagccg	ccctgggctg	cctcgtgaag	gactactttc	ccgagcccgt	gaccgtgtcc	480
tggaactctg	gcgctctgac	aagcggcgtg	cacacctttc	cagccgtgct	ccagagcagc	540
ggcctgtact	ctctgagcag	cgctcgtgac	gtgcccagca	gcagcctggg	caccaagacc	600
tacacctgta	acgtggacca	caagcccagc	aacaccaagg	tggacaagcg	ggtggaatct	660
aagtacggcc	ctccctgccc	tccttgccc	gcccctgaat	ttctgggcgg	accctccgtg	720
ttcctgttcc	ccccaaagcc	caaggacacc	ctgatgatca	gccggacccc	cgaagtgacc	780
tgcgtggtgg	tggatgtgtc	ccaggaagat	cccagaggtg	agttcaattg	gtacgtggac	840
ggcgtggaag	tgcacaacgc	caagaccaag	cccagagagg	aacagttcaa	cagcacctac	900
cgggtggtgt	ccgtgctgac	cgtgctgcac	caggactggc	tgaacggcaa	agagtacaag	960
tgcaaggtgt	ccaacaaggg	cctgcccagc	tccatcgaga	aaaccatcag	caaggccaag	1020
ggccagcccc	gcgagcctca	agtgtatacc	ctgccccctt	gccaggaaga	gatgaccaag	1080
aaccagggtgt	ccctgtggtg	tctcgtgaaa	ggcttctacc	ccagcgacat	tgccgtggaa	1140
tgggagagca	acggccagcc	cgagaacaac	tacaagacca	ccccccctgt	gctggacagc	1200
gacggctcat	tcttcctgta	ctccaagctg	accgtggaca	agagccggtg	gcaggaaggc	1260
aacgtgttca	gctgctccgt	gatgcacgag	gccctgcaca	accactacac	ccagaagtcc	1320
ctgtctctgt	ccctgggcaa	g				1341

<210> 363
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 363

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4. __183952027041SEQLIST.TXT

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atcacctgtc aggccagcca gaacatctac gtgtggctga actggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacaag gccagcaacc tgcacaccgg cgtgcccagc 180
agattttctg gcagcggctc cggcaccgac ttcaccctga caatcagctc cctgcagccc 240
gaggacattg ccacctacta ctgccagcag ggccagacct acccctacac ctttggccag 300
ggcaccaagc tggaaatcaa gcgtacgggtg gccgctccca gcgtgttcat cttcccacct 360
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 420
ccccgcgagg ccaaggtgca gtggaaggtg gacaatgccc tgcagagcgg caacagccag 480
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600
ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 642

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<210> 364

<211> 1740

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 364

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tcctgtcaga caagcggcta caccttcacc gccacatcc tgttctgggtt ccggcaggcc 120
cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
ggcggaggct tccgggatag agtgaccctg acccgggacg tgtaccgcga gatcgacctac 240
atggacatcc ggggcctgaa gcccgatgac accgccgtgt actactgcgc cagagacaga 300
agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtggtggtg 360
tctgccgaca aaaccatac ccaggtgcag ctggtggaat ctggcggcgg agtggtgcag 420
cctggcagaa gcctgagact gagctgtgcc gccagcggct tcaccttcac caaggcctgg 480
atgcaactggg tgcgccaggc ccctggaaag cagctggaat gggtggcca gatcaaggac 540
aagagcaaca gctacgccac ctactacgcc gacagcgtga agggccgggtt caccatcagc 600
cgggacgaca gcaagaacac cctgtacctg cagatgaaca gcctgcgggc cgaggacacc 660
gccgtgtact actgtcgggg cgtgtactat gccctgagcc ctttcgatta ctggggccag 720
ggaaccctcg tgaccgtgtc tagtgataag acccacaccg cttcgaccaa gggcccatcg 780
gtgttccctc tggccccttg cagcagaagc accagcgaat ctacagccgc cctgggctgc 840
ctcgtgaagg actactttcc cgagcccgtg accgtgtcct ggaactcttg cgctctgaca 900
agcggcgtgc acacctttcc agccgtgctc cagagcagcg gcctgtactc tctgagcagc 960
gtcgtgacag tgcccagcag cagcctgggc accaagacct acacctgtaa cgtggaccac 1020
aagcccagca acaccaaggt ggacaagcgg gtggaatcta agtacggccc tccctgccct 1080
ccttgcccag cccctgaatt tctgggcgga ccctccgtgt tcctgttccc cccaaagccc 1140
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caggaagatc ccgaggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc 1260
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ctgcccagct ccctcgagaa aaccatcagc aaggccaagg gccagccccg cgagcctcaa 1440
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gccgtgaaag gcttctaccc cagcgacatt gccgtggaat gggagagcaa cggccagccc 1560
gagaacaact acaagaccac cccccctgtg ctggacagcg acggctcatt cttcctggtg 1620
tccaagctga ccgtggacaa gagccggtgg caggaaggca acgtgttcag ctgctccgtg 1680
atgcacgagg ccctgcacaa ccactacacc cagaagtccc tgtctctgtc cctgggcaag 1740

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<210> 365

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<211> 996
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 365
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atcagctgca agagcagcca gagcctgggtg cacaacaacg ccaacaccta cctgagctgg 120
tatctgcaga agcccggcca gagccccag tccctgatct acaaggtgtc caacagattc 180
agcggcgtgc ccgacagatt ctccggcagc ggctctggca ccgacttcac cctgaagatc 240
agccgggtgg aagccgagga cgtgggcgtg tactattgtg gccagggcac ccagtacccc 300
ttcacctttg gcagcggcac caaggtggaa atcaaggaca aaaccatac ctacatccac 360
gtgaccaga gcccagcag cctgtccgtg tccatcggcg acagagtga catcaactgc 420
cagaccttc agggcgtggg cagcgacctg cactgggtatc agcacaagcc tggcagagcc 480
cccaagctgc tgatccacca cacaagcagc gtggaagatg gcgtgccag cagattttcc 540
ggcagcggct tccacaccag cttcaacctg accatcagcg atctgcaggc cgacgacatt 600
gccacctact attgtcaggt gctgcagttc ttcggcagag gcagcagact gcacatcaag 660
gataagacct ataccgtac ggtggccgct cccagcgtgt tcattttccc acctagcgac 720
gagcagctga agtccggcac agcctctgtc gtgtgcctgc tgaacaactt ctacccccgc 780
gaggccaaag tgcagtggaa ggtggacaac gccctgcaga gcggcaacag ccaggaaagc 840
gtgaccgagc aggacagcaa ggactccacc tacagcctga gcagcaccct gacactgagc 900
aaggccgact acgagaagca caaggtgtac gcctgcgaag tgaccacca gggcctgtct 960
agccccgtga ccaagagctt caaccggggc gagtgt 996

<210> 366
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

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

4.__183952027041SEQLIST.TXT

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

<210> 368

<211> 573

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 368

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

4. 183952027041SEQLIST.TXT

		115					120				125				
Ser	Gly	Thr	Ala	Met	Lys	Lys	Pro	Gly	Ala	Ser	Val	Arg	Val	Ser	Cys
	130					135					140				
Gln	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Ala	His	Ile	Leu	Phe	Trp	Phe	Arg
145					150					155					160
Gln	Ala	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Val	Gly	Trp	Ile	Lys	Pro	Gln
				165					170					175	
Tyr	Gly	Ala	Val	Asn	Phe	Gly	Gly	Gly	Phe	Arg	Asp	Arg	Val	Thr	Leu
			180					185					190		
Thr	Arg	Asp	Val	Tyr	Arg	Glu	Ile	Ala	Tyr	Met	Asp	Ile	Arg	Gly	Leu
		195					200					205			
Lys	Pro	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Arg	Ser	Tyr
	210					215					220				
Gly	Asp	Ser	Ser	Trp	Ala	Leu	Asp	Ala	Trp	Gly	Gln	Gly	Thr	Thr	Val
225					230					235					240
Val	Val	Ser	Ala	Arg	Thr	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro
				245					250					255	
Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly
			260					265					270		
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn
		275					280					285			
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
	290					295					300				
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
305					310					315					320
Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser
				325					330					335	
Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys
			340					345					350		
Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu
		355					360					365			
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu
	370					375					380				
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln
385					390					395					400
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys
				405					410					415	
Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu
			420					425					430		
Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys
		435					440					445			
Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys
	450					455					460				
Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Cys	Thr	Leu	Pro	Pro	Ser
465					470			</							

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530		535		540	
Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn					
545		550		555	560
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys					
	565		570		

<210> 369

<211> 334

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 369

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

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Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
 290 295 300
 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
 305 310 315 320
 Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 325 330

<210> 370
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 370
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 cctggacagg gactggaatg gatcggcagc atctacccc gcaacgtgaa caccaactac 180
 gcccagaagt tccagggcag agccaccctg accgtggaca ccagcatcag caccgcctac 240
 atggaactga gccggctgag aagcgacgac accgccgtgt actactgcac ccggtccac 300
 tacggcctgg attggaactt cgacgtgtgg ggcaagggca ccaccgtgac agtgtctagc 360
 gcgtcgacca agggccctc ggtgttccct ctggcccctt gcagcagaag caccagcgaa 420
 tctacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc 480
 tggaactctg gcgctctgac aagcggcgtg cacaccttc cagccgtgct ccagagcagc 540
 ggcctgtact ctctgagcag cgtcgtgaca gtgcccagca gcagcctggg caccaagacc 600
 tacacctgta acgtggacca caagcccagc aacaccaagg tggacaagcg ggtggaatct 660
 aagtacggcc ctccctgccc tccttgccc gcccctgaat ttctgggcgg accctccgtg 720
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 tgcaagggtg ccaacaaggg cctgcccagc tccatcgaga aaaccatcag caaggccaag 1020
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 aaccaggtgt ccctgtggtg tctcgtgaaa ggcttctacc ccagcgacat tgccgtggaa 1140
 tgggagagca acggccagcc cgagaacaac tacaagacca cccccctgt gctggacagc 1200
 gacggctcat tcttcctgta ctccaagctg accgtggaca agagccggtg gcaggaaggc 1260
 aacgtgttca gctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc 1320
 ctgtctctgt ccctgggcaa g 1341

<210> 371
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 371
 gacatccaga tgacccagag ccccagcagc ctgtctgcc a gcgtgggcga cagagtgacc 60
 atcacctgtc aggcagcca gaacatctac gtgtggctga actggtatca gcagaagccc 120

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```

ggcaaggccc ccaagctgct gatctacaag gccagcaacc tgcacaccgg cgtgcccagc 180
agatttttctg gcagcggctc cggcaccgac ttcaccctga caatcagctc cctgcagccc 240
gaggacattg ccacctacta ctgccagcag ggccagacct acccctacac ctttggccag 300
ggcaccaagc tggaaatcaa gcgtacgggtg gccgctccca gcgtgttcat cttcccacct 360
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 420
ccccgcgagg ccaaggtgca gtggaaggtg gacaatgccc tgcagagcgg caacagccag 480
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600
ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 642

```

<210> 372

<211> 1719

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 372

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caggtgcagc tgggtggaatc tggcggcgga gtggtgcagc ctggcagaag cctgagactg 60
agctgtgccg ccagcggctt caccttcacc aaggcctgga tgcactgggt gcgccaggcc 120
cctggaaagc agctggaatg ggtggcccag atcaaggaca agagcaacag ctacgccacc 180
tactacgccg acagcgtgaa gggccggttc accatcagcc gggacgacag caagaacacc 240
ctgtacctgc agatgaacag cctgcggggc gaggacaccg ccgtgtacta ctgtcggggc 300
gtgtactatg ccctgagccc cttcgattac tggggccagg gaaccctcgt gaccgtgtct 360
agtagcagag cccacctggg gcagtctggc accgccatga agaaaccagg cgcctctgtg 420
cgggtgtcct gtcagacaag cggctacacc ttcaccgccc acatcctgtt ctggttcagg 480
caggcccctg gcagaggact ggaatgggtg ggatggatca agccccagta tggcgccgtg 540
aacttcggcg gaggcttcgg ggatagagt accctgacc gggacgtgta ccgcgagatc 600
gcctacatgg acatccgggg cctgaagccc gatgacaccg ccgtgtacta ctgcgccaga 660
gacagaagct acggcgacag cagctgggct ctggatgctt ggggcccagg cacaaccgtg 720
gtggtgtctg cccggaccgc cagcacaag ggcccatcgg tgttccctct ggccccttgc 780
agcagaagca ccagcgaatc tacagccgcc ctgggctgcc tcgtgaagga ctactttccc 840
gagcccgtga ccgtgtcctg gaactctggc gctctgacaa gcggcgtgca cacctttcca 900
gccgtgtccc agagcagcgg cctgtactct ctgagcagcg tcgtgacagt gcccagcagc 960
agcctgggca ccaagacctt cacctgtaac gtggaccaca agcccagcaa caccaagggtg 1020
gacaagcggg tggaaatctaa gtacggccct ccctgccctc cttgcccagc ccctgaattt 1080
ctgggcggac cctccgtgtt cctgttcccc ccaaagccca aggacaccct gatgatcagc 1140
cggacccccg aagtgcacct cgtggtgggt gatgtgtccc aggaagatcc cgagggtgcag 1200
ttcaattggg acgtggacgg cgtggaagt cacaacgcca agaccaagcc cagagaggaa 1260
cagttcaaca gcacctaccg ggtggtgtcc gtgctgaccg tgctgcacca ggactggctg 1320
aacggcaaag agtacaagt caaggtgtcc aacaagggcc tgcccagctc catcgagaaa 1380
accatcagca aggccaaggg ccagccccgc gagcctcaag tgtgtaccct gccccctagc 1440
caggaagaga tgaccaagaa ccaggtgtcc ctgagctgtg ccgtgaaagg cttctacccc 1500
agcgacattg ccgtggaatg ggagagcaac ggccagcccg agaacaacta caagaccacc 1560
ccccctgtgc tggacagcga cggctcattc ttctgtgtgt ccaagctgac cgtggacaag 1620
agccggtggc aggaaggcaa cgtgttcagc tgctccgtga tgcacgaggc cctgcacaac 1680
cactacaccc agaagtcctt gtctctgtcc ctgggcaag 1719

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<210> 373

<211> 1002

<212> DNA

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<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 373

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atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgcccagc 180
agattttccg gcagcggtt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagg gccagcccaa ggccgcccc gacatcgtga tgacccagac cccctgagc 360
ctgagcgtga cacctggaca gcctgccagc atcagctgca agagcagcca gagcctgggtg 420
cacaacaacg ccaacaccta cctgagctgg tatctgcaga agcccgcca gagccccag 480
tccctgatct acaaggtgtc caacagattc agcggcgtgc ccgacagatt ctccggcagc 540
ggctctggca ccgacttcac cctgaagatc agccgggtgg aagccgagga cgtgggcgtg 600
tactattgtg gccagggcac ccagtacccc ttcaccttg gcagcggcac caaggtggaa 660
atcaagacca agggccccag ccgtacgggtg gccgctccca gcgtgttcat cttccacct 720
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 780
ccccgcgagg ccaaagtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag 840
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgaca 900
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 960
ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 1002
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<210> 374

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 374

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

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145					150					155				160	
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165					170					175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
		195					200				205				
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
	210					215				220					
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225				230				235						240	
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
			245					250					255		
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
	260							265				270			
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
	275						280					285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
	290					295				300					
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305				310					315					320	
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
			325					330					335		
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
		340						345				350			
Pro	Cys	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu
	355					360				365					
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	370				375				380						
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385				390					395					400	
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg
			405					410					415		
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
		420						425				430			
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
	435					440				445					

<210> 375

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 375

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10						15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Gln	Ala	Ser	Gln	Asn	Ile	Tyr	Val	Trp
		20					25						30		

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```

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

```

<210> 376

<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 376

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

```

130					135					140				
Val	Ser	Cys	Gln	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Ala	His	Ile	Leu
				150					155					
Trp	Phe	Arg	Gln	Ala	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Val	Gly	Trp
				165					170					
Lys	Pro	Gln	Tyr	Gly	Ala	Val	Asn	Phe	Gly	Gly	Gly	Phe	Arg	Asp
				180					185					
Val	Thr	Leu	Thr	Arg	Asp	Val	Tyr	Arg	Glu	Ile	Ala	Tyr	Met	Asp
				195					200					
Arg	Gly	Leu	Lys	Pro	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg
210					215					220				
Arg	Ser	Tyr	Gly	Asp	Ser	Ser	Trp	Ala	Leu	Asp	Ala	Trp	Gly	Gln
				230					235					
Thr	Thr	Val	Val	Val	Ser	Ala	Asp	Lys	Thr	His	Thr	Ala	Ser	Thr
				245					250					
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser
				260					265					
Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu
				275					280					
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His
290					295					300				
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser
				310					315					
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys
				325					330					
Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu
				340					345					
Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu
				355					360					
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
370					375					380				
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
				390					395					
Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
				405					410					
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr
				420					425					
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
				435					440					
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser
450					455					460				
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
				470					475					
Cys	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val
				485					490					
Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val
				500					505					
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro
				515					520					
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr
530					535					540				
Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val

545 550 555 560
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 565 570 575
Ser Leu Gly Lys
 580

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<210> 377
<211> 332
<212> PRT
<213> Artificial Sequence
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<220>
<223> Synthetic Construct

◀400> 377															
Tyr 1	Ile	His	Val	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Val	Ser	Ile 15	Gly
Asp	Arg	Val	Thr 20	Ile	Asn	Cys	Gln	Thr 25	Ser	Gln	Gly	Val	Gly 30	Ser	Asp
Leu	His	Trp 35	Tyr	Gln	His	Lys	Pro 40	Gly	Arg	Ala	Pro	Lys 45	Leu	Leu	Ile
His 50	His	Thr	Ser	Ser	Val	Glu 55	Asp	Gly	Val	Pro	Ser 60	Arg	Phe	Ser	Gly
Ser 65	Gly	Phe	His	Thr	Ser 70	Phe	Asn	Leu	Thr	Ile 75	Ser	Asp	Leu	Gln	Ala 80
Asp	Asp	Ile	Ala	Thr 85	Tyr	Tyr	Cys	Gln	Val 90	Leu	Gln	Phe	Phe	Gly 95	Arg
Gly	Ser	Arg	Leu 100	His	Ile	Lys	Asp	Lys 105	Thr	His	Thr	Asp	Ile 110	Val	Met
Thr	Gln	Thr 115	Pro	Leu	Ser	Leu	Ser 120	Val	Thr	Pro	Gly	Gln 125	Pro	Ala	Ser
Ile 130	Ser	Cys	Lys	Ser	Ser	Gln 135	Ser	Leu	Val	His	Asn 140	Asn	Ala	Asn	Thr
Tyr 145	Leu	Ser	Trp	Tyr	Leu 150	Gln	Lys	Pro	Gly	Gln 155	Ser	Pro	Gln	Ser	Leu 160
Ile	Tyr	Lys	Val 165	Ser	Asn	Arg	Phe	Ser	Gly 170	Val	Pro	Asp	Arg	Phe 175	Ser
Gly	Ser	Gly	Ser 180	Gly	Thr	Asp	Phe	Thr 185	Leu	Lys	Ile	Ser	Arg 190	Val	Glu
Ala	Glu	Asp 195	Val	Gly	Val	Tyr	Tyr 200	Cys	Gly	Gln	Gly	Thr 205	Gln	Tyr	Pro
Phe 210	Thr	Phe	Gly	Ser	Gly	Thr 215	Lys	Val	Glu	Ile	Lys 220	Asp	Lys	Thr	His
Thr 225	Arg	Thr	Val	Ala	Ala 230	Pro	Ser	Val	Phe	Ile 235	Phe	Pro	Pro	Ser	Asp 240
Glu	Gln	Leu	Lys 245	Ser	Gly	Thr	Ala	Ser	Val 250	Val	Cys	Leu	Leu	Asn 255	Asn
Phe	Tyr	Pro	Arg 260	Glu	Ala	Lys	Val	Gln 265	Trp	Lys	Val	Asp	Asn 270	Ala	Leu
Gln	Ser	Gly 275	Asn	Ser	Gln	Glu	Ser 280	Val	Thr	Glu	Gln	Asp 285	Ser	Lys	Asp

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Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr
290						295					300				
Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser
305					310					315					320
Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				
				325					330						

<210> 378
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 378
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 tcctgcaagg ccagcggcta cacctttacc agctactaca tccactgggt gcgccaggcc 120
 cctggacagg gactggaatg gatcggcagc atctacccc gcaacgtgaa caccaactac 180
 gcccagaagt tccagggcag agccaccctg accgtggaca ccagcatcag caccgcctac 240
 atggaactga gccggctgag aagcgacgac accgccgtgt actactgcac ccggtccac 300
 tacggcctgg attggaactt cgacgtgtgg ggcaaggga ccaccgtgac agtgtctagc 360
 gcgtcgacca agggccctc ggtgttcct ctggcccctt gcagcagaag caccagcgaa 420
 tctacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc 480
 tggaactctg gcgctctgac aagcggcgtg cacaccttc cagccgtgct ccagagcagc 540
 ggcctgtact ctctgagcag cgtcgtgaca gtgcccagca gcagcctggg caccaagacc 600
 tacacctgta acgtggacca caagcccagc aacaccaagg tggacaagcg ggtggaatct 660
 aagtacggcc ctccctgccc tccttgccc gcccctgaat ttctgggcgg accctccgtg 720
 ttctgtttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc 780
 tgcgtggtgg tggatgtgtc ccaggaagat cccgaggtgc agttcaattg gtacgtggac 840
 ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagttcaa cagcacctac 900
 cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agagtacaag 960
 tgcaagggtg ccaacaaggg cctgcccagc tccatcgaga aaaccatcag caaggccaag 1020
 ggccagcccc gcgagcctca agtgtatacc ctgccccctt gccaggaaga gatgaccaag 1080
 aaccaggtgt ccctgtggtg tctcgtgaaa ggcttctacc ccagcgacat tgccgtggaa 1140
 tgggagagca acggccagcc cgagaacaac tacaagacca cccccctgt gctggacagc 1200
 gacggctcat tcttcctgta ctccaagctg accgtggaca agagccggtg gcaggaaggc 1260
 aacgtgttca gctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc 1320
 ctgtctctgt ccctgggcaa g 1341

<210> 379
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 379
 gacatccaga tgacccagag ccccagcagc ctgtctgcc a gcgtgggcga cagagtgacc 60
 atcacctgtc aggcagcca gaacatctac gtgtggctga actggtatca gcagaagccc 120

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ggcaaggccc ccaagctgct gatctacaag gccagcaacc tgcacaccgg cgtgcccagc 180
agatttttctg gcagcggctc cggcaccgac ttcaccctga caatcagctc cctgcagccc 240
gaggacattg ccacctacta ctgccagcag ggccagacct acccctacac ctttggccag 300
ggcaccaagc tggaaatcaa gcgtacggtg gccgctccca gcgtgttcat cttcccacct 360
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 420
ccccgcgagg ccaaggtgca gtggaagggt gacaatgccc tgcaagcgg caacagccag 480
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600
ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 642

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<210> 380

<211> 1740

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 380

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agctgtgccg ccagcggctt caccttcacc aaggcctgga tgcactgggt gcgccaggcc 120
cctggaaagc agctggaatg ggtggcccag atcaaggaca agagcaacag ctacgccacc 180
tactacgccg acagcgtgaa gggccggttc accatcagcc gggacgacag caagaacacc 240
ctgtacctgc agatgaacag cctgcggggc gaggacaccg ccgtgtacta ctgtcggggc 300
gtgtactatg ccctgagccc cttcgattac tggggccagg gaaccctcgt gaccgtgtct 360
agtgcacaaa cccataccag agcccacctg gtgcagtctg gcaccgccat gaagaaacca 420
ggcgccctctg tgcgggtgtc ctgtcagaca agcggctaca ctttcaccgc ccacatcctg 480
ttctggttcc ggcaggcccc tggcagagga ctggaatggg tgggatggat caagccccag 540
tatggcgccg tgaacttcgg cggaggcttc cgggatagag tgaccctgac ccgggacgtg 600
taccgcgaga tcgcctacat ggacatccgg ggcctgaagc ccgatgacac cgccgtgtac 660
tactgcgcca gagacagaag ctacggcgac agcagctggg ctctggatgc ttggggccag 720
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gtgtttccctc tggccccttg cagcagaagc accagcgaat ctacagccgc cctgggctgc 840
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agcggcgtgc acacctttcc agccgtgtc cagagcagcg gcctgtactc tctgagcagc 960
gtcgtgacag tgcccagcag cagcctgggc accaagacct acacctgtaa cgtggaccac 1020
aagcccagca acaccaaggt ggacaagcgg gtggaatcta agtacggccc tccctgccct 1080
ccttgcccag cccctgaatt tctgggcgga ccctccgtgt tcctgttccc cccaaagccc 1140
aaggacaccc tgatgatcag ccggaccccc gaagtgcct gcgtgggtgg ggatgtgtcc 1200
caggaagatc ccgaggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc 1260
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gccgtgaaag gcttctaccc cagcgacatt gccgtggaat gggagagcaa cggccagccc 1560
gagaacaact acaagaccac cccccctgtg ctggacagcg acggctcatt cttcctgggtg 1620
tccaagctga ccgtggacaa gagccggtgg caggaaggca acgtgttcag ctgctccgtg 1680
atgcacgagg ccctgcacaa ccactacacc cagaagtccc tgtctctgtc cctgggcaag 1740

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<210> 381

<211> 996

4.__183952027041SEQLIST.TXT

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 381

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ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgcccagc 180
agattttccg gcagcggcctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcagggt ctgcagttct tcggcagagg cagcagactg 300
cacatcaagg acaaaaccca taccgacatc gtgatgacct agacccccct gagcctgagc 360
gtgacacctg gacagcctgc cagcatcagc tgcaagagca gccagagcct ggtgcacaac 420
aacgccaaca cctacctgag ctggtatctg cagaagcccg gccagagccc ccagtccctg 480
atctacaagg tgtccaacag attcagcggc gtgcccgcga gattctccgg cagcggctct 540
ggcaccgact tcacctgaa gatcagccgg gtggaagccg aggacgtggg cgtgtactat 600
tgtggccagg gcacccagta ccccttcacc tttggcagcg gcaccaaggt ggaaatcaag 660
gataagaccc atacccttac ggtggccgct cccagcgtgt tcattctccc acctagcgac 720
gagcagctga agtccggcac agcctctgtc gtgtgcctgc tgaacaactt ctacccccgc 780
gaggccaaag tgcagtggaa ggtggacaac gccctgcaga gcggcaacag ccaggaaagc 840
gtgaccgagc aggacagcaa ggactccacc tacagcctga gcagcaccct gacactgagc 900
aaggccgact acgagaagca caaggtgtac gcctgcgaag tgaccaccca gggcctgtct 960
agccccgtga ccaagagctt caaccggggc gagtgt 996
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<210> 382

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 382

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

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```

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                150                155                160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                170                175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
                180                185                190
Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
                195                200                205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
                210                215                220
Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
225                230                235                240
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                250                255
Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
                260                265                270
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                275                280                285
Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
                290                295                300
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                310                315                320
Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
                325                330                335
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
                340                345                350
Pro Cys Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
                355                360                365
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                370                375                380
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                390                395                400
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                410                415
Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
                420                425                430
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
                435                440                445

```

<210> 383

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 383

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Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Pro Gly
1                5                10                15
Gln Arg Ala Thr Ile Thr Cys Arg Ala Ser Glu Ser Val Glu Tyr Tyr

```

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```

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

```

<210> 384

<211> 573

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 384

```

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

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Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser
130						135					140				
Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Thr	Lys	Ala	Trp	Met	His	Trp	Val
145				150						155					160
Arg	Gln	Ala	Pro	Gly	Lys	Gln	Leu	Glu	Trp	Val	Ala	Gln	Ile	Lys	Asp
				165					170					175	
Lys	Ser	Asn	Ser	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg
			180					185					190		
Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met
		195					200					205			
Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Arg	Gly	Val
		210				215					220				
Tyr	Tyr	Ala	Leu	Ser	Pro	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val
225					230					235					240
Thr	Val	Ser	Ser	Arg	Thr	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro
				245					250					255	
Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly
			260					265					270		
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn
		275					280					285			
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
290					295						300				
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
305					310					315					320
Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser
				325					330					335	
Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys
			340					345					350		
Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu
		355					360						365		
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu
						375					380				
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln
385					390					395					400
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys
				405				410						415	
Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu
			420					425					430		
Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys
		435					440					445			
Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys
		450				455					460				
Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Cys	Thr	Leu	Pro	Pro	Ser
465					470					475					480
Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Ser	Cys	Ala	Val	Lys
				485					490					495	
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln
			500					505					510		
Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly
		515					520					525			
Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln
		530				535					540				

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Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 545 550 555 560
 His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 565 570

<210> 385
 <211> 334
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 385
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Val His Asn
 20 25 30
 Asn Ala Asn Thr Tyr Leu Ser Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Ser Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gly Gln Gly
 85 90 95
 Thr Gln Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys
 100 105 110
 Gly Gln Pro Lys Ala Ala Pro Tyr Ile His Val Thr Gln Ser Pro Ser
 115 120 125
 Ser Leu Ser Val Ser Ile Gly Asp Arg Val Thr Ile Asn Cys Gln Thr
 130 135 140
 Ser Gln Gly Val Gly Ser Asp Leu His Trp Tyr Gln His Lys Pro Gly
 145 150 155 160
 Arg Ala Pro Lys Leu Ile His His Thr Ser Ser Val Glu Asp Gly
 165 170 175
 Val Pro Ser Arg Phe Ser Gly Ser Gly Phe His Thr Ser Phe Asn Leu
 180 185 190
 Thr Ile Ser Asp Leu Gln Ala Asp Asp Ile Ala Thr Tyr Tyr Cys Gln
 195 200 205
 Val Leu Gln Phe Phe Gly Arg Gly Ser Arg Leu His Ile Lys Thr Lys
 210 215 220
 Gly Pro Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
 225 230 235 240
 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
 245 250 255
 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
 260 265 270
 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
 275 280 285
 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala

4.__183952027041SEQLIST.TXT

290	295	300
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly		
305	310	315
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys		320
	325	330

<210> 386
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 386
 caggtgcagc tgcaggaatc tggccctggc ctcgtgaagc ctagccagac cctgagcctg 60
 acctgtaccg tgtccggctt cagcctgagc gactacggcg tgcactgggt gcgccagcca 120
 cctggaaaag gcctggaatg gctgggcgtg atctgggctg gcggaggcac caactacaac 180
 cccagcctga agtccagaaa gaccatcagc aaggacacca gcaagaacca ggtgtccctg 240
 aagctgagca gcgtgacagc cgccgatacc gccgtgtact actgcgccag agacaagggc 300
 tacagctact actacagcat ggactactgg ggccagggca ccaccgtgac cgtgtcatcc 360
 gcgtcgacca agggcccctc ggtgttccct ctggcccctt gcagcagaag caccagcgaa 420
 tctacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc 480
 tggaactctg gcgctctgac aagcggcgtg cacacctttc cagccgtgct ccagagcagc 540
 ggcctgtact ctctgagcag cgtcgtgaca gtgcccagca gcagcctggg caccaagacc 600
 tacacctgta acgtggacca caagcccagc aacaccaagg tggacaagcg ggtggaatct 660
 aagtacggcc ctccctgccc tccttgcccga gccctgaat ttctgggcgg accctccgtg 720
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 cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agagtacaag 960
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 ggccagcccc gcgagcctca agtgtatacc ctgccccctt gccaggaaga gatgaccaag 1080
 aaccaggtgt ccctgtggtg tctcgtgaaa ggcttctacc ccagcgacat tgccgtggaa 1140
 tgggagagca acggccagcc cgagaacaac tacaagacca cccccctgt gctggacagc 1200
 gacggctcat tcttctgta ctccaagctg accgtggaca agagccggtg gcaggaaggc 1260
 aacgtgttca gctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc 1320
 ctgtctctgt ccctgggcaa g 1341

<210> 387
 <211> 654
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 387
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 atcacctgta gagccagcga gagcgtggaa tattacgtga ccagcctgat gcagtgggtat 120
 cagcagaagc ccggccagcc cccaagctg ctgattttcg ccgccagcaa cgtggaaagc 180

4. __183952027041SEQLIST.TXT

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acctttggcc agggcaccaa gctggaaatc aagcgtacgg tggccgctcc cagcgtgttc 360
atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 420
aacaacttct acccccgcga ggccaagggtg cagtggaaagg tggacaatgc cctgcagagc 480
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 540
agcacctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 600
accaccagg gcctgtctag ccccgtagacc aagagcttca accggggcga gtgt 654

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<210> 388

<211> 1719

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 388

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cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
ggcggaggct tccgggatag agtgaccctg acccgggacg tgtaccgcga gatcgctac 240
atggacatcc ggggcctgaa gcccgatgac accgccgtgt actactgcgc cagagacaga 300
agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtggtggtg 360
tctgcctctc aggtgcagct ggtggaatct ggcgggcgag tgggtgcagc tggcagaagc 420
ctgagactga gctgtgccgc cagcggcttc acctcacca aggcctggat gcactgggtg 480
cgccaggccc ctggaagca gctggaatgg gtggcccaga tcaaggacaa gagcaacagc 540
tacgccacct actacgccga cagcgtgaag ggccggttca ccatcagccg ggacgacagc 600
aagaacaccc tgtacctgca gatgaacagc ctgcggggcc aggacaccgc cgtgtactac 660
tgtcggggcg tgtactatgc cctgagcccc ttcgattact gggggccaggg aaccctcgtg 720
accgtgtcta gtcggaccgc ttcgaccaag ggcccatcgg tgttccctct ggccccttgc 780
agcagaagca ccagcgaatc tacagccgcc ctgggctgcc tcgtgaagga ctactttccc 840
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gccgtgtccc agagcagcgg cctgtactct ctgagcagcg tcgtgacagt gccagcagc 960
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cagttcaaca gcacctaccg ggtggtgtcc gtgctgaccg tgctgcacca ggactggctg 1320
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agccgggtggc aggaaggcaa cgtgttcagc tgctccgtga tgcacgaggc cctgcacaac 1680
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<210> 389

<211> 1002

<212> DNA

<213> Artificial Sequence

4.__183952027041SEQLIST.TXT

<220>

<223> Synthetic Construct

<400> 389

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gacatcgtga tgacccagac ccccctgagc ctgagcgtga cacctggaca gcctgccagc 60
atcagctgca agagcagcca gagcctggtg cacaacaacg ccaacaccta cctgagctgg 120
tatctgcaga agcccggcca gagcccccag tccctgatct acaaggtgtc caacagattc 180
agcggcgtgc ccgacagatt ctccggcagc ggctctggca ccgacttcac cctgaagatc 240
agccgggttg aagccgagga cgtgggcgtg tactattgtg gccagggcac ccagtacccc 300
ttcacctttg gcagcggcac caaggtggaa atcaagggcc agcccaaggc cgccccctac 360
atccacgtga cccagagccc cagcagcctg tccgtgtcca tcggcgacag agtgaccatc 420
aactgccaga cctctcaggg cgtgggcagc gacctgcact ggtatcagca caagcctggc 480
agagccccc aagctgctgat ccaccacaca agcagcgtgg aagatggcgt gccagcaga 540
ttttccggca gcggtttcca caccagcttc aacctgacca tcagcgatct gcaggccgac 600
gacattgcc a cctactattg tcaggtgctg cagttcttcg gcagaggcag cagactgcac 660
atcaagacca agggccccag ccgtacggtg gccgctccca gcgtgttcat cttccacct 720
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 780
ccccgcgagg ccaaagtgc gtggaaggtg gacaacgccc tgcagagcgg caacagccag 840
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgaca 900
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 960
ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 1002

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<210> 390

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 390

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

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4.__183952027041SEQLIST.TXT

Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165					170					175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
	210					215					220				
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225					230					235					240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
				245					250					255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
			260					265					270		
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
		275					280					285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
		290				295					300				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305					310					315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
				325					330					335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
			340					345					350		
Pro	Cys	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu
		355					360					365			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	370					375					380				
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385					390					395					400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg
			405						410					415	
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
			420					425					430		
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
		435					440					445			

<210> 391

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 391

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

4._183952027041SEQLIST.TXT

```

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

```

<210> 392

<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 392

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

```

4._183952027041SEQLIST.TXT

Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Thr	Lys	Ala	Trp
145					150					155					160
Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gln	Leu	Glu	Trp	Val	Ala
				165					170					175	
Gln	Ile	Lys	Asp	Lys	Ser	Asn	Ser	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp	Ser
			180					185					190		
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Leu
		195					200					205			
Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr
	210					215					220				
Cys	Arg	Gly	Val	Tyr	Tyr	Ala	Leu	Ser	Pro	Phe	Asp	Tyr	Trp	Gly	Gln
225					230					235					240
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Ala	Ser	Thr
				245					250					255	
Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser
			260					265					270		
Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu
		275					280					285			
Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His
	290					295					300				
Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser
305					310					315					320
Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys
				325					330					335	
Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu
			340					345					350		
Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu
		355				360					365				
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
	370					375					380				
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
385					390					395					400
Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
				405					410					415	
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr
			420					425					430		
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
		435				440						445			
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser
	450					455					460				
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
465					470					475					480
Val	Cys	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val
				485					490					495	
Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val
			500					505					510		
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro
		515					520					525			
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr
	530					535					540				
Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val
545					550					555					560

4._183952027041SEQLIST.TXT

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
565 570 575
Ser Leu Gly Lys
580

<210> 393
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 393
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Val His Asn
20 25 30
Asn Ala Asn Thr Tyr Leu Ser Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Gln Ser Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gly Gln Gly
85 90 95
Thr Gln Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys
100 105 110
Asp Lys Thr His Thr Tyr Ile His Val Thr Gln Ser Pro Ser Ser Leu
115 120 125
Ser Val Ser Ile Gly Asp Arg Val Thr Ile Asn Cys Gln Thr Ser Gln
130 135 140
Gly Val Gly Ser Asp Leu His Trp Tyr Gln His Lys Pro Gly Arg Ala
145 150 155 160
Pro Lys Leu Leu Ile His His Thr Ser Ser Val Glu Asp Gly Val Pro
165 170 175
Ser Arg Phe Ser Gly Ser Gly Phe His Thr Ser Phe Asn Leu Thr Ile
180 185 190
Ser Asp Leu Gln Ala Asp Asp Ile Ala Thr Tyr Tyr Cys Gln Val Leu
195 200 205
Gln Phe Phe Gly Arg Gly Ser Arg Leu His Ile Lys Asp Lys Thr His
210 215 220
Thr Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
225 230 235 240
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
245 250 255
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
260 265 270
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
275 280 285
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr

4.__183952027041SEQLIST.TXT

290		295		300	
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser					
305		310		315	320
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys					
	325		330		

<210> 394
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 394
 caggtgcagc tgcaggaatc tggccctggc ctcgtgaagc ctagccagac cctgagcctg 60
 acctgtaccg tgtccggctt cagcctgagc gactacggcg tgcactgggt gcgccagcca 120
 cctggaaaag gcctggaatg gctgggcgtg atctgggctg gcggaggcac caactacaac 180
 cccagcctga agtccagaaa gaccatcagc aaggacacca gcaagaacca ggtgtccctg 240
 aagctgagca gcgtgacagc cgccgatacc gccgtgtact actgcgccag agacaagggc 300
 tacagctact actacagcat ggactactgg ggccagggca ccaccgtgac cgtgtcatcc 360
 gcgtcgacca agggcccctc ggtgttccct ctggcccctt gcagcagaag caccagcgaa 420
 tctacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc 480
 tggaactctg gcgctctgac aagcggcgtg cacacctttc cagccgtgct ccagagcagc 540
 ggcctgtact ctctgagcag cgtcgtgaca gtgcccagca gcagcctggg caccaagacc 600
 tacacctgta acgtggacca caagcccagc aacaccaagg tggacaagcg ggtggaatct 660
 aagtacggcc ctccctgccc tccttgccca gcccctgaat ttctgggcgg accctccgtg 720
 ttctgtttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc 780
 tgcgtggtgg tggatgtgtc ccaggaagat cccgaggtgc agttcaattg gtacgtggac 840
 ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagttcaa cagcacctac 900
 cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agagtacaag 960
 tgcaaggtgt ccaacaaggg cctgcccagc tccatcgaga aaaccatcag caaggccaag 1020
 ggccagcccc gcgagcctca agtgtatacc ctgccccctt gccaggaaga gatgaccaag 1080
 aaccaggtgt ccctgtggtg tctcgtgaaa ggcttctacc ccagcgacat tgccgtggaa 1140
 tgggagagca acggccagcc cgagaacaac tacaagacca cccccctgt gctggacagc 1200
 gacggctcat tcttcctgta ctccaagctg accgtggaca agagccggtg gcaggaaggc 1260
 aacgtgttca gctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc 1320
 ctgtctctgt ccctgggcaa g 1341

<210> 395
 <211> 654
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 395
 gacatcgtgc tgacacagag ccctgctagc ctggccgtgt ctcctggaca gagggccacc 60
 atcacctgta gagccagcga gagcgtggaa tattacgtga ccagcctgat gcagtgggtat 120
 cagcagaagc ccggccagcc cccaagctg ctgattttcg ccgccagcaa cgtggaaagc 180

4. __183952027041SEQLIST.TXT

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ggcgtgccag ccagattttc cggcagcggc tctggcaccg acttcaccct gaccatcaac 240
cccgtggaag ccaacgacgt ggccaactac tactgccagc agagccggaa ggtgccctac 300
acctttggcc agggcaccaa gctggaaatc aagcgtacgg tggccgctcc cagcgtgttc 360
atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 420
aacaacttct acccccgcga ggccaaggtg cagtggaaagg tggacaatgc cctgcagagc 480
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 540
agcacctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 600
accaccagg gcctgtctag ccccgtagacc aagagcttca accggggcga gtgt 654

```

<210> 396

<211> 1740

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 396

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agagcccacc tgggtgcagtc tggcaccgcc atgaagaaac caggcgcctc tgtgcgggtg 60
tcctgtcaga caagcggcta caccttcacc gcccacatcc tgttcttggtt ccggcaggcc 120
cctggcagag gactggaatg ggtgggatgg atcaagcccc agtatggcgc cgtgaacttc 180
ggcggaggct tccgggatat agtgaccctg acccgggacg tgtaccgcga gatcgacctac 240
atggacatcc ggggcctgaa gcccgatgac accgccgtgt actactgcgc cagagacaga 300
agctacggcg acagcagctg ggctctggat gcttggggcc agggcacaac cgtggtggtg 360
tctgccgaca aaaccatac ccagggtgcag ctggtggaat ctggcggcgg agtggtgcag 420
cctggcagaa gcctgagact gagctgtgcc gccagcggct tcaccttcac caaggcctgg 480
atgcaactggg tgcgccaggc ccctggaaag cagctggaat ggggtggcca gatcaaggac 540
aagagcaaca gctacgccac ctactacgcc gacagcgtga agggccggtt caccatcagc 600
cgggacgaca gcaagaacac cctgtacctg cagatgaaca gcctgcgggc cgaggacacc 660
gccgtgtact actgtcgggg cgtgtactat gccctgagcc ctttcgatta ctggggccag 720
ggaaccctcg tgaccgtgtc tagtgataag acccacaccg cttcgaccaa gggcccatcg 780
gtgttccctc tggccccttg cagcagaagc accagcgaat ctacagccgc cctgggctgc 840
ctcgtgaagg actactttcc cgagcccgtg accgtgtcct ggaactctgg cgctctgaca 900
agcggcgtgc acacctttcc agccgtgctc cagagcagcg gcctgtactc tctgagcagc 960
gtcgtgacag tgcccagcag cagcctgggc accaagacct acacctgtaa cgtggaccac 1020
aagcccagca acaccaaggt ggacaagcgg gtggaatcta agtacggccc tccctgccct 1080
ccttgcccag cccctgaatt tctgggcgga ccctccgtgt tcctgttccc cccaaagccc 1140
aaggacaccc tgatgatcag ccggaccccc gaagtgcct gcgtggtggt ggatgtgtcc 1200
caggaagatc ccgaggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc 1260
aagaccaagc ccagagagga acagttcaac agcacctacc ggggtggtgtc cgtgctgacc 1320
gtgctgcacc aggactggct gaacggcaaa gagtacaagt gcaagggtgtc caacaagggc 1380
ctgcccagct ccatcgagaa aaccatcagc aaggccaagg gccagccccg cgagcctcaa 1440
gtgtgtaccc tgccccctag ccaggaagag atgaccaaga accaggtgtc cctgagctgt 1500
gccgtgaaag gcttctaccc cagcgacatt gccgtggaat gggagagcaa cggccagccc 1560
gagaacaact acaagaccac cccccctgtg ctggacagcg acggctcatt cttcctgggtg 1620
tccaagctga ccgtggacaa gagccggtgg caggaaggca acgtgttcag ctgctccgtg 1680
atgcacgagg ccctgcacaa ccactacacc cagaagtccc tgtctctgtc cctgggcaag 1740

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<210> 397

<211> 996

<212> DNA

4.__183952027041SEQLIST.TXT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 397

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atcagctgca agagcagcca gagcctggtg cacaacaacg ccaacaccta cctgagctgg 120
tatctgcaga agcccggcca gagcccccag tccctgatct acaaggtgtc caacagattc 180
agcggcgtgc ccgacagatt ctccggcagc ggctctggca ccgacttcac cctgaagatc 240
agccgggttg aagccgagga cgtgggcgtg tactattgtg gccagggcac ccagtacccc 300
ttcacctttg gcagcggcac caaggtggaa atcaaggaca aaaccatac ctacatccac 360
gtgaccaga gcccagcag cctgtccgtg tccatcggcg acagagtgc catcaactgc 420
cagacctctc agggcgtggg cagcgacctg cactggtatc agcacaagcc tggcagagcc 480
cccaagctgc tgatccacca cacaagcagc gtggaagatg gcgtgcccag cagattttcc 540
ggcagcggct tccacaccag cttcaacctg accatcagcg atctgcaggc cgacgacatt 600
gccacctact attgtcaggt gctgcagttc ttcggcagag gcagcagact gcacatcaag 660
gataagaccc atacccttac ggtggccgct cccagcgtgt tcatcttccc acctagcgac 720
gagcagctga agtccggcac agcctctgtc gtgtgcctgc tgaacaactt ctacccccgc 780
gaggccaaag tgcagtggaa ggtggacaac gccctgcaga gcggcaacag ccaggaaagc 840
gtgaccgagc aggacagcaa ggactccacc tacagcctga gcagcaccct gacactgagc 900
aaggccgact acgagaagca caaggtgtac gcctgcgaag tgaccacca gggcctgtct 960
agccccgtga ccaagagctt caaccggggc gagtgt 996

```

<210> 398

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 398

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

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4.__183952027041SEQLIST.TXT

145					150					155				160	
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165					170					175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
		195					200				205				
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
	210					215				220					
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225				230				235						240	
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
			245					250					255		
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
		260						265					270		
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
	275						280					285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
	290					295					300				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305				310					315					320	
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
			325					330					335		
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
		340						345				350			
Pro	Cys	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu
	355					360				365					
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	370				375				380						
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385				390					395					400	
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg
			405					410					415		
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
		420					425					430			
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
	435					440				445					

<210> 399

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 399

Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val	Ser	Pro	Gly
1				5				10					15		
Gln	Arg	Ala	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Glu	Ser	Val	Glu	Tyr	Tyr
		20					25						30		

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```

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

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<210> 400

<211> 573

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 400

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

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130 135 140

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545 550 555 560
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
565 570

```
<210> 401
<211> 334
<212> PRT
<213> Artificial Sequence
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<220>
<223> Synthetic Construct

<400> 401															
Tyr 1	Ile	His	Val	Thr 5	Gln	Ser	Pro	Ser 10	Ser	Leu	Ser	Val	Ser 15	Ile	Gly
Asp	Arg	Val	Thr 20	Ile	Asn	Cys	Gln	Thr 25	Ser	Gln	Gly	Val	Gly 30	Ser	Asp
Leu	His	Trp	Tyr 35	Gln	His	Lys	Pro	Gly 40	Arg	Ala	Pro	Lys 45	Leu	Leu	Ile
His	His	Thr	Ser 50	Ser	Val	Glu 55	Asp	Gly	Val	Pro	Ser	Arg 60	Phe	Ser	Gly
Ser 65	Gly	Phe	His	Thr	Ser	Phe	Asn	Leu	Thr	Ile	Ser	Asp	Leu	Gln	Ala 80
Asp	Asp	Ile	Ala	Thr 85	Tyr	Tyr	Cys	Gln	Val	Leu	Gln	Phe	Phe	Gly 95	Arg
Gly	Ser	Arg	Leu 100	His	Ile	Lys	Gly	Gln 105	Pro	Lys	Ala	Ala	Pro	Asp	Ile
Val	Met	Thr	Gln 115	Thr	Pro	Leu	Ser	Leu 120	Ser	Val	Thr	Pro	Gly 125	Gln	Pro
Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Val	His	Asn	Asn	Ala
Asn 145	Thr	Tyr	Leu	Ser	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Gln 160
Ser	Leu	Ile	Tyr	Lys 165	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg
Phe	Ser	Gly	Ser	Gly 180	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg
Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Gly	Gln	Gly	Thr	Gln
Tyr	Pro	Phe	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Val	Glu	Ile	Lys	Thr	Lys
Gly 225	Pro	Ser	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro
Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu
Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn
Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser
Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala
>300															

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Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
 305 310 315 320
 Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 325 330

<210> 402
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 402
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 acctgtaccg tgtccggctt cagcctgagc gactacggcg tgcactgggt gcgccagcca 120
 cctggaaaag gcctggaatg gctgggctgt atctgggctg gcggaggcac caactacaac 180
 cccagcctga agtccagaaa gaccatcagc aaggacacca gcaagaacca ggtgtccctg 240
 aagctgagca gcgtgacagc cgccgatacc gccgtgtact actgcgccag agacaagggc 300
 tacagctact actacagcat ggactactgg ggccagggca ccaccgtgac cgtgtcatcc 360
 gcgtcgacca agggcccctc ggtgttccct ctggcccctt gcagcagaag caccagcgaa 420
 tctacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc 480
 tggaactctg gcgctctgac aagcggcgtg cacacctttc cagccgtgct ccagagcagc 540
 ggcctgtact ctctgagcag cgtcgtgaca gtgccagca gcagcctggg caccaagacc 600
 tacacctgta acgtggacca caagcccagc aacaccaagg tggacaagcg ggtggaatct 660
 aagtacggcc ctccctgccc tccttgcca gccctgaat ttctgggcgg accctccgtg 720
 ttctgtttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc 780
 tgcgtgggtg tggatgtgtc ccaggaagat cccgaggtgc agttcaattg gtacgtggac 840
 ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagttcaa cagcacctac 900
 cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agagtacaag 960
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 ggccagcccc gcgagcctca agtgtatacc ctgccccctt gccaggaaga gatgaccaag 1080
 aaccaggtgt ccctgtggtg tctcgtgaaa ggcttctacc ccagcgacat tgccgtggaa 1140
 tgggagagca acggccagcc cgagaacaac tacaagacca cccccctgt gctggacagc 1200
 gacggctcat tcttcctgta ctccaagctg accgtggaca agagccggtg gcaggaaggc 1260
 aacgtgttca gctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc 1320
 ctgtctctgt ccctgggcaa g 1341

<210> 403
 <211> 654
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 403
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 cagcagaagc ccggccagcc cccaagctg ctgattttcg ccgccagcaa cgtggaaagc 180
 ggcgtgccag ccagattttc cggcagcggc tctggcaccg acttcaccct gaccatcaac 240

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cccgtggaag ccaacgacgt ggccaactac tactgccagc agagccggaa ggtgccctac 300
acctttggcc agggcaccaa gctggaaatc aagcgtacgg tggccgctcc cagcgtgttc 360
atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 420
aacaacttct acccccgcga ggccaagggtg cagtgggaagg tggacaatgc cctgcagagc 480
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 540
agcacctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 600
accaccagg gcctgtctag ccccgtagc aagagcttca accggggcga gtgt 654

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<210> 404

<211> 1719

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 404

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agctgtgccg ccagcggctt caccttcacc aaggcctgga tgcactgggt gcgccaggcc 120
cctgaaaagc agctggaatg ggtggcccag atcaaggaca agagcaacag ctacgccacc 180
tactacgccg acagcgtgaa gggccggttc accatcagcc gggacgacag caagaacacc 240
ctgtacctgc agatgaacag cctgcggggc gaggacaccg ccgtgtacta ctgtcggggc 300
gtgtactatg ccctgagccc cttcgattac tggggccagg gaaccctcgt gaccgtgtct 360
agtagcagag ccacactggg gcagtctggc accgccatga agaaaccagg cgcctctgtg 420
cgggtgtcct gtcagacaag cggctacacc ttcaccgcc acatcctgtt ctggttccgg 480
caggcccctg gcagaggact ggaatgggtg ggatggatca agcccagta tggcgccgtg 540
aacttcggcg gaggcttcg ggatagagt accctgacc gggacgtgta ccgcgagatc 600
gcctacatgg acatccgggg cctgaagccc gatgacacc ccgtgtacta ctgcgccaga 660
gacagaagct acggcgacag cagctgggct ctggatgctt ggggcccagg cacaaccgtg 720
gtggtgtctg cccggaccgc cagcacaag ggcccatcgg tgttccctct ggccccttgc 780
agcagaagca ccagcgaatc tacagccgcc ctgggctgcc tcgtgaagga ctactttccc 840
gagcccgtga ccgtgtcctg gaactctggc gctctgacaa gcggcgtgca cacctttcca 900
gccgtgtccc agagcagcgg cctgtactct ctgagcagcg tcgtgacagt gccagcagc 960
agcctgggca ccaagaccta cacctgtaac gtggaccaca agcccagcaa caccaagggtg 1020
gacaagcggg tggaaatctaa gtacggccct ccctgccctc cttgcccagc ccctgaattt 1080
ctgggcggac cctccgtgtt cctgttcccc ccaaagccca aggacaccct gatgatcagc 1140
cggacccccg aagtgaacct cgtggtgggt gatgtgtccc aggaagatcc cgagggtcag 1200
ttcaattggg acgtggacgg cgtggaagtg cacaacgcc agaccaagcc cagagaggaa 1260
cagttcaaca gcacctaccg ggtggtgtcc gtgctgaccg tgctgcacca ggactggctg 1320
aacggcaaag agtacaagt caaggtgtcc aacaagggcc tgcccagctc catcgagaaa 1380
accatcagca agggcaaggg ccagccccgc gagcctcaag tgtgtaccct gccccctagc 1440
caggaagaga tgaccaagaa ccagggtgtc ctgagctgtg ccgtgaaagg cttctacccc 1500
agcgacattg ccgtggaatg ggagagcaac ggccagcccg agaacaacta caagaccacc 1560
ccccctgtgc tggacagcga cggctcattc ttcctggtgt ccaagctgac cgtggacaag 1620
agccgggtggc aggaaggcaa cgtgttcagc tgctccgtga tgcacgaggc cctgcacaac 1680
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<210> 405

<211> 1002

<212> DNA

<213> Artificial Sequence

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<220>

<223> Synthetic Construct

<400> 405

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atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgcccagc 180
agatthttccg gcagcggctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagg gccagcccaa ggccgcccc gacatcgtga tgacccagac ccccctgagc 360
ctgagcgtga cacctggaca gcctgccagc atcagctgca agagcagcca gagcctgggtg 420
cacaacaacg ccaacaccta cctgagctgg tatctgcaga agcccggcca gagccccag 480
tccctgatct acaaggtgtc caacagattc agcggcgtgc ccgacagatt ctccggcagc 540
ggctctggca ccgacttcac cctgaagatc agccgggtgg aagccgagga cgtgggcgtg 600
tactattgtg gccagggcac ccagtacccc ttcacctttg gcagcggcac caaggtggaa 660
atcaagacca agggccccag ccgtacggtg gccgctccca gcgtgttcat cttccacct 720
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 780
ccccgcgagg ccaaagtgc gtggaagggtg gacaacgccc tgcagagcgg caacagccag 840
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgaca 900
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgc ccaccagggc 960
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<210> 406

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 406

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


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				165				170					175		
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
	210					215					220				
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225				230						235					240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
				245				250						255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
			260					265					270		
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
		275					280					285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
	290					295					300				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305				310						315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
				325				330						335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
		340						345					350		
Pro	Cys	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu
		355					360					365			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	370					375				380					
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385				390						395					400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg
				405				410						415	
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
			420					425				430			
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
		435					440					445			

<210> 407

<211> 218

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 407

Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val	Ser	Pro	Gly
1				5					10					15	
Gln	Arg	Ala	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Glu	Ser	Val	Glu	Tyr	Tyr
			20					25					30		
Val	Thr	Ser	Leu	Met	Gln	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro
		35					40					45			

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

<210> 408

<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 408

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

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145					150					155				160
Phe	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Val	Gly
				165					170					175
Ile	Lys	Pro	Gln	Tyr	Gly	Ala	Val	Asn	Phe	Gly	Gly	Gly	Phe	Arg
			180					185					190	Asp
Arg	Val	Thr	Leu	Thr	Arg	Asp	Val	Tyr	Arg	Glu	Ile	Ala	Tyr	Met
		195					200					205		Asp
Ile	Arg	Gly	Leu	Lys	Pro	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
	210					215					220			Arg
Asp	Arg	Ser	Tyr	Gly	Asp	Ser	Ser	Trp	Ala	Leu	Asp	Ala	Trp	Gly
225					230					235				240
Gly	Thr	Thr	Val	Val	Val	Ser	Ala	Asp	Lys	Thr	His	Thr	Ala	Ser
			245					250						255
Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr
			260					265					270	Ser
Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro
		275					280					285		Glu
Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val
	290					295						300		His
Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser
305					310					315				320
Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr
			325						330					335
Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val
			340					345					350	Glu
Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe
		355					360					365		Leu
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr
	370					375					380			Leu
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
385					390					395				400
Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val
			405						410					415
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser
			420					425					430	Thr
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu
		435					440					445		Asn
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser
	450					455					460			Ser
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro
465					470					475				480
Val	Cys	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln
			485						490					495
Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala
			500					505					510	Val
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr
		515					520					525		Pro
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu
	530					535						540		Thr
Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser
545					550					555				560
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser
													Leu	Leu

Ser Leu Gly Lys 565 570 575
580

<210> 409
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 409
Tyr Ile His Val Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ile Gly
1 5 10 15
Asp Arg Val Thr Ile Asn Cys Gln Thr Ser Gln Gly Val Gly Ser Asp
20 25 30
Leu His Trp Tyr Gln His Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
35 40 45
His His Thr Ser Ser Val Glu Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Phe His Thr Ser Phe Asn Leu Thr Ile Ser Asp Leu Gln Ala
65 70 75 80
Asp Asp Ile Ala Thr Tyr Tyr Cys Gln Val Leu Gln Phe Phe Gly Arg
85 90 95
Gly Ser Arg Leu His Ile Lys Asp Lys Thr His Thr Asp Ile Val Met
100 105 110
Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly Gln Pro Ala Ser
115 120 125
Ile Ser Cys Lys Ser Ser Gln Ser Leu Val His Asn Asn Ala Asn Thr
130 135 140
Tyr Leu Ser Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Ser Leu
145 150 155 160
Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser
165 170 175
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu
180 185 190
Ala Glu Asp Val Gly Val Tyr Tyr Cys Gly Gln Gly Thr Gln Tyr Pro
195 200 205
Phe Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys Asp Lys Thr His
210 215 220
Thr Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
225 230 235 240
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
245 250 255
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
260 265 270
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
275 280 285
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
290 295 300

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Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 305 310 315 320
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 325 330

<210> 410
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 410
 cagggtgcagc tgcaggaatc tggccctggc ctctgtgaagc ctagccagac cctgagcctg 60
 acctgtaccg tgtccggctt cagcctgagc gactacggcg tgcactgggt gcgccagcca 120
 cctggaaaag gcctggaatg gctggggctg atctgggctg gcggaggcac caactacaac 180
 cccagcctga agtccagaaa gaccatcagc aaggacacca gcaagaacca ggtgtccctg 240
 aagctgagca gcgtgacagc cgccgatacc gccgtgtact actgcgccag agacaagggc 300
 tacagctact actacagcat ggactactgg ggccagggca ccaccgtgac cgtgtcatcc 360
 gcgtcgacca agggcccctc ggtgttccct ctggcccctt gcagcagaag caccagcgaa 420
 tctacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc 480
 tggaactctg gcgctctgac aagcggcgtg cacacctttc cagccgtgct ccagagcagc 540
 ggcctgtact ctctgagcag cgtcgtgaca gtgcccagca gcagcctggg caccaagacc 600
 tacacctgta acgtggacca caagcccagc aacaccaagg tggacaagcg ggtggaatct 660
 aagtacggcc ctccctgccc tccttgcca gccctgaat ttctgggcgg accctccgtg 720
 ttctgtttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc 780
 tgcgtgggtg tggatgtgtc ccaggaagat cccgaggtgc agttcaattg gtacgtggac 840
 ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagttcaa cagcacctac 900
 cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agagtacaag 960
 tgcaaggtgt ccaacaaggg cctgcccagc tccatcgaga aaaccatcag caaggccaag 1020
 ggccagcccc gcgagcctca agtgtatacc ctgccccctt gccaggaaga gatgaccaag 1080
 aaccaggtgt ccctgtggtg tctcgtgaaa ggcttctacc ccagcgacat tgccgtggaa 1140
 tgggagagca acggccagcc cgagaacaac tacaagacca cccccctgt gctggacagc 1200
 gacggctcat tcttcctgta ctccaagctg accgtggaca agagccggtg gcaggaaggc 1260
 aacgtgttca gctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc 1320
 ctgtctctgt ccctgggcaa g 1341

<210> 411
 <211> 654
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 411
 gacatcgtgc tgacacagag ccctgctagc ctggccgtgt ctcttggaaca gagggccacc 60
 atcacctgta gagccagcga gagcgtggaa tattacgtga ccagcctgat gcagtgggtat 120
 cagcagaagc ccggccagcc cccaagctg ctgattttcg ccgccagcaa cgtggaaagc 180
 ggcgtgccag ccagattttc cggcagcggc tctggcaccg acttcaccct gaccatcaac 240

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cccgtggaag ccaacgacgt ggccaactac tactgccagc agagccggaa ggtgccctac 300
acctttggcc agggcaccaa gctggaaatc aagcgtacgg tggccgctcc cagcgtgttc 360
atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 420
aacaacttct acccccgcga ggccaaggtg cagtgggaagg tggacaatgc cctgcagagc 480
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 540
agcaccctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 600
accaccagg gcctgtctag ccccgtagc aagagcttca accggggcga gtgt 654

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<210> 412

<211> 1740

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 412

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caggtgcagc tgggtggaatc tggcggcgga gtggtgcagc ctggcagaag cctgagactg 60
agctgtgccg ccagcggctt caccttcacc aaggcctgga tgcactgggt gcgccaggcc 120
cctgaaaagc agctggaatg ggtggcccag atcaaggaca agagcaacag ctacgccacc 180
tactacgccg acagcgtgaa gggccggttc accatcagcc gggacgacag caagaacacc 240
ctgtacctgc agatgaacag cctgcggggc gaggacaccg ccgtgtacta ctgtcggggc 300
gtgtactatg ccctgagccc cttcgattac tggggccagg gaaccctcgt gaccgtgtct 360
agtgcacaaa cccataccag agcccacctg gtgcagtctg gcaccgccat gaagaaacca 420
ggcgcctctg tgcgggtgtc ctgtcagaca agcggctaca ccttcaccgc ccacatcctg 480
ttctggttcc ggcaggcccc tggcagagga ctggaatggg tgggatggat caagccccag 540
tatggcgccg tgaacttcgg cggaggcttc cgggatagag tgaccctgac ccgggacgtg 600
taccgcgaga tcgcctacat ggacatccgg ggcctgaagc ccgatgacac cgcctgttac 660
tactgcgcca gagacagaag ctacggcgac agcagctggg ctctggatgc ttggggccag 720
ggcacaaccg tgggtgtgtc tgccgataag acccacaccg ccagcacaaa gggcccatcg 780
gtgttccctc tggccccttg cagcagaagc accagcgaat ctacagccgc cctgggctgc 840
ctcgtgaagg actactttcc cgagcccgtg accgtgtcct ggaactctgg cgctctgaca 900
agcggcgtgc acacctttcc agccgtgtc cagagcagcg gcctgtactc tctgagcagc 960
gtcgtgacag tgcccagcag cagcctgggc accaagacct acacctgtaa cgtggaccac 1020
aagcccagca acaccaaggt ggacaagcgg gtggaatcta agtacggccc tccctgccct 1080
ccttgcccag cccctgaatt tctgggcgga ccctccgtgt tcctgttccc cccaaagccc 1140
aaggacaccc tgatgatcag ccggaccccc gaagtgaact gcgtgggtgg ggatgtgtcc 1200
caggaagatc ccgaggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc 1260
aagaccaagc ccagagagga acagttcaac agcacctacc ggggtggtgtc cgtgtctgacc 1320
gtgctgcacc aggactggct gaacggcaaa gagtacaagt gcaaggtgtc caacaagggc 1380
ctgcccagct ccatcgagaa aaccatcagc aaggccaagg gccagccccg cgagcctcaa 1440
gtgtgtaccc tgccccctag ccaggaagag atgaccaaga accaggtgtc cctgagctgt 1500
gccgtgaaag gcttctaccc cagcgacatt gccgtggaat gggagagcaa cggccagccc 1560
gagaacaact acaagaccac cccccctgtg ctggacagcg acggctcatt cttcctgggtg 1620
tccaagctga ccgtggacaa gagccggtgg caggaaggca acgtgttcag ctgctccgtg 1680
atgcacgagg ccctgcacaa ccactacacc cagaagtccc tgtctctgtc cctgggcaag 1740

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<210> 413

<211> 996

<212> DNA

<213> Artificial Sequence

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<220>

<223> Synthetic Construct

<400> 413

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tacatccacg tgacccagag ccccagcagc ctgtccgtgt ccatcggcga cagagtgacc 60
atcaactgcc agacctctca gggcgtgggc agcgacctgc actggtatca gcacaagcct 120
ggcagagccc ccaagctgct gatccaccac acaagcagcg tggaagatgg cgtgcccagc 180
agattttccg gcagcggctt ccacaccagc ttcaacctga ccatcagcga tctgcaggcc 240
gacgacattg ccacctacta ttgtcaggtg ctgcagttct tcggcagagg cagcagactg 300
cacatcaagg acaaaaccca taccgacatc gtgatgacct agacccccct gagcctgagc 360
gtgacacctg gacagcctgc cagcatcagc tgcaagagca gccagagcct ggtgcacaac 420
aacgccaaca cctacctgag ctggtatctg cagaagcccc gccagagccc ccagtccctg 480
atctacaagg tgtccaacag attcagcggc gtgcccgcga gattctccgg cagcggctct 540
ggcaccgact tcaccctgaa gatcagccgg gtggaagccg aggacgtggg cgtgtactat 600
tgtggccagg gcacccagta ccccttcacc tttggcagcg gcaccaaggt ggaaatcaag 660
gataagaccc ataccctgac ggtggccgct cccagcgtgt tcatcttccc acctagcgac 720
gagcagctga agtccggcac agcctctgtc gtgtgcctgc tgaacaactt ctacccccgc 780
gaggccaaag tgcagtggaa ggtggacaac gccctgcaga gcggcaacag ccaggaaagc 840
gtgaccgagc aggacagcaa ggactccacc tacagcctga gcagcaccct gacactgagc 900
aaggccgact acgagaagca caaggtgtac gcctgcgaag tgaccacca gggcctgtct 960
agccccgtga ccaagagctt caaccggggc gagtgt 996
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<210> 414

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 414

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Val Lys Pro Gly Ala
 1          5          10          15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20          25          30
Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35          40          45
Gly Ser Ile Tyr Pro Gly Asn Val Asn Thr Asn Tyr Ala Gln Lys Phe
 50          55          60
Gln Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
 65          70          75          80
Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85          90          95
Thr Arg Ser His Tyr Gly Leu Asp Trp Asn Phe Asp Val Trp Gly Lys
100          105          110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115          120          125
Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130          135          140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145          150          155          160
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Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165					170					175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
	210					215					220				
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225					230					235					240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
				245					250					255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
			260					265					270		
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
		275					280					285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
		290				295					300				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305					310					315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
				325					330					335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
			340					345					350		
Pro	Cys	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu
		355					360					365			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	370					375					380				
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385					390					395					400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg
			405						410					415	
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
			420					425					430		
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
		435					440					445			

<210> 415

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 415

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

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```

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

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<210> 416

<211> 592

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 416

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

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Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	145	150	155	160
Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Thr	Lys	Ala	Trp	Met	165	170	175	
His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gln	Leu	Glu	Trp	Val	Ala	Gln	180	185	190	
Ile	Lys	Asp	Lys	Ser	Asn	Ser	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	195	200	205	
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Leu	Tyr	210	215	220	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	225	230	235	240
Arg	Gly	Val	Tyr	Tyr	Ala	Leu	Ser	Pro	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	245	250	255	
Thr	Leu	Val	Thr	Val	Ser	Ser	Arg	Thr	Ala	Ser	Thr	Lys	Gly	Pro	Ser	260	265	270	
Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	275	280	285	
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	290	295	300	
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	305	310	315	320
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	325	330	335	
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	340	345	350	
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	355	360	365	
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	370	375	380	
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	385	390	395	400
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	405	410	415	
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	420	425	430	
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	435	440	445	
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	450	455	460	
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	465	470	475	480
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Cys	Thr	Leu	485	490	495	
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Ser	Cys	500	505	510	
Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	515	520	525	
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	530	535	540	
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	545	550	555	560

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Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
565 570 575
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
580 585 590

<210> 417
<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 417
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Val His Asn
20 25 30
Asn Ala Asn Thr Tyr Leu Ser Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Gln Ser Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gly Gln Gly
85 90 95
Thr Gln Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys
100 105 110
Gly Gln Pro Lys Ala Ala Pro Asp Phe Val Leu Thr Gln Ser Pro His
115 120 125
Ser Leu Ser Val Thr Pro Gly Glu Ser Ala Ser Ile Ser Cys Lys Ser
130 135 140
Ser His Ser Leu Ile His Gly Asp Arg Asn Asn Tyr Leu Ala Trp Tyr
145 150 155 160
Val Gln Lys Pro Gly Arg Ser Pro Gln Leu Leu Ile Tyr Leu Ala Ser
165 170 175
Ser Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Asp
180 185 190
Lys Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Thr Glu Asp Val Gly
195 200 205
Thr Tyr Tyr Cys Met Gln Gly Arg Glu Ser Pro Trp Thr Phe Gly Gln
210 215 220
Gly Thr Lys Val Asp Ile Lys Thr Lys Gly Pro Ser Arg Thr Val Ala
225 230 235 240
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
245 250 255
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
260 265 270
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
275 280 285
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu

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290		295		300	
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val					
305		310		315	320
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys					
	325		330		335
Ser Phe Asn Arg Gly Glu Cys					
340					

<210> 418
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 418

caggtgcagc	tggtgcagtc	tggcgccgag	gtcgtgaaac	ctggcgccctc	tgtgaagggtg	60
tcctgcaagg	ccagcggcta	cacctttacc	agctactaca	tccactgggt	gcgccaggcc	120
cctggacagg	gactggaatg	gatcggcagc	atctacccc	gcaacgtgaa	caccaactac	180
gcccagaagt	tccagggcag	agccaccctg	accgtggaca	ccagcatcag	caccgcctac	240
atggaactga	gccggctgag	aagcgacgac	accgccgtgt	actactgcac	ccgggtccac	300
tacggcctgg	attggaactt	cgacgtgtgg	ggcaagggca	ccaccgtgac	agtgtctagc	360
gcgtcgacca	agggccccctc	ggtgttccct	ctggccccctt	gcagcagaag	caccagcgaa	420
tctacagccg	ccctgggctg	cctcgtgaag	gactactttc	ccgagcccgt	gaccgtgtcc	480
tggaactctg	gcgctctgac	aagcggcgtg	cacacctttc	cagccgtgct	ccagagcagc	540
ggcctgtact	ctctgagcag	cgctcgtgaca	gtgcccagca	gcagcctggg	caccaagacc	600
tacacctgta	acgtggacca	caagcccagc	aacaccaagg	tggacaagcg	ggtggaatct	660
aagtacggcc	ctccctgccc	tccttgccc	gcccctgaat	ttctgggcgg	accctccgtg	720
ttcctgttcc	ccccaaagcc	caaggacacc	ctgatgatca	gccggacccc	cgaagtgacc	780
tgcgtggtgg	tggatgtgtc	ccaggaagat	cccagaggtg	agttcaattg	gtacgtggac	840
ggcgtggaag	tgcacaacgc	caagaccaag	cccagagagg	aacagttcaa	cagcacctac	900
cgggtggtgt	ccgtgctgac	cgtgctgcac	caggactggc	tgaacggcaa	agagtacaag	960
tgcaaggtgt	ccaacaaggg	cctgcccagc	tccatcgaga	aaaccatcag	caaggccaag	1020
ggccagcccc	gcgagcctca	agtgtatacc	ctgccccctt	gccaggaaga	gatgaccaag	1080
aaccagggtgt	ccctgtggtg	tctcgtgaaa	ggcttctacc	ccagcgacat	tgccgtggaa	1140
tgggagagca	acggccagcc	cgagaacaac	tacaagacca	ccccccctgt	gctggacagc	1200
gacggctcat	tcttcctgta	ctccaagctg	accgtggaca	agagccggtg	gcaggaaggc	1260
aacgtgttca	gctgctccgt	gatgcacgag	gccctgcaca	accactacac	ccagaagtcc	1320
ctgtctctgt	ccctgggcaa	g				1341

<210> 419
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 419

gacatccaga	tgacccagag	ccccagcagc	ctgtctgcca	gcgtgggcga	cagagtgacc	60
------------	------------	------------	------------	------------	------------	----

4. __183952027041SEQLIST.TXT

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atcacctgtc aggccagcca gaacatctac gtgtggctga actggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacaag gccagcaacc tgcacaccgg cgtgcccagc 180
agattttctg gcagcggctc cggcaccgac ttcaccctga caatcagctc cctgcagccc 240
gaggacattg ccacctacta ctgccagcag ggccagacct acccctacac ctttggccag 300
ggcaccaagc tggaaatcaa gcgtacgggtg gccgctccca gcgtgttcat cttcccacct 360
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 420
ccccgcgagg ccaaggtgca gtggaagggtg gacaatgccc tgcagagcgg caacagccag 480
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600
ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 642

```

<210> 420

<211> 1776

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 420

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cagggtgcacc tgacacagag cggacccgaa gtgcggaagc ctggcacctc tgtgaagggtg 60
tcctgcaagg cccctggcaa caccctgaaa acctacgacc tgcactgggt gcgcagcgtg 120
ccaggacagg gactgcagtg gatgggctgg atcagccacg agggcgacaa gaaagtgatc 180
gtggaacggg tcaaggccaa agtgaccatc gactgggaca gaagcaccaa caccgcctac 240
ctgcagctga gcggcctgac ctctggcgat accgccgtgt actactgcgc caagggcagc 300
aagcaccggc tgagagacta cgccctgtac gacgatgacg gcgccctgaa ctgggcccgtg 360
gatgtggact acctgagcaa cctggaattc tggggccagg gcacagccgt gaccgtgtca 420
tcttctcagg tgcagctggg ggaatctggc ggcggagtgg tgcagcctgg cagaagcctg 480
agactgagct gtgccgccag cggcttcacc ttcaccaagg cctggatgca ctgggtgcgc 540
caggccccctg gaaagcagct ggaatgggtg gccagatca aggacaagag caacagctac 600
gccacctact acgccgacag cgtgaagggc cggttcacca tcagccggga cgacagcaag 660
aacaccctgt acctgcagat gaacagcctg cgggcccagg acaccgccgt gtactactgt 720
cggggcgctgt actatgccct gagccccttc gattactggg gccagggaac cctcgtgacc 780
gtgtctagtc ggaccgcttc gaccaagggc ccatcggtgt tccctctggc cccttgacgc 840
agaagcacca gcgaatctac agccgccctg ggctgcctcg tgaaggacta ctttcccag 900
cccgtagacc tgtcctggaa ctctggcgct ctgacaagcg gcgtgcacac ctttccagcc 960
gtgtctcaga gcagcggcct gtactctctg agcagcgtcg tgacagtgcc cagcagcagc 1020
ctgggcacca agacctacac ctgtaacgtg gaccacaagc ccagcaacac caaggtggac 1080
aagcgggtgg aatctaagta cggccctccc tgccctcctt gcccagcccc tgaatttctg 1140
ggcggaccct ccgtgttcct gttcccccca aagcccaagg acaccctgat gatcagccgg 1200
acccccgaag tgacctgcgt ggtggtggat gtgtcccagg aagatcccga ggtgcagttc 1260
aattgggtacg tggacggcgt ggaagtgcac aacgccaaga ccaagcccag agaggaacag 1320
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gaagagatga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccccagc 1560
gacattgccg tggaatggga gagcaacggc cagcccagaga acaactacaa gaccaccccc 1620
cctgtgtctgg acagcgacgg ctcatcttc ctggtgtcca agctgaccgt ggacaagagc 1680
cgggtggcagg aaggcaacgt gttcagctgc tccgtgatgc acgaggccct gcacaaccac 1740
tacaccacga agtccctgtc tctgtccctg ggcaag 1776

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<210> 421

4.__183952027041SEQLIST.TXT

<211> 1029

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 421

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gacatcgtga tgacccagac ccccttgagc ctgagcgtga cacctggaca gcctgccagc 60
atcagctgca agagcagcca gagcctgggtg cacaacaacg ccaacaccta cctgagctgg 120
tatctgcaga agcccggcca gagccccagc tccctgatct acaaggtgtc caacagattc 180
agcggcgtgc ccgacagatt ctccggcagc ggctctggca ccgacttcac cctgaagatc 240
agccgggtgg aagccgagga cgtgggcgtg tactattgtg gccagggcac ccagtacccc 300
ttcacctttg gcagcggcac caaggtggaa atcaagggcc agcccaaggc cgcccccgac 360
ttcgtgctga cccagagccc tcacagcctg agcgtgacac ctggcgagag cgccagcatc 420
agctgcaaga gcagccactc cctgatccac ggcgaccgga acaactacct ggcttggtac 480
gtgcagaagc ccggcagatc cccccagctg ctgatctacc tggccagcag cagagccagc 540
ggcgtgcccg atagattttc tggcagcggc agcgacaagg acttcaccct gaagatcagc 600
cgggtggaaa ccgaggacgt gggcacctac tactgtatgc agggcagaga gagcccctgg 660
acctttggcc agggcaccaa ggtggacatc aagaccaagg gccccagccg tacggtggcc 720
gtctccagcg tgttcatctt cccacctagc gacgagcagc tgaagtccgg cacagcctct 780
gtcgtgtgcc tgctgaacaa cttctacccc cgcgaggcca aagtgcagtg gaaggtggac 840
aacgccctgc agagcggcaa cagccaggaa agcgtgaccg agcaggacag caaggactcc 900
acctacagcc tgagcagcac cctgacactg agcaaggccg actacgagaa gcacaagggtg 960
tacgcctgcg aagtgaccca ccagggcctg tctagccccg tgaccaagag cttcaaccgg 1020
ggcgagtgt 1029

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<210> 422

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 422

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

```

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Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala
130						135					140				
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
			165						170					175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
		210				215					220				
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225					230					235					240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
			245						250					255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
			260					265					270		
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
		275					280					285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
	290					295					300				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305					310					315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
				325					330					335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
			340					345					350		
Pro	Cys	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu
		355					360					365			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	370					375					380				
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385					390					395					400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg
			405						410					415	
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
			420					425					430		
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
		435					440					445			

<210> 423

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 423

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

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```

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

```

<210> 424

<211> 599

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 424

```

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

```


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Asp	Gly	Ala	Leu	Asn	Trp	Ala	Val	Asp	Val	Asp	Tyr	Leu	Ser	Asn	Leu	115	120	125
Glu	Phe	Trp	Gly	Gln	Gly	Thr	Ala	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	130	135	140
His	Thr	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	145	150	155
Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Thr	165	170	175
Lys	Ala	Trp	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gln	Leu	Glu	180	185	190
Trp	Val	Ala	Gln	Ile	Lys	Asp	Lys	Ser	Asn	Ser	Tyr	Ala	Thr	Tyr	Tyr	195	200	205
Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	210	215	220
Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	225	230	235
Val	Tyr	Tyr	Cys	Arg	Gly	Val	Tyr	Tyr	Ala	Leu	Ser	Pro	Phe	Asp	Tyr	245	250	255
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	260	265	270
Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	275	280	285
Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	290	295	300
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	305	310	315
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	325	330	335
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	340	345	350
Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	355	360	365
Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	370	375	380
Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	385	390	395
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	405	410	415
Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	420	425	430
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	435	440	445
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	450	455	460
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	465	470	475
Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	485	490	495
Glu	Pro	Gln	Val	Cys	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	500	505	510
Asn	Gln	Val	Ser	Leu	Ser	Cys	Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	515	520	525

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Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
530 535 540
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser
545 550 555 560
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
565 570 575
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
580 585 590
Leu Ser Leu Ser Leu Gly Lys
595

<210> 425

<211> 341

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 425

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

4. 183952027041SEQLIST.TXT

[illegible]

<210> 426

<211> 1341

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 426

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tcctgcaagg	ccagcggcta	cacctttacc	agctactaca	tccactgggt	gcgccaggcc	120
cctggacagg	gactggaatg	gatcggcagc	atctaccccg	gcaacgtgaa	caccaactac	180
gcccagaagt	tccagggcag	agccaccctg	accgtggaca	ccagcatcag	caccgcctac	240
atggaactga	gccggctgag	aagcgacgac	accgccgtgt	actactgcac	ccggtcccac	300
tacggcctgg	attggaactt	cgacgtgtgg	ggcaagggca	ccaccgtgac	agtgtctagc	360
gcgtcgacca	agggccctc	ggtgttccct	ctggccctt	gcagcagaag	caccagcgaa	420
tctacagccg	ccctgggctg	cctcgtgaag	gactactttc	ccgagcccgt	gaccgtgtcc	480
tggaactctg	gcgctctgac	aagcggcgtg	cacacctttc	cagccgtgct	ccagagcagc	540
ggcctgtact	ctctgagcag	cgtcgtgaca	gtgcccagca	gcagcctggg	caccaagacc	600
tacacctgta	acgtggacca	caagcccagc	aacaccaagg	tggacaagcg	ggtggaatct	660
aagtacggcc	ctccctgccc	tccttgcccc	gcccctgaat	ttctggggcg	accctccgtg	720
ttcctgttcc	ccccaaagcc	caaggacacc	ctgatgatca	gccggacccc	cgaagtgacc	780
tgctgtggtg	tggatgtgtc	ccaggaagat	cccgaggtgc	agttcaattg	gtacgtggac	840
ggcgtggaag	tgcacaacgc	caagaccaag	cccagagagg	aacagttcaa	cagcacctac	900
cgggtggtgt	ccgtgctgac	cgtgctgcac	caggactggc	tgaacggcaa	agagtacaag	960
tgcaaggtgt	ccaacaaggg	cctgcccagc	tccatcgaga	aaaccatcag	caaggccaag	1020
ggccagcccc	gcgagcctca	agtgtatacc	ctgccccctt	gccaggaaga	gatgaccaag	1080
aaccaggtgt	ccctgtggtg	tctcgtgaaa	ggcttctacc	ccagcgacat	tgccgtggaa	1140
tgggagagca	acggccagcc	cgagaacaac	tacaagacca	ccccccctgt	gctggacagc	1200
gacggctcat	tcttctgtga	ctccaagctg	accgtggaca	agagccggtg	gcaggaaggc	1260
aacgtgttca	gctgctcctg	gatgcacgag	gccctgcaca	accactacac	ccagaagtcc	1320
ctgtctctgt	ccctgggcaa	g				1341

<210> 427

<211> 642

<212> DNA

<213> Artificial Sequence

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<220>

<223> Synthetic Construct

<400> 427

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gacatccaga tgacccagag ccccagcagc ctgtctgcca gcgtgggcga cagagtgacc 60
atcacctgtc aggccagcca gaacatctac gtgtggctga actggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacaag gccagcaacc tgcacaccgg cgtgcccagc 180
agattttctg gcagcggctc cggcaccgac ttcaccctga caatcagctc cctgcagccc 240
gaggacattg ccacctacta ctgccagcag ggccagacct acccctacac ctttggccag 300
ggcaccaagc tggaaatcaa gcgtacggtg gccgctccca gcgtgttcat cttcccacct 360
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 420
ccccgcgagg ccaagggtgca gtggaagggt gacaatgccc tgcagagcgg caacagccag 480
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600
ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt 642
```

<210> 428

<211> 1797

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 428

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caggtgcacc tgacacagag cggacccgaa gtgcggaagc ctggcacctc tgtgaagggtg 60
tcctgcaagg cccctggcaa caccctgaaa acctacgacc tgcactgggt gcgcagcgtg 120
ccaggacagg gactgcagtg gatgggctgg atcagccacg agggcgacaa gaaagtgatc 180
gtggaacggg tcaaggccaa agtgaccatc gactgggaca gaagcaccaa caccgcctac 240
ctgcagctga gcggcctgac ctctggcgat accgccgtgt actactgcgc caagggcagc 300
aagcacccggc tgagagacta cgccctgtac gacgatgacg gcgccctgaa ctgggcccgtg 360
gatgtggact acctgagcaa cctggaattc tggggccagg gcacagccgt gaccgtgtca 420
tctgacaaaa cccataccca ggtgcagctg gtggaatctg gcggcggagt ggtgcagcct 480
ggcagaagcc tgagactgag ctgtgccgcc agcggcttca ctttcaccaa ggcctggatg 540
cactgggtgc gccaggcccc tggaaagcag ctggaatggg tggcccagat caaggacaag 600
agcaacagct acgccaccta ctacgccgac agcgtgaagg gccggttcac catcagccgg 660
gacgacagca agaacaccct gtacctgcag atgaacagcc tgcggggcca ggacaccgcc 720
gtgtactact gtcggggcgt gtactatgcc ctgagcccct tcgattactg gggccaggga 780
accctcgtga ccgtgtctag tgataagacc cacaccgctt cgaccaaggg cccatcggtg 840
ttccctctgg ccccttgtag cagaagcacc agcgaatcta cagccgccct gggctgcctc 900
gtgaaggact actttcccga gcccgtgacc gtgtcctgga actctggcgc tctgacaagc 960
ggcgtgcaca cttttccagc cgtgctccag agcagcggcc tgtactctct gagcagcgtc 1020
gtgacagtgc ccagcagcag cctgggcacc aagacctaca cctgtaacgt ggaccacaag 1080
cccagcaaca ccaagggtga caagcgggtg gaatctaagt acggccctcc ctgccctcct 1140
tgcccagccc ctgaatttct gggcggaccc tccgtgttcc tgttcccccc aaagcccaag 1200
gacaccctga tgatcagccg gacccccgaa gtgacctgcg tgggtggtgga tgtgtcccag 1260
gaagatcccg aggtgcagtt caattggtac gtggacggcg tggaaagtga caacgccaaag 1320
accaagcccc gagaggaaca gttcaacagc acctaccggg tgggtgtccgt gctgaccgtg 1380
ctgcaccagg actggctgaa cggcaaaagag tacaagtga aggtgtccaa caagggcctg 1440
cccagctcca tcgagaaaac catcagcaag gccaaaggcc agccccgcga gcctcaagtg 1500
tgtaccctgc cccctagcca ggaagagatg accaagaacc aggtgtccct gagctgtgcc 1560
```

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gtgaaaggct tctaccccag cgacattgcc gtggaatggg agagcaacgg ccagcccag 1620
aacaactaca agaccacccc ccctgtgctg gacagcgacg gctcattctt cctgggtgtcc 1680
aagctgaccg tggacaagag ccggtggcag gaaggcaacg tgttcagctg ctccgtgatg 1740
cacgaggccc tgcacaacca ctacaccag aagtcctgt ctctgtccct gggcaag 1797
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<210> 429

<211> 1023

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 429

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gacatcgtga tgaccagac cccctgagc ctgagcgtga cacctggaca gcctgccagc 60
atcagctgca agagcagcca gagcctgggtg cacaacaacg ccaacaccta cctgagctgg 120
tatctgcaga agcccggcca gagccccag tccctgatct acaaggtgtc caacagattc 180
agcggcgtgc ccgacagatt ctccggcagc ggctctggca ccgacttcac cctgaagatc 240
agccgggtgg aagccgagga cgtgggcgtg tactattgtg gccagggcac ccagtacccc 300
ttcacctttg gcagcggcac caaggtggaa atcaaggaca aaaccatac cgacttcgtg 360
ctgaccaga gccctcacag cctgagcgtg acacctggcg agagcgccag catcagctgc 420
aagagcagcc actccctgat ccacggcgac cggaacaact acctggcttg gtacgtgcag 480
aagcccggca gatcccccca gctgctgac tacctggcca gcagcagagc cagcggcgtg 540
cccgatagat tttctggcag cggcagcgac aaggacttca ccctgaagat cagccgggtg 600
gaaaccgagg acgtgggcac ctactactgt atgcagggca gagagagccc ctggaccttt 660
ggccagggca ccaaggtgga catcaaggat aagaccata cccgtacggg ggccgctccc 720
agcgtgttca tcttccacc tagcgacgag cagctgaagt ccggcacagc ctctgtcgtg 780
tgcctgctga acaacttcta ccccgcgag gccaaagtgc agtggaaagg ggacaacgcc 840
ctgcagagcg gcaacagcca ggaaagcgtg accgagcagg acagcaagga ctccacctac 900
agcctgagca gcacctgac actgagcaag gccgactacg agaagcaca ggtgtacgcc 960
tgcgaagtga cccaccaggg cctgtctagc cccgtgacca agagcttcaa ccggggcgag 1020
tgt 1023
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<210> 430

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 430

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Val Lys Pro Gly Ala
 1          5          10         15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20         25         30
Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35         40         45
Gly Ser Ile Tyr Pro Gly Asn Val Asn Thr Asn Tyr Ala Gln Lys Phe
 50         55         60
Gln Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Ile Ser Thr Ala Tyr
 65         70         75         80
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Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85				90					95			
Thr	Arg	Ser	His	Tyr	Gly	Leu	Asp	Trp	Asn	Phe	Asp	Val	Trp	Gly	Lys	
			100				105					110				
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	
		115				120					125					
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	
	130				135					140						
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	
145				150					155						160	
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	
			165					170						175		
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	
		180					185					190				
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	
		195				200					205					
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	
	210				215					220						
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	
225				230				235							240	
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	
			245					250						255		
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	
		260						265				270				
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	
		275					280					285				
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	
	290					295					300					
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	
305				310				315							320	
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	
			325					330						335		
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	
		340						345					350			
Pro	Cys	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu	
	355					360					365					
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	
	370				375			380								
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	
385				390				395						400		
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	
			405					410						415		
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	
		420					425					430				
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys		
		435				440						445				

<210> 431

<211> 214

<212> PRT

<213> Artificial Sequence

4.___183952027041SEQLIST.TXT

<220>

<223> Synthetic Construct

<400> 431

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

<210> 432

<211> 592

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 432

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

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Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65          70          75          80
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
          85          90          95
Tyr Cys Arg Gly Val Tyr Tyr Ala Leu Ser Pro Phe Asp Tyr Trp Gly
          100         105         110
Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gln Val His Leu Thr Gln
          115         120         125
Ser Gly Pro Glu Val Arg Lys Pro Gly Thr Ser Val Lys Val Ser Cys
          130         135         140
Lys Ala Pro Gly Asn Thr Leu Lys Thr Tyr Asp Leu His Trp Val Arg
145          150         155         160
Ser Val Pro Gly Gln Gly Leu Gln Trp Met Gly Trp Ile Ser His Glu
          165         170         175
Gly Asp Lys Lys Val Ile Val Glu Arg Phe Lys Ala Lys Val Thr Ile
          180         185         190
Asp Trp Asp Arg Ser Thr Asn Thr Ala Tyr Leu Gln Leu Ser Gly Leu
          195         200         205
Thr Ser Gly Asp Thr Ala Val Tyr Tyr Cys Ala Lys Gly Ser Lys His
          210         215         220
Arg Leu Arg Asp Tyr Ala Leu Tyr Asp Asp Asp Gly Ala Leu Asn Trp
225          230         235         240
Ala Val Asp Val Asp Tyr Leu Ser Asn Leu Glu Phe Trp Gly Gln Gly
          245         250         255
Thr Ala Val Thr Val Ser Ser Arg Thr Ala Ser Thr Lys Gly Pro Ser
          260         265         270
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
          275         280         285
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
          290         295         300
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
305          310         315         320
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
          325         330         335
Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
          340         345         350
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
          355         360         365
Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
          370         375         380
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
385          390         395         400
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
          405         410         415
Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
          420         425         430
Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
          435         440         445
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
          450         455         460
Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
465          470         475         480

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Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Cys	Thr	Leu
				485					490					495	
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Ser	Cys
			500					505					510		
Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
		515					520					525			
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Val	Leu	Asp	
	530					535					540				
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser
545					550					555					560
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
				565					570					575	
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys
			580					585						590	

<210> 433

<211> 343

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 433

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

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210	215	220
Gly Thr Lys Val Glu Ile Lys Thr Lys Gly Pro Ser Arg Thr Val Ala		
225	230	235
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser		
	245	250
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu		
	260	265
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser		
	275	280
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu		
	290	295
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val		
305	310	315
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys		
	325	330
Ser Phe Asn Arg Gly Glu Cys		
340		

<210> 434

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 434

caggtgcagc	tgggtgcagtc	tggcgccgag	gtcgtgaaac	ctggcgcctc	tgtgaagggtg	60
tcctgcaagg	ccagcggcta	cacctttacc	agctactaca	tccactgggt	gcgccaggcc	120
cctggacagg	gactggaatg	gatcggcagc	atctacccc	gcaacgtgaa	caccaactac	180
gcccagaagt	tccagggcag	agccaccctg	accgtggaca	ccagcatcag	caccgcctac	240
atggaactga	gccggctgag	aagcgacgac	accgccgtgt	actactgcac	ccgggtcccac	300
tacggcctgg	attggaactt	cgacgtgtgg	ggcaagggca	ccaccgtgac	agtgtctagc	360
gcgtcgacca	agggcccctc	ggtgttccct	ctggccccct	gcagcagaag	caccagcgaa	420
tctacagccg	ccctgggctg	cctcgtgaag	gactactttc	ccgagcccgt	gaccgtgtcc	480
tggaactctg	gcgctctgac	aagcggcgtg	cacacctttc	cagccgtgct	ccagagcagc	540
ggcctgtact	ctctgagcag	cgctcgtgaca	gtgcccagca	gcagcctggg	caccaagacc	600
tacacctgta	acgtggacca	caagcccagc	aacaccaagg	tggacaagcg	ggtggaatct	660
aagtacggcc	ctccctgccc	tccttgccca	gcccctgaat	ttctgggcgg	accctccgtg	720
ttcctgttcc	ccccaaagcc	caaggacacc	ctgatgatca	gccggacccc	cgaagtgacc	780
tgcgtgggtg	tggatgtgtc	ccaggaagat	cccagaggtg	agttcaattg	gtacgtggac	840
ggcgtggaag	tgcacaacgc	caagaccaag	cccagagagg	aacagttcaa	cagcacctac	900
cgggtgggtg	ccgtgctgac	cgtgctgcac	caggactggc	tgaacggcaa	agagtacaag	960
tgcaagggtg	ccaacaaggg	cctgcccagc	tccatcgaga	aaaccatcag	caaggccaag	1020
ggccagcccc	gcgagcctca	agtgtatacc	ctgccccctt	gccaggaaga	gatgaccaag	1080
aaccagggtg	ccctgtgggtg	tctcgtgaaa	ggcttctacc	ccagcgacat	tgccgtggaa	1140
tgggagagca	acggccagcc	cgagaacaac	tacaagacca	ccccccctgt	gctggacagc	1200
gacggctcat	tcttctctgta	ctccaagctg	accgtggaca	agagccggtg	gcaggaaggc	1260
aacgtgttca	gctgctccgt	gatgcacgag	gccctgcaca	accactacac	ccagaagtcc	1320
ctgtctctgt	ccctgggcaa	g				1341

4.__183952027041SEQLIST.TXT

<210> 435
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 435
 gacatccaga tgacccagag ccccagcagc ctgtctgccg gcgtgggcga cagagtgacc 60
 atcacctgtc aggccagcca gaacatctac gtgtggctga actggtatca gcagaagccc 120
 ggcaaggccc ccaagctgct gatctacaag gccagcaacc tgcacaccgg cgtgcccagc 180
 agattttctg gcagcggctc cggcaccgac ttcaccctga caatcagctc cctgcagccc 240
 gaggacattg ccacctacta ctgccagcag ggccagacct acccctacac ctttggccag 300
 ggcaccaagc tggaaatcaa gcgtacggtg gccgctccca gcgtgttcat cttccacct 360
 agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 420
 ccccgcgagg ccaaggtgca gtggaaggtg gacaatgccc tgcagagcgg caacagccag 480
 gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540
 ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgc ccaccagggc 600
 ctgtctagcc ccgtgaccaa gagcttcaac cggggcaggt gt 642

<210> 436
 <211> 1776
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 436
 caggtgcagc tgggtggaatc tggcggcgga gtggtgcagc ctggcagaag cctgagactg 60
 agctgtgccg ccagcggctt caccttcacc aaggcctgga tgcactgggt gcgccaggcc 120
 cctggaaagc agctggaatg ggtggcccag atcaaggaca agagcaacag ctacgccacc 180
 tactacgccg acagcgtgaa gggccggttc accatcagcc gggacgacag caagaacacc 240
 ctgtacctgc agatgaacag cctgcggggc gaggacaccg ccgtgtacta ctgtcggggc 300
 gtgtactatg ccctgagccc cttcgattac tggggccagg gaaccctcgt gaccgtgtct 360
 agtagccagg tgcacctgac acagagcggg cccgaagtgc ggaagcctgg cacctctgtg 420
 aaggtgtcct gcaaggcccc tggcaacacc ctgaaaacct acgacctgca ctgggtgcgc 480
 agcgtgccag gacagggact gcagtggatg ggctggatca gccacgaggg cgacaagaaa 540
 gtgatcgtgg aacggttcaa ggccaaagtg accatcgact gggacagaag caccaacacc 600
 gcctacctgc agctgagcgg cctgacctct ggcgataccg ccgtgtacta ctgcgccaag 660
 ggcagcaagc accggctgag agactacgcc ctgtacgacg atgacggcgc cctgaactgg 720
 gccgtggatg tggactacct gagcaacctg gaattctggg gccagggcac agccgtgacc 780
 gtgtcatctc ggaccgccag cacaaggggc ccacggtgt tccctctggc cccttgacgc 840
 agaagcacca gcgaatctac agccgccctg ggctgcctcg tgaaggacta ctttcccag 900
 cccgtgaccg tgtcctggaa ctctggcgct ctgacaagcg gcgtgcacac ctttccagcc 960
 gtgctccaga gcagcggcct gtactctctg agcagcgtcg tgacagtgcc cagcagcagc 1020
 ctgggcacca agacctacac ctgtaacctg gaccacaagc ccagcaacac caaggtggac 1080
 aagcgggtgg aatctaagta cggccctccc tgccctcctt gccagcccc tgaatttctg 1140
 ggcggaccct ccgtgttcct gttccccca aagcccaagg acaccctgat gatcagccgg 1200
 acccccgaag tgacctgcgt ggtggtggat gtgtcccagg aagatcccga ggtgcagttc 1260
 aattggtacg tggacggcgt ggaagtgcac aacgccaaga ccaagcccag agaggaacag 1320

4. __183952027041SEQLIST.TXT

```

ttcaacagca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ctggctgaac 1380
ggcaaagagt acaagtgcaa ggtgtccaac aagggcctgc ccagctccat cgagaaaacc 1440
atcagcaagg ccaagggcca gccccgcgag cctcaagtgt gtaccctgcc ccctagccag 1500
gaagagatga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccccagc 1560
gacattgccg tggaatggga gagcaacggc cagcccgaga acaactacaa gaccaccccc 1620
cctgtgctgg acagcgacgg ctcatcttc ctggtgtcca agctgaccgt ggacaagagc 1680
cgggtggcagg aaggcaacgt gttcagctgc tccgtgatgc acgaggccct gcacaaccac 1740
tacaccaga agtccctgtc tctgtccctg ggcaag 1776

```

<210> 437

<211> 1029

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 437

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atcagctgca agagcagcca ctccctgatc cacggcgacc ggaacaacta cctggcttgg 120
tacgtgcaga agcccgagc atccccccag ctgctgatct acctggccag cagcagagcc 180
agcggcgtgc ccgatagatt ttctggcagc ggcagcgaca aggacttcac cctgaagatc 240
agccgggtgg aaaccgagga cgtgggcacc tactactgta tgcagggcag agagagcccc 300
tggaaccttg gccagggcac caaggtggac atcaagggcc agcccaaggc cgcccccgac 360
atcgtgatga ccagaccccc cctgagcctg agcgtgacac ctggacagcc tgccagcatc 420
agctgcaaga gcagccagag cctggtgcac aacaacgcca acacctacct gagctggtat 480
ctgcagaagc ccggccagag cccccagtcc ctgatctaca aggtgtccaa cagattcagc 540
ggcgtgccc acagattctc cggcagcggc tctggcaccg acttcaccct gaagatcagc 600
cgggtggaag ccgaggacgt gggcgtgtac tattgtggcc agggcaccca gtacccttc 660
acctttggca gcggcaccaa ggtggaaatc aagaccaagg gccccagccg tacggtggcc 720
gctcccagcg tgttcattctt cccacctagc gacgagcagc tgaagtccgg cacagcctct 780
gtcgtgtgcc tgctgaacaa cttctacccc cgcgaggcca aagtgcagtg gaaggtggac 840
aacgccctgc agagcggcaa cagccaggaa agcgtgaccg agcaggacag caaggactcc 900
acctacagcc tgagcagcac cctgacactg agcaaggccg actacgagaa gcacaagggtg 960
tacgcctgcg aagtgaccca ccagggcctg tctagccccg tgaccaagag cttcaaccgg 1020
ggcagtggt 1029

```

<210> 438

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 438

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Val Lys Pro Gly Ala
 1             5             10             15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
      20             25             30
Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
      35             40             45

```

4. __183952027041SEQLIST.TXT

Gly	Ser	Ile	Tyr	Pro	Gly	Asn	Val	Asn	Thr	Asn	Tyr	Ala	Gln	Lys	Phe
50						55					60				
Gln	Gly	Arg	Ala	Thr	Leu	Thr	Val	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Thr	Arg	Ser	His	Tyr	Gly	Leu	Asp	Trp	Asn	Phe	Asp	Val	Trp	Gly	Lys
			100					105					110		
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
			115					120				125			
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala
						135					140				
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165					170					175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
		210				215					220				
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225					230					235					240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
				245					250					255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
			260					265					270		
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
		275					280					285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
		290				295					300				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305					310					315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
				325					330					335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
			340					345					350		
Pro	Cys	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu
		355					360					365			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
		370				375					380				
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385					390					395					400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg
				405					410					415	
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
			420					425					430		
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
		435					440					445			

4.___183952027041SEQLIST.TXT

<210> 439
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 439
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asn Ile Tyr Val Trp
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Thr Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
 210

<210> 440
 <211> 599
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 440
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Lys Ala
 20 25 30

4.__183952027041SEQLIST.TXT

Trp	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gln	Leu	Glu	Trp	Val
	35						40					45			
Ala	Gln	Ile	Lys	Asp	Lys	Ser	Asn	Ser	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp
	50					55					60				
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr
65					70					75					80
Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr
				85					90					95	
Tyr	Cys	Arg	Gly	Val	Tyr	Tyr	Ala	Leu	Ser	Pro	Phe	Asp	Tyr	Trp	Gly
			100				105						110		
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	Gln	Val
			115				120					125			
His	Leu	Thr	Gln	Ser	Gly	Pro	Glu	Val	Arg	Lys	Pro	Gly	Thr	Ser	Val
	130					135					140				
Lys	Val	Ser	Cys	Lys	Ala	Pro	Gly	Asn	Thr	Leu	Lys	Thr	Tyr	Asp	Leu
145					150					155					160
His	Trp	Val	Arg	Ser	Val	Pro	Gly	Gln	Gly	Leu	Gln	Trp	Met	Gly	Trp
				165					170					175	
Ile	Ser	His	Glu	Gly	Asp	Lys	Lys	Val	Ile	Val	Glu	Arg	Phe	Lys	Ala
			180					185					190		
Lys	Val	Thr	Ile	Asp	Trp	Asp	Arg	Ser	Thr	Asn	Thr	Ala	Tyr	Leu	Gln
		195					200					205			
Leu	Ser	Gly	Leu	Thr	Ser	Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys
	210					215					220				
Gly	Ser	Lys	His	Arg	Leu	Arg	Asp	Tyr	Ala	Leu	Tyr	Asp	Asp	Asp	Gly
225					230					235					240
Ala	Leu	Asn	Trp	Ala	Val	Asp	Val	Asp	Tyr	Leu	Ser	Asn	Leu	Glu	Phe
				245					250					255	
Trp	Gly	Gln	Gly	Thr	Ala	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr
			260					265						270	
Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg
		275					280						285		
Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
	290					295					300				
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
305					310					315					320
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
				325					330					335	
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr
			340					345					350		
Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
		355					360						365		
Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro
	370					375						380			
Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys
385					390					395					400
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val
				405					410					415	
Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp
			420				425						430		
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe
		435					440					445			

4.__183952027041SEQLIST.TXT

```

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 450                      455                      460
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
465                      470                      475                      480
Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
                      485                      490                      495
Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
                      500                      505                      510
Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp
                      515                      520                      525
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                      530                      535                      540
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser
545                      550                      555                      560
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
                      565                      570                      575
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
                      580                      585                      590
Leu Ser Leu Ser Leu Gly Lys
                      595

```

<210> 441

<211> 341

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 441

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

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4. 183952027041SEQLIST.TXT

[illegible]

<210> 442

<211> 1341

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 442

caggtgcagc	tggtgcagtc	tggcgccgag	gtcgtgaaac	ctggcgcctc	tgtgaagggtg	60
tcctgcaagg	ccagcggcta	cacctttacc	agctactaca	tccactgggt	gcgccaggcc	120
cctggacagg	gactggaatg	gatcggcagc	atctaccccg	gcaacgtgaa	caccaactac	180
gcccagaagt	tccagggcag	agccaccctg	accgtggaca	ccagcatcag	caccgcctac	240
atggaactga	gccggctgag	aagcgacgac	accgccgtgt	actactgcac	ccggtcccac	300
tacggcctgg	attggaactt	cgacgtgtgg	ggcaagggca	ccaccgtgac	agtgtctagc	360
gcgtcgacca	agggccctc	ggtgttccct	ctggccctt	gcagcagaag	caccagcgaa	420
tctacagccg	ccctgggctg	cctcgtgaag	gactactttc	ccgagcccgt	gaccgtgtcc	480
tggaactctg	gcgctctgac	aagcggcgtg	cacacctttc	cagccgtgct	ccagagcagc	540
ggcctgtact	ctctgagcag	cgtcgtgaca	gtgcccagca	gcagcctggg	caccaagacc	600
tacacctgta	acgtggacca	caagcccagc	aacaccaagg	tggacaagcg	ggtggaatct	660
aagtacggcc	ctccctgccc	tccttgccca	gcccctgaat	ttctggggcg	accctccgtg	720
ttcctgttcc	ccccaaagcc	caaggacacc	ctgatgatca	gccggacccc	cgaagtgacc	780
tgcgtgggtg	tggatgtgtc	ccaggaagat	cccaggtgac	agttcaattg	gtacgtggac	840
ggcgtggaag	tgcacaacgc	caagaccaag	cccagagagg	aacagttcaa	cagcacctac	900
cgggtgggtgt	ccgtgctgac	cgtgctgcac	caggactggc	tgaacggcaa	agagtacaag	960
tgcaaggtgt	ccaacaaggg	cctgcccgac	tccatcgaga	aaaccatcag	caaggccaag	1020
ggccagcccc	gcgagcctca	agtgtatacc	ctgccccctt	gccaggaaga	gatgaccaag	1080

4. __183952027041SEQLIST.TXT

```
aaccagggtgt ccctgtggtg tctcgtgaaa ggcttctacc ccagcgacat tgccgtggaa 1140
tgggagagca acggccagcc cgagaacaac tacaagacca cccccctgt gctggacagc 1200
gacggctcat tcttcctgta ctccaagctg accgtggaca agagccggtg gcaggaaggc 1260
aacgtgttca gctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc 1320
ctgtctctgt ccctgggcaa g                                     1341
```

<210> 443

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 443

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gacatccaga tgacccagag ccccagcagc ctgtctgccg gcgtgggcca cagagtgacc 60
atcacctgtc agggcagcca gaacatctac gtgtggctga actggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacaag gccagcaacc tgcacaccgg cgtgccccagc 180
agattttctg gcagcggctc cggcaccgac ttcaccctga caatcagctc cctgcagccc 240
gaggacattg ccacctacta ctgccagcag ggccagacct acccctacac ctttggccag 300
ggcaccaagc tggaaatcaa gcgtacggtg gccgctccca gcgtgttcat cttcccacct 360
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 420
ccccgcgagg ccaagggtgca gtggaagggt gacaatgccc tgcaagagcg caacagccag 480
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtga ccaccagggc 600
ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt                                     642
```

<210> 444

<211> 1797

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 444

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cagggtgcagc tgggtggaatc tggcggcgga gtggtgcagc ctggcagaag cctgagactg 60
agctgtgccg ccagcggctt caccttcacc aaggcctgga tgcactgggt gcgccaggcc 120
cctggaaagc agctggaatg ggtggcccag atcaaggaca agagcaacag ctacgccacc 180
tactacgccg acagcgtgaa gggccggttc accatcagcc gggacgacag caagaacacc 240
ctgtacctgc agatgaacag cctgcggggc gaggacaccg ccgtgtacta ctgtcggggc 300
gtgtactatg ccctgagccc cttcgattac tggggccagg gaaccctcgt gaccgtgtct 360
agtgacaaaa cccataccca ggtgcacctg acacagagcg gaccggaagt gcggaagcct 420
ggcacctctg tgaagggtgc ctgcaaggcc cctggcaaca ccctgaaaac ctacgacctg 480
cactgggtgc gcagcgtgcc aggacaggga ctgcagtgga tgggctggat cagccacgag 540
ggcgacaaga aagtgatcgt ggaacggttc aaggccaaag tgaccatcga ctgggacaga 600
agcaccaaca ccgcctacct gcagctgagc ggcctgacct ctggcgatac cgccgtgtac 660
tactgcgcca agggcagcaa gcaccggctg agagactacg ccctgtacga cgatgacggc 720
gccctgaact gggccgtgga tgtggactac ctgagcaacc tgggaattctg gggccagggc 780
acagccgtga ccgtgtcatc tgataagacc cacaccgcca gcacaaaggg cccatcggtg 840
ttccctctgg ccccttgagc cagaagcacc agcgaatcta cagccgccct gggctgcctc 900
gtgaaggact actttcccga gccctgacc gtgtcctgga actctggcgc tctgacaagc 960
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4. __183952027041SEQLIST.TXT

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ggcgtgcaca cctttccagc cgtgctccag agcagcggcc tgtactctct gagcagcgtc 1020
gtgacagtgc ccagcagcag cctggggcacc aagacctaca cctgtaacgt ggaccacaag 1080
cccagcaaca ccaaggtgga caagcgggtg gaatctaagt acggccctcc ctgccctcct 1140
tgcccagccc ctgaatttct gggcgggacc tccgtgttcc tgttcccccc aaagcccaag 1200
gacaccctga tgatcagccg gacccccgaa gtgacctgcg tgggtggtgga tgtgtcccag 1260
gaagatcccg aggtgcagtt caattggtac gtggacggcg tggaaagtgc caacgccaag 1320
accaagcccc gagaggaaca gttcaacagc acctaccggg tgggtgtccgt gctgaccgtg 1380
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cccagctcca tcgagaaaac catcagcaag gccaaaggcc agccccgcga gcctcaagtg 1500
tgtaccctgc cccctagcca ggaagagatg accaagaacc aggtgtccct gagctgtgcc 1560
gtgaaaggct tctaccccag cgacattgcc gtggaatggg agagcaacgg ccagcccag 1620
aacaactaca agaccacccc ccctgtgctg gacagcgacg gctcattctt cctggtgtcc 1680
aagctgaccg tggacaagag ccggtggcag gaaggcaacg tgttcagctg ctccgtgatg 1740
cacgaggccc tgcacaacca ctacaccag aagtccctgt ctctgtccct gggcaag 1797

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<210> 445

<211> 1023

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 445

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atcagctgca agagcagcca ctccctgatc cacggcgacc ggaacaacta cctggcttgg 120
tacgtgcaga agcccggcag atccccccag ctgctgatct acctggccag cagcagagcc 180
agcggcgtgc ccgatagatt ttctggcagc ggcagcgaca aggacttcac cctgaagatc 240
agccgggtgg aaaccgagga cgtgggcacc tactactgta tgcagggcag agagagcccc 300
tggaaccttg gccagggcac caaggtggac atcaaggaca aaaccatac cgacatcgtg 360
atgaccagga cccccctgag cctgagcgtg acacctggac agcctgccag catcagctgc 420
aagagcagcc agagcctggt gcacaacaac gccaacacct acctgagctg gtatctgcag 480
aagcccggcc agagccccca gtccctgatc tacaagggtg ccaacagatt cagcggcgtg 540
cccagacgat tctccggcag cggctctggc accgacttca ccctgaagat cagccgggtg 600
gaagccgagg acgtgggcgt gtactattgt ggccagggca cccagtacc cttcaccttt 660
ggcagcggca ccaaggtgga aatcaaggat aagaccata cccgtacggt ggccgctccc 720
agcgtgttca tcttcccacc tagcgacgag cagctgaagt ccggcacagc ctctgtcgtg 780
tgcctgctga acaacttcta cccccgcgag gccaaagtgc agtggaagggt ggacaacgcc 840
ctgcagagcg gcaacagcca ggaaagcgtg accgagcagg acagcaagga ctccacctac 900
agcctgagca gcaccctgac actgagcaag gccgactacg agaagcaca ggtgtacgcc 960
tgcgaagtga cccaccaggg cctgtctagc cccgtgacca agagcttcaa ccggggcgag 1020
tgt 1023

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<210> 446

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 446

4._183952027041SEQLIST.TXT

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gln	1	5	10	15
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Ser	Asp	Tyr	20	25	30	
Gly	Val	His	Trp	Val	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu	35	40	45	
Gly	Val	Ile	Trp	Ala	Gly	Gly	Gly	Thr	Asn	Tyr	Asn	Pro	Ser	Leu	Lys	50	55	60	
Ser	Arg	Lys	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	Asn	Gln	Val	Ser	Leu	65	70	75	80
Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	85	90	95	
Arg	Asp	Lys	Gly	Tyr	Ser	Tyr	Tyr	Tyr	Ser	Met	Asp	Tyr	Trp	Gly	Gln	100	105	110	
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	115	120	125	
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	130	135	140	
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	145	150	155	160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	165	170	175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	180	185	190	
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	195	200	205	
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	210	215	220	
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	225	230	235	240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	245	250	255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	260	265	270	
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	275	280	285	
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	290	295	300	
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	305	310	315	320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	325	330	335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	340	345	350	
Pro	Cys	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu	355	360	365	
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	370	375	380	
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	385	390	395	400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	405	410	415	

4.__183952027041SEQLIST.TXT

Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
			420					425					430		
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
		435					440					445			

<210> 447
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 447

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

<210> 448
 <211> 592
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

4.__183952027041SEQLIST.TXT

<400> 448

Gln	Val	His	Leu	Thr	Gln	Ser	Gly	Pro	Glu	Val	Arg	Lys	Pro	Gly	Thr
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Pro	Gly	Asn	Thr	Leu	Lys	Thr	Tyr
			20					25					30		
Asp	Leu	His	Trp	Val	Arg	Ser	Val	Pro	Gly	Gln	Gly	Leu	Gln	Trp	Met
		35					40					45			
Gly	Trp	Ile	Ser	His	Glu	Gly	Asp	Lys	Lys	Val	Ile	Val	Glu	Arg	Phe
	50					55					60				
Lys	Ala	Lys	Val	Thr	Ile	Asp	Trp	Asp	Arg	Ser	Thr	Asn	Thr	Ala	Tyr
65					70				75						80
Leu	Gln	Leu	Ser	Gly	Leu	Thr	Ser	Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Lys	Gly	Ser	Lys	His	Arg	Leu	Arg	Asp	Tyr	Ala	Leu	Tyr	Asp	Asp
			100					105					110		
Asp	Gly	Ala	Leu	Asn	Trp	Ala	Val	Asp	Val	Asp	Tyr	Leu	Ser	Asn	Leu
		115					120					125			
Glu	Phe	Trp	Gly	Gln	Gly	Thr	Ala	Val	Thr	Val	Ser	Ser	Ser	Gln	Val
	130					135					140				
Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu
145					150					155					160
Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Thr	Lys	Ala	Trp	Met
			165					170						175	
His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gln	Leu	Glu	Trp	Val	Ala	Gln
		180						185					190		
Ile	Lys	Asp	Lys	Ser	Asn	Ser	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp	Ser	Val
	195						200					205			
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Leu	Tyr
	210					215					220				
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
225					230					235					240
Arg	Gly	Val	Tyr	Tyr	Ala	Leu	Ser	Pro	Phe	Asp	Tyr	Trp	Gly	Gln	Gly
			245						250					255	
Thr	Leu	Val	Thr	Val	Ser	Ser	Arg	Thr	Ala	Ser	Thr	Lys	Gly	Pro	Ser
		260						265					270		
Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala
	275						280					285			
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
	290					295					300				
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
305					310					315					320
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
				325					330					335	
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His
			340					345					350		
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly
		355					360					365			
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser
	370					375					380				
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
385					390					395					400

4._183952027041SEQLIST.TXT

Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
				405					410					415	
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
			420					425					430		
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
		435					440					445			
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
	450					455					460				
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
465					470					475					480
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Cys	Thr	Leu
			485						490					495	
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Ser	Cys
			500					505					510		
Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
		515					520					525			
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
	530					535					540				
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser
545					550					555					560
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
			565					570						575	
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys
			580					585					590		

<210> 449

<211> 343

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 449

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

4.__183952027041SEQLIST.TXT

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

<210> 450

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 450

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acctgtaccg tgtccggctt cagcctgagc gactacggcg tgcactgggt gcgccagcca 120
cctggaaaag gcctggaatg gctgggcgtg atctgggctg gcggaggcac caactacaac 180
cccagcctga agtccagaaa gaccatcagc aaggacacca gcaagaacca ggtgtccctg 240
aagctgagca gcgtgacagc cgccgatacc gccgtgtact actgcgccag agacaagggc 300
tacagctact actacagcat ggactactgg ggccagggca ccaccgtgac cgtgtcatcc 360
gcgtcgacca agggccctc ggtgttccct ctggcccctt gcagcagaag caccagcgaa 420
tctacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc 480
tggaactctg gcgctctgac aagcggcgtg cacacctttc cagccgtgct ccagagcagc 540
ggcctgtact ctctgagcag cgtcgtgaca gtgcccagca gcagcctggg caccaagacc 600
tacacctgta acgtggacca caagcccagc aacaccaagg tggacaagcg ggtggaatct 660
aagtacggcc ctccctgccc tccttgccca gccctgaat ttctgggcgg accctccgtg 720
ttcctgttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc 780
tgcgtggtgg tggatgtgtc ccaggaagat cccgaggtgc agttcaattg gtacgtggac 840

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4. __183952027041SEQLIST.TXT

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ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagttcaa cagcacctac 900
cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agagtacaag 960
tgcaaggtgt ccaacaaggg cctgcccagc tccatcgaga aaaccatcag caaggccaag 1020
ggccagcccc gcgagcctca agtgtatacc ctgccccctt gccaggaaga gatgaccaag 1080
aaccaggtgt ccctgtggtg tctcgtgaaa ggcttctacc ccagcgacat tgccgtggaa 1140
tgggagagca acggccagcc cgagaacaac tacaagacca cccccctgt gctggacagc 1200
gacggctcat tcttcctgta ctccaagctg accgtggaca agagccggtg gcaggaaggc 1260
aacgtgttca gctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc 1320
ctgtctctgt ccctgggcaa g                                     1341

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<210> 451

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 451

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gacatcgtgc tgacacagag ccctgctagc ctggccgtgt ctcttggaaca gagggccacc 60
atcacctgta gagccagcga gagcgtggaa tattacgtga ccagcctgat gcagtgggtat 120
cagcagaagc ccggccagcc cccaagctg ctgattttcg ccgccagcaa cgtggaaagc 180
ggcgtgccag ccagattttc cggcagcggc tctggcaccg acttcaccct gaccatcaac 240
cccgtggaag ccaacgacgt ggccaactac tactgccagc agagccggaa ggtgccctac 300
acctttggcc agggcaccaa gctggaaatc aagcgtacgg tggccgctcc cagcgtgttc 360
atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 420
aacaacttct acccccgcga ggccaaggtg cagtggaaagg tggacaatgc cctgcagagc 480
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 540
agcacctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 600
accaccagg gcctgtctag ccccgtagc aagagcttca accggggcga gtgt 654

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<210> 452

<211> 1776

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 452

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tcctgcaagg cccctggcaa caccctgaaa acctacgacc tgcactgggt gcgcagcgtg 120
ccaggacagg gactgcagtg gatgggctgg atcagccacg agggcgacaa gaaagtgatc 180
gtggaacggt tcaaggccaa agtgaccatc gactgggaca gaagcaccaa caccgcctac 240
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aagcaccggc tgagagacta cgccctgtac gacgatgacg gcgcccctgaa ctgggcccgtg 360
gatgtggact acctgagcaa cctggaattc tggggccagg gcacagccgt gaccgtgtca 420
tcttctcagg tgcagctggg ggaatctggc ggcgagtggt tgcagcctgg cagaagcctg 480
agactgagct gtgccgccag cggcttcacc ttcaccaagg cctggatgca ctgggtgcgc 540
caggccccctg gaaagcagct ggaatgggtg gccagatca aggacaagag caacagctac 600
gccacctact acgccgacag cgtgaagggc cggttcacca tcagccggga cgacagcaag 660
aacaccctgt acctgcagat gaacagcctg cgggcccagg acaccgccgt gtactactgt 720

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4. __183952027041SEQLIST.TXT

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cggggcgtgt actatgccct gagccccttc gattactggg gccagggaac cctcgtgacc 780
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agaagcacca gcgaatctac agccgccctg ggctgcctcg tgaaggacta ctttcccagag 900
cccgtgaccg tgccttgaa ctctggcgct ctgacaagcg gcgtgcacac ctttccagcc 960
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gaagagatga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccccagc 1560
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cctgtgctgg acagcgacgg ctcatcttc ctggtgtcca agctgaccgt ggacaagagc 1680
cggtggcagg aaggcaacgt gttcagctgc tccgtgatgc acgaggccct gcacaaccac 1740
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<210> 453

<211> 1029

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 453

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tatctgcaga agcccgcca gagccccag tccctgatct acaagggtgtc caacagattc 180
agcggcgtgc ccgacagatt ctccggcagc ggctctggca ccgacttcac cctgaagatc 240
agccgggtgg aagccgagga cgtgggcgtg tactattgtg gccagggcac ccagtacccc 300
ttcacctttg gcagcggcac caaggtggaa atcaagggcc agcccaaggc cgccccgac 360
ttcgtgctga cccagagccc tcacagcctg agcgtgacac ctggcgagag cgccagcatc 420
agctgcaaga gcagccactc cctgatccac ggcgaccgga acaactacct ggcttggtac 480
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acctttggcc agggcaccaa ggtggacatc aagaccaagg gcccagccg tacggtggcc 720
gtctccagcg tgttcatctt cccacctagc gacgagcagc tgaagtccgg cacagcctct 780
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aacgccctgc agagcggcaa cagccaggaa agcgtgaccg agcaggacag caaggactcc 900
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<210> 454

<211> 447

<212> PRT

<213> Artificial Sequence

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<220>

<223> Synthetic Construct

<400> 454

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Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Ser	Asp	Tyr
			20					25					30		
Gly	Val	His	Trp	Val	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu
		35					40					45			
Gly	Val	Ile	Trp	Ala	Gly	Gly	Gly	Thr	Asn	Tyr	Asn	Pro	Ser	Leu	Lys
		50				55					60				
Ser	Arg	Lys	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	Asn	Gln	Val	Ser	Leu
65					70					75					80
Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
				85					90					95	
Arg	Asp	Lys	Gly	Tyr	Ser	Tyr	Tyr	Tyr	Ser	Met	Asp	Tyr	Trp	Gly	Gln
			100					105					110		
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
		115					120					125			
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala
		130				135					140				
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165					170					175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
		210				215					220				
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225					230					235					240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
				245					250					255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
			260					265					270		
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
		275					280					285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
		290				295					300				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305					310					315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
				325					330					335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
			340					345					350		
Pro	Cys	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu
		355					360					365			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
		370				375					380				

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Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385					390					395					400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg
				405					410					415	
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
			420					425					430		
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
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<210> 455
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 455

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

<210> 456
 <211> 599
 <212> PRT

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<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 456

Gln	Val	His	Leu	Thr	Gln	Ser	Gly	Pro	Glu	Val	Arg	Lys	Pro	Gly	Thr	1	5	10	15
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Pro	Gly	Asn	Thr	Leu	Lys	Thr	Tyr	20	25	30	
Asp	Leu	His	Trp	Val	Arg	Ser	Val	Pro	Gly	Gln	Gly	Leu	Gln	Trp	Met	35	40	45	
Gly	Trp	Ile	Ser	His	Glu	Gly	Asp	Lys	Lys	Val	Ile	Val	Glu	Arg	Phe	50	55	60	
Lys	Ala	Lys	Val	Thr	Ile	Asp	Trp	Asp	Arg	Ser	Thr	Asn	Thr	Ala	Tyr	65	70	75	80
Leu	Gln	Leu	Ser	Gly	Leu	Thr	Ser	Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Ala	Lys	Gly	Ser	Lys	His	Arg	Leu	Arg	Asp	Tyr	Ala	Leu	Tyr	Asp	Asp	100	105	110	
Asp	Gly	Ala	Leu	Asn	Trp	Ala	Val	Asp	Val	Asp	Tyr	Leu	Ser	Asn	Leu	115	120	125	
Glu	Phe	Trp	Gly	Gln	Gly	Thr	Ala	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	130	135	140	
His	Thr	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	145	150	155	160
Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Thr	165	170	175	
Lys	Ala	Trp	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gln	Leu	Glu	180	185	190	
Trp	Val	Ala	Gln	Ile	Lys	Asp	Lys	Ser	Asn	Ser	Tyr	Ala	Thr	Tyr	Tyr	195	200	205	
Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	210	215	220	
Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	225	230	235	240
Val	Tyr	Tyr	Cys	Arg	Gly	Val	Tyr	Tyr	Ala	Leu	Ser	Pro	Phe	Asp	Tyr	245	250	255	
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Asp	Lys	Thr	His	Thr	260	265	270	
Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	275	280	285	
Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	290	295	300	
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	305	310	315	320
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	325	330	335	
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	340	345	350	
Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	355	360	365	

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Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
370 375 380
Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
385 390 395 400
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
405 410 415
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
420 425 430
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
435 440 445
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
450 455 460
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
465 470 475 480
Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
485 490 495
Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
500 505 510
Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp
515 520 525
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
530 535 540
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser
545 550 555 560
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
565 570 575
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
580 585 590
Leu Ser Leu Ser Leu Gly Lys
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<210> 457

<211> 341

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 457

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

4. 183952027041SEQLIST.TXT

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

<210> 458

<211> 1341

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 458

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cctggaaaag	gcctggaatg	gctggggctg	atctgggctg	gcggaggcac	caactacaac	180
cccagcctga	agtccagaaa	gaccatcagc	aaggacacca	gcaagaacca	ggtgtccctg	240
aagctgagca	gcgtgacagc	cgccgatacc	gccgtgtact	actgcgccag	agacaagggc	300
tacagctact	actacagcat	ggactactgg	ggccagggca	ccaccgtgac	cgtgtcatcc	360
gcgtcgacca	agggccctc	ggtgtttccct	ctggccctt	gcagcagaag	caccagcgaa	420
tctacagccg	ccctgggctg	cctcgtgaag	gactactttc	ccgagcccgt	gaccgtgtcc	480

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ggcctgtact ctctgagcag cgtcgtgaca gtgcccagca gcagcctggg caccaagacc 600
tacacctgta acgtggacca caagcccagc aacaccaagg tggacaagcg ggtggaatct 660
aagtacggcc ctccctgccc tccttgccc a gcccctgaat ttctgggcgg accctccgtg 720
ttcctgttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc 780
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ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagttcaa cagcacctac 900
cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agagtacaag 960
tgcaaggtgt ccaacaaggg cctgcccagc tccatcgaga aaaccatcag caaggccaag 1020
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aaccaggtgt ccctgtggtg tctcgtgaaa ggcttctacc ccagcgacat tgccgtggaa 1140
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gacggctcat tcttctgta ctccaagctg accgtggaca agagccggtg gcaggaaggc 1260
aacgtgttca gctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc 1320
ctgtctctgt ccctgggcaa g                                     1341

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<210> 459

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 459

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atcacctgta gagccagcga gagcgtggaa tattacgtga ccagcctgat gcagtgggat 120
cagcagaagc ccggccagcc cccaagctg ctgattttcg ccgccagcaa cgtggaaagc 180
ggcgtgccag ccagattttc cggcagcggc tctggcaccg acttcaccct gaccatcaac 240
cccgtggaag ccaacgacgt ggccaactac tactgccagc agagccggaa ggtgccctac 300
acctttggcc agggcaccaa gctggaaatc aagcgtacgg tggccgctcc cagcgtgttc 360
atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 420
aacaacttct acccccgcga ggccaaggtg cagtggagg tggacaatgc cctgcagagc 480
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 540
agcaccctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 600
accaccagg gcctgtctag ccccgtagc aagagcttca accggggcga gtgt 654

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<210> 460

<211> 1797

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 460

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tcctgcaagg cccctggcaa caccctgaaa acctacgacc tgcactgggt gcgcagcgtg 120
ccaggacagg gactgcagtg gatgggctgg atcagccacg agggcgacaa gaaagtgatc 180
gtggaacggt tcaaggccaa agtgaccatc gactgggaca gaagcaccaa caccgcctac 240
ctgcagctga gcggcctgac ctctggcgat accgccgtgt actactgcgc caagggcagc 300
aagcaccggc tgagagacta cgccctgtac gacgatgacg gcgccctgaa ctgggccgtg 360

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4. __183952027041SEQLIST.TXT

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gatgtggact acctgagcaa cctggaattc tggggccagg gcacagccgt gaccgtgtca 420
tctgacaaaa cccataccca ggtgcagctg gtggaatctg gcggcggagt ggtgcagcct 480
ggcagaagcc tgagactgag ctgtgccgcc agcggcttca ccttcaccaa ggcctggatg 540
cactgggtgc gccaggcccc tggaaagcag ctggaatggg tggcccagat caaggacaag 600
agcaacagct acgccaccta ctacgccgac agcgtgaagg gccggttcac catcagccgg 660
gacgacagca agaacaccct gtacctgcag atgaacagcc tgcgggccga ggacaccgcc 720
gtgtactact gtcggggcgt gtactatgcc ctgagcccct tcgattactg gggccaggga 780
accctcgtga cgtgtcttag tgataagacc cacaccgctt cgaccaaggg cccatcgggtg 840
ttccctctgg ccccttgtag cagaagcacc agcgaatcta cagccgccct gggctgcctc 900
gtgaaggact actttcccga gcccgtgacc gtgtcctgga actctggcgc tctgacaagc 960
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aagctgaccg tggacaagag ccggtggcag gaaggcaacg tgttcagctg ctccgtgatg 1740
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<210> 461

<211> 1023

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 461

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atcagctgca agagcagcca gagcctgggt cacaacaacg ccaacaccta cctgagctgg 120
tatctgcaga agcccggcca gagccccag tccctgatct acaaggtgtc caacagattc 180
agcggcgtgc ccgacagatt ctccggcagc ggctctggca ccgacttcac cctgaagatc 240
agccgggtgg aagccgagga cgtgggcgtg tactattgtg gccagggcac ccagtacccc 300
ttcacctttg gcagcggcac caaggtggaa atcaaggaca aaaccatac cgacttcgtg 360
ctgaccaga gccctcacag cctgagcgtg acacctggcg agagcgccag catcagctgc 420
aagagcagcc actccctgat ccacggcgac cggaacaact acctggcttg gtacgtgcag 480
aagcccggca gatccccca gctgctgac tacctggcca gcagcagagc cagcggcgtg 540
ccgatagat tttctggcag cggcagcgac aaggacttca ccctgaagat cagccgggtg 600
gaaaccgagg acgtgggcac ctactactgt atgcagggca gagagagccc ctggaccttt 660
ggccagggca ccaaggtgga catcaaggat aagaccata cccgtacggg ggccgctccc 720
agcgtgttca tcttccacc tagcgacgag cagctgaagt ccggcacagc ctctgtcgtg 780
tgcctgctga acaacttcta ccccgcgag gccaaagtgc agtggaagggt ggacaacgcc 840
ctgcagagcg gcaacagcca ggaaagcgtg accgagcagg acagcaagga ctccacctac 900
agcctgagca gcaccctgac actgagcaag gccgactacg agaagcaca ggtgtacgcc 960
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tgt 1023

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4.__183952027041SEQLIST.TXT

<210> 462
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 462
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 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
 20 25 30
 Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45
 Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Lys Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335

4. __183952027041SEQLIST.TXT

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Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    340                      345                      350
Pro Cys Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
    355                      360                      365
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                      375                      380
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
    385                      390                      395                      400
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
    405                      410                      415
Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
    420                      425                      430
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
    435                      440                      445

```

<210> 463

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 463

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

```

210

215

<210> 464
 <211> 592
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 464
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Lys Ala
 20 25 30
 Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gln Leu Glu Trp Val
 35 40 45
 Ala Gln Ile Lys Asp Lys Ser Asn Ser Tyr Ala Thr Tyr Tyr Ala Asp
 50 55 60
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
 65 70 75 80
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 85 90 95
 Tyr Cys Arg Gly Val Tyr Tyr Ala Leu Ser Pro Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser Ser Gln Val His Leu Thr Gln
 115 120 125
 Ser Gly Pro Glu Val Arg Lys Pro Gly Thr Ser Val Lys Val Ser Cys
 130 135 140
 Lys Ala Pro Gly Asn Thr Leu Lys Thr Tyr Asp Leu His Trp Val Arg
 145 150 155 160
 Ser Val Pro Gly Gln Gly Leu Gln Trp Met Gly Trp Ile Ser His Glu
 165 170 175
 Gly Asp Lys Lys Val Ile Val Glu Arg Phe Lys Ala Lys Val Thr Ile
 180 185 190
 Asp Trp Asp Arg Ser Thr Asn Thr Ala Tyr Leu Gln Leu Ser Gly Leu
 195 200 205
 Thr Ser Gly Asp Thr Ala Val Tyr Tyr Cys Ala Lys Gly Ser Lys His
 210 215 220
 Arg Leu Arg Asp Tyr Ala Leu Tyr Asp Asp Asp Gly Ala Leu Asn Trp
 225 230 235 240
 Ala Val Asp Val Asp Tyr Leu Ser Asn Leu Glu Phe Trp Gly Gln Gly
 245 250 255
 Thr Ala Val Thr Val Ser Ser Arg Thr Ala Ser Thr Lys Gly Pro Ser
 260 265 270
 Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
 275 280 285
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 290 295 300
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 305 310 315 320

4.__183952027041SEQLIST.TXT

Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val		
				325					330					335			
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His		
			340					345					350				
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly		
		355					360					365					
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser		
		370				375					380						
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg		
385					390				395						400		
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro		
				405					410					415			
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala		
			420					425					430				
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val		
		435					440					445					
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr		
		450				455					460						
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr		
465					470					475					480		
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Cys	Thr	Leu		
			485					490						495			
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Ser	Cys		
			500					505					510				
Ala	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser		
		515					520					525					
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp		
	530					535					540						
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Val	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser		
545					550					555					560		
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala		
				565					570					575			
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys		
			580					585					590				

<210> 465

<211> 343

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 465

Asp	Phe	Val	Leu	Thr	Gln	Ser	Pro	His	Ser	Leu	Ser	Val	Thr	Pro	Gly		
1				5					10					15			
Glu	Ser	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	His	Ser	Leu	Ile	His	Gly		
			20					25					30				
Asp	Arg	Asn	Tyr	Leu	Ala	Trp	Tyr	Val	Gln	Lys	Pro	Gly	Arg	Ser			
	35					40					45						
Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Ala	Ser	Ser	Arg	Ala	Ser	Gly	Val	Pro		

4.__183952027041SEQLIST.TXT

```

50          55          60
Asp Arg Phe Ser Gly Ser Gly Ser Asp Lys Asp Phe Thr Leu Lys Ile
65          70          75          80
Ser Arg Val Glu Thr Glu Asp Val Gly Thr Tyr Tyr Cys Met Gln Gly
85          90          95
Arg Glu Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
100         105         110
Gly Gln Pro Lys Ala Ala Pro Asp Ile Val Met Thr Gln Thr Pro Leu
115         120         125
Ser Leu Ser Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser
130         135         140
Ser Gln Ser Leu Val His Asn Asn Ala Asn Thr Tyr Leu Ser Trp Tyr
145         150         155         160
Leu Gln Lys Pro Gly Gln Ser Pro Gln Ser Leu Ile Tyr Lys Val Ser
165         170         175
Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
180         185         190
Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly
195         200         205
Val Tyr Tyr Cys Gly Gln Gly Thr Gln Tyr Pro Phe Thr Phe Gly Ser
210         215         220
Gly Thr Lys Val Glu Ile Lys Thr Lys Gly Pro Ser Arg Thr Val Ala
225         230         235         240
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
245         250         255
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
260         265         270
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
275         280         285
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
290         295         300
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
305         310         315         320
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
325         330         335
Ser Phe Asn Arg Gly Glu Cys
340

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<210> 466

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 466

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caggtgcagc tgcaggaatc tggccctggc ctcgtgaagc ctagccagac cctgagcctg 60
acctgtaccg tgtccggctt cagcctgagc gactacggcg tgcactgggt gcgccagcca 120
cctggaaaag gcctggaatg gctgggcgtg atctgggctg gcggaggcac caactacaac 180
cccagcctga agtccagaaa gaccatcagc aaggacacca gcaagaacca ggtgtccctg 240

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4. __183952027041SEQLIST.TXT

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aagctgagca gcgtgacagc cgccgatacc gccgtgtact actgcgccag agacaagggc 300
tacagctact actacagcat ggactactgg gccagggca ccaccgtgac cgtgtcatcc 360
gcgtcgacca agggccctc ggtgttcctt ctggcccctt gcagcagaag caccagcgaa 420
tctacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc 480
tggaactctg gcgctctgac aagcggcgtg cacacctttc cagccgtgct ccagagcagc 540
ggcctgtact ctctgagcag cgtcgtgaca gtgcccagca gcagcctggg caccaagacc 600
tacacctgta acgtggacca caagcccagc aacaccaagg tggacaagcg ggtggaatct 660
aagtacggcc ctccctgccc tccttgccc aacacctgaat ttctgggagg accctccgtg 720
ttcctgttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc 780
tgctgtggtg tggatgtgtc ccaggaagat cccgaggtgc agttcaattg gtacgtggac 840
ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagttcaa cagcacctac 900
cgggtggtgt ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agagtacaag 960
tgcaagggtg ccaacaaggg cctgcccagc tccatcgaga aaaccatcag caaggccaag 1020
ggccagcccc gcgagcctca agtgtatacc ctgccccctt gccaggaaga gatgaccaag 1080
aaccaggtgt ccctgtggtg tctcgtgaaa ggcttctacc ccagcgacat tgccgtggaa 1140
tgaggagagca acggccagcc cgagaacaac tacaagacca cccccctgt gctggacagc 1200
gacggctcat tcttctgta ctccaagctg accgtggaca agagccggtg gcaggaaggc 1260
aacgtgttca gctgctccgt gatgcacgag gccctgcaca accactacac ccagaagtcc 1320
ctgtctctgt ccctgggcaa g                                     1341

```

<210> 467

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 467

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gacatcgtgc tgacacagag ccctgctagc ctggccgtgt ctcttggaaca gagggccacc 60
atcacctgta gagccagcga gagcgtggaa tattacgtga ccagcctgat gcagtggat 120
cagcagaagc ccggccagcc ccccaagctg ctgattttcg ccgccagcaa cgtggaaagc 180
ggcgtgccag ccagattttc cggcagcggc tctggcaccg acttcaccct gaccatcaac 240
cccgtggaag ccaacgacgt ggccaactac tactgccagc agagccggaa ggtgccctac 300
acctttggcc agggcaccaa gctggaaatc aagcgtacgg tggccgctcc cagcgtgttc 360
atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 420
aacaacttct acccccgcga ggccaaggtg cagtggaaagg tggacaatgc cctgcagagc 480
ggcaacagcc aggaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 540
agcaccctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 600
accaccagg gcctgtctag cccctgacc aagagcttca accggggcga gtgt 654

```

<210> 468

<211> 1776

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 468

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caggtgcagc tgggtggaatc tggcggcgga gtggtgcagc ctggcagaag cctgagactg 60
agctgtgccg ccagcggtt caccttcacc aaggcctgga tgcactgggt gcgccaggcc 120

```

4. __183952027041SEQLIST.TXT

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cctggaaagc agctggaatg ggtggcccag atcaaggaca agagcaacag ctacgccacc 180
tactacgccg acagcgtgaa gggccggttc accatcagcc gggacgacag caagaacacc 240
ctgtacctgc agatgaacag cctgcggggc gaggacaccg ccgtgtacta ctgtcggggc 300
gtgtactatg ccctgagccc cttcgattac tggggccagg gaaccctcgt gaccgtgtct 360
agtagccagg tgcacctgac acagagcggg cccgaagtgc ggaagcctgg cacctctgtg 420
aaggtgtcct gcaaggcccc tggcaacacc ctgaaaacct acgacctgca ctgggtgcgc 480
agcgtgccag gacagggact gcagtggatg ggctggatca gccacgaggg cgacaagaaa 540
gtgatcgtgg aacggttcaa ggccaaagtg accatcgact gggacagaag caccaacacc 600
gcctacctgc agctgagcgg cctgacctct ggcgataccg ccgtgtacta ctgcgccaa 660
ggcagcaagc accggtgag agactacgcc ctgtacgacg atgacggcgc cctgaactgg 720
gccgtggatg tggactacct gagcaacctg gaattctggg gccagggcac agccgtgacc 780
gtgtcatctc ggaccgccag cacaaggggc ccatcggtgt tccctctggc cccttgacgc 840
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gtgctccaga gcagggcct gtactctctg agcagcgtcg tgacagtgcc cagcagcagc 1020
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aagcgggtgg aatctaagta cggccctccc tgccctcctt gcccagcccc tgaatttctg 1140
ggcggaccct ccgtgttcct gttccccca aagcccaagg acaccctgat gatcagccgg 1200
acccccgaag tgacctgctg ggtggtggat gtgtcccagg aagatcccga ggtgcagttc 1260
aattggtacg tggacggcgt ggaagtgcac aacgccaaga ccaagcccag agaggaacag 1320
ttcaacagca cctaccgggt ggtgtccgtg ctgaccgtgc tgcaccagga ctggctgaac 1380
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atcagcaagg ccaagggcca gccccgcgag cctcaagtgt gtaccctgcc ccctagccag 1500
gaagagatga ccaagaacca ggtgtccctg agctgtgccg tgaaaggctt ctaccccagc 1560
gacattgccg tggaatggga gagcaacggc cagcccagaga acaactacaa gaccaccccc 1620
cctgtgtctg acagcgacgg ctcatctctc ctggtgtcca agctgaccgt ggacaagagc 1680
cggtggcagg aaggcaacgt gttcagctgc tccgtgatgc acgaggccct gcacaaccac 1740
tacaccaga agtccctgtc tctgtccctg ggcaag 1776

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<210> 469

<211> 1029

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 469

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gacttcgtgc tgaccagag ccctcacagc ctgagcgtga cacctggcga gagcgccagc 60
atcagctgca agagcagcca ctccctgatc cacggcgacc ggaacaacta cctggcttgg 120
tacgtgcaga agcccggcag atccccccag ctgctgatct acctggccag cagcagagcc 180
agcggcgtgc ccgatagatt ttctggcagc ggcagcgaca aggacttcac cctgaagatc 240
agccgggtgg aaaccgagga cgtgggcacc tactactgta tgcagggcag agagagcccc 300
tggacctttg gccagggcac caaggtggac atcaagggcc agcccaaggc ccccccgac 360
atcgtgatga cccagacccc cctgagcctg agcgtgacac ctggacagcc tgccagcatc 420
agctgcaaga gcagccagag cctggtgcac aacaacgcca acacctacct gagctggtat 480
ctgcagaagc ccggccagag cccccagtcc ctgatctaca aggtgtccaa cagattcagc 540
ggcgtgcccg acagattctc cggcagcggc tctggcaccg acttcaccct gaagatcagc 600
cgggtggaag ccgaggacgt gggcgtgtac tattgtggcc agggcaccca gtacccttc 660
acctttggca gcggcaccaa ggtggaaatc aagaccaagg gccccagccg tacggtggcc 720
gtccccagcg tgttcatctt cccacctagc gacgagcagc tgaagtccgg cacagcctct 780
gtcgtgtgcc tgctgaacaa cttctacccc cgcgaggcca aagtgcagtg gaaggtggac 840

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aacgccctgc	agagcggcaa	cagccaggaa	agcgtgaccg	agcaggacag	caaggactcc	900
acctacagcc	tgagcagcac	cctgacactg	agcaaggccg	actacgagaa	gcacaaggtg	960
tacgcctgcg	aagtgaccca	ccagggcctg	tctagccccg	tgaccaagag	cttcaaccgg	1020
ggcgagtgt						1029

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<210> 470
<211> 447
<212> PRT
<213> Artificial Sequence
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<220>
<223> Synthetic Construct

<400> 470															
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Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly 25	Phe	Ser	Leu	Ser	Asp	Tyr
Gly	Val	His 35	Trp	Val	Arg	Gln	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu	
Gly 50	Val	Ile	Trp	Ala	Gly	Gly 55	Gly	Thr	Asn	Tyr	Asn	Pro	Ser	Leu	Lys
Ser 65	Arg	Lys	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	Asn	Gln	Val	Ser	Leu
Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
Arg	Asp	Lys	Gly	Tyr	Ser	Tyr	Tyr	Tyr	Ser	Met	Asp	Tyr	Trp	Gly	Gln
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala
Leu 145	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
Pro 225	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser

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

<210> 471

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 471

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

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His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 180 185 190
 195 200 205
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 472

<211> 599

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 472

Gln 1	Val 2	Gln 3	Leu 4	Val 5	Glu 6	Ser 7	Gly 8	Gly 9	Gly 10	Val 11	Val 12	Gln 13	Pro 14	Gly 15	Arg 16
Ser	Leu	Arg	Leu 20	Ser 21	Cys 22	Ala 23	Ala 24	Ser 25	Gly 26	Phe 27	Thr 28	Phe 29	Thr 30	Lys 31	Ala 32
Trp	Met 33	His 34	Trp 35	Val 36	Arg 37	Gln 38	Ala 39	Pro 40	Gly 41	Lys 42	Gln 43	Leu 44	Glu 45	Trp 46	Val 47
Ala 48	Gln 49	Ile 50	Lys 51	Asp 52	Lys 53	Ser 54	Asn 55	Ser 56	Tyr 57	Ala 58	Thr 59	Tyr 60	Tyr 61	Ala 62	Asp 63
Ser 64	Val 65	Lys 66	Gly 67	Arg 68	Phe 69	Thr 70	Ile 71	Ser 72	Arg 73	Asp 74	Asp 75	Ser 76	Lys 77	Asn 78	Thr 79
Leu 80	Tyr 81	Leu 82	Gln 83	Met 84	Asn 85	Ser 86	Leu 87	Arg 88	Ala 89	Glu 90	Asp 91	Thr 92	Ala 93	Val 94	Tyr 95
Tyr 96	Cys 97	Arg 98	Gly 99	Val 100	Tyr 101	Tyr 102	Ala 103	Leu 104	Ser 105	Pro 106	Phe 107	Asp 108	Tyr 109	Trp 110	Gly 111
Gln 112	Gly 113	Thr 114	Leu 115	Val 116	Thr 117	Val 118	Ser 119	Ser 120	Asp 121	Lys 122	Thr 123	His 124	Thr 125	Gln 126	Val 127
His 128	Leu 129	Thr 130	Gln 131	Ser 132	Gly 133	Pro 134	Glu 135	Val 136	Arg 137	Lys 138	Pro 139	Gly 140	Thr 141	Ser 142	Val 143
Lys 144	Val 145	Ser 146	Cys 147	Lys 148	Ala 149	Pro 150	Gly 151	Asn 152	Thr 153	Leu 154	Lys 155	Thr 156	Tyr 157	Asp 158	Leu 159
His 160	Trp 161	Val 162	Arg 163	Ser 164	Val 165	Pro 166	Gly 167	Gln 168	Gly 169	Leu 170	Gln 171	Trp 172	Met 173	Gly 174	Trp 175
Ile 176	Ser 177	His 178	Glu 179	Gly 180	Asp 181	Lys 182	Lys 183	Val 184	Ile 185	Val 186	Glu 187	Arg 188	Phe 189	Lys 190	Ala 191
Lys 192	Val 193	Thr 194	Ile 195	Asp 196	Trp 197	Asp 198	Arg 199	Ser 200	Thr 201	Asn 202	Thr 203	Ala 204	Tyr 205	Leu 206	Gln 207
Leu 208	Ser 209	Gly 210	Leu 211	Thr 212	Ser 213	Gly 214	Asp 215	Thr 216	Ala 217	Val 218	Tyr 219	Tyr 220	Cys 221	Ala 222	Lys 223
Gly 224	Ser 225	Lys 226	His 227	Arg 228	Leu 229	Arg 230	Asp 231	Tyr 232	Ala 233	Leu 234	Tyr 235	Asp 236	Asp 237	Asp 238	Gly 239
Ala 240	Leu 241	Asn 242	Trp 243	Ala 244	Val 245	Asp 246	Val 247	Asp 248	Tyr 249	Leu 250	Ser 251	Asn 252	Leu 253	Glu 254	Phe 255
Trp 256	Gly 257	Gln 258	Gly 259	Thr 260	Ala 261	Val 262	Thr 263	Val 264	Ser 265	Ser 266	Asp 267	Lys 268	Thr 269	His 270	Thr 271
Ala 272	Ser 273	Thr 274	Lys 275	Gly 276	Pro 277	Ser 278	Val 279	Phe 280	Pro 281	Leu 282	Ala 283	Pro 284	Cys 285	Ser 286	Arg 287

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Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 290                295                300
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
305                310                315                320
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
                325                330                335
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
 340                345                350
Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 355                360                365
Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
 370                375                380
Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
385                390                395                400
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
                405                410                415
Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 420                425                430
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 435                440                445
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 450                455                460
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
465                470                475                480
Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
                485                490                495
Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 500                505                510
Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp
 515                520                525
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 530                535                540
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser
545                550                555                560
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
                565                570                575
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 580                585                590
Leu Ser Leu Ser Leu Gly Lys
 595

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<210> 473

<211> 341

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 473

Asp Phe Val Leu Thr Gln Ser Pro His Ser Leu Ser Val Thr Pro Gly

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			20				25						30			
Asp	Arg	Asn	Asn	Tyr	Leu	Ala	Trp	Tyr	Val	Gln	Lys	Pro	Gly	Arg	Ser	
		35			40						45					
Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Ala	Ser	Ser	Arg	Ala	Ser	Gly	Val	Pro	
		50			55						60					
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Asp	Lys	Asp	Phe	Thr	Leu	Lys	Ile	
65				70						75			80			
Ser	Arg	Val	Glu	Thr	Glu	Asp	Val	Gly	Thr	Tyr	Tyr	Cys	Met	Gln	Gly	
				85				90				95				
Arg	Glu	Ser	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Asp	Ile	Lys	
			100				105				110					
Asp	Lys	Thr	His	Thr	Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	
		115				120						125				
Ser	Val	Thr	Pro	Gly	Gln	Pro	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	Gln	
		130				135				140						
Ser	Leu	Val	His	Asn	Asn	Ala	Asn	Thr	Tyr	Leu	Ser	Trp	Tyr	Leu	Gln	
145				150						155				160		
Lys	Pro	Gly	Gln	Ser	Pro	Gln	Ser	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	
				165				170				175				
Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	
			180				185				190					
Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	
		195				200				205						
Tyr	Cys	Gly	Gln	Gly	Thr	Gln	Tyr	Pro	Phe	Thr	Phe	Gly	Ser	Gly	Thr	
		210				215				220						
Lys	Val	Glu	Ile	Lys	Asp	Lys	Thr	His	Thr	Arg	Thr	Val	Ala	Ala	Pro	
225				230						235				240		
Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	
				245				250				255				
Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	
			260				265				270					
Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	
		275				280				285						
Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	
		290				295				300						
Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	
305				310						315				320		
Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	
				325				330				335				
Asn	Arg	Gly	Glu	Cys												
			340													

<223> Synthetic Construct

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<400> 474

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cctggaaaag gcctggaatg gctgggctg atctgggctg gcggaggcac caactacaac 180
cccagcctga agtccagaaa gaccatcagc aaggacacca gcaagaacca ggtgtccctg 240
aagctgagca gcgtgacagc cgccgatacc gccgtgtact actgcgccag agacaagggc 300
tacagctact actacagcat ggactactgg ggccagggca ccaccgtgac cgtgtcatcc 360
gcgtcgacca agggccctc ggtgttccct ctggcccctt gcagcagaag caccagcgaa 420
tctacagccg ccctgggctg cctcgtgaag gactactttc ccgagcccgt gaccgtgtcc 480
tggaactctg gcgctctgac aagcggcgtg cacacctttc cagccgtgct ccagagcagc 540
ggcctgtact ctctgagcag cgtcgtgaca gtgcccagca gcagcctggg caccaagacc 600
tacacctgta acgtggacca caagcccagc aacaccaagg tggacaagcg ggtggaatct 660
aagtacggcc ctccctgccc tccttgccca gccctgaat ttctgggcgg accctccgtg 720
ttcctgttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc 780
tgctgtgtgg tggatgtgtc ccaggaagat cccgaggtgc agttcaattg gtacgtggac 840
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cgggtgtgtg ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agagtacaag 960
tgcaaggtgt ccaacaaggg cctgcccagc tccatcgaga aaaccatcag caaggccaag 1020
ggccagcccc gcgagcctca agtgtatacc ctgccccctt gccaggaaga gatgaccaag 1080
aaccaggtgt ccctgtgtgt tctcgtgaaa ggcttctacc ccagcgacat tgccgtggaa 1140
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gacggctcat tcttctgtga ctccaagctg accgtggaca agagccggtg gcaggaaggc 1260
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<210> 475

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 475

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atcacctgta gagccagcga gagcgtggaa tattacgtga ccagcctgat gcagtgggtat 120
cagcagaagc ccggccagcc cccaagctg ctgattttcg ccgccagcaa cgtggaaagc 180
ggcgtgccag ccagattttc cggcagcggc tctggcaccg acttcaccct gaccatcaac 240
cccgtggaag ccaacgacgt ggccaactac tactgccagc agagccggaa ggtgccctac 300
acctttggcc agggcaccaa gctggaaatc aagcgtacgg tggccgctcc cagcgtgttc 360
atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 420
aacaacttct acccccgcga ggccaaggtg cagtggaaagg tggacaatgc cctgcagagc 480
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 540
agcaccctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagtg 600
accaccagg gcctgtctag ccccgtagc aagagcttca accggggcga gtgt 654
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<210> 476

<211> 1797

<212> DNA

<213> Artificial Sequence

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<220>

<223> Synthetic Construct

<400> 476

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cctggaaagc agctggaatg ggtggcccag atcaaggaca agagcaacag ctacgccacc 180
tactacgccg acagcgtgaa gggccggttc accatcagcc gggacgacag caagaacacc 240
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tactgcgcca agggcgacaa gcaccggctg agagactacg ccctgtacga cgatgacggc 720
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cccagctcca tcgagaaaac catcagcaag gccaaaggcc agccccgcga gcctcaagtg 1500
tgtaccctgc cccctagcca ggaagagatg accaagaacc aggtgtccct gagctgtgcc 1560
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aagctgaccg tggacaagag ccggtggcag gaaggcaacg tgttcagctg ctccgtgatg 1740
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<210> 477

<211> 1023

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 477

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tacgtgcaga agcccggcag atccccccag ctgctgatct acctggccag cagcagagcc 180
agcggcgtgc ccgatagatt ttctggcagc ggcagcgaca aggacttcac cctgaagatc 240
agccgggtgg aaaccgagga cgtgggcacc tactactgta tgcagggcag agagagcccc 300
tggacctttg gccagggcac caaggtggac atcaaggaca aaaccatac cgacatcgtg 360
atgaccagga cccccctgag cctgagcgtg acacctggac agcctgccag catcagctgc 420
aagagcagcc agagcctggt gcacaacaac gccaacacct acctgagctg gtatctgcag 480

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aagcccgcc agagcccca gtccctgac tacaagggtg ccaacagatt cagcggcgtg 540
cccgcagat tctccggcag cggctctggc accgacttca ccctgaagat cagccgggtg 600
gaagccgagg acgtgggctg gtactattgt ggccaggcca cccagtaccc cttcaccttt 660
ggcagcggca ccaagggtga aatcaaggat aagaccata cccgtacggg ggccgctccc 720
agcgtgttca tcttcccacc tagcgacgag cagctgaagt ccggcacagc ctctgtcgtg 780
tgcctgctga acaacttcta ccccgcgag gccaaagtgc agtggaagggt ggacaacgcc 840
ctgcagagcg gcaacagcca ggaaagcgtg accgagcagg acagcaagga ctccacctac 900
agcctgagca gcaccctgac actgagcaag gccgactacg agaagcaca ggtgtacgcc 960
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Gly Tyr Thr Phe Thr Ser Tyr Tyr

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Ile Tyr Pro Gly Asn Val Asn Thr

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Thr Arg Ser His Tyr Gly Leu Asp Trp Asn Phe Asp Val
1 5 10

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Gly Phe Ser Leu Ser Asp Tyr Gly
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Ile Trp Ala Gly Gly Gly Thr
1 5

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

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Gly Phe Thr Phe Thr Lys Ala Trp
1 5

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<400> 486
Ile Lys Asp Lys Ser Asn Ser
1 5

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<400> 487
Arg Gly Val Tyr Tyr Ala Leu Ser Pro Phe Asp Tyr
1 5 10

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<400> 488
Gln Asn Ile Tyr Val Trp
1 5

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<400> 489

Lys Ala Ser

1

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<213> Artificial Sequence

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<223> Synthetic Construct

<400> 490

Gln Gln Gly Gln Thr Tyr Pro Tyr Thr

1

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<212> PRT

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<223> Synthetic Construct

<400> 491

Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu

1

5

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Ala Ala Ser

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<212> PRT

<213> Artificial Sequence

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<223> Synthetic Construct

<400> 493

4.__183952027041SEQLIST.TXT

Gln Gln Ser Arg Lys Val Pro Tyr Thr
1 5

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<212> PRT
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<400> 494
Gln Ser Leu Val His Asn Asn Ala Asn Thr Tyr
1 5 10

<210> 495
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<400> 495
Lys Val Ser
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<400> 496
Gly Gln Gly Thr Gln Tyr Pro
1 5

<210> 497
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<220>
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<400> 497

4.__183952027041SEQLIST.TXT

Leu Lys Pro Arg Gly Gly Ala Val Asn Tyr Ala Arg Pro Leu Gln
 1 5 10 15

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 <213> Artificial Sequence

<220>
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<400> 498
 Thr Gly Lys Tyr Tyr Asp Phe Trp Trp Gly Tyr Pro Pro Gly Glu Glu
 1 5 10 15
 Tyr Phe Gln Asp
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<210> 499
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 <212> PRT
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<220>
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<400> 499
 Gly Ala Ser Ile Ser Asp Ser Tyr
 1 5

<210> 500
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 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 500
 Ser Leu Arg Ser His Tyr
 1 5

<210> 501
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<400> 501

Gly Lys Asn

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<212> PRT

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<223> Synthetic Construct

<400> 502

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

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<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 503

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

4.__183952027041SEQLIST.TXT

Met Asp Ile Arg Gly Leu Lys Pro Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp Arg Ser Tyr Gly Asp Ser Ser Trp Ala Leu Asp Ala Trp
100 105 110
Gly Gln Gly Thr Thr Val Val Val Ser Ala
115 120

<210> 504
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 504
Glu Val Arg Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Asp Asn Ala
20 25 30
Trp Met Thr Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Gly Arg Ile Thr Gly Pro Gly Glu Gly Trp Ser Val Asp Tyr Ala Glu
50 55 60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Asn Thr
65 70 75 80
Leu Tyr Leu Glu Met Asn Asn Val Arg Thr Glu Asp Thr Gly Tyr Tyr
85 90 95
Phe Cys Ala Arg Thr Gly Lys Tyr Tyr Asp Phe Trp Ser Gly Tyr Pro
100 105 110
Pro Gly Glu Glu Tyr Phe Gln Asp Trp Gly Gln Gly Thr Leu Val Ile
115 120 125
Val Ser Ser
130

<210> 505
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 505
Glu Val Arg Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Asp Asn Ala
20 25 30
Trp Met Thr Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

4.__183952027041SEQLIST.TXT

Gly Arg Ile Thr Gly Pro Gly Glu Gly Trp Ser Val Asp Tyr Ala Glu
 50 55 60
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Lys Asn Thr
 65 70 75 80
 Leu Tyr Leu Glu Met Asn Asn Val Arg Thr Glu Asp Thr Gly Tyr Tyr
 85 90 95
 Phe Cys Ala Arg Thr Gly Lys Tyr Tyr Asp Phe Trp Trp Gly Tyr Pro
 100 105 110
 Pro Gly Glu Glu Tyr Phe Gln Asp Trp Gly Gln Gly Thr Leu Val Ile
 115 120 125
 Val Ser Ser
 130

<210> 506

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 506

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

<210> 507

<211> 145

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 507

4.__183952027041SEQLIST.TXT

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

<210> 508

<211> 132

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 508

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

<210> 509

4.__183952027041SEQLIST.TXT

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 509

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

<210> 510

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 510

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

4.___183952027041SEQLIST.TXT

<210> 511
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 511
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Lys Ala
 20 25 30
 Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gln Leu Glu Trp Val
 35 40 45
 Ala Gln Ile Lys Asp Lys Ser Asn Ser Tyr Ala Thr Tyr Tyr Ala Asp
 50 55 60
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
 65 70 75 80
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 85 90 95
 Tyr Cys Arg Gly Val Tyr Tyr Ala Leu Ser Pro Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 512
 <211> 103
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 512
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Thr Ala Ile Ile Ser Cys Arg Thr Ser Gln Tyr Gly Ser Leu Ala
 20 25 30
 Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Val Ile Tyr Ser
 35 40 45
 Gly Ser Thr Arg Ala Ala Gly Ile Pro Asp Arg Phe Ser Gly Ser Arg
 50 55 60
 Trp Gly Pro Asp Tyr Asn Leu Thr Ile Ser Asn Leu Glu Ser Gly Asp
 65 70 75 80
 Phe Gly Val Tyr Tyr Cys Gln Gln Tyr Glu Phe Phe Gly Gln Gly Thr
 85 90 95
 Lys Val Gln Val Asp Ile Lys
 100

4.__183952027041SEQLIST.TXT

<210> 513
 <211> 103
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 513
 Tyr Ile His Val Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ile Gly
 1 5 10 15
 Asp Arg Val Thr Ile Asn Cys Gln Thr Ser Gln Gly Val Gly Ser Asp
 20 25 30
 Leu His Trp Tyr Gln His Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
 35 40 45
 His His Thr Ser Ser Val Glu Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Phe His Thr Ser Phe Asn Leu Thr Ile Ser Asp Leu Gln Ala
 65 70 75 80
 Asp Asp Ile Ala Thr Tyr Tyr Cys Gln Val Leu Gln Phe Phe Gly Arg
 85 90 95
 Gly Ser Arg Leu His Ile Lys
 100

<210> 514
 <211> 103
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 514
 Tyr Ile His Val Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ile Gly
 1 5 10 15
 Asp Arg Val Thr Ile Asn Cys Gln Thr Ser Gln Gly Val Gly Ser Asp
 20 25 30
 Leu His Trp Tyr Gln His Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
 35 40 45
 His His Thr Ser Ser Val Glu Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Phe His Thr Ser Phe Gln Leu Thr Ile Ser Asp Leu Gln Ala
 65 70 75 80
 Asp Asp Ile Ala Thr Tyr Tyr Cys Gln Val Leu Gln Phe Phe Gly Arg
 85 90 95
 Gly Ser Arg Leu His Ile Lys
 100

<210> 515

4.__183952027041SEQLIST.TXT

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

<220>
<223> Synthetic Construct

<400> 515
Tyr Ile His Val Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ile Gly
1 5 10 15
Asp Arg Val Thr Ile Asn Cys Gln Thr Ser Gln Gly Val Gly Ser Asp
20 25 30
Leu His Trp Tyr Gln His Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
35 40 45
His His Thr Ser Ser Val Glu Glu Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Phe His Thr Ser Phe Asn Leu Thr Ile Ser Asp Leu Gln Ala
65 70 75 80
Asp Asp Ile Ala Thr Tyr Tyr Cys Gln Val Leu Gln Phe Phe Gly Arg
85 90 95
Gly Ser Arg Leu His Ile Lys
100

<210> 516
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 516
Tyr Ile His Val Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ile Gly
1 5 10 15
Asp Arg Val Thr Ile Asn Cys Gln Thr Ser Gln Gly Val Gly Ser Asp
20 25 30
Leu His Trp Tyr Gln His Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
35 40 45
His His Thr Ser Ser Val Glu Asp Ala Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Phe His Thr Ser Phe Asn Leu Thr Ile Ser Asp Leu Gln Ala
65 70 75 80
Asp Asp Ile Ala Thr Tyr Tyr Cys Gln Val Leu Gln Phe Phe Gly Arg
85 90 95
Gly Ser Arg Leu His Ile Lys
100

<210> 517
<211> 103
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 517

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

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<210> 518

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 518

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

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<210> 519

<211> 112

<212> PRT

<213> Artificial Sequence

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<220>

<223> Synthetic Construct

<400> 519

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

<210> 520

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 520

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

<210> 521

<211> 105

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

4.___183952027041SEQLIST.TXT

<400> 521

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

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<210> 522

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 522

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

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<210> 523

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 523

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