

SEQUENCE LISTING

<110> YANG, Zhi-yong
NABEL, Gary J.
WU, Lan
SEUNG, Edward
WEI, Ronnie
BENINGA, Jochen
RAO, Ercole
LEUSCHNER, Wulf Dirk
BEIL, Christian
LANGE, Christian
CORVEY, Carsten

<120> TRISPECIFIC AND/OR TRIVALENT BINDING
PROTEINS

<130> 183952027140

<140> Not Yet Assigned

<141> Concurrently Herewith

<150> US 62/322,036

<151> 2016-04-13

<150> US 62/331,191

<151> 2016-05-03

<150> US 62/412,187

<151> 2016-10-24

<150> EP 17305298.6

<151> 2017-03-17

<160> 179

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 1

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
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Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Thr

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

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435

440

445

<210> 2
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 2
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
20 25 30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val 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> 3
<211> 571
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 3
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Val Lys Pro Gly Ala

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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
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 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
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
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
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
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

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

$\langle 210 \rangle$ 4

<211> 338

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

 $\langle 400 \rangle$ 4

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

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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> 5

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 5

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agctgtgccg ccagcggctt caacatcaag gacacctaca tccactgggt gcgccaggcc 120
cctggcaagg gactggaatg ggtggccaga atctacccca ccaacggcta caccagatac 180
gccgacagcg tgaagggccg gttcaccatc agcgccgaca ccagcaagaa caccgcctac 240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgtag tagatgggga 300
ggcgacggct tctacgcat ggactattgg ggccagggca ccctcgtgac cgtgtctagt 360
gcgtcgacca agggcccac tgggtttcct 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 tccttgccca gccctgaat ttctgggcgg accctccgtg 720
ttcctgttcc 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

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183952027140SEQLISTING

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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> 6

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 6

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atcacctgta gagccagcca ggacgtgaac accgccgtgg cctggatatca gcagaagcct 120
ggcaaggccc ccaagctgct gatctacagc gccagcttcc tgtacagcgg cgtgcccagc 180
agattcagcg gaagcagaag cggcacagc ttcaccctga ccatcagctc cctgcagccc 240
gaggacttcg ccacctacta ctgccagcag cactacacca cccccccac atttgccag 300
ggcaccaagg tggaaatcaa gcgtacggtg gccgctccca gcgtgttcat cttcccacct 360
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 420
ccccgcgagg ccaaagtga gtggaagggt gacaacgccc tgcagagcgg caacagccag 480
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgaca 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtga ccaccagggc 600
ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt                                     642

```

<210> 7

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 7

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caggtgcagc tgggtgcagtc tggcgccgag gtcgtgaaac ctggcgcctc tgtgaagggtg 60
tcctgcaagg ccagcggcta cacctttacc agctactaca tccactgggt gcgccaggcc 120
cctggacagg gactggaatg gatcggcagc atctacccc gcaacgtgaa caccaactac 180
gccagaagt tccagggcag agccaccctg accgtggaca ccagcatcag caccgcctac 240
atggaactga gccggctgag aagcgacgac accgccgtgt actactgcac ccggtccac 300
tacggcctgg attggaactt cgacgtgtgg ggcaagggca ccaccgtgac agtgtctagc 360
agccagggtg 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 ccgccagcac aaagggccca tcggtgttcc ctctggcccc ttgcagcaga 780
agcaccagcg aatctacagc cgccctgggc tgcctcgtga aggactactt tcccagagccc 840
gtgaccgtgt cctggaactc tggcgctctg acaagcggcg tgcacacctt tccagccgtg 900
ctccagagca gcggcctgta ctctctgagc agcgtcgtga cagtgccag cagcagcctg 960
ggcaccaaga cctacacctg taacgtggac cacaagccca gcaacaccaa ggtggacaag 1020

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183952027140SEQLISTING

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cgggtggaat ctaagtacgg ccctccctgc ctccttgcc cagcccctga atttctgggc 1080
ggaccctccg tgttctgtt cccccc aaag cccaaggaca ccctgatgat cagccggacc 1140
cccgaagtga cctgctgtgt ggtggatgtg tcccaggaag atcccagagt gcagttcaat 1200
tggtagctgg acggcgtgga agtgcacaac gccaaagaca agcccagaga ggaacagttc 1260
aacagcacct accgggtggt gtccgtgctg accgtgctgc 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 attcttctct gtgtccaagc tgaccgtgga caagagccgg 1620
tggcaggaag gcaacgtgtt cagctgctcc gtgatgcacg aggcctgca caaccactac 1680
accagaagt ccctgtctct gtccctgggc aag 1713

```

<210> 8

<211> 1014

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 8

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gacatcgtga tgaccagac ccccctgagc ctgagcgtga cacctggaca gcctgccagc 60
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 cgcccccgac 360
atccagatga cccagagccc cagcagcctg tctgccagcg tgggcgacag agtgaccatc 420
acctgtcagg ccagccagaa catctacgtg tggctgaact ggtatcagca gaagcccggc 480
aaggcccca agctgctgat ctacaaggcc agcaacctgc acaccggcgt gccagcaga 540
ttttctggca gcggctccgg caccgacttc accctgacaa tcagctccct gcagcccag 600
gacattgcca cctactactg ccagcagggc cagacctacc cctacacctt tggccagggc 660
accaagctgg aaatcaagac caagggcccc agccgtacgg tggccgctcc cagcgtgttc 720
atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 780
aacaacttct accccgcga ggccaaagt cagtggaaagg tggacaacgc cctgcagagc 840
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccaccta cagcctgagc 900
agcacctga cactgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagt 960
accaccagg gcctgtctag cccgtgacc aagagcttca accggggcga gtgt 1014

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<210> 9

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 9

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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

```

183952027140SEQLISTING

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

183952027140SEQLISTING

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

<210> 10

<211> 342

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 10

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly	
1	5
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Val His Asn	
20	25
Asn Ala Asn Thr Tyr Leu Ser Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
35	40
Pro Gln Ser Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro	
50	55
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	
65	70
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gly Gln Gly	
85	90
Thr Gln Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys	
100	105
Gly Gln Pro Lys Ala Ala Pro Asp Ile Val Leu Thr Gln Ser Pro Ala	
115	120
Ser Leu Ala Val Ser Pro Gly Gln Arg Ala Thr Ile Thr Cys Arg Ala	
130	135
Ser Glu Ser Val Glu Tyr Tyr Val Thr Ser Leu Met Gln Trp Tyr Gln	
145	150
Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Phe Ala Ala Ser Asn	
165	170
Val Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr	
180	185
	190

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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> 11

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 11

caggtgcagc tgcaggaatc tggccctggc ctctgtgaagc ctagccagac cctgagcctg 60
 acctgtaccg tgtccggcctt cagcctgagc gactacggcg tgcactgggt gcgccagcca 120
 cctggaaaag gcctggaatg gctgggctgtg 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 ggagtgggtgc agcctggcag aagcctgaga 420
 ctgagctgtg ccgccagcgg cttcaccttc accaaggcct ggatgcactg ggtgcccag 480
 gcccctggaa agcagctgga atgggtggcc cagatcaagg acaagagcaa cagctacgcc 540
 acctactacg ccgacagcgt gaagggccgg ttcacatca gccgggacga cagcaagaac 600
 accctgtacc tgcagatgaa cagcctgcgg gccgaggaca ccgccgtgta ctactgtcgg 660
 ggctgtact atgccctgag ccccttcgat tactggggcc agggaaacct cgtgaccgtg 720
 tctagtcgga ccgcttcgac caagggccca tcggtgttcc ctctggcccc ttgcagcaga 780
 agcaccagcg aatctacagc cgccctgggc tgcctcgtga aggactactt tcccagagccc 840
 gtgaccgtgt cctggaactc tggcgctctg acaagcggcg tgcacacctt tccagccgtg 900
 ctccagagca gcggcctgta ctctctgagc agcgtcgtga cagtggccag cagcagcctg 960
 ggacaccaaga cctacacctg taacgtggac cacaagccca gcaacaccaa ggtggacaag 1020
 cgggtggaat ctaagtacgg ccctccctgc cctccttgcc cagcccctga atttctgggc 1080
 ggaccctccg tgttcctgtt cccccaaaag cccaaggaca ccctgatgat cagccggacc 1140
 cccgaagtga cctgcgtggt ggtggatgtg tcccaggaag atcccagagt gcagttcaat 1200
 tggtagctgg acggcgtgga agtgcacaac gccaaagacca agcccagaga ggaacagttc 1260

183952027140SEQLISTING

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aacagcacct accgggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc 1320
aaagagtaca agtgcaaggt gtccaacaag ggcctgccc a gctccatcga gaaaaccatc 1380
agcaaggcca agggccagcc ccgcgagcct caagtgtgta ccctgcccc tagccaggaa 1440
gagatgacca agaaccaggt gtccctgagc tgtgccgtga aaggcttcta cccagcgac 1500
attgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cccccccct 1560
gtgctggaca gcgacggctc attcttcctg gtgtccaagc tgaccgtgga caagagccgg 1620
tggcaggaag gcaacgtgtt cagctgctcc gtgatgcacg aggccctgca caaccactac 1680
accagaagt ccctgtctct gtccctgggc aag                                     1713

```

<210> 12

<211> 1026

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 12

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gacatcgtga tgaccagac ccccctgagc ctgagcgtga cacctggaca gcctgccagc 60
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 cgcctccgac 360
atcgtgctga cacagagccc tgctagcctg gccgtgtctc ctggacagag ggccaccatc 420
acctgtagag ccagcgagag cgtggaatat tacgtgacca gcctgatgca gtggtatcag 480
cagaagcccg 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
gtgtgcctgc tgaacaactt ctacccccgc gaggccaaag tgcagtggaa ggtggacaac 840
gccctgcaga gcggcaacag ccaggaaagc gtgaccgagc aggacagcaa ggactccacc 900
tacagcctga gcagcaccct gacactgagc aaggccgact acgagaagca caaggtgtac 960
gcctgcgaag tgaccacca gggcctgtct agccccgtga ccaagagctt caaccggggc 1020
gagtgt                                     1026

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<210> 13

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 13

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

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183952027140SEQLISTING

Gly	Gln	Ile	Trp	Pro	Gly	Asp	Gly	Asp	Thr	Asn	Tyr	Asn	Gln	Lys	Phe
50						55					60				
Lys	Gly	Arg	Ala	Thr	Leu	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Arg	Glu	Thr	Thr	Thr	Val	Gly	Arg	Tyr	Tyr	Tyr	Ala	Met	Asp
			100					105					110		
Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys
		115					120					125			
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu
	130					135					140				
Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro
145					150					155					160
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr
				165					170					175	
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val
			180					185					190		
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn
		195					200					205			
Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser
	210					215					220				
Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	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	Gln
			260					265					270		
Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
		275					280					285			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	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	Gly	Leu	Pro	Ser	Ser	Ile
				325					330					335	
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
		340						345					350		
Tyr	Thr	Leu	Pro	Pro	Cys	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser
		355					360					365			
Leu	Trp	Cys	Leu	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	Tyr	Ser	Lys	Leu	Thr	Val
				405					410					415	
Asp	Lys	Ser	Arg	Trp	Gln	Glu	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			
Leu	Gly	Lys													
450															

183952027140SEQLISTING

<210> 14
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 14
 Asp Leu 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 Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30
 Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45
 Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val 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 Thr Ala Asn Tyr Tyr Cys Gln Gln Ser Thr
 85 90 95
 Glu Asp Pro Trp 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> 15
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 15
 caggtgcagc tgggtgcagag cggcgccgaa gtgaagaagc ctggcagcag cgtgaaggtg 60
 agctgcaagg ccagcggcta tgccttcagc agctactgga tgaactgggt gaggcaggca 120

183952027140SEQLISTING

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cctggccagg gcctggagtg gataggccaa atatggcctg gcgatggcga caccaactac 180
aaccagaagt tcaagggcag agcgaccttg accgccgacg agagcaccag caccgcgtac 240
atggagctga gcagcctgag gagcgaggac accgccgtgt actattgcgc cagaagggag 300
accaccaccg tgggcaggta ctactacgcc atggactact ggggccaggg aaccaccgtg 360
accgtgagca gcgcctcgac caagggccca tcggtgttcc ctctggcccc ttgcagcaga 420
agcaccagcg aatctacagc cgccctgggc tgcctcgtga aggactactt tcccagagcc 480
gtgaccgtgt cctggaaactc tggcgctctg acaagcggcg tgcacacctt tccagccgtg 540
ctccagagca gcggcctgta ctctctgagc agcgtcgtga cagtgtcccag cagcagcctg 600
ggcaccaaga cctacacctg taacgtggac cacaagccca gcaacaccaa ggtggacaag 660
cgggtggaat ctaagtacgg ccctccctgc cctccttgcc cagcccctga atttctgggc 720
ggaccctccg tgttcctgtt cccccaaaag cccaaggaca ccctgatgat cagccggacc 780
cccgaagtga cctgcgtggt ggtggatgtg tcccaggaag atcccagggt gcagttcaat 840
tggtacgtgg acggcgtgga agtgcacaac gccaaagaca agcccagaga ggaacagttc 900
aacagcacct accgggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc 960
aaagagtaca agtgcaaggt gtccaacaag ggcctgcca gctccatcga gaaaaccatc 1020
agcaaggcca agggccagcc ccgcgagcct caagtgtata ccctgcccc ttgccaggaa 1080
gagatgacca agaaccaggt gtccctgtgg tgtctcgtga aaggcttcta cccagcgac 1140
attgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cccccccct 1200
gtgctggaca gcgacggctc attcttctg tactccaagc tgaccgtgga caagagccgg 1260
tggcaggaag gcaacgtgtt cagctgctcc gtgatgcacg aggccctgca caaccactac 1320
accagaagt ccctgtctct gtccctgggc aag 1353

```

<210> 16

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 16

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atcacctgca aagccagcca gagcgtggac tacgacggcg acagctacct caactggtac 120
cagcagaagc ctggccagcc cccaagctg ctgatttacg atgccagcaa cctggtgagc 180
ggcgtgcctg ctagattcag cggctccggc agcggcaccg acttcaccct gaccatcaac 240
cccgtggagg ccaacgacac cgccaactac tactgccagc agagcacgga ggacccttg 300
accttcggcc agggcacaaa gctggagatc aagcgtacgg tggccgctcc cagcgtgttc 360
atcttccac ctagcgacga gcagctgaag tccggcacag cctctgtcgt gtgcctgctg 420
aacaacttct accccgcga ggccaaagt cagtggaaagg tggacaacgc cctgcagagc 480
ggcaacagcc aggaaagcgt gaccgagcag gacagcaagg actccacct cagcctgagc 540
agcacctga cactgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaagt 600
accaccagg gcctgtctag ccccgtagac aagagcttca accggggcga gtgt 654

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<210> 17

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 17

183952027140SEQLISTING

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

183952027140SEQLISTING

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> 18
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18
Asp Ile Val Met Thr Gln Ser His Leu Ser Met Ser Thr Ser Leu Gly
1 5 10 15
Asp Pro Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Thr Val
20 25 30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Arg Arg Leu Ile
35 40 45
Tyr Ser Ala Ser Tyr Arg Tyr Ile Gly Val Pro Asp Arg Phe Thr Gly
50 55 60
Ser Gly Ala Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Ala
65 70 75 80
Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Ser Pro Pro Tyr
85 90 95
Thr Phe Gly Gly 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> 19
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

183952027140SEQLISTING

<400> 19

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caggtgcagc tgggtgcagtc tggcgccgaa gtggccaagc ctggcacaag cgtgaagctg 60
agctgcaagg ccagcggcta caccttcacc gactactgga tgcagtgggt caagcagagg 120
ccaggccagg gcctggaatg gatcggcaca atctatcccg gcgacggcga taccggctac 180
gcccagaagt ttcagggcaa ggccaccctg accgccgaca agagcagcaa gaccgtgtac 240
atgcacctga gcagcctggc cagcaggagc agcgccgtgt actattgcgc cagaggcgac 300
tactacggca gcaacagcct ggactattgg ggccagggca ccagcgtgac agtgtctagt 360
gcgtcgacca agggcccata ggtgttcctt 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 tccttgcccga gccctgaat ttctgggcgg accctccgtg 720
ttcctgttcc ccccaaagcc caaggacacc ctgatgatca gccggacccc cgaagtgacc 780
tgcgtgggtg tggatgtgtc ccaggaagat cccgaggtgc agttcaattg gtacgtggac 840
ggcgtggaag tgcacaacgc caagaccaag cccagagagg aacagttcaa cagcacctac 900
cgggtgggtg ccgtgctgac cgtgctgcac caggactggc tgaacggcaa agagtacaag 960
tgcaagggtg ccaacaaggg cctgccagc tccatcgaga aaaccatcag caaggccaag 1020
ggccagcccc gcgagcctca agtgtatacc ctgccccctt gccaggaaga gatgaccaag 1080
aaccagggtg ccctgtgggt 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

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<210> 20

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 20

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atcacctgta aagccagcca ggacgtgtcc accgtggtgg cctggtatca gcagaagcct 120
ggccagagcc ccagacggct gatctacagc gccagctatc ggtacatcgg cgtgcccgcac 180
agattcaccg gaagcggagc cggcaccgac ttcaccttca ccatcagctc tgtgcaggcc 240
gaggacctgg ccgtgtacta ctgccagcag cactacagcc ccccctacac ctttggcgga 300
ggcaccaagc tggaaatcaa gcgtacggtg gccgtccca gcgtgttcat cttccacct 360
agcgacgagc agctgaagtc cggcacagcc tctgtcgtgt gcctgctgaa caacttctac 420
ccccgcgagg ccaaagtga gtggaagggt gacaacgccc tgcagagcgg caacagccag 480
gaaagcgtga ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgaca 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaagtgac ccaccagggc 600
ctgtctagcc ccgtgaccaa gagcttcaac cggggcgagt gt                                     642

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<210> 21

<211> 445

<212> PRT

<213> Artificial Sequence

183952027140SEQLISTING

<220>

<223> Synthetic Construct

<400> 21

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

183952027140SEQLISTING

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

<210> 22

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 22

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

<210> 23

<211> 1335

<212> DNA

183952027140SEQLISTING

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 23

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ccaggccagg gcctggaatg gatcggcgcc atctatccc gaaacggcga cgccccttac 180
agccagaagt tccagggcaa ggccaccctg accgccgata ccagcacctc caccacctac 240
atggaactga gcagcctgcg gagcgaggac accgccgtgt actattgcgt gcgggccaac 300
tgggatgtgg ctttcgccta ttggggccag ggcacactcg tgaccgtgtc ctctgcgtcg 360
accaagggcc catcgggtgtt ccctctggcc cttgcagca gaagcaccag cgaatctaca 420
gccgccctgg gctgcctcgt gaaggactac tttcccgagc ccgtgaccgt gtcctggaac 480
tctggcgctc tgacaagcgg cgtgcacacc tttccagccg tgctccagag cagcggcctg 540
tactctctga gcagcgtcgt gacagtggcc agcagcagcc tgggcaccaa gacctacacc 600
tgtaacgtgg accacaagcc cagcaacacc aaggtggaca agcgggtgga atctaagtac 660
ggccctccct gccctccttg cccagcccct gaatttctgg gcggaccctc cgtgttcctg 720
ttcccccaa agcccaagga caccctgatg atcagccgga ccccgaagt gacctgcgtg 780
gtggtggatg tgtcccagga agatcccag gtgcagttca attggtacgt ggacggcgtg 840
gaagtgcaca acgccaagac caagcccaga gaggaacagt tcaacagcac ctaccgggtg 900
gtgtccgtgc tgaccgtgct gcaccaggac tggctgaacg gcaaagagta caagtgaag 960
gtgtccaaca agggcctgcc cagctccatc gagaaaacca tcagcaaggc caagggccag 1020
ccccgcgagc ctcaagtgtg tacctgccc cttgcccagg aagagatgac caagaaccag 1080
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agcaacggcc agcccagaaa caactacaag accaccccc ctgtgctgga cagcgacggc 1200
tcattcttcc tgtactccaa gctgaccgtg gacaagagcc ggtggcagga aggcaacgtg 1260
ttcagctgct ccgtgatgca cgaggccctg cacaaccact acaccagaa gtccctgtct 1320
ctgtcccctgg gcaag                                     1335

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<210> 24

<211> 639

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 24

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atcacatgca aggccagcca ggacatcgat cggtagatgg cctggtatca ggacaagccc 120
ggcaaggccc ccagactgct gatccacgat accagcacac tgcagagcgg cgtgcccagc 180
agattttccg gctctggcag cggcagagac tacaccctga ccatcagcaa cctggaaccc 240
gaggacttcg ccacctacta ctgcctgcag tacgacaacc tgtggacctt cggcggaggc 300
accaaggtgg aaatcaagcg tacggtggcc gctcccagcg tgttcatctt cccacctagc 360
gacgagcagc tgaagtccgg cacagcctct gtcgtgtgcc tgctgaacaa cttctacccc 420
cgcgaggcca aagtgcagtg gaaggtggac aacgccctgc agagcggcaa cagccaggaa 480
agcgtgaccg agcaggacag caaggactcc acctacagcc tgagcagcac cctgacactg 540
agcaaggccg actacgagaa gcacaagggtg tacgcctgcg aagtgacca ccagggcctg 600
tctagccccg tgaccaagag cttcaaccgg ggcgagtgt                                     639

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<210> 25

183952027140SEQLISTING

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 25

Gly Phe Asn Ile Lys Asp Thr Tyr
1 5

<210> 26

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 26

Ile Tyr Pro Thr Asn Gly Tyr Thr
1 5

<210> 27

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 27

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr
1 5 10

<210> 28

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 28

Gly Tyr Thr Phe Thr Ser Tyr Tyr
1 5

<210> 29

183952027140SEQLISTING

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 29

Ile Tyr Pro Gly Asn Val Asn Thr
1 5

<210> 30

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 30

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

<210> 31

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 31

Gly Phe Ser Leu Ser Asp Tyr Gly
1 5

<210> 32

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 32

Ile Trp Ala Gly Gly Gly Thr
1 5

<210> 33

183952027140SEQLISTING

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 33

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

<210> 34

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 34

Gly	Phe	Thr	Phe	Thr	Lys	Ala	Trp
1				5			

<210> 35

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 35

Ile	Lys	Asp	Lys	Ser	Asn	Ser
1				5		

<210> 36

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 36

Arg	Gly	Val	Tyr	Tyr	Ala	Leu	Ser	Pro	Phe	Asp	Tyr
1				5					10		

<210> 37

183952027140SEQLISTING

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 37

Gly Tyr Ala Phe Ser Ser Tyr Trp
1 5

<210> 38

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 38

Ile Trp Pro Gly Asp Gly Asp Thr
1 5

<210> 39

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 39

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
1 5 10 15

<210> 40

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 40

Gly Tyr Thr Phe Thr Asp Tyr Trp
1 5

<210> 41

183952027140SEQLISTING

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 41

Ile Tyr Pro Gly Asp Gly Asp Thr
1 5

<210> 42

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 42

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

<210> 43

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 43

Gln Asp Val Asn Thr Ala
1 5

<210> 44

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 44

Ser Ala Ser
1

<210> 45

183952027140SEQLISTING

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 45

Gln Gln His Tyr Thr Thr Pro Pro Thr
1 5

<210> 46

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 46

Gln Asn Ile Tyr Val Trp
1 5

<210> 47

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 47

Lys Ala Ser
1

<210> 48

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 48

Gln Gln Gly Gln Thr Tyr Pro Tyr Thr
1 5

<210> 49

183952027140SEQLISTING

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 49

Glu	Ser	Val	Glu	Tyr	Tyr	Val	Thr	Ser	Leu
1				5					10

<210> 50

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 50

Ala	Ala	Ser
1		

<210> 51

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 51

Gln	Gln	Ser	Arg	Lys	Val	Pro	Tyr	Thr
1				5				

<210> 52

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 52

Gln	Ser	Leu	Val	His	Asn	Asn	Ala	Asn	Thr	Tyr
1				5					10	

<210> 53

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

<220>
<223> Synthetic Construct

<400> 53
Lys Val Ser
1

<210> 54
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 54
Gly Gln Gly Thr Gln Tyr Pro
1 5

<210> 55
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 55
Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr
1 5 10

<210> 56
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 56
Asp Ala Ser
1

<210> 57

183952027140SEQLISTING

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 57

Gln Gln Ser Thr Glu Asp Pro Trp Thr
1 5

<210> 58

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 58

Gln Asp Val Ser Thr Val
1 5

<210> 59

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 59

Gln Gln His Tyr Ser Pro Pro Tyr Thr
1 5

<210> 60

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 60

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

183952027140SEQLISTING

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

183952027140SEQLISTING

450

<210> 61
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 61
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gln Pro Lys Ala
 100 105 110
 Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala
 115 120 125
 Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala
 130 135 140
 Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val
 145 150 155 160
 Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
 165 170 175
 Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 180 185 190
 Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala
 195 200 205
 Pro Thr Glu Cys Ser
 210

<210> 62
 <211> 570
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 62
 Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala

183952027140SEQLISTING

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

183952027140SEQLISTING

420					425					430					
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
435					440					445					
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
450					455					460					
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Cys	Arg	Asp
465					470					475					
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Trp	Cys	Leu	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	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
530					535					540					
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	Arg	Phe
545					550					555					
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly						
565					570										

<210> 63

<211> 345

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 63

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

183952027140SEQLISTING

Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Gly	Phe
		180						185					190		
Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr
		195					200					205			
Cys	Gln	Gln	Ala	His	Ser	Tyr	Pro	Phe	Thr	Phe	Gly	Gly	Gly	Thr	Lys
		210				215					220				
Leu	Glu	Ile	Lys	Gly	Gly	Ser	Gly	Ser	Ser	Gly	Ser	Gly	Gly	Arg	Thr
225				230						235				240	
Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu
			245						250					255	
Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro
		260						265					270		
Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly
		275					280					285			
Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr
	290					295					300				
Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His
305					310					315					320
Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val
			325						330					335	
Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys							
		340						345							

<210> 64

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 64

```

gagggtgcagc  tgggtggaaag  cggcggagga  ctggtgcagc  ccggcagaag  cctgagactg  60
agctgcgccg  ccagcggcctt  caccttcgac  gactacgcc  tgcactgggt  ccgccaggcc  120
cctggcaagg  gcctggaatg  ggtgtccgcc  atcacctgga  acagcggcca  catcgactac  180
gccgacagcg  tggaaggccg  gttcaccatc  agccgggaca  acgccaagaa  cagcctgtac  240
ctgcagatga  acagcctgcg  ggccgaggac  accgccgtgt  actactgcgc  caaggtgtcc  300
tacctgagca  ccgccagcag  cctggactac  tggggccagg  gcaccctggt  gacagtgtcc  360
agcgcttcca  ccaagggccc  cagcgtgttc  cccctggccc  ctagcagcaa  gagcacatct  420
ggcggcacag  ccgccctggg  ctgcctggtc  aaggactact  tccccgagcc  cgtgacagtg  480
tcctggaact  ctggcgccct  gaccagcgga  gtgcatacct  tccctgccgt  gctgcagtcc  540
agcggcctgt  acagcctgag  cagcgtggtc  acagtgccca  gcagcagcct  gggcacccag  600
acctacatct  gcaacgtgaa  ccacaagccc  agcaacacca  aggtggacaa  gaaggtggaa  660
cccaagagct  gcgacaagac  ccacacctgt  cccccctgcc  ctgcccctga  actgctgggc  720
ggaccctccg  tgttcctgtt  cccccaaaag  cccaaggaca  ccctgatgat  cagccggacc  780
cccgaagtga  cctgcgtggt  ggtggacgtg  tcccacgagg  accctgaagt  gaagttcaat  840
tggtacgtgg  acggcgtgga  agtgcataac  gccaaagacca  agcccagaga  ggaacagtac  900
aacagcacct  accgggtggt  gtccgtgctg  accgtgctgc  accaggactg  gctgaacggc  960
aaagagtaca  agtgcaaggt  gtccaacaag  gccctgcctg  ccccatcga  gaaaaccatc  1020
agcaaggcca  agggccagcc  tagagagccc  caagtctgca  ccctgcccc  cagcagagat  1080
gagctgacca  agaaccaggt  gtccctgagc  tgcgccgtga  agggcttcta  cccagcgat  1140

```

183952027140SEQLISTING

```

atcgccgtgg aatgggagag caacggccag cccgagaaca actacaagac cccccccct 1200
gtgctggaca gcgacggctc attcttcctg gtgtccaagc tgacagtgga caagagccgg 1260
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccttgca caaccattac 1320
accagaagt ccctgagcct gagccccggc                                     1350

```

<210> 65

<211> 639

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 65

```

gacatccaga tgaccagag ccccagcagc ctgagcgcca gcgtgggcga cagagtgacc 60
atcacctgtc gggccagcca gggcatccgg aactacctgg cctggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacgcc gccagcacac tgcagagcgg cgtgcccagc 180
agattcagcg gcagcggctc cggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacgtgg ccacctacta ctgccagcgg tacaacagag ccccctacac cttcgccag 300
ggcaccaagg tggaaatcaa gggacagccc aaggctgccc cctcggtcac cctgttcccc 360
ccaagcagcg aggaactgca ggccaacaag gccaccctcg tgtgcctgat cagcgacttc 420
taccctggcg ccgtgaccgt ggcctggaag gccgatagct ctcccgtgaa ggccggcgtg 480
gaaaccacca ccccagcaa gcagagcaac aacaaatacg ccgcctccag ctacctgagc 540
ctgacccccg agcagtggaa gtcccaccgg tcctacagct gccaggtcac acacgagggc 600
agcaccgtgg aaaagaccgt ggccccacc gagtgcagc                                     639

```

<210> 66

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 66

```

caggtgcagc tgcagcagag cggccctgag ctggtcaagc ctggcgccag cgtgaagatc 60
agctgcaagg ccagcggcta cagcttcacc agctactgga tccactggat caagcagcgg 120
cctggccagg gcctggaatg gatcggcatg atcgacccca gcgacggcga gacacggctg 180
aaccagagat tccagggcag agccaccctg accgtggacg agagcaccag caccgcctac 240
atgcagctgc ggagccccac cagcgaggac agcgcctgtg actactgcac ccggctgaaa 300
gagtacggca actacgacag cttctacttc gacgtgtggg gagccggcac cctggtcacc 360
gtgtccagcg aagtgcagct gaaagaaagc ggccctggcc tgggtggccc tggcggcagc 420
ctgagcatca cctgtaccgt gtccggcttc agcctgaccg acagcagcat caactgggtc 480
cgacagcccc ctggcaaggg cctcgagtgg ctgggaatga tctggggcga cggccgcatc 540
gactacgccg acgccctgaa gtcccggctg agcatcagca aggacagcag caagagccag 600
gtgttcctgg aaatgaccag cctgcggacc gacgacaccg ccacctacta ctgcgccagg 660
gacggctact tcccctacgc catggatttc tggggccagg gcaccagcgt gaccgtgtcc 720
tctgcttcca ccaagggccc cagcgtgttc cctctggccc ctagcagcaa gagcacatct 780
ggcgggaacag ccgccctggg ctgcctggtc aaggactact ttcccagacc cgtgaccgtg 840
tcctggaaact ctggtgccct gacaagcgga gtgcatacct tccctgccgt gctgcagagc 900
agcggcctgt actctctgag cagcgtggtc accgtgcaa gcagcagcct gggcaccagg 960
acctacatct gcaacgtgaa ccacaagccc tccaacacca aggtggacaa gaaggtggaa 1020

```

183952027140SEQLISTING

```

cccaagagct gcgacaagac ccacacctgt cctccctgtc ctgcccctga actgctgggc 1080
ggaccctccg tgttcctggt ccctccaaag cccaaggata ccctgatgat cagccggacc 1140
cctgaagtga cctgcgtggg ggtggacgtg tcccacgagg atcccgaagt gaagttcaat 1200
tggtagctgg acggcgtgga agtgcataac gccaaagaca agcccagaga ggaacagtac 1260
aacagcacct accgggtggg gtccgtgctg acagtgtgc accaggactg gctgaacggc 1320
aaagagtaca agtgcaagggt gtccaacaag gccctgccag cccctatcga gaaaaccatc 1380
agcaaggcca agggccagcc ccgcgagcct caggtgtaca cactgcctcc atgccgggac 1440
gagctgacca agaaccagggt gtccctgtgg tgcctcgtga agggcttcta cccctccgat 1500
atgccgtgg aatgggagag caacggccag cccgagaaca actacaagac caccctccc 1560
gtgctggaca gcgacggctc attcttcctg tacagcaagc tgaccgtgga caagtcccgg 1620
tggcagcagg gcaacgtgtt cagctgctct gtgatgcacg aggccttgca caaccggttc 1680
accagaagt ccctgagcct gagccctggc 1710

```

<210> 67

<211> 1035

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 67

```

gacatcgtgc tgaccagag ccctgccagc ctggccgtgt ctctgggcca gagagccacc 60
atcagctgcc gggccagcga gagcgtggac agctacggcc agagctacat gcactggtat 120
cagcagaagg ccggccagcc cccaagctg ctgatctacc tggccagcaa cctggaaagc 180
ggcgtgcccc ccagattcag cggcagcggc agcagaaccg acttcaccct gaccatcgac 240
cccgtgcagg ccgaggacgc cgccacctac tactgccagc agaacgccga ggacagccgg 300
accttcggcg gaggcacaa gctggaaatc aagggcggct ccggcagcag cggctctggc 360
ggcgatatcc agatgacca gtccccgcc tccctgagcg tgtccgtggg cgacaccatc 420
accctgacat gccacgccag ccagaacatc gacgtgtggc tgagctggtt ccagcagaag 480
cctggcaaca tccctaagct gctcatctat aaggcctcca acctgcacac cggcgtgcc 540
agcaggtttt ccggctctgg cagcggcacc ggctttacc tgacaatcag cagcctgcag 600
cccgaggata tcgccacata ttactgtcag caggcccaca gctaccctt cacccttggc 660
ggcggaacaa agctcgagat taagggcggc agcggaagct ccggctccgg cggacgtacg 720
gtggccgctc cttccgtgtt catcttcct ccctccgacg agcagctgaa gtccggcacc 780
gcctccgtgg tgtgtctgct gaacaacttc taccctcggg aggccaagg gtagtggaag 840
gtggacaacg ccctgcagtc cggcaactcc caggagtccg tcaccgagca ggactccaag 900
gacagcacct actccctgtc ctccaccctg accctgtcca aggccgacta cgagaagcac 960
aaggtgtacg cctgtgaggt gaccaccag ggcctgtcca gccctgtgac caagtccttc 1020
aaccggggcg agtgc 1035

```

<210> 68

<211> 570

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 68

```

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

```

183952027140SEQLISTING

```

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

```

183952027140SEQLISTING

```

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
    435                      440                      445
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    450                      455                      460
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys Arg Asp
465                      470                      475                      480
Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu 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 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    530                      535                      540
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe
545                      550                      555                      560
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
    565                      570

```

<210> 69

<211> 345

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 69

```

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

```

183952027140SEQLISTING

Thr	Leu	Thr	Ile	Asp	Pro	Val	Gln	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr
		195					200					205			
Cys	Gln	Gln	Asn	Ala	Glu	Asp	Ser	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys
	210					215					220				
Leu	Glu	Ile	Lys	Gly	Gly	Ser	Gly	Ser	Ser	Gly	Ser	Gly	Gly	Arg	Thr
225					230					235					240
Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu
				245					250					255	
Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro
			260					265					270		
Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly
			275				280					285			
Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr
	290					295					300				
Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His
305					310					315					320
Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val
				325					330					335	
Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys							
			340					345							

$\langle 210 \rangle$ 70

<211> 1035

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 70

gacatccaga	tgaccagag	ccccgccagc	ctgagcgtgt	ccgtgggcga	taccatcacc	60
ctgacctgcc	acgccagcca	gaacatcgac	gtgtggctga	gctggttcca	gcagaagccc	120
ggcaacatcc	ccaagctgct	gatctacaag	gccagcaacc	tgacacccgg	cgtgcccagc	180
agattcagcg	gctctggcag	cggcaccggc	tttaccctga	ccatcagcag	cctgcagccc	240
gaggatatcg	ccacctacta	ctgccagcag	gcccacagct	accccttcac	cttcggcgga	300
ggcaccaagc	tggaatcaa	gggcggcagc	ggcagctccg	gctctggcgg	cgatatcgtg	360
ctgaccagtg	ctccgcctc	cctggccgtg	tctctgggcc	agagagccac	catcagctgc	420
cgggccagcg	agagcgtgga	cagctacggc	cagagctaca	tgactggta	tcagcagaag	480
gccggacagc	cccctaaact	gctcatctac	ctggcctcca	acctggaaag	cggcgtgccc	540
gccagggtttt	ccggcagcgg	ctccagaacc	gacttcaccc	tgacaatcga	ccccgtgcag	600
gccgaggacg	ccgccacata	ttactgtcag	cagaacgccg	aggacagcag	aacctttggc	660
ggcggaacaa	agctcgagat	taagggcggc	tccggctcca	gcggatctgg	cggacgtacg	720
gtggccgctc	cttccgtgtt	catcttcctt	ccctccgacg	agcagctgaa	gtccggcacc	780
gcctccgtgg	tgtgtctgct	gaacaacttc	taccctcggg	aggccaaggt	gcagtggaag	840
gtggacaacg	ccctgcagtc	cggcaactcc	caggagtccg	tcaccgagca	ggactccaag	900
gacagcacct	actccctgtc	ctccaccctg	accctgtcca	aggccgacta	cgagaagcac	960
aagggtgtacg	cctgtgaggt	gaccaccag	ggcctgtcca	gccctgtgac	caagtccttc	1020
aaccggggcg	agtg					1035

<210> 71

183952027140SEQLISTING

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

<220>
 <223> Synthetic Construct

<400> 71

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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 Arg Ala Ser Gln Gly Ile Arg Asn Tyr
          20           25           30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45
Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50           55           60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80
Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
          85           90           95
Thr Phe Gly Gln Gly Thr Lys Val 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> 72
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 72

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gacatccaga tgaccagag cccagcagc ctgagcgcca gcgtgggcga cagagtgacc 60
atcacctgtc gggccagcca gggcatccgg aactacctgg cctggatatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacgcc gccagcacac tgcagagcgg cgtgcccagc 180
agattcagcg gcagcggctc cggcaccgac ttcacctga ccatcagcag cctgcagccc 240
gaggacgtgg ccacctacta ctgccagcgg tacaacagag cccctacac cttcgccag 300

```

183952027140SEQLISTING

```

ggcaccaagg tggaaatcaa gcgtacggtg gccgctcctt ccgtgttcat cttccctccc 360
tccgacgagc agctgaagtc cggcaccgcc tccgtggtgt gtctgctgaa caacttctac 420
cctcgggagg ccaaggtgca gtggaagggtg gacaacgccc tgcagtccgg caactcccag 480
gagtccgtca ccgagcagga ctccaaggac agcacctact ccctgtcctc caccctgacc 540
ctgtccaagg ccgactacga gaagcacaag gtgtacgcct gtgaggtgac ccaccagggc 600
ctgtccagcc ctgtgaccaa gtccttcaac cggggcgagt gc 642

```

<210> 73

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 73

```

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

```

183952027140SEQLISTING

```

Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro Ile Glu Lys Thr
                325                330                335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu
                340                345                350
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys
                355                360                365
Ala 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 Val Ser Lys Leu Thr Val Asp Lys Ser
                405                410                415
Arg Trp Gln Gln 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 Pro Gly
                435                440                445

```

<210> 74

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 74

```

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

```

183952027140SEQLISTING

				165				170					175			
Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	Ser	
			180					185					190			
His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	Glu	
		195					200					205				
Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser								
	210					215										

<210> 75

<211> 573

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 75

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

183952027140SEQLISTING

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

<210> 76

<211> 341

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 76

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

183952027140SEQLISTING

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

<210> 77

<211> 1341

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 77

183952027140SEQLISTING

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gaggtgcagc tgaaggagag cggccccggc ctggtggccc ccggcggcag cctgagcatc 60
acctgcaccg tgagcggctt cagcctgacc gacagcagca tcaactgggt gcgccagccc 120
cccggcaagg gcctggagtg gctgggcatg atctggggcg acggccgcat cgactacgcc 180
gacgccctga agagccgcct gagcatcagc aaggacagca gcaagagcca ggtgttcctg 240
gagatgacca gcctgcgcac cgacgacacc gccacctact actgcgcccg cgacggctac 300
ttcccctacg ccatggactt ctggggccag ggcaccagcg tgaccgtgag cagcgccagc 360
accaagggcc ccagcgtggt ccccctggcc cctagcagca agagcacatc tggcggcaca 420
gccgccctgg gctgcctggt caaggactac ttccccgagc ccgtgacagt gtcctggaac 480
tctggcgccc tgaccagcgg agtgcatacc ttccctgccg tgctgcagtc cagcggcctg 540
tacagcctga gcagcgtggt cacagtgcct agcagcagcc tgggcaccca gacctacatc 600
tgcaacgtga accacaagcc cagcaacacc aaggtggaca agaaggtgga acccaagagc 660
tgcgacaaga cccacacctg tccccctgc cctgcccctg aactgctggg cggaccctcc 720
gtgttcctgt tcccccaaa gcccaaggac accctgatga tcagccggac cccgaagtg 780
acctgcgtgg tgggtggact gtcccacgag gacctgaag tgaagttcaa ttggtacgtg 840
gacggcgtgg aagtgcataa cgccaagacc aagcccagag aggaacagta caacagcacc 900
taccgggtgg tgtccgtgct gaccgtgctg caccaggact ggctgaacgg caaagagtac 960
aagtgcagg tgtccaacaa ggccctgcct gcccccatcg agaaaaccat cagcaaggcc 1020
aaggggccag ctagagagcc ccaagtctgc accctgcccc ccagcagaga tgagctgacc 1080
aagaaccagg tgtccctgag ctgcgccgtg aagggttctt accccagcga tatcgccgtg 1140
gaatgggaga gcaacggcca gcccgagaac aactacaaga ccaccccccc tgtgctggac 1200
agcgacggct cattcttcct ggtgtccaag ctgacagtgg acaagagccg gtggcagcag 1260
ggcaacgtgt tcagctgcag cgtgatgcac gaggccctgc acaaccatta caccagaag 1320
tccctgagcc tgagccccgg c                                     1341

```

<210> 78

<211> 651

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 78

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gacatcgtgc tgaccagag ccctgccagc ctggccgtgt ctctgggcca gagagccacc 60
atcagctgcc gggccagcga gagcgtggac agctacggcc agagctacat gcactggtat 120
cagcagaagg ccggccagcc cccaagctg ctgatctacc tggccagcaa cctggaaagc 180
ggcgtgcccc ccagattcag cggcagcggc agcagaaccg acttcaccct gaccatcgac 240
cccgtgcagg ccgaggacgc cgccacctac tactgccagc agaacgccga ggacagccgg 300
accttcggcg gaggcacaa gctggaaatc aagggacagc ccaaggctgc cccctcggtc 360
accctgttcc cccaagcag cgaggaactg caggccaaca aggccaccct cgtgtgcctg 420
atcagcgact tctaccctgg cgccgtgacc gtggcctgga aggccgatag ctctcccgtg 480
aaggccggcg tggaaccac cccccagc aagcagagca acaacaata cgccgccagc 540
agctacctga gcctgacccc cgagcagtgg aagtcccacc ggtcctacag ctgccaggtc 600
acacacgagg gcagcaccgt ggaaaagacc gtggccccc cagagtgcag c 651

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<210> 79

<211> 1719

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

183952027140SEQLISTING

<400> 79

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caggtgcagc tgcagcagag cggccctgag ctggtcaagc ctggcgccag cgtgaagatc 60
agctgcaagg ccagcggcta cagcttcacc agctactgga tccactggat caagcagcgg 120
cctggccagg gcctggaatg gatcggcatg atcgacccca gcgacggcga gacacggctg 180
aaccagagat tccagggcag agccaccctg accgtggacg agagcaccag caccgcctac 240
atgcagctgc ggagccccac cagcaggagc agcgccgtgt actactgcac ccggctgaaa 300
gagtacggca actacgacag cttctacttc gacgtgtggg gagccggcac cctggtcacc 360
gtgtccagcg aagtgcagct ggtggaaagc ggcgagggcc tgggtgcagcc cggcagaagc 420
ctgagactga gctgcgccgc cagcggcctt accttcgacg actacgccat gcactgggtc 480
cgacaggccc ctggcaaagg actggaatgg gtgtccgcca tcacctggaa cagcggccac 540
atcgactacg ccgacagcgt ggaaggccgg ttcacatca gccgggacaa cgccaagaac 600
agcctgtacc tgcagatgaa cagcctgcgg gccgaggata ccgccgtgta ttattgcgcc 660
aaggtgtcct acctgagcac cgccagcagc ctggactact ggggcccagg caccctcgtg 720
acagtgtcct ccgcttcac caagggcccc agcgtgttcc ctctggcccc tagcagcaag 780
agcacatctg gcggaacagc cgccctgggc tgcctggtca aggactactt tcccagagcc 840
gtgaccgtgt cctggaactc tgggtgccctg acaagcggag tgcatacctt ccctgccgtg 900
ctgcagagca gcggcctgta ctctctgagc agcgtggtca ccgtgccaag cagcagcctg 960
ggcaccaga cctacatctg caacgtgaac cacaagccct ccaacaccaa ggtggacaag 1020
aaggtggaac ccaagagctg cgacaagacc cacacctgtc ctccctgtcc tgcccctgaa 1080
ctgctgggcg gaccctccgt gttcctgttc cctccaaagc ccaaggatac cctgatgata 1140
agccggaccc ctgaagtac ctgctgggtg gtggacgtgt cccacgagga tcccgaagtg 1200
aagttcaatt ggtacgtgga cggcgtggaa gtgcataacg ccaagaccaa gcccagagag 1260
gaacagtaca acagcaccta ccgggtgggtg tccgtgctga cagtgtgca ccaggactgg 1320
ctgaacggca aagagtacaa gtgcaagggtg tccaacaagg ccctgccagc ccctatcgag 1380
aaaacatca gcaaggccaa gggccagccc cgcgagcctc aggtgtacac actgcctcca 1440
tgccgggacg agctgaccaa gaaccagggtg tccctgtggt gcctcgtgaa gggcttctac 1500
ccctccgata tcgccgtgga atgggagagc aacggccagc ccgagaacaa ctacaagacc 1560
acccctcccg tgctggacag cgacggctca ttcttcctgt acagcaagct gaccgtggac 1620
aagtcccggg ggacgaggc caacgtgttc agctgctctg tgatgcacga ggccctgcac 1680
aaccggttca cccagaagtc cctgagcctg agccctggc 1719

```

<210> 80

<211> 1023

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 80

```

gacatccaga tgaccagag ccccagcagc ctgagcgcca gcgtgggcga cagagtgacc 60
atcacctgtc gggccagcca gggcatccgg aactacctgg cctggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacgcc gccagcacac tgcagagcgg cgtgcccagc 180
agattcagcg gcagcggctc cggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacgtgg ccacctacta ctgccagcgg tacaacagag cccctacac cttcgccag 300
ggcaccaagg tggaaatcaa gggcggctct ggcagctccg gcagcggcgg agacattcag 360
atgacacagt ccccgccag cctgtccgtg tccgtgggag ataccatcac cctgacatgc 420
cacgccagcc agaacatcga cgtgtggctg agctggttcc agcagaaacc tggcaacatc 480
cctaagctgc tcatctataa ggccagcaac ctgcacacag gcgtgccctc cagattctcc 540
ggctctggct ctggcaccgg ctttacactg acaatcagtt ctctgcagcc tgaggatatc 600
gccacatatt actgtcagca ggcccacagc taccctttca ccttcggagg cggcaccaag 660

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183952027140SEQLISTING

```

ctcgagatta agggcggaag cggctcctcc ggctccggcg gacgtacggt ggccgctcct 720
tccgtgttca tcttcctcc ctccgacgag cagctgaagt ccggcaccgc ctccgtggtg 780
tgtctgctga acaacttcta ccctcgggag gccaaaggtgc agtggaaggt ggacaacgcc 840
ctgcagtccg gcaactccca ggagtccgtc accgagcagg actccaagga cagcacctac 900
tccctgtcct ccaccctgac cctgtccaag gccgactacg agaagcaca ggtgtacgcc 960
tgtgaggtga cccaccaggg cctgtccagc cctgtgacca agtccttcaa ccggggcgag 1020
tgc 1023

```

<210> 81

<211> 573

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 81

```

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

```

183952027140SEQLISTING

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

<210> 82

<211> 341

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 82

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

183952027140SEQLISTING

```

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

```

<210> 83

<211> 1719

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 83

gaggtgcagc tgggtggaaag cggcggagga ctggtgcagc ccggcagaag cctgagactg 60

183952027140SEQLISTING

```

agctgcgccg ccagcggcctt caccttcgac gactacgcca tgcactgggt cgcacaggcc 120
cctggcaagg gcctggaatg ggtgtccgcc atcacctgga acagcggcca catcgactac 180
gccgacagcg tggaaggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcmc caaggtgtcc 300
tacctgagca ccgccagcag cctggactac tggggccagg gcaccctggg caccgtgtcc 360
agtcaggctc agctgcagca gagcggccct gagctggtca agcctggcmc cagcgtgaag 420
atcagctgca aggccagcgg ctacagcttc accagctact ggatccactg gatcaagcag 480
cggcctggcc agggcctcga gtggatcggc atgatcgacc ccagcgacgg cgagacacgg 540
ctgaaccaga gattccaggg cagagccacc ctgaccgtgg acgagagcac cagcaccgcc 600
tacatgcagc tgcggagccc caccagcgag gatagcgccg tgtattattg caccgggctg 660
aaagagtacg gcaactacga cagcttctac ttcgacgtgt ggggagccgg caccctcgtg 720
acagtgtcct ccgcttcac caagggcccc agcgtgttcc ctctggcccc tagcagcaag 780
agcacatctg gcggaacagc cgccctgggc tgcctggtca aggactactt tcccgagccc 840
gtgaccgtgt cctggaactc tgggtccctg acaagcggag tgcatacctt ccctgccgtg 900
ctgcagagca gcggcctgta ctctctgagc agcgtggtca ccgtgccaag cagcagcctg 960
ggcaccacga cctacatctg caacgtgaac cacaagccct ccaacaccaa ggtggacaag 1020
aaggtggaac ccaagagctg cgacaagacc cacacctgtc ctccctgtcc tgcccctgaa 1080
ctgctgggcm gaccctccgt gttcctgttc cctccaaagc ccaaggatac cctgatgatc 1140
agccggaccc ctgaagtga cctgcgtggtg gtggacgtgt cccacgagga tccgaagtg 1200
aagttcaatt ggtacgtgga cggcgtggaa gtgcataacg ccaagaccaa gccagagag 1260
gaacagtaca acagcaccta ccgggtggtg tccgtgctga cagtgtctga ccaggactgg 1320
ctgaacggca aagagtacaa gtgcaagggtg tccaacaagg ccctgccagc ccctatcgag 1380
aaaaccatca gcaaggccaa gggccagccc cgcgagcctc aggtgtacac actgcctcca 1440
tgccgggacg agctgaccaa gaaccagggtg tccctgtggt gcctcgtgaa gggcttctac 1500
ccctccgata tcgccgtgga atgggagagc aacggccagc ccgagaacaa ctacaagacc 1560
acccctcccg tgctggacag cgacggctca ttcttcctgt acagcaagct gaccgtggac 1620
aagtcctggg ggcagcaggg caacgtgttc agctgctctg tgatgcacga ggccctgcac 1680
aaccggttca cccagaagtc cctgagcctg agccctggc 1719

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<210> 84

<211> 1023

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 84

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gacatccaga tgaccagag ccccgccagc ctgagcgtgt ccgtgggcmg taccatcacc 60
ctgacctgcc acgccagcca gaacatcgac gtgtggctga gctggttcca gcagaagccc 120
ggcaacatcc ccaagctgct gatctacaag gccagcaacc tgcacaccgg cgtgccagc 180
agattcagcg gctctggcag cggcaccggc tttaccctga ccatcagcag cctgcagccc 240
gaggatatcg ccacctacta ctgccagcag gcccacagct accccttcac cttcggcgga 300
ggcaccaagc tggaatcaa gggcggcagc ggcagctccg gcagcggcmg agacattcag 360
atgacacagt ccccgagcag cctgtccgcc agcgtgggcm acagagtga ccatcactgt 420
cgggcccagc agggcatccg gaactacctg gcctggtatc agcagaaacc tggcaaggcc 480
cctaaactgc tcatctacgc cgccagcaca ctgcagtctg gcgtgccctc cagattctcc 540
ggaagcggct ccggcaccga tttcaccctg acaatctcat ctctgcagcc tgaggacgtg 600
gccacatatt actgccagag atacaacaga gcccctaca cctttggcca gggcaccaag 660
gtcgagatta agggcgatc cggctccagc ggcagcggag gacgtacggg ggccgctcct 720
tccgtgttca tcttccctcc ctccgacgag cagctgaagt ccggcaccgc ctccgtgggt 780
tgtctgctga acaacttcta ccctcgggag gccaaaggtg agtggaaagt ggacaacgcc 840

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183952027140SEQLISTING

ctgcagtccg gcaactccca ggagtccgtc accgagcagg actccaagga cagcacctac 900
 tccctgtcct ccaccctgac cctgtccaag gccgactacg agaagcaciaa ggtgtacgcc 960
 tgtgaggtga cccaccaggg cctgtccagc cctgtgacca agtccttcaa ccggggcgag 1020
 tgc 1023

<210> 85

<211> 452

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 85

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

183952027140SEQLISTING

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

```

<210> 86

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 86

```

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

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183952027140SEQLISTING

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

<210> 87

<211> 568

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 87

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

183952027140SEQLISTING

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

<210> 88

<211> 344

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 88

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

183952027140SEQLISTING

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

<210> 89

<211> 1356

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 89

183952027140SEQLISTING

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cccggccagg gcctggagtg gatcggcatg atcgacccca gcgacggcga gacccgcctg 180
aaccagcgct tccagggccg cgccaccctg accgtggacg agagcaccag caccgcctac 240
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gagtacggca actacgacag cttctacttc gacgtgtggg gcgccggcac cctggtgacc 360
gtgagcagcg ccagcaccaa gggccccagc gtgttcccc tggccccctag cagcaagagc 420
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acccagacct acatctgcaa cgtgaaccac aagcccagca acaccaaggt ggacaagaag 660
gtggaacca agagctgcga caagaccac acctgtcccc cctgccctgc ccctgaactg 720
ctgggaggac cctccgtgtt cctgttcccc ccaaagccca aggacaccct gatgatcagc 780
cggacccccg aagtgacctg cgtggtggtg gacgtgtccc acgaggacc tgaagtgaag 840
ttcaattggt acgtggacgg cgtggaagtg cataacgcca agaccaagcc cagagaggaa 900
cagtacaaca gcacctaccg ggtggtgtcc gtgctgaccg tgctgcacca ggactggctg 960
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accatcagca aggccaaggg ccagcctaga gagcccaag tctgcaccct gccccccagc 1080
agagatgagc tgaccaagaa ccaggtgtcc ctgagctgcg ccgtgaaggg cttctacccc 1140
agcgatatcg ccgtggaatg ggagagcaac ggccagcccg agaacaacta caagaccacc 1200
ccccctgtgc tggacagcga cggctcattc ttcctggtgt ccaagctgac agtggacaag 1260
agccggtggc agcagggcaa cgtgttcagc tgcagcgtga tgcacgaggc cctgcacaac 1320
cattacacc agaagtccct gacccctgagc cccggc 1356

```

<210> 90

<211> 639

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 90

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ggcaacatcc ccaagctgct gatctacaag gccagcaacc tgcacaccgg cgtgcccagc 180
agattcagcg gctctggcag cggcaccggc tttaccctga ccatcagcag cctgcagccc 240
gaggatatcg ccacctacta ctgccagcag gccacagct accccttcac cttcggcgga 300
ggcaccaagc tggaaatcaa gggacagccc aaggctgccc cctcggtcac cctgttcccc 360
ccaagctctg aggaactgca ggccaacaag gccaccctcg tgtgcctgat cagcgacttc 420
taccctggcg ccgtgaccgt ggcctggaag gccgatagct ctcccgtgaa ggccggcgtg 480
gaaaccacca ccccagcaa gcagagcaac aacaaatacg ccgccagcag ctacctgagc 540
ctgacccccg agcagtggaa gtcccaccgg tcctacagct gccaggtcac acacgagggc 600
agcaccgtgg aaaagaccgt ggccccacc gagtgcagc 639

```

<210> 91

<211> 1704

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

183952027140SEQLISTING

<400> 91

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cctggcaagg gcctggaatg gctgggcatg atctggggcg acggccggat cgactacgcc 180
gacgccctga agtcccggct gagcatcagc aaggacagca gcaagagcca ggtgttcctg 240
gaaatgacca gcctgcggac cgacgacacc gccacctact actgcgccag ggacggctac 300
ttcccctacg ccatggattt ctggggccag ggcaccagcg tgaccgtgtc ctccgaagtg 360
cagctggtgg aaagcggcgg aggcctggtg cagcccggca gaagcctgag actgagctgc 420
gccgccagcg gcttcacctt cgacgactac gccatgcact gggtccgcca ggctcccgga 480
aagggactcg agtgggtgtc cgccatcacc tggaacagcg gccacatcga ttacgccgat 540
agcgtggaag gccgggtcac catcagccgg gacaacgcca agaacagcct gtacctgcag 600
atgaacagcc tgagagccga ggataccgcc gtgtactact gtgccaaggt gtcctacctg 660
agcaccgcca gcagcctgga ctactgggga cagggaaccc tggtcaccgt gtccagcgct 720
tccaccaagg gccccagcgt gttccctctg gcccttagca gcaagagcac atctggcgga 780
acagccgccc tgggctgcct ggtcaaggac tactttcccg agcccgtgac cgtgtcctgg 840
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gtggacggcg tggaagtgca taacgccaag accaagccca gagaggaaca gtacaacagc 1260
acctaccggg tgggtgtccg gctgacagtg ctgcaccagg actggctgaa cggcaaagag 1320
tacaagtgca aggtgtccaa caaggccctg ccagccccta tcgagaaaac catcagcaag 1380
gccaagggcc agccccgcga gcctcaggtg tacacactgc ctccatgccg ggacgagctg 1440
accaagaacc aggtgtccct gtggtgcctc gtgaagggtc tctaccctc cgatatcgcc 1500
gtggaatggg agagcaacgg ccagcccag aacaactaca agaccacccc tcccgtgctg 1560
gacagcgacg gctcattctt cctgtacagc aagctgaccg tggacaagtc ccggtggcag 1620
cagggcaacg tgttcagctg ctctgtgatg cacgaggccc tgcacaaccg gttcacccag 1680
aagtccttga gcctgagccc tggc 1704

```

<210> 92

<211> 1035

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 92

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atcacctgtc gggccagcca gggcatccgg aactacctgg cctggtatca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacgcc gccagcacac tgacagcgcg cgtgcccagc 180
agattcagcg gcagcggctc cggcaccgac ttaccctga ccatcagcag cctgcagccc 240
gaggacgtgg ccacctacta ctgccagcgg tacaacagag ccccctacac cttcgccag 300
ggcaccaagg tggaaatcaa gggcggctct ggcagctccg gctctggcgg cgatatcgctg 360
ctgaccaggt ctcccgccag cctggccgtg tctctgggcc agagagccac catcagctgc 420
agagccagcg agagcgtgga cagctacggc cagagctaca tgcattggta tcagcagaaa 480
gccggccagc ctctaaact gctcatctac ctggccagca acctggaatc cggcgtgccc 540
gccaggtttt ccggcagcgg cagcagaacc gatttcacac tgacaatcga ccccgctgcag 600
gccgaggatg ccgccacata ttactgtcag cagaacgccg aggacagccg gaccttcggc 660

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183952027140SEQLISTING

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ggaggcacca agctcgagat taagggcgga agcggctcca gcggcagtgg cggacgtacg 720
gtggccgctc cttccgtgtt catcttcctt ccctccgacg agcagctgaa gtccggcacc 780
gcctccgtgg tgtgtctgct gaacaacttc taccctcggg aggccaaggt gcagtggaag 840
gtggacaacg ccctgcagtc cggcaactcc caggagtccg tcaccgagca ggactccaag 900
gacagcacct actccctgtc ctccaccctg accctgtcca aggccgacta cgagaagcac 960
aaggtgtacg cctgtgaggt gaccaccag ggctgtcca gccctgtgac caagtccttc 1020
aaccggggcg agtgc 1035

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<210> 93

<211> 568

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 93

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

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

<210> 94

<211> 345

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 94

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

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

<210> 95

<211> 1704

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 95

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183952027140SEQLISTING

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gccgacagcg tggaaggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caaggtgtcc 300
tacctgagca ccgccagcag cctggactac tggggccagg gcaccctggt caccgtgtcc 360
tccgaagtgc agctgaaaga gtccggccct ggccctggtg cccctggcgg cagcctgagc 420
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cctcccggaa agggactcga gtggctgggc atgatctggg gcgacggccg gatcgattac 540
gccgatgccc tgaagtcccg gctgagcatc agcaaggaca gcagcaagag ccaggtgttc 600
ctggaaatga ccagcctgag aaccgacgac accgccacct actactgtgc ccgggacggc 660
tacttcccct acgccatgga tttctgggga cagggaacca gcgtgaccgt gtccagcgct 720
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gacagcgacg gctcattctt cctgtacagc aagctgaccg tggacaagtc ccggtggcag 1620
cagggcaacg tgttcagctg ctctgtgatg cacgaggccc tgcacaaccg gttcaccag 1680
aagtcctga gcctgagccc tggc 1704

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<210> 96

<211> 1035

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 96

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cagcagaagg ccggccagcc ccccaagctg ctgatctacc tggccagcaa cctggaaagc 180
ggcgtgcccg ccagattcag cggcagcggc agcagaaccg acttcaccct gaccatcgac 240
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accttcggcg gaggcaccaa gctggaaatc aagggcggct ccggcagcag cggctctggc 360
ggcgatatcc agatgaccca gtccccagc agcctgagcg ccagcgtggg cgacagagtg 420
accatcacct gtagagccag ccagggcatc cggaactacc tggcttggtg tcagcagaaa 480
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cagggcacca aggtcgagat taagggcgga agcggcagct ccggctccgg cgacgtacg 720
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183952027140SEQLISTING

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aaggtgtacg cctgtgaggt gaccaccag ggcctgtcca gccctgtgac caagtccttc 1020
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<210> 97

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 97

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gacgccctga agtcccggct gagcatcagc aaggacagca gcaagagcca ggtgttcctg 240
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cagctgcagc agagcggccc tgagctggtc aagcctggcg ccagcgtgaa gatcagctgc 420
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<210> 98

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 98

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<210> 99

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 99

Gly Gly Gly Gly Gly

1

5

<210> 100

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 100

Gly Gly Gly Gly Gly Gly

1

5

<210> 101

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 101

Gly Gly Gly Gly Gly Gly Gly

1

5

<210> 102

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

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<400> 102

Gly Gly Gly Gly Gly Gly Gly Gly
1 5

<210> 103

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 103

Gly Gly Gly Gly Ser
1 5

<210> 104

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 104

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 105

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 105

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 106

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 106

Thr Lys Gly Pro Ser
1 5

<210> 107

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 107

Thr Val Ala Ala Pro
1 5

<210> 108

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 108

Gln Pro Lys Ala Ala
1 5

<210> 109

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 109

Gln Arg Ile Glu Gly
1 5

<210> 110

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 110

Ala Ser Thr Lys Gly Pro Ser
1 5

<210> 111

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 111

Arg Thr Val Ala Ala Pro Ser
1 5

<210> 112

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 112

Gly Gln Pro Lys Ala Ala Pro
1 5

<210> 113

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 113

His Ile Asp Ser Pro Asn Lys
1 5

<210> 114

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

183952027140SEQLISTING

<400> 114

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

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				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> 115

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 115

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

<210> 116

<211> 1344

<212> DNA

<213> Artificial Sequence

<220>

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<223> Synthetic Construct

<400> 116

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cccggcagag gcctggaatg gatcggcgcc atctaccccg gcaacggcga cacctcctac 180
aaccagaagt tcaagggcaa ggccaccctg accgccgaca agagcagcag cacagcctac 240
atgcagctgt ccagcctgac cagcgaggac agcgccgtgt actactgctc cagaagcacc 300
tactacggcg gcgactggta cttcaacgtg tggggagccg gcaccaccgt gacagtgtct 360
gctgcttcga ccaagggccc atcgggtgttc cctctggccc cttgcagcag aagcaccagc 420
gaatctacag ccgccctggg ctgcctctgt aaggactact ttcccagacc 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
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agcgacggct cattcttctt gtactccaag ctgaccgtgg acaagagccg gtggcaggaa 1260
ggcaacgtgt tcagctgctc cgtgatgcac gaggccctgc acaaccacta caccagaag 1320
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<210> 117

<211> 639

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 117

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atgacctgca gagccagcag cagcgtgtcc tacatccact gggtccagca gaagcccggc 120
agcagcccca agccttggat ctacgccacc agcaatctgg ccagcggagt gcctgtgcgg 180
tttagcggct ctggcagcgg cacaagctac agcctgacca tcagccgggt ggaagccgaa 240
gatgccgcca ctactactg ccagcagtgg accagcaacc cccccacatt tggcggaggc 300
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gacgagcagc tgaagtccgg cacagcctct gtcgtgtgct tgctgaacaa cttctacccc 420
cgcgaggcca aagtgcagtg gaaggtggac aacgccctgc agagcggcaa cagccaggaa 480
agcgtgaccg agcaggacag caaggactcc acctacagcc tgagcagcac cctgacactg 540
agcaaggccg actacgagaa gcacaaggtg tacgcctgcg aagtgacca ccagggcctg 600
tctagccccg tgaccaagag cttcaaccgg ggcgagtgt                                     639

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<210> 118

<211> 1713

<212> DNA

<213> Artificial Sequence

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<220>

<223> Synthetic Construct

<400> 118

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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 agctgggtgga atctggcggc ggagtgggtgc agcctggcag aagcctgaga 420
ctgagctgtg ccgccagcgg cttcaccttc accaaggcct ggatgactg ggtgcgccag 480
gcccctggaa agcagctgga atgggtggcc cagatcaagg acaagagcaa cagctacgcc 540
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accagaagt ccctgtctct gtccctgggc aag 1713

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<210> 119

<211> 1026

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 119

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atcagctgca agagcagcca gagcctggtg cacaacaacg ccaacaccta cctgagctgg 120
tatctgcaga agcccggcca gagccccag tccctgatct acaagggtgtc caacagattc 180
agcggcgtgc ccgacagatt ctccggcagc ggctctggca ccgacttcac cctgaagatc 240
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ttcaccttg gcagcggcac caaggtggaa atcaagggcc agcccaaggc cgccccgcac 360
atcgtgctga cacagagccc tgctagcctg gccgtgtctc ctggacagag ggccaccatc 420
acctgtagag ccagcgagag cgtggaatat tacgtgacca gcctgatgca gtggtatcag 480

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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
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<210> 120
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 120
 Gly Tyr Thr Phe Thr Ser Tyr Asn
 1 5

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

<220>
 <223> Synthetic Construct

<400> 121
 Ile Tyr Pro Gly Asn Gly Asp Thr
 1 5

<210> 122
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 122
 Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val
 1 5 10

<210> 123
 <211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 123

Ser	Ser	Val	Ser	Tyr
1				5

<210> 124

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 124

Ala	Thr	Ser
1		

<210> 125

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 125

Gln	Gln	Trp	Thr	Ser	Asn	Pro
1					5	

<210> 126

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 126

Gly	Tyr	Ile	Phe	Thr	Asn	Tyr	Asn	Ile	His
1					5				10

<210> 127

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 127

Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Ala	Pro
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<210> 128

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 128

Ala	Asn	Trp	Asp	Val	Ala	Phe	Ala	Tyr
1				5				

<210> 129

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 129

Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Ala	Met	His
1				5					10

<210> 130

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 130

Ala	Ile	Thr	Trp	Asn	Ser	Gly	His	Ile	Asp
1				5					10

<210> 131

<211> 12

183952027140SEQLISTING

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 131

Val	Ser	Tyr	Leu	Ser	Thr	Ala	Ser	Ser	Leu	Asp	Tyr
1				5					10		

<210> 132

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 132

Gly	Tyr	Ser	Phe	Thr	Ser	Tyr	Trp	Ile	His
1				5					10

<210> 133

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 133

Met	Ile	Asp	Pro	Ser	Asp	Gly	Glu	Thr
1				5				

<210> 134

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 134

Leu	Lys	Glu	Tyr	Gly	Asn	Tyr	Asp	Ser	Phe	Tyr	Phe	Asp	Val
1				5								10	

<210> 135

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 135

Gly	Phe	Ser	Leu	Thr	Asp	Ser	Ser	Ile	Asn
1				5					10

<210> 136

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 136

Met	Ile	Trp	Gly	Asp	Gly	Arg	Ile	Asp
1				5				

<210> 137

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 137

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

<210> 138

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 138

Lys	Ala	Ser	Gln	Asp	Ile	Asp	Arg	Tyr	Met	Ala
1				5						10

<210> 139

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 139

Asp	Thr	Ser	Thr	Leu	Gln	Ser
1				5		

<210> 140

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 140

Leu	Gln	Tyr	Asp	Asn	Leu	Trp	Thr
1				5			

<210> 141

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 141

Arg	Ala	Ser	Gln	Gly	Ile	Arg	Asn	Tyr	Leu	Ala
1				5					10	

<210> 142

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 142

Gln	Arg	Tyr	Asn	Arg	Ala	Pro	Tyr	Thr
1				5				

<210> 143

<211> 11

183952027140SEQLISTING

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 143

His	Ala	Ser	Gln	Asn	Ile	Asp	Val	Trp	Leu	Ser
1				5					10	

<210> 144

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 144

Gln	Gln	Ala	His	Ser	Tyr	Pro	Phe	Thr
1				5				

<210> 145

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 145

Arg	Ala	Ser	Glu	Ser	Val	Asp	Ser	Tyr	Gly	Gln	Ser	Tyr	Met	His
1				5					10					15

<210> 146

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 146

Leu	Ala	Ser	Asn	Leu	Glu	Ser
1				5		

<210> 147

<211> 9

183952027140SEQLISTING

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 147

Gln	Gln	Asn	Ala	Glu	Asp	Ser	Arg	Thr
1				5				

<210> 148

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 148

Gly	Gly	Ser	Gly	Ser	Ser	Gly	Ser	Gly	Gly
1				5					10

<210> 149

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 149

Gln	Ser	Leu	Val	His	Asn	Asn	Gly	Asn	Thr	Tyr
1				5						10

<210> 150

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 150

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

183952027140SEQLISTING

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

<210> 151

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 151

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

<210> 152

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 152

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

183952027140SEQLISTING

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> 153

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 153

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

<210> 154

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 154

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 Gly Leu Glu Trp Val
 35 40 45

183952027140SEQLISTING

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 Asn 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> 155

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 155

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 Gly Asn Thr Tyr Leu Ser Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Leu 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 Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 156

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 156

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

183952027140SEQLISTING

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

<210> 157

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 157

Asp Leu 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 Lys Ala Ser Gln Ser Val Asp Tyr Asp
 20 25 30
 Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45
 Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val 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 Thr Ala Asn Tyr Tyr Cys Gln Gln Ser Thr
 85 90 95
 Glu Asp Pro Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 158

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 158

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

183952027140SEQLISTING

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

<210> 159

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 159

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

<210> 160

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 160

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

183952027140SEQLISTING

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> 161

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 161

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

<210> 162

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 162

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 Gly Lys Gly Leu Glu Trp Leu
 35 40 45

183952027140SEQLISTING

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

<210> 163

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 163

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
 100 105 110

<210> 164

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 164

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

183952027140SEQLISTING

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

<210> 165

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 165

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

<210> 166

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 166

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

183952027140SEQLISTING

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Ala Pro Tyr Ser Gln Lys Phe
 50 55 60
 Gln Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Thr Ser Thr Thr Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Val Arg Ala Asn Trp Asp Val Ala Phe Ala Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser
 115

<210> 167

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 167

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

<210> 168

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 168

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

183952027140SEQLISTING

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

<210> 169

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 169

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

<210> 170

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 170

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

183952027140SEQLISTING

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

<210> 171

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 171

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

<210> 172

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 172

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

183952027140SEQLISTING

Gly Met Ile Trp Gly Asp Gly Arg Ile Asp Tyr Ala Asp Ala Leu Lys
50 55 60
Ser Arg Leu Ser Ile Ser Lys Asp Ser Ser Lys Ser Gln Val Phe Leu
65 70 75 80
Glu Met Thr Ser Leu Arg Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95
Arg Asp Gly Tyr Phe Pro Tyr Ala Met Asp Phe Trp Gly Gln Gly Thr
100 105 110
Ser Val Thr Val Ser Ser
115

<210> 173
<211> 111
<212> PRT
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<220>
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<400> 173
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1 5 10 15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr
20 25 30
Gly Gln Ser Tyr Met His Trp Tyr Gln Gln Lys Ala Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60
Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp
65 70 75 80
Pro Val Gln Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Ala
85 90 95
Glu Asp Ser Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 174
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> VARIANT
<222> (1)...(5)
<223> Can be absent or present, or present in repeats
of up to 5 times

<400> 174

Gly Gly Gly Gly Ser
1 5

<210> 175
<211> 7
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<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 175
Gly Gln Pro Lys Ala Ala Pro
1 5

<210> 176
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<220>
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<400> 176
Asp Lys Thr His Thr
1 5

<210> 177
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<220>
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<400> 177
Thr Lys Gly Pro Ser Arg
1 5

<210> 178
<211> 7
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<220>
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<400> 178

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Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 179

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 179

Lys Ala Ser Asn Leu His Thr
1 5