

SEQUENCE LISTING

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<120> MULTISPECIFIC CHIMERIC RECEPTORS COMPRISING AN NKG2D DOMAIN AND METHODS OF USE THEREOF

<130> 76142-20009.41

<140> Not Yet Assigned

<141> Concurrently Herewith

<150> PCT/CN2017/119397

<151> 2017-12-28

<160> 45

<170> FastSEQ for Windows Version 4.0

 $\langle 210 \rangle$ 1

<211> 19

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

 $\langle 400 \rangle$ 1

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

 $\langle 210 \rangle$ 2

<211> 21

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Synthetic Construct

 $\langle 400 \rangle$ 2

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15
His Ala Ala Arg Pro
20

<210> 3
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 3
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15
Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30
Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
35 40 45

<210> 4
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 4
Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1 5 10 15
Ser Leu Val Ile Thr Leu Tyr Cys
20

<210> 5
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 5
Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15
Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30
Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
35 40

<210> 6
<211> 112
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 6

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

<210> 7

<211> 128

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 7

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

<210> 8

<211> 128

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 8

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

<210> 9

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 9

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

<210> 10

<211> 25

<212> PRT

<213> Artificial Sequence

<210> 14
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15
Ser Gly Gly Gly Gly Ser
20

<210> 15
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 15
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly
1 5 10 15
Ser Gly Ser Gly Gly Gly Gly Ser
20

<210> 16
<211> 704
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16
Met Ser Arg Leu Pro Val Leu Leu Leu Leu Gln Leu Leu Val Arg Pro
1 5 10 15
Gly Leu Gln Ala Pro Met Thr Gln Thr Thr Pro Leu Lys Thr Ser Trp
20 25 30
Val Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln
35 40 45
Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln
50 55 60
Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe
65 70 75 80
Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile
85 90 95
Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr

			100				105				110				
Arg	His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg
			115				120				125				
Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln
			130				135				140				
Thr	Thr	Leu	Ser	Leu	Ala	Ile	Phe	Thr	Ser	Gly	Gly	Gly	Gly	Ser	Gly
			145				150				155				
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Gly	Gly	Ser
			165				170				175				
Arg	Arg	Val	Thr	Arg	Gln	Met	Cys	Ile	Tyr	Thr	Asn	Pro	Thr	Ser	Cys
			180				185				190				
Asn	Glu	Ile	Tyr	Gly	Lys	Phe	Ser	Ser	Ala	Tyr	Leu	Ala	Cys	Asp	Gly
			195				200				205				
Lys	Gln	Met	Glu	Ile	Ile	Thr	Leu	Leu	Asn	Pro	Ser	Leu	Ile	Ser	Gly
			210				215				220				
Asp	Glu	Trp	Gln	Trp	Ser	Gly	Asn	Thr	Pro	Ile	His	Val	Leu	Gly	Met
			225				230				235				
Trp	His	Tyr	Ser	Lys	Val	Leu	Lys	Leu	Leu	Asp	Gln	Asp	Glu	Lys	Ser
			245				250				255				
Tyr	Val	Lys	Leu	Leu	Ser	Ala	Asn	Gln	Ser	Met	Cys	Ser	Ala	Gln	Ser
			260				265				270				
Glu	Tyr	Trp	Asn	Lys	Ser	Glu	Asp	Phe	Phe	Gln	Tyr	Cys	Asn	Asn	Lys
			275				280				285				
Tyr	Cys	Ile	Trp	Asn	Lys	Pro	Cys	Pro	Gly	Cys	Tyr	Ser	Glu	Thr	Leu
			290				295				300				
Pro	Ile	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
			305				310				315				
Gly	Ser	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ile	Pro	Leu	Thr	Glu	Ser	Tyr
			325				330				335				
Cys	Gly	Pro	Cys	Pro	Lys	Asn	Trp	Ile	Cys	Tyr	Lys	Asn	Asn	Cys	Tyr
			340				345				350				
Gln	Phe	Phe	Asp	Glu	Ser	Lys	Asn	Trp	Tyr	Glu	Ser	Gln	Ala	Ser	Cys
			355				360				365				
Met	Ser	Gln	Asn	Ala	Ser	Leu	Leu	Lys	Val	Tyr	Ser	Lys	Glu	Asp	Gln
			370				375				380				
Asp	Leu	Leu	Lys	Leu	Val	Lys	Ser	Tyr	His	Trp	Met	Gly	Leu	Val	His
			385				390				395				
Ile	Pro	Thr	Asn	Gly	Ser	Trp	Gln	Trp	Glu	Asp	Gly	Ser	Ile	Leu	Ser
			405				410				415				
Pro	Asn	Leu	Leu	Thr	Ile	Ile	Glu	Met	Gln	Lys	Gly	Asp	Cys	Ala	Leu
			420				425				430				
Tyr	Ala	Ser	Ser	Phe	Lys	Gly	Tyr	Ile	Glu	Asn	Cys	Ser	Thr	Pro	Asn
			435				440				445				
Thr	Tyr	Ile	Cys	Met	Gln	Arg	Thr	Val	Asp	Asp	Ser	Gly	Gly	Gly	Gly
			450				455				460				
Ser	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
			465				470				475				
Gly	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile
			485				490				495				
Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala
			500				505				510				
Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr
			515				520				525				
Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu

530		535		540
Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile				
545		550		555
Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp				
	565		570	575
Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu				
	580		585	590
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly				
	595		600	605
Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr				
	610		615	620
Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys				
625		630		635
Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys				
	645		650	655
Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg				
	660		665	670
Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala				
	675		680	685
Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg				
	690		695	700

<210> 17

<211> 700

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 17

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

Val	Thr	Arg	Gln	Met	Cys	Ile	Tyr	Thr	Asn	Pro	Thr	Ser	Cys	Asn	Glu
			180					185					190		
Ile	Tyr	Gly	Lys	Phe	Ser	Ser	Ala	Tyr	Leu	Ala	Cys	Asp	Gly	Lys	Gln
		195					200					205			
Met	Glu	Ile	Ile	Thr	Leu	Leu	Asn	Pro	Ser	Leu	Ile	Ser	Gly	Asp	Glu
	210					215					220				
Trp	Gln	Trp	Ser	Gly	Asn	Thr	Pro	Ile	His	Val	Leu	Gly	Met	Trp	His
225					230					235					240
Tyr	Ser	Lys	Val	Leu	Lys	Leu	Leu	Asp	Gln	Asp	Glu	Lys	Ser	Tyr	Val
			245					250						255	
Lys	Leu	Leu	Ser	Ala	Asn	Gln	Ser	Met	Cys	Ser	Ala	Gln	Ser	Glu	Tyr
			260					265					270		
Trp	Asn	Lys	Ser	Glu	Asp	Phe	Phe	Gln	Tyr	Cys	Asn	Asn	Lys	Tyr	Cys
		275					280						285		
Ile	Trp	Asn	Lys	Pro	Cys	Pro	Gly	Cys	Tyr	Ser	Glu	Thr	Leu	Pro	Ile
	290					295					300				
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
305					310					315					320
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ile	Pro	Leu	Thr	Glu	Ser	Tyr	Cys	Gly
				325					330					335	
Pro	Cys	Pro	Lys	Asn	Trp	Ile	Cys	Tyr	Lys	Asn	Asn	Cys	Tyr	Gln	Phe
			340					345					350		
Phe	Asp	Glu	Ser	Lys	Asn	Trp	Tyr	Glu	Ser	Gln	Ala	Ser	Cys	Met	Ser
		355					360					365			
Gln	Asn	Ala	Ser	Leu	Leu	Lys	Val	Tyr	Ser	Lys	Glu	Asp	Gln	Asp	Leu
	370					375					380				
Leu	Lys	Leu	Val	Lys	Ser	Tyr	His	Trp	Met	Gly	Leu	Val	His	Ile	Pro
385					390					395					400
Thr	Asn	Gly	Ser	Trp	Gln	Trp	Glu	Asp	Gly	Ser	Ile	Leu	Ser	Pro	Asn
			405					410						415	
Leu	Leu	Thr	Ile	Ile	Glu	Met	Gln	Lys	Gly	Asp	Cys	Ala	Leu	Tyr	Ala
			420					425					430		
Ser	Ser	Phe	Lys	Gly	Tyr	Ile	Glu	Asn	Cys	Ser	Thr	Pro	Asn	Thr	Tyr
		435					440					445			
Ile	Cys	Met	Gln	Arg	Thr	Val	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Gly
	450					455					460				
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Thr	Thr	Thr
465					470					475					480
Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro
			485					490						495	
Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val
			500					505					510		
His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro
		515					520					525			
Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu
	530					535					540				
Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro
545					550					555					560
Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys
			565						570					575	
Arg	Phe	Pro	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	
		580					585					590			
Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu
		595					600					605			

Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp
610						615					620				
Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys
625					630					635					640
Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala
				645					650					655	
Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys
			660				665						670		
Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr
	675					680						685			
Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg				
690						695					700				

<210> 18

<211> 552

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 18

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

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

<210> 19

<211> 527

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 19

Met	Ser	Arg	Leu	Pro	Val	Leu	Leu	Leu	Leu	Gln	Leu	Leu	Val	Arg	Pro	
1				5					10					15		
Gly	Leu	Gln	Ala	Pro	Met	Thr	Gln	Thr	Thr	Pro	Leu	Lys	Thr	Ser	Trp	
			20					25					30			

Val	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln
		35					40					45			
Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln
	50					55					60				
Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe
65					70					75					80
Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile
				85					90					95	
Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr
		100						105					110		
Arg	His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg
		115					120					125			
Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln
	130					135					140				
Thr	Thr	Leu	Ser	Leu	Ala	Ile	Phe	Thr	Ser	Gly	Gly	Gly	Gly	Ser	Gly
145					150					155					160
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Gly
				165					170					175	
Gly	Ser	Val	Thr	Arg	Gln	Met	Cys	Ile	Tyr	Thr	Asn	Pro	Thr	Ser	Cys
			180					185					190		
Asn	Glu	Ile	Tyr	Gly	Lys	Phe	Ser	Ser	Ala	Tyr	Leu	Ala	Cys	Asp	Gly
	195						200					205			
Lys	Gln	Met	Glu	Ile	Ile	Thr	Leu	Leu	Asn	Pro	Ser	Leu	Ile	Ser	Gly
	210					215					220				
Asp	Glu	Trp	Gln	Trp	Ser	Gly	Asn	Thr	Pro	Ile	His	Val	Leu	Gly	Met
225					230				235						240
Trp	His	Tyr	Ser	Lys	Val	Leu	Lys	Leu	Leu	Asp	Gln	Asp	Glu	Lys	Ser
				245				250						255	
Tyr	Val	Lys	Leu	Leu	Ser	Ala	Asn	Gln	Ser	Met	Cys	Ser	Ala	Gln	Ser
			260					265					270		
Glu	Tyr	Trp	Asn	Lys	Ser	Glu	Asp	Phe	Phe	Gln	Tyr	Cys	Asn	Asn	Lys
		275					280					285			
Tyr	Cys	Ile	Trp	Asn	Lys	Pro	Cys	Pro	Gly	Cys	Tyr	Ser	Glu	Thr	Leu
	290					295					300				
Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala
305					310					315					320
Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly
				325					330					335	
Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile
			340					345					350		
Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val
		355					360					365			
Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe
						375					380				
Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly
385					390					395					400
Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg
				405					410					415	
Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln
			420					425					430		
Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp
		435					440					445			
Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro
	450					455					460				

Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp
465					470					475					480
Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg
				485					490					495	
Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr
			500					505					510		
Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg	
		515					520					525			

<210> 20

<211> 554

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 20

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

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<210> 22

<211> 2094

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 22

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gagatcatca	cacacctgaa	gcagccccct	ctgccactgc	tggatttcaa	caatctgaac	180
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gggatgaaag	gcgagcgccg	gaggggcaag	gggcacgatg	gcctttacca	gggtctcagt	2040
acagccacca	aggacaccta	cgacgccctt	cacatgcagg	ccctgcccc	tcgc	2094

<210> 23

<211> 1656

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 23

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<210> 24

<211> 1581

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 24

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cacgatggcc	tttaccaggg	tctcagtaca	gccaccaagg	acacctacga	cgcccttcac	1560
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<210> 25

<211> 1662

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 25

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gagatcatca	cacacctgaa	gcagccccct	ctgcctctgc	tggatttcaa	caatctgaac	180
ggcgaggacc	aggatatcct	gatggagaac	aatctgagac	ggcccaacct	ggaggccttt	240

aatcgcgccg	tgaagagcct	gcagaacgcc	agcgccatcg	agtcctatcct	gaagaatctg	300
ctgcccttgtc	tgccactggc	aaccgcagca	ccaacacggc	accctatcca	catcaaggac	360
ggcgattgga	acgagttcag	gcgcaagctg	acctttttacc	tgaagacact	ggagaatgcc	420
caggccccagc	agaccacact	gtccctggcc	atcttcacct	ccggcggcgg	cggctctgga	480
ggaggaggaa	gcggcggagg	aggaggaggc	tctggcagcg	gcggcggcgg	ctctaaggag	540
gagctggagg	ccgagaagcg	ggacctgac	agaaccaacg	agaggctgag	ccaggagctg	600
gagtacctga	tccccctgac	agagtcctat	tgcgggccat	gtcccaagaa	ttggatctgc	660
tacaagaaca	actgttacca	gttctttgat	gagtccaaga	actggtacga	gtcccaggcc	720
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cgtggccggg	accctgagat	ggggggaaaag	ccgagaagga	agaaccctca	ggaaggcctg	1500
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gagcgccgga	ggggcaaggg	gcacgatggc	ctttaccagg	gtctcagtac	agccaccaag	1620
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<210> 26

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 26

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aagttcagct	ccgcctatct	ggcctgtgac	ggcaagcaga	tggagatcat	caccctgctg	180
aacccatctc	tgatcagcgg	cgatgagtgg	cagtggctcg	gcaatacacc	catccacgtg	240
ctgggcatgt	ggcactactc	taaggtgctg	aagctgctgg	accaggatga	gaagtcttat	300
gtgaagctgc	tgagcgccaa	ccagtccatg	tgctctgccc	agagcgagta	ctggaataag	360
tccgaggact	tctttcagta	ctgcaacaat	aagtattgta	tctggaacaa	gccatgcccc	420
ggctgttatt	ctgagacact	gccccatcagc	ggaggaggag	gatccggcgg	aggaggctct	480
ggcggcggcg	gctccggctc	tggaggagga	ggatccatcc	ctctgacaga	gtcttactgc	540
ggcccttgtc	caaagaattg	gatctgctac	aagaacaact	gttaccagtt	ctttgatgag	600
tccaagaact	ggtatgagtc	ccaggcctct	tgtatgagcc	agaatgccag	cctgctgaag	660
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gcctattctg	agatcggcat	gaaggagag	aggcgccggg	gcaagggaca	cgatggcctg	1500
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gcacctcgcc	ccccaaactc	tgccccaaca	atcgcacccc	agccactgtc	tctgcgcccc	2160
gaggcatgca	ggcctgcagc	aggcggcgcc	gtgcacaccc	ggggcctgga	ctttgcctgt	2220
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<210> 27

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 27

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aacaattgtt	atcagttctt	tgacgagtct	aagaactggt	acgagtcca	ggcctcttgt	180
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gattgcgccc	tgtacgccag	ctccttcaag	ggctatatcg	agaactgcag	caccccaaat	420
acatacatct	gtatgcagag	gaccgtgacc	acaaccctg	caccacggcc	ccctacccca	480
gcacctacaa	tcgcaagcca	gccactgtcc	ctgcgccccg	aggcatgtag	gcctgcagca	540
ggcggcgccg	tgacaccag	aggcctggac	tttgctgctg	atatctatat	ctgggcacct	600
ctggcaggaa	cctgtggcgt	gctgctgctg	agcctggcca	tcaccctgta	ctgcaagaga	660
ggcaggaaga	agctgctgta	tatcttcaag	cagcctttta	tgcgcccagt	gcagacaacc	720
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gagctgcaga	aggacaagat	ggccgaggcc	tattctgaga	tcggcatgaa	gggagagagg	1020
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cagcctccac	tgccctgct	ggatttcaac	aatctgaatg	gcgaggacca	ggatatcctg	1380
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accgcagcac ccacaaggca ccctatccac atcaaggacg gcgattggaa cgagttccgc 1560
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<210> 28

<211> 1

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> (1)...(1)

<223> can be present in repeat of at least 1

<400> 28

Gly

1

<210> 29

<211> 2

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> (1)...(2)

<223> can be present in repeat of at least 1

<400> 29

Gly Ser

1

<210> 30

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> (1)...(5)

<223> can be present in repeat of at least 1

<400> 30

Gly Ser Gly Gly Ser
1 5

<210> 31

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> (1)...(4)

<223> can be present in repeat of at least 1

<400> 31

Gly Gly Gly Ser
1

<210> 32

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> VARIANT

<222> (1)...(5)

<223> can be present in repeat of at least 1

<400> 32

Gly Gly Gly Gly Ser
1 5

<210> 33

<211> 516

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 33

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

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

Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn
	450					455					460				
Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met
465					470					475					480
Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly
				485					490					495	
Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala
			500					505					510		
Leu	Pro	Pro	Arg												
			515												

<210> 34

<211> 523

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 34

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

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

<210> 36

<211> 765

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 36

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

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

465					470					475					480
Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly
				485					490					495	
His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr
			500					505					510		
Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg	Gly	Ser	Gly	Glu	Gly
		515					520					525			
Arg	Gly	Ser	Leu	Leu	Thr	Cys	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro
	530					535					540				
Met	Ser	Arg	Leu	Pro	Val	Leu	Leu	Leu	Leu	Gln	Leu	Leu	Val	Arg	Pro
545					550					555					560
Gly	Leu	Gln	Ala	Pro	Met	Thr	Gln	Thr	Thr	Pro	Leu	Lys	Thr	Ser	Trp
				565					570						575
Val	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln
			580					585					590		
Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln
		595					600					605			
Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe
	610					615					620				
Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile
625					630					635					640
Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr
				645					650					655	
Arg	His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg
			660					665				670			
Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln
		675					680					685			
Thr	Thr	Leu	Ser	Leu	Ala	Ile	Phe	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro
	690					695					700				
Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro
705					710					715					720
Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu
				725					730					735	
Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys
			740					745					750		
Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys			
		755					760					765			

<210> 37

<211> 606

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 37

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

Glu	Ser	Lys	Asn	Trp	Tyr	Glu	Ser	Gln	Ala	Ser	Cys	Met	Ser	Gln	Asn
50						55					60				
Ala	Ser	Leu	Leu	Lys	Val	Tyr	Ser	Lys	Glu	Asp	Gln	Asp	Leu	Leu	Lys
65					70					75					80
Leu	Val	Lys	Ser	Tyr	His	Trp	Met	Gly	Leu	Val	His	Ile	Pro	Thr	Asn
				85					90					95	
Gly	Ser	Trp	Gln	Trp	Glu	Asp	Gly	Ser	Ile	Leu	Ser	Pro	Asn	Leu	Leu
			100					105					110		
Thr	Ile	Ile	Glu	Met	Gln	Lys	Gly	Asp	Cys	Ala	Leu	Tyr	Ala	Ser	Ser
		115					120					125			
Phe	Lys	Gly	Tyr	Ile	Glu	Asn	Cys	Ser	Thr	Pro	Asn	Thr	Tyr	Ile	Cys
130						135					140				
Met	Gln	Arg	Thr	Val	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro
145					150					155					160
Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys
				165					170					175	
Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala
			180					185					190		
Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu
		195					200					205			
Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys
						215					220				
Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr
225					230					235					240
Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly
				245					250					255	
Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala
			260					265					270		
Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg
			275				280					285			
Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu
	290					295					300				
Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn
305					310					315					320
Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met
				325					330					335	
Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly
			340					345					350		
Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala
		355					360					365			
Leu	Pro	Pro	Arg	Gly	Ser	Gly	Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr	Cys
						375					380				
Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Ser	Arg	Leu	Pro	Val	Leu
385					390					395					400
Leu	Leu	Leu	Gln	Leu	Leu	Val	Arg	Pro	Gly	Leu	Gln	Ala	Pro	Met	Thr
				405					410					415	
Gln	Thr	Thr	Pro	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys	Ser	Asn	Met	Ile
			420					425					430		
Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro	Pro	Leu	Pro	Leu	Leu	Asp
		435					440					445			
Phe	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp	Ile	Leu	Met	Glu	Asn	Asn	
450					455					460					
Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn	Arg	Ala	Val	Lys	Ser	Leu
465					470					475					480

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

<210> 38

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 38

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aacaattgtt atcagttctt tgacgagtct aagaactggg acgagtccca ggcctcttgt 180
atgagccaga atgcctctct gctgaaggtg tacagcaagg aggaccagga tctgctgaag 240
ctggtgaaga gctatcactg gatgggcctg gtgcacatcc ccaccaacgg ctcttgccag 300
tgggaggacg gctccatcct gtctccta atctgctgacaa tcatcgagat gcagaagggc 360
gattgcgccc tgtacgccag ctccttcaag ggctatatcg agaactgcag caccctaat 420
acatacatct gtatgcagag gaccgtggga ggaggaagcg gaggaggatc cggaggcggc 480
tctggcgggc gcagcatccc tctgactgaa tcatactgtg gcccatgccc caagaactgg 540
atctgtaca agaacaattg ttatcagttc tttgacgagt ctaagaactg gtacgagtcc 600
caggcctctt gtatgagcca gaatgcctct ctgctgaagg tgtacagcaa ggaggaccag 660
gatctgtgta agctggtgaa gagctatcac tggatgggcc tgggtgcacat cccaccaaac 720
ggctcctggc agtgggagga cggctccatc ctgtctccta atctgctgac aatcatcgag 780
atgcagaagg gcgattgcgc cctgtacgcc agctccttca agggctatat cgagaactgc 840
agcaccctca atacatacat ctgtatgcag aggaccgtga ctagtaccac gacgccagcg 900
ccgcgaccac caacaccggc gccaccatc gcgtcgcagc ccctgtccct gcgcccagag 960
gcgtgccggc cagcggcggg gggcgagtg cacacgaggg ggctggactt cgcctgtgat 1020
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accctttact gcaaacgggg cagaaagaaa ctctgtata tattcaaaca accatttatg 1140
agaccagtac aaactactca agaggaagat ggctgtagct gccgatttcc agaagaagaa 1200
gaaggaggat gtgaactgag agtgaagttc agcaggagcg cagacgcccc cgcgtaccag 1260
cagggccaga accagctcta taacgagctc aatctaggac gaagagagga gtacgatgtt 1320
ttggacaaga gacgtggccg ggaccctgag atggggggaa agccgagaag gaagaacctt 1380
caggaaggcc tgtacaatga actgcagaaa gataagatgg cggaggccta cagtgaagatt 1440
gggatgaaag gcgagcgccg gaggggcaag gggcacgatg gcctttacca gggtctcagt 1500
acagccacca aggacaccta cgacgccctt cacatgcagg ccctgcccc tcgc 1554

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<210> 39
<211> 1569
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 39
atggctctgc ccgtgaccgc cctgctgctg cccctggctc tgctgctgca cgccgcccgc 60
cctgtgacaa gacagatgtg catctatacc aacccacat cctgcaatga gatctacggc 120
aagttcagct ccgcctatct ggcctgtgac ggcaagcaga tggagatcat caccctgctg 180
aacccatctc tgatcagcgg cgatgagtgg cagtgggtccg gcaatacacc catccacgtg 240
ctgggcatgt ggcactactc taagggtgctg aagctgctgg accaggatga gaagtcttat 300
gtgaagctgc tgagcgccaa ccagtccatg tgctctgccc agagcgagta ctggaataag 360
tccgaggact tctttcagta ctgcaacaat aagtattgta tctggaacaa gccatgcccc 420
ggctgttatt ctgagacact gcccatcagc ggaggaggag gatccggcgg aggaggctct 480
ggcggcggcg gctccggctc tggaggagga ggatccatcc ctctgacaga gtcttactgc 540
ggcccttgct caaagaattg gatctgctac aagaacaact gttaccagtt ctttgatgag 600
tccaagaact ggtatgagtc ccaggcctct tgtatgagcc agaatgccag cctgctgaag 660
gtgtactcca aggaggacca ggatctgctg aagctggtga agagctatca ctggatgggc 720
ctggtgcaca tccctacca cggctcctgg cagtgggagg acggctccat cctgtctcca 780
aatctgctga caatcatcga gatgcagaag ggcgattgct ccctgtacgc ctctagcttc 840
aagggtata tcgagaactg cagcaccca aatacatata tctgtatgca gcgcaccgtg 900
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gaggagtacg acgtgctgga taagaggagg ggacgggacc ccgagatggg aggcaagcct 1380
cggagaaaga acccacagga gggcctgtac aatgagctgc agaaggacaa gatggccgag 1440
gcctattctg agatcggcat gaaggagag aggcgccggg gcaagggaca cgatggcctg 1500
taccagggcc tgagcaccgc cacaaggac acctatgat ccctgcacat gcaggccctg 1560
ccaccaaga 1569

<210> 40
<211> 1122
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 40
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ccaatccctc tgactgaatc atactgtggc ccatgcccc agaactggat ctgctacaag 120
aacaattgtt atcagttctt tgacgagtct aagaactggt acgagtccca ggcctcttgt 180
atgagccaga atgcctctct gctgaagggt tacagcaagg aggaccagga tctgctgaag 240
ctggtgaaga gctatcactg gatgggcctg gtgcacatcc ccaccaacgg ctctggcag 300
tgaggagacg gctccatcct gtctcctaag ctgctgacaa tcatcgagat gcagaagggc 360
gattgcgccc tgtacgccag ctcttcaag ggctatatcg agaactgcag caccctaat 420
acatacatct gtatgcagag gaccgtgact agtaccacga cgccagcgcc gcgaccacca 480

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acaccggcgc ccaccatcgc gtcgcagccc ctgtccctgc gcccagaggc gtgccggcca 540
gcggcggggg gcgcagtgca cacgaggggg ctggacttcg cctgtgatat ctacatctgg 600
gcgcccttgg ccgggacttg tggggtcctt ctcctgtcac tggttatcac cttttactgc 660
aaacggggca gaaagaaact cctgtatata ttcaaacaac catttatgag accagtacaa 720
actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 780
gaactgagag tgaagttcag caggagcgca gacgccccg cgtaccagca gggccagaac 840
cagctctata acgagctcaa tctaggacga agagaggagt acgatgtttt ggacaagaga 900
cgtggccggg accctgagat ggggggaaag ccgagaagga agaaccctca ggaaggcctg 960
tacaatgaac tgcagaaaga taagatggcg gaggcctaca gtgagattgg gatgaaaggc 1020
gagcgccgga ggggcaaggg gcacgatggc ctttaccagg gtctcagtac agccaccaag 1080
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<210> 41
 <211> 221
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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<400> 41
Met Ser Arg Leu Pro Val Leu Leu Leu Leu Gln Leu Leu Val Arg Pro
1          5          10          15
Gly Leu Gln Ala Pro Met Thr Gln Thr Thr Pro Leu Lys Thr Ser Trp
20          25          30
Val Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln
35          40          45
Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln
50          55          60
Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe
65          70          75          80
Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile
85          90          95
Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr
100          105          110
Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg
115          120          125
Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
130          135          140
Thr Thr Leu Ser Leu Ala Ile Phe Thr Thr Thr Pro Ala Pro Arg Pro
145          150          155          160
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
165          170          175
Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
180          185          190
Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
195          200          205
Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
210          215          220

```

<210> 42
 <211> 213
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 42

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Met Ser Arg Leu Pro Val Leu Leu Leu Leu Gln Leu Leu Val Arg Pro
 1           5           10           15
Gly Leu Gln Ala Pro Met Thr Gln Thr Thr Pro Leu Lys Thr Ser Trp
 20           25           30
Val Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln
 35           40           45
Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln
 50           55           60
Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe
 65           70           75           80
Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile
 85           90           95
Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr
100           105           110
Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg
115           120           125
Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
130           135           140
Thr Thr Leu Ser Leu Ala Ile Phe Thr Thr Thr Pro Ala Pro Arg Pro
145           150           155           160
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
165           170           175
Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
180           185           190
Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
195           200           205
Gly Val Leu Leu Leu
210
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<210> 43

<211> 663

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 43

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caggcccagc agacaaccct gagcctggcc atcttcacaa ccacaccagc acctcgcccc 480
ccaactcctg cccaacaat cgcattccag ccactgtctc tgcgccccga ggcatgcagg 540
```

```
cctgcagcag gcggcgccgt gcacacccgg ggcctggact ttgcctgtga tatctacatc 600
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<212> DNA

<213> Artificial Sequence

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<223> Synthetic Construct

<400> 44

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