

SEQUENCE LISTING

<110> iCell Gene Therapeutics LLC

<120> Chimeric Antigen Receptors (CARs), Compositions and Methods of Use

<130> 2541-3 PCT

<140> 00000000

<141> 2016-06-24

<150> 62/184,321

<151> 2015-06-25

<160> 36

<170> PatentIn version 3.5

<210> 1

<211> 830

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

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Ala Val Ser Leu Gly Glu Arg Val Thr Met Asn Cys Lys Ser Ser Gln
35 40 45

Ser Leu Leu Tyr Ser Thr Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln
50 55 60

Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr
65 70 75 80

Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
85 90 95

Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Val Ala Val

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

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
325 330 335

Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
340 345 350

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
355 360 365

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg
370 375 380

Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln
385 390 395 400

Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu
405 410 415

Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
420 425 430

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
435 440 445

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
450 455 460

Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly
465 470 475 480

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
485 490 495

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
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Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
515 520 525

Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu

530

535

540

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg
 545 550 555 560

Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn
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Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro
 580 585 590

Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile
 595 600 605

Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu
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Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu
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Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His
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Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser
 660 665 670

Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu
 675 680 685

Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln
 690 695 700

Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
 705 710 715 720

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln
 725 730 735

Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala Leu
 740 745 750

Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr Cys
755 760 765

Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr
770 775 780

Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg
785 790 795 800

Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr
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Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
820 825 830

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<220>
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<213> Artificial Sequence

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His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
20 25 30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

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

145		150		155		160									
Leu	Ser	Val	Thr	Cys	Thr	Val	Ser	Gly	Val	Ser	Leu	Pro	Asp	Tyr	Gly
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Val	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Arg	Lys	Gly	Leu	Glu	Trp	Leu	Gly
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Val	Ile	Trp	Gly	Ser	Glu	Thr	Thr	Tyr	Tyr	Asn	Ser	Ala	Leu	Lys	Ser
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Arg	Leu	Thr	Ile	Ile	Lys	Asp	Asn	Ser	Lys	Ser	Gln	Val	Phe	Leu	Lys
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Met	Asn	Ser	Leu	Gln	Thr	Asp	Asp	Thr	Ala	Ile	Tyr	Tyr	Cys	Ala	Lys
225					230					235					240
His	Tyr	Tyr	Tyr	Gly	Gly	Ser	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly
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Thr	Ser	Val	Thr	Val	Ser	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro
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Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu
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Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp
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Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly
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Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg
				325					330					335	
Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro	Val	Gln
			340					345					350		
Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu
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Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
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Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
 385 390 395 400

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
 405 410 415

Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly
 420 425 430

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
 435 440 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
 450 455 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
 465 470 475 480

Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu
 485 490 495

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu
 500 505 510

Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala
 515 520 525

Arg Pro Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser
 530 535 540

Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser
 545 550 555 560

Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp
 565 570 575

Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser

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595	600	605
Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn Pro		
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Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly		
625	630	635
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln		
645	650	655
Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser		
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Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val		
675	680	685
Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro		
690	695	700
Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr		
705	710	715
Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser		
725	730	735
Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser Thr Tyr		
740	745	750
Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly Thr Thr Val		
755	760	765
Thr Val Ser Ala Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala		
770	775	780
Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg		
785	790	795
		800

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
805 810 815

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
820 825 830

Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu
835 840 845

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
850 855 860

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
865 870 875 880

Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
885 890 895

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
900 905 910

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
915 920 925

Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
930 935 940

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
945 950 955 960

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
965 970 975

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
980 985 990

Pro Pro Arg
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3004

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Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala
35 40 45

Ser Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp
50 55 60

Gly Thr Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly
65 70 75 80

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
85 90 95

Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln
100 105 110

Gln Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
115 120 125

Ile Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Glu Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser
145 150 155 160

Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp

175

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
370 375 380

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
 385 390 395 400

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
 405 410 415

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
 420 425 430

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
 435 440 445

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
 450 455 460

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
 465 470 475 480

His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser
 485 490 495

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
 500 505 510

Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala
 515 520 525

Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
 530 535 540

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Ile
 545 550 555 560

Val His Ser Val Gly Asn Thr Phe Leu Glu Trp Tyr Gln Gln Lys Pro
 565 570 575

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
 580 585 590

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

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Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys
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Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
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Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Glu	Phe	Ser
		675					680					685			
Arg	Ser	Trp	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu
		690				695					700				
Trp	Val	Gly	Arg	Ile	Tyr	Pro	Gly	Asp	Gly	Asp	Thr	Asn	Tyr	Ser	Gly
705					710					715					720
Lys	Phe	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr
				725					730					735	
Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr
			740					745					750		
Tyr	Cys	Ala	Arg	Asp	Gly	Ser	Ser	Trp	Asp	Trp	Tyr	Phe	Asp	Val	Trp
		755					760					765			
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Thr	Thr	Thr	Pro	Ala	Pro
		770					775					780			
Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu
785					790					795					800
Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg
				805					810				815		

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
820 825 830

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys
835 840 845

Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg
850 855 860

Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro
865 870 875 880

Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser
885 890 895

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
900 905 910

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
915 920 925

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
930 935 940

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
945 950 955 960

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
965 970 975

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
980 985 990

Leu His Met Gln Ala Leu Pro Pro Arg
995 1000

<210> 6
<211> 3016
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 6

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acagagtc	ac catcagtt	gc agggcaag	tc aggacatt	ag taaatatt	ta aatttggt	atc	180
agcagaaa	acc agatgga	act gttaaact	cc tgatctac	ca tacatca	aga ttacact	cag	240
gagtccca	tc aagggtc	agt ggagtg	gggt ctggaac	aga ttatttct	ctc accattag	ca	300
acctggag	ca agaagata	tt gccactt	act tttgcca	aca gggtaat	acg cttccgt	taca	360
cgttcgga	gg ggggacca	ag ctggagat	ca caggtggc	gg tggtcggg	c ggtgggtg	ggt	420
cgggtggc	gg cggatctg	ag gtgaaact	gc aggagtc	cagg acctgg	cctg gtggcg	ccct	480
cacagagc	ct gtccgtca	ca tgcactgt	ctc caggggt	ctc attaccc	gac tatggtg	taa	540
gctggatt	cg ccagcctc	ca cgaaagg	gtc tggagtg	gct gggagta	ata tggggtag	tg	600
aaaccaca	ta ctataatt	ca gctctcaa	at ccagact	gac catcatca	ag gacaact	cca	660
agagcca	agt tttctta	aaaa atgaac	agtc tgcaaact	ga tgacacag	cc atttact	act	720
gtgccaa	aca ttattact	ac ggtggtag	ct atgctat	gga ctactggg	gc caaggaac	cct	780
cagtcacc	gt ctctca	acc acgacgc	cag cgccgcg	acc accaac	cgc gcgccc	acca	840
tcgcgtcg	ca gcccctgt	cc ctgcgccc	ag aggcgtg	ccg gccagcgg	cg gggggcgc	cag	900
tgcacacg	ag ggggctgg	ac ttgcctgt	g atatctac	at ctgggcgc	ccc ttggccgg	ga	960
cttgtggg	gt ccttctc	ctg tcactgg	tta tcaccctt	ta ctgcaa	acgg ggcagaa	aga	1020
aactcctg	ta tatattc	aaa caaccatt	ta tgagacc	agt acaaact	act caagagga	ag	1080
atggctgt	tag ctgccgat	tt ccagaaga	ag aagaagg	agg atgtga	actg agagtga	agt	1140
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gctccctgtc cgcattccgtg ggcgacagag tgacaattac ctgtagaagc agccaaagca	1680
tcgtgcatag cgtcggcaac acttttctgg agtggtatca acagaagccc gggaaggccc	1740
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gcagcggctc cgggactgac ttcaccctga ccattagcag cctgcagcca gaggacttcg	1860
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tggagatcaa agggggggga ggaagcggcg gaggaggag cggaggcggg ggatccgaag	1980
tgcaactggc cgaatccgga ggggggctgg tccagcctgg agggtcctg agactgagct	2040
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gaaaagggtc ggaatgggtg ggcaggatct accctggcga cggcgatacc aactactccg	2160
gaaagttaa gggcaggttc actatcagcg ccgacactag caagaatacc gcctacctgc	2220
agatgaatag cctgagggcc gaggacaccg ccgtgtatta ctgcgctaga gacggcagca	2280
gctgggattg gtacttcgac gtgtggggcc agggcactct ggtgactgtg agcagcacca	2340
cgacgccagc gccgcgacca ccaacaccgg cgcccacat cgcgtcgcag cccctgtccc	2400
tgcgcccaga ggcgtgccgg ccagcggcgg ggggcgcagt gcacacgagg gggctggact	2460
tcgcctgtga tatctacatc tgggcgccct tggccgggac ttgtggggtc cttctcctgt	2520
cactggttat caccctttac tgcaaacggg gcagaaagaa actcctgtat atattcaaac	2580
aaccatttat gagaccagta caaactactc aagaggaaga tggctgtagc tgccgatttc	2640
cagaagaaga agaaggagga tgtgaactga gagtgaagtt cagcaggagc gcagacgccc	2700
ccgcgtacca gcagggccag aaccagctct ataacgagct caatctagga cgaagagagg	2760
agtacgatgt tttggacaag agacgtggcc gggaccctga gatgggggga aagccgagaa	2820
ggaagaacct tcaggaaggc ctgtacaatg aactgcagaa agataagatg gcggaggcct	2880
acagtgagat tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat ggcctttacc	2940
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ctcgctaagt ttaaac	3016

<210> 7

<211> 990
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 7

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 20 25 30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
 35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
 50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
 65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
 85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
 100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
 130 135 140

Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
 145 150 155 160

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
 165 170 175

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly

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

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
405 410 415

Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly
420 425 430

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
435 440 445

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
450 455 460

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
465 470 475 480

Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu
485 490 495

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu
500 505 510

Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala
515 520 525

Arg Pro Asp Val Gln Ile Thr Gln Ser Pro Ser Tyr Leu Ala Ala Ser
530 535 540

Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser
545 550 555 560

Lys Asp Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Leu
565 570 575

Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe
580 585 590

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
595 600 605

Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His Asn Lys Tyr

610		615		620
Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly				
625		630		635
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Gln Leu				
		645		650
				655
Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Ala Ser Val Lys Leu				
		660		665
				670
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Met Asn Trp				
		675		680
				685
Val Lys Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile Gly Arg Ile Asp				
		690		695
				700
Pro Tyr Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys Asp Lys Ala				
705		710		715
				720
Ile Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser				
		725		730
				735
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Asn				
		740		745
				750
Trp Asp Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Thr				
		755		760
				765
Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser				
		770		775
				780
Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly				
785		790		795
				800
Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp				
		805		810
				815
Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile				
		820		825
				830

Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
835 840 845

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
850 855 860

Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys
865 870 875 880

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
885 890 895

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
900 905 910

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg
915 920 925

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
930 935 940

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
945 950 955 960

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
965 970 975

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
980 985 990

<210> 8

<211> 2989

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 8

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acagagtcac catcagttgc agggcaagtc aggacattag taaatattta aattggtatc	180
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gagtcccatc aaggttcagt ggcagtgggt ctggaacaga ttattctctc accattagca	300
acctggagca agaagatatt gccacttact tttgccaaca gggtaatacg cttccgtaca	360
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gccggagggg caaggggcac gatggccttt accagggtct cagtacagcc accaaggaca	2940
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<210> 9
 <211> 1066
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 9

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

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

Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
 225 230 235 240

Gly Gly Gly Val Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
 245 250 255

Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
 260 265 270

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
 275 280 285

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
 290 295 300

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
 305 310 315 320

Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His
 325 330 335

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
 340 345 350

His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
 355 360 365

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
 370 375 380

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
 385 390 395 400

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
 405 410 415

Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn
 420 425 430

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg

435		440		445
Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro	450	455	460	
Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala	465	470	475	480
Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His	485	490	495	
Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp	500	505	510	
Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn	515	520	525	
Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro	530	535	540	
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu	545	550	555	560
His Ala Ala Arg Pro Asp Val Gln Ile Thr Gln Ser Pro Ser Tyr Leu	565	570	575	
Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys	580	585	590	
Ser Ile Ser Lys Asp Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr	595	600	605	
Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro	610	615	620	
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile	625	630	635	640
Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His	645	650	655	

Asn Lys Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
660 665 670

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
675 680 685

Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Ala Ser
690 695 700

Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp
705 710 715 720

Met Asn Trp Val Lys Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile Gly
725 730 735

Arg Ile Asp Pro Tyr Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys
740 745 750

Asp Lys Ala Ile Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
755 760 765

Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
770 775 780

Arg Gly Asn Trp Asp Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
785 790 795 800

Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
805 810 815

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
820 825 830

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
835 840 845

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
850 855 860

Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His

865		870		875		880									
Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys
			885						890					895	
His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser
		900						905					910		
Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met
		915					920					925			
Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe
	930					935					940				
Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg
945					950					955					960
Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Lys	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn
			965						970					975	
Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg
		980						985					990		
Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro
	995						1000					1005			
Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	
	1010					1015					1020				
Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	
	1025					1030					1035				
Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	
	1040					1045					1050				
Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg			
	1055					1060					1065				

<210> 10
 <211> 3217
 <212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 10

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agaaggtgac catcacctgc agcgccagca gcagcatcag ctacatgcac tggttccagc	180
agaagcccgg caccagcccc aagctgtgga tctacaccac cagcaacctg gccagcggcg	240
tgcccgccag attcagcggc agcggcagcg gcaccagcta cagcctgacc atcagcagaa	300
tggaggccga ggacgccgc acctactact gccaccagag aagcacctac cccctgacct	360
tcggcagcgg caccaagctg gagctgaagg gagggggggg atccggggga ggaggctccg	420
gcggaggcgg aagccagggtg cagctgcagc agagcggcgc cgagctggcc aagcccggcg	480
ccagcgtgaa gatgagctgc aaggccagcg gctacacctt caccagctac agaatgcact	540
gggtgaagca gagaccggc cagggcctgg agtggatcgg ctacatcaac cccagcaccg	600
gctacaccga gtacaaccag aagttcaagg acaaggccac cctgaccgcc gacaagagca	660
gcagcaccgc ctacatgcag ctgagcagcc tgaccttcga ggacagcgcc gtgtactact	720
gcgccagagg cggcggcgtg ttcgactact ggggccaggg caccaccctg accgtgagca	780
gcaccacgac gccagcgccg cgaccaccaa caccggcgcc caccatcgcg tcgcagcccc	840
tgtccctgcg cccagaggcg tgccggccag cggcgggggg cgcagtgac acgagggggc	900
tggacttcgc ctgtgatatc tacatctggg cgcccttggc cgggacttgt ggggtccttc	960
tcctgtcact ggttatcacc ctttactgca ggagtaagag gagcaggctc ctgcacagt	1020
actacatgaa catgactccc cgccgccccg ggcccacccg caagcattac cagccctatg	1080
ccccaccacg cgacttcgca gcctatcgct ccaaacgggg cagaaagaaa ctctgtata	1140
tattcaaaca accatttatg agaccagtac aaactactca agaggaagat ggctgtagct	1200
gccgatttcc agaagaagaa gaaggaggat gtgaactgag agtgaagttc agcaggagcg	1260
cagacgcccc cgcgtacaag cagggccaga accagctcta taacgagctc aatctaggac	1320
gaagagagga gtacgatgtt ttggacaaga gacgtggccg ggaccctgag atggggggaa	1380
agccgagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa gataagatgg	1440

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gcctttacca ggggtctcagt acagccacca aggacaccta cgacgccctt cacatgcagg	1560
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tggaggagaa ccctggacct atggccttac cagtgaccgc cttgctcctg ccgctggcct	1680
tgctgctcca cgccgccagg ccggacgtgc agatcaccca gagccccagc tacctggccg	1740
ccagccccgg cgagaccatc accatcaact gcagagccag caagagcatc agcaaggacc	1800
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tgaccatcag cagcctggag cccgaggact tcgccatgta ctactgccag cagcacaaca	1980
agtacccta caccttcggc ggcggcacca agctggagat caaggaggagg gggggatccg	2040
ggggaggagg ctccggcgga ggcggaagcc aggtgcagct gcagcagccc ggcgccgagc	2100
tggtagagacc cggcgccagc gtgaagctga gctgcaaggc cagcggctac accttcacca	2160
gctactggat gaactgggtg aagcagagac ccgaccaggg cctggagtgg atcggcagaa	2220
tcgacctta cgacagcgag acccactaca accagaagtt caaggacaag gccatcctga	2280
ccgtggacaa gagcagcagc accgcctaca tgcagctgag cagcctgacc agcgaggaca	2340
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tgaccgtgag cagcaccacg acgccagcgc cgcgaccacc aacaccggcg cccaccatcg	2460
cgtcgcagcc cctgtccctg cgcccagagg cgtgccggcc agcggcgggg ggcgcagtgc	2520
acacgagggg gctggacttc gcctgtgata tctacatctg ggcgcccttg gccgggactt	2580
gtggggtcct tctcctgtca ctggttatca ccctttactg caggagtaag aggagcaggc	2640
tcctgcacag tgactacatg aacatgactc cccgccgccc cggggcccacc cgcaagcatt	2700
accagcccta tgccccacca cgcgacttcg cagcctatcg ctccaaacgg ggcagaaaga	2760
aactcctgta tatattcaaa caaccattta tgagaccagt acaaactact caagaggaag	2820
atggctgtag ctgccgattt ccagaagaag aagaaggagg atgtgaactg agagtgaagt	2880
tcagcaggag cgcagacgcc cccgcgtaca agcagggccca gaaccagctc tataacgagc	2940
tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc cgggaccctg	3000
agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat gaactgcaga	3060

aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc cggaggggca 3120
 aggggcacga tggcctttac caggggtctca gtacagccac caaggacacc tacgacgccc 3180
 ttcacatgca ggccctgccc cctcgctaag tttaaac 3217

<210> 11
 <211> 985
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 11

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 Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met
 20 25 30

Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser
 35 40 45

Ser Ile Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro
 50 55 60

Lys Leu Trp Ile Tyr Thr Thr Ser Asn Leu Ala Ser Gly Val Pro Ala
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
 85 90 95

Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser
 100 105 110

Thr Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys Gly
 115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
 130 135 140

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

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

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
 370 375 380

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
 385 390 395 400

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
 405 410 415

Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
 420 425 430

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
 435 440 445

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
 450 455 460

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
 465 470 475 480

Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
 485 490 495

Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu
 500 505 510

Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asp Val Gln
 515 520 525

Ile Thr Gln Ser Pro Ser Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile
 530 535 540

Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Asp Leu Ala Trp
 545 550 555 560

Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly
 565 570 575

Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser

580	585	590
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe		
595	600	605
Ala Met Tyr Tyr Cys Gln Gln His Asn Lys Tyr Pro Tyr Thr Phe Gly		
610	615	620
Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly		
625	630	635
Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Pro Gly Ala		
645	650	655
Glu Leu Val Arg Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser		
660	665	670
Gly Tyr Thr Phe Thr Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro		
675	680	685
Asp Gln Gly Leu Glu Trp Ile Gly Arg Ile Asp Pro Tyr Asp Ser Glu		
690	695	700
Thr His Tyr Asn Gln Lys Phe Lys Asp Lys Ala Ile Leu Thr Val Asp		
705	710	715
Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu		
725	730	735
Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Asn Trp Asp Asp Tyr Trp		
740	745	750
Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Thr Thr Thr Pro Ala Pro		
755	760	765
Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu		
770	775	780
Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg		
785	790	795
		800

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
805 810 815

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg
820 825 830

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
835 840 845

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
850 855 860

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala
865 870 875 880

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu
885 890 895

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
900 905 910

Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln
915 920 925

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
930 935 940

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
945 950 955 960

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
965 970 975

Leu His Met Gln Ala Leu Pro Pro Arg
980 985

<210> 12
<211> 2974
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 12

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ccgccagg	cc gcagatcg	tg ctgacccag	a gccccgcc	at catgagcg	cc agccccgg	c	120
agaaggtg	ac catcacct	gc agcgccag	ca gcagcatc	ag ctacatgc	ac tggttccag	c	180
agaagccc	gg caccagccc	aa aagctgtg	ga tctacacc	ac cagcaacct	g gccagcg	g	240
tgcccgcc	ag attcagcg	gc agcggcag	cg gcaccagc	ta cagcctga	cc atcagcag	aa	300
tggaggcc	ga ggacgccg	cc acctacta	ct gccaccag	ag aagcacct	ac cccctga	cc	360
tcggcagc	gg caccaagc	tg gagctga	agg gagggggg	gg atccgggg	ga ggaggctc	cg	420
gcggaggc	gg aagccagg	tg cagctgc	agc agagcgg	cgc cgagctg	gcc aagccc	gg	480
ccagcgtg	aa gatgagc	tgc aaggcc	ag cg gctacac	ctt caccagc	ta agaatgc	act	540
gggtgaag	ca gagacccg	gc cagggc	cttg agtggat	cgg ctacatc	aa cccagc	acc	600
gctacacc	ga gtacaacc	ag aagttca	agg acaagg	cc cctgacc	gcc gacaag	ag	660
gcagcacc	gc ctacatgc	ag ctgagc	agcc tgacct	tcga ggacag	cgc gtgtact	act	720
gcgccag	agg cggcggc	gtg ttcgact	act ggggcc	agg caccacc	ctg accgtg	ag	780
gcaccacg	ac gccagcg	ccg cgaccac	caa caccgg	cgc caccat	cgc tgcagc	ccc	840
tgtccctg	cgc cccagag	gcg tgccgg	ccag cggcgg	ggg cgagtg	cac acgagg	ggg	900
tggacttc	gc ctgtgata	tc tacatct	ggg cgccct	tggc cgggac	ttgt ggggtc	cttc	960
tcctgtca	ct ggttatc	acc ctttact	gca aacggg	gcag aaagaa	actc ctgtata	tat	1020
tcaaaca	acc atttatg	aga ccagtaca	aaa ctactca	aga ggaagat	ggc tgtagct	gcc	1080
gatttcca	ga agaaga	aa ggaggat	gtg aactgag	agt gaagtt	cagc aggagc	gc	1140
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cgcagaga	ag gaagaacc	ct caggaagg	cc tgtaca	atga actgc	agaaa gataag	at	1320
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gcctttac	ca gggctc	agt acagcc	acca aggaca	cta cgacgc	ctt cacatg	cagg	1440
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acatgcaggc cctgccccct cgctaagttt aaac	2974

<210> 13
 <211> 546
 <212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 13

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
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His Ala Ala Arg Pro Ser Asp Ile Val Leu Thr Gln Ser Pro Ala Ser
20 25 30

Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser
35 40 45

Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln
50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu
65 70 75 80

Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr
100 105 110

Tyr Cys Gln His Ser Arg Glu Leu Pro Phe Thr Phe Gly Ser Gly Thr
115 120 125

Lys Leu Glu Ile Lys Lys Ile Ser Gly Gly Gly Gly Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
165 170 175

Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg
180 185 190

Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
195 200 205

Ile Gly Glu Ile Asn Pro Thr Ser Ser Thr Ile Asn Phe Thr Pro Ser
210 215 220

Leu Lys Asp Lys Val Phe Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu
225 230 235 240

Tyr Leu Gln Met Ser Lys Val Arg Ser Glu Asp Thr Ala Leu Tyr Tyr
245 250 255

Cys Ala Arg Gly Asn Tyr Tyr Arg Tyr Gly Asp Ala Met Asp Tyr Trp
260 265 270

Gly Gln Gly Thr Ser Val Thr Val Ser Thr Thr Thr Pro Ala Pro Arg
275 280 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
290 295 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305 310 315 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
325 330 335

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser
340 345 350

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
355 360 365

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
370 375 380

Asp Phe Ala Ala Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr
385 390 395 400

Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu

405

410

415

Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu
 420 425 430

Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
 435 440 445

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
 450 455 460

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
 465 470 475 480

Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
 485 490 495

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
 500 505 510

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
 515 520 525

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
 530 535 540

Pro Arg
 545

<210> 14
 <211> 1657
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 14
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 ccgccaggcc gagcgacatc gtgctgaccc agagccccgc cagcctggcc gtgagcctgg 120
 gccagagagc caccatcagc tgcagagcca gcaagagcgt gagcaccagc ggctacagct 180

acctgcactg gtaccagcag aagccccggcc agccccccaa gctgctgatac tacctggcca	240
gcaacctgga gagcggcgtg cccgccagat tcagcggcag cggcagcggc accgacttca	300
ccctgaacat ccacccccgtg gaggaggagg acgccgccac ctactactgc cagcacagca	360
gagagctgcc cttcaccttc ggacgcggca ccaagctgga gatcaagaag atcagcggcg	420
gcggcggcag cggcggcggc ggacgcggcg gcggcggcag cggcggcggc ggacgcggcg	480
gcggcggcag ccaggtgcag ctggtggaga gcggcggcgg cctggtgcag cccggcggca	540
gcctgaagct gagctgcgcc gccacggcgt tcgacttcag cagatactgg atgagctggg	600
tgagacaggc ccccggcaag ggcttgaggt ggatcggcga gatcaacccc accagcagca	660
ccatcaactt cacccccagc ctgaaggaca aggtgttcat cagcagagac aacgccaaga	720
acaccctgta cctgcagatg agcaaggtga gaagcgagga caccgccctg tactactgcg	780
ccagaggcaa ctactacaga tacggcgacg ccatggacta ctggggccag ggcaccagcg	840
tgaccgtgag caccacgacg ccagcgccgc gaccaccaac accggcgccc accatcgct	900
cgagccccct gtccctgcgc ccagaggcgt gccggccagc ggccggggggc gcagtgcaca	960
cgagggggct ggacttcgcc tgtgatatct acatctgggc gcccttggcc gggacttgtg	1020
gggtccttct cctgtcactg gttatcacc tttactgcag gagtaagagg agcaggctcc	1080
tgcacagtga ctacatgaac atgactcccc gccgccccgg gccacccgc aagcattacc	1140
agccctatgc cccaccacgc gacttcgcag cctatcgctc caaacggggc agaaagaaac	1200
tcctgtatat attcaaaca ccatttatga gaccagtaca aactactcaa gaggaagatg	1260
gctgtagctg ccgatttcca gaagaagaag aaggaggatg tgaactgaga gtgaagttca	1320
gcaggagcgc agacgcccc gcgtaccagc agggccagaa ccagctctat aacgagctca	1380
atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg gaccctgaga	1440
tggggggaaa gccgcagaga aggaagaacc ctcaggaagg cctgtacaat gaactgcaga	1500
aagataagat ggcgagggcc tacagtgaga ttgggatgaa aggcgagcgc cggaggggca	1560
aggggcacga tggcctttac cagggctctca gtacagccac caaggacacc tacgacgcc	1620
ttcacatgca ggccctgccc cctcgctaag tttaaac	1657

<210> 15
 <211> 490
 <212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 15

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 Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu
20 25 30

Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys
35 40 45

Ser Val Ser Thr Ser Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu
65 70 75 80

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr
100 105 110

Cys Gln His Ser Arg Glu Leu Pro Phe Thr Phe Gly Ser Gly Thr Lys
115 120 125

Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
145 150 155 160

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe
165 170 175

Ser Arg Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
180 185 190

Glu Trp Ile Gly Glu Ile Asn Pro Thr Ser Ser Thr Ile Asn Phe Thr
195 200 205

Pro Ser Leu Lys Asp Lys Val Phe Ile Ser Arg Asp Asn Ala Lys Asn
210 215 220

Thr Leu Tyr Leu Gln Met Ser Lys Val Arg Ser Glu Asp Thr Ala Leu
225 230 235 240

Tyr Tyr Cys Ala Arg Gly Asn Tyr Tyr Arg Tyr Gly Asp Ala Met Asp
245 250 255

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Thr Thr Thr Pro Ala
260 265 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
275 280 285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
325 330 335

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
340 345 350

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
355 360 365

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
370 375 380

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
385 390 395 400

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg

405

410

415

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro
 420 425 430

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
 435 440 445

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
 450 455 460

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
 465 470 475 480

Ala Leu His Met Gln Ala Leu Pro Pro Arg
 485 490

<210> 16
 <211> 1489
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 16
 gcgatcgcat ggccttacca gtgaccgcct tgctcctgcc gctggccttg ctgctccacg 60
 ccgccaggcc ggacatcgtg ctgaccaga gccccgccag cctggccgtg agcctgggcc 120
 agagggccac catcagctgc agggccagca agagcgtgag caccagcggc tacagctacc 180
 tgactggta ccagcagaag cccggccagc cccccaagct gctgatctac ctggccagca 240
 acctggagag cggcgtgccc gccaggttca gcggcagcgg cagcggcacc gacttcaccc 300
 tgaacatcca ccccgaggag gaggaggacg ccgccaccta ctactgccag cacagcaggg 360
 agctgccctt caccttcggc agcggcacca agctggagat caagggaggg gggggatccg 420
 ggggaggagg ctccggcgga ggcggaagcc aggtgcagct ggtggagagc ggcggcggcc 480
 tgggtgcagcc cggcggcagc ctgaagctga gctgcgccgc cagcggcttc gacttcagca 540
 ggtactggat gagctgggtg aggcaggccc ccggcaaggg cctggagtgg atcggcgaga 600
 tcaacccac cagcagcacc atcaacttca ccccgagcct gaaggacaag gtgttcatca 660

gcagggacaa cgccaagaac accctgtacc tgcagatgag caaggtgagg agcgaggaca 720
ccgccctgta ctactgcgcc aggggcaact actacaggta cggcgacgcc atggactact 780
ggggccaggg caccagcgtg accgtgagca ccacgacgcc agcgccgcga ccaccaacac 840
cggcgccac catcgcgtcg cagcccctgt ccctgcgccc agaggcgtgc cggccagcgg 900
cggggggcgc agtgcacacg agggggctgg acttcgcctg tgatatctac atctgggcgc 960
ccttggccgg gacttgtggg gtccttctcc tgtcactggt taccacctt tactgcagga 1020
gtaagaggag caggctcctg cacagtgact acatgaacat gactccccgc cgccccgggc 1080
ccaccgcaa gcattaccag ccctatgccc caccacgcga cttcgcagcc tatcgtcca 1140
gagtgaagtt cagcaggagc gcagacgccc ccgcgtacca gcagggccag aaccagctct 1200
ataacgagct caatctagga cgaagagagg agtacgatgt tttggacaag agacgtggcc 1260
gggaccctga gatgggggga aagccgcaga gaaggaagaa ccctcaggaa ggcctgtaca 1320
atgaactgca gaaagataag atggcggagg cctacagtga gattgggatg aaagcgagc 1380
gccggagggg caaggggcac gatggccttt accagggtct cagtacagcc accaaggaca 1440
cctacgacgc cttcacatg caggccctgc cccctcgcta agtttaaac 1489

<210> 17
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 17

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 Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu
20 25 30

Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys
35 40 45

Ser Val Ser Thr Ser Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu
65 70 75 80

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr
100 105 110

Cys Gln His Ser Arg Glu Leu Pro Phe Thr Phe Gly Ser Gly Thr Lys
115 120 125

Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
145 150 155 160

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe
165 170 175

Ser Arg Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
180 185 190

Glu Trp Ile Gly Glu Ile Asn Pro Thr Ser Ser Thr Ile Asn Phe Thr
195 200 205

Pro Ser Leu Lys Asp Lys Val Phe Ile Ser Arg Asp Asn Ala Lys Asn
210 215 220

Thr Leu Tyr Leu Gln Met Ser Lys Val Arg Ser Glu Asp Thr Ala Leu
225 230 235 240

Tyr Tyr Cys Ala Arg Gly Asn Tyr Tyr Arg Tyr Gly Asp Ala Met Asp
245 250 255

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Thr Thr Thr Pro Ala
260 265 270

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser

275

280

285

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
 290 295 300

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
 305 310 315 320

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
 325 330 335

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
 340 345 350

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
 355 360 365

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
 370 375 380

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
 385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
 405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn
 420 425 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
 435 440 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
 450 455 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
 465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 485 490

<210> 18
 <211> 1492
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 18
 gcgatcgcac ggccttacca gtgaccgcct tgctcctgcc gctggccttg ctgctccacg 60
 ccgccaggcc ggacatcgtg ctgaccaga gccccgccag cctggccgtg agcctgggcc 120
 agagggccac catcagctgc agggccagca agagcgtgag caccagcggc tacagctacc 180
 tgactggta ccagcagaag cccggccagc cccccaagct gctgatctac ctggccagca 240
 acctggagag cggcgtgccc gccagggttca gcggcagcgg cagcggcacc gacttcaccc 300
 tgaacatcca ccccgaggag gaggaggacg ccgccaccta ctactgccag cacagcaggg 360
 agctgccctt caccttcggc agcggcacca agctggagat caaggaggagg gggggatccg 420
 ggggaggagg ctccggcggg ggcggaagcc aggtgcagct ggtggagagc ggcggcggcc 480
 tgggtgcagcc cggcggcagc ctgaagctga gctgcgccgc cagcggcttc gacttcagca 540
 ggtactggat gagctgggtg aggcaggccc ccggcaaggg cctggagtgg atcggcgaga 600
 tcaacccac cagcagcacc atcaacttca ccccgagcct gaaggacaag gtgttcatca 660
 gcagggacaa cgccaagaac accctgtacc tgcagatgag caaggtagagg agcaggagaca 720
 ccgccctgta ctactgcgcc agggggaact actacaggta cggcgacgcc atggactact 780
 ggggcccaggg caccagcgtg accgtgagca ccacgacgcc agcggcgga ccaccaacac 840
 cggcgccac catcgcgtcg cagcccctgt ccctgcgccc agaggcgtgc cggccagcgg 900
 cggggggcgc agtgcacacg agggggctgg acttcgcctg tgatatctac atctgggcgc 960
 ccttggccgg gacttgtggg gtccttctcc tgtcactggt tatcaccctt tactgcaaac 1020
 ggggcagaaa gaaactcctg tatatatcca aacaaccatt tatgagacca gtacaaacta 1080
 ctcaagagga agatggctgt agctgccgat ttccagaaga agaagaagga ggatgtgaac 1140
 tgagagtga gttcagcagg agcgcagacg ccccgcgta ccagcagggc cagaaccagc 1200
 tctataacga gctcaatcta ggacgaagag aggagtacga tgttttgac aagagacgtg 1260
 gccgggaccc tgagatgggg ggaaagccgc agagaaggaa gaaccctcag gaagcctgt 1320

acaatgaact gcagaaagat aagatggcgg aggcctacag tgagattggg atgaaaggcg 1380
agcgccggag gggcaagggg cacgatggcc tttaccaggg tctcagtaca gccaccaagg 1440
acacctacga cgcccttcac atgcaggccc tgccccctcg ctaagtttaa ac 1492

<210> 19
<211> 997
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 19

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 Asp Val Val Met Thr Gln Ser His Arg Phe Met
20 25 30

Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Gln
35 40 45

Asp Val Asn Thr Ala Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser
50 55 60

Pro Lys Leu Leu Ile Phe Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro
65 70 75 80

Asp Arg Phe Thr Gly Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr Ile
85 90 95

Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His
100 105 110

Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
130 135 140

Ile Gln Leu Val Gln Ser Gly Pro Asp Leu Lys Lys Pro Gly Glu Thr

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

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg
370 375 380

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
385 390 395 400

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
405 410 415

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn
420 425 430

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
435 440 445

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
450 455 460

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
465 470 475 480

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr
485 490 495

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
500 505 510

Pro Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
515 520 525

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
530 535 540

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln
545 550 555 560

Asp Val Gly Ile Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val
565 570 575

Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro

580	585	590
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile		
595	600	605
Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr		
610	615	620
Ser Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys		
625	630	635
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu		
645	650	655
Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser		
660	665	670
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr Trp		
675	680	685
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly		
690	695	700
Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys		
705	710	715
Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu		
725	730	735
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala		
740	745	750
Arg Pro Asp Gly Asn Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr		
755	760	765
Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr		
770	775	780
Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala		
785	790	795
		800

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
805 810 815

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
820 825 830

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser
835 840 845

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
850 855 860

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
865 870 875 880

Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
885 890 895

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
900 905 910

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
915 920 925

Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
930 935 940

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
945 950 955 960

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
965 970 975

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
980 985 990

Ala Leu Pro Pro Arg
995

<210> 20

<211> 2994
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 20
 atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
 ccggatgtgg tgatgaccca gagccatcgc tttatgagca ccagcgtggg cgatcgcgtg 120
 agcattacct gccgcgcgag ccaggatgtg aacaccgcgg tgagctggta tcagcagaaa 180
 ccggggcaga gcccgaact gctgattttt agcgcgagct atcgctatac cggcgtgccg 240
 gatcgcttta ccggcagcgg cagcggcgcg gattttaccc tgaccattag cagcgtgcag 300
 gcggaagatc tggcgggtga ttattgccag cagcattata gcaccccggtg gacctttggc 360
 ggcggcacca aactggaaat taaaggaggg gggggatccg ggggaggagg ctccggcgga 420
 ggcggaagcc agattcagct ggtgcagagc ggcccggatc tgaaaaaacc gggcgaaacc 480
 gtgaaactga gctgcaaagc gagcggctat acctttacca actttggcat gaactgggtg 540
 aaacaggcgc cgggcaaagg ctttaaattg atggcgtgga ttaacaccac ccgctatacc 600
 ggcgaaagct attttgcgga tgattttaaa ggccgctttg cgtttagcgt ggaaaccagc 660
 gcgaccaccg cgtatctgca gattaacaac ctgaaaaccg aagataccgc gacctatfff 720
 tgcgcgcgcg gcgaaattta ttatggctat gatggcggct ttgcgtattg gggccagggc 780
 accctgggtga ccgtgagcgc gaccacgacg ccagcgccgc gaccaccaac accggcgccc 840
 accatcgcgt cgagcccct gtccctgcgc ccagaggcgt gccggccagc ggcggggggc 900
 gcagtgcaca cgagggggct ggacttcgcc tgtgatattt acatctgggc gcccttggcc 960
 gggactttgtg gggtccttct cctgtcactg gttatcacc cttactgcaa acggggcaga 1020
 aagaaactcc tgtatatatt caaacaacca tttatgagac cagtacaaac tactcaagag 1080
 gaagatggct gtagctgccg atttccagaa gaagaagaag gaggatgtga actgagagtg 1140
 aagttcagca ggagcgcaga cgccccgcg taccagcagg gccagaacca gctctataac 1200
 gagctcaatc taggacgaag agaggagtac gatgttttgg acaagagacg tggccgggac 1260
 cctgagatgg ggggaaagcc gcagagaagg aagaaccctc aggaaggcct gtacaatgaa 1320
 ctgcagaaaag ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg 1380

aggggcaagg ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac	1440
gacgcccttc acatgcaggc cctgccccct cgcggaagcg gagccaccaa cttcagcctg	1500
ctgaagcagg ccggcgacgt ggaggagaac cccggccccg ccttaccagt gaccgccttg	1560
ctcctgccgc tggccttgct gctccacgcc gccaggccgg atattcagat gaccagagc	1620
ccgagcagcc tgagcgcgag cgtgggcgat cgcgtgacca ttacctgcaa agcgagccag	1680
gatgtgggca ttgcggtggc gtggtatcag cagaaaccgg gcaaagtgcc gaaactgctg	1740
atttattggg cgagcacccg ccataccggc gtgccggatc gctttagcgg cagcggcagc	1800
ggcaccgatt ttaccctgac cattagcagc ctgcagccgg aagatgtggc gacctattat	1860
tgccagcagt atagcagcta tccgtatacc tttggccagg gcaccaaagt ggaaattaaa	1920
ggaggggggg gatccggggg aggaggctcc ggcggaggcg gaagcgaagt gcagctggtg	1980
gaaagcggcg gcggcctggt gcagccgggc ggcagcctgc gcctgagctg cgcggcgagc	2040
ggctttgatt ttagccgcta ttggatgagc tgggtgcgcc aggcgccggg caaaggcctg	2100
gaatggattg gcgaaattaa cccggatagc agcaccatta actatgcgcc gagcctgaaa	2160
gataaattta ttattagccg cgataacgcg aaaaacagcc tgtatctgca gatgaacagc	2220
ctgcgcgcgg aagataccgc ggtgtattat tgcgcgcgcc cgcatggcaa ctattggtat	2280
tttgatgtgt ggggccaggg caccctggtg accgtgagca gcaccacgac gccagcgccg	2340
cgaccaccaa caccggcgcc caccatcgcg tcgcagcccc tgtccctgcg cccagaggcg	2400
tgccggccag cggcgggggg cgcagtgcac acgagggggc tggacttcgc ctgtgatatc	2460
tacatctggg cgcccttggc cgggacttgt ggggtccttc tcctgtcact ggttatcacc	2520
ctttactgca ggagtaagag gagcaggctc ctgcacagtg actacatgaa catgactccc	2580
cgccgccccg ggcccacccg caagcattac cagccctatg ccccaccag cgacttcgca	2640
gcctatcgct ccagagtga gttcagcagg agcgcagacg ccccgcgta ccagcagggc	2700
cagaaccagc tctataacga gctcaatcta ggacgaagag aggagtacga tgttttggac	2760
aagagacgtg gccgggaccc tgagatgggg ggaaagccgc agagaaggaa gaaccctcag	2820
gaaggcctgt acaatgaact gcagaaagat aagatggcgg aggcctacag tgagattggg	2880
atgaaaggcg agcgccggag gggcaagggg cacgatggcc tttaccaggg tctcagtaca	2940
gccaccaagg acacctacga cgcccttcac atgcaggccc tgccccctcg ctaa	2994

<210> 21
 <211> 997
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 21

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 Asp Val Val Met Thr Gln Ser His Arg Phe Met
 20 25 30

Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Gln
 35 40 45

Asp Val Asn Thr Ala Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser
 50 55 60

Pro Lys Leu Leu Ile Phe Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro
 65 70 75 80

Asp Arg Phe Thr Gly Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr Ile
 85 90 95

Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His
 100 105 110

Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Asp Ile Lys
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
 130 135 140

Ile Gln Leu Val Gln Ser Gly Pro Asp Leu Lys Lys Pro Gly Glu Thr
 145 150 155 160

Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Phe Gly
 165 170 175

Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Phe Lys Trp Met Ala
180 185 190

Trp Ile Asn Thr Tyr Thr Gly Glu Ser Tyr Phe Ala Asp Asp Phe Lys
195 200 205

Gly Arg Phe Ala Phe Ser Val Glu Thr Ser Ala Thr Thr Ala Tyr Leu
210 215 220

Gln Ile Asn Asn Leu Lys Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala
225 230 235 240

Arg Gly Glu Ile Tyr Tyr Gly Tyr Asp Gly Gly Phe Ala Tyr Trp Gly
245 250 255

Gln Gly Thr Leu Val Thr Val Ser Ala Thr Thr Thr Pro Ala Pro Arg
260 265 270

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
275 280 285

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
290 295 300

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
305 310 315 320

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg
325 330 335

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
340 345 350

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
355 360 365

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
370 375 380

Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu

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

Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser
610 615 620

Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly
625 630 635 640

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
645 650 655

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
660 665 670

Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr Trp Met
675 680 685

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu
690 695 700

Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp
705 710 715 720

Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
725 730 735

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
740 745 750

Pro Asp Gly Asn Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu
755 760 765

Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
770 775 780

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
785 790 795 800

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
805 810 815

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu

820	825	830
Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys		
835	840	845
Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr		
850	855	860
Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly		
865	870	880
Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala		
885	890	895
Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg		
900	905	910
Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu		
915	920	925
Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr		
930	935	940
Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly		
945	950	955
Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln		
965	970	975
Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln		
980	985	990
Ala Leu Pro Pro Arg		
995		

<210> 22
 <211> 3009
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 22

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cgccaggccg	gatgtggtga	tgaccagag	ccatcgcttt	atgagcacca	gcgtgggaga	120
tcgagtgagc	attacctgcc	gcgcgagcca	ggatgtgaac	accgcggtga	gctggtatca	180
gcagaaaccg	ggccagagcc	cgaaactgct	gatttttagc	gcgagctatc	gctataaccgg	240
cgtgccggat	cgctttaccg	gcagcggcag	cggcgcggat	tttacctga	ccattagcag	300
cgtgcaggcg	gaagatctgg	cggtgtatta	ttgccagcag	cattatagca	ccccgtggac	360
ctttggcggc	ggcaccaa	ac tggatattaa	aggagggggg	ggatccgggg	gaggaggctc	420
cggcggaggc	ggaagccaga	ttcagctggt	gcagagcggc	ccggatctga	aaaaaccggg	480
cgaaaccgtg	aaactgagct	gcaaagcgag	cggctatacc	tttaccaact	ttggcatgaa	540
ctgggtgaaa	caggcgccgg	gcaaaggctt	taaatggatg	gcgtggatta	acacctatac	600
cggcgaaaagc	tattttgcgg	atgattttta	aggccgcttt	gcgttttagcg	tggaaaccag	660
cgcgaccacc	gcgtatctgc	agattaacaa	cctgaaaacc	gaagataccg	cgacctat	720
ttgcgcgcgc	ggcgaaat	ttt attatggcta	tgatggcggc	tttgcgtatt	ggggccaggg	780
caccttggtg	accgtgagcg	cgaccacgac	gccagcgccg	cgaccaccaa	caccggcgcc	840
caccatcgcg	tcgcagcccc	tgtccctgcg	cccagaggcg	tgccggccag	cggcgggggg	900
cgcagtgcac	acgagggggc	tggacttcgc	ctgtgatatc	tacatctggg	cgcccttggc	960
cgggacttgt	ggggtccttc	tcctgtcact	ggttatcacc	ctttactgca	aacggggcag	1020
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ggaagatggc	tgtagctgcc	gattttccaga	agaagaagaa	ggaggatgtg	aactgagagt	1140
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cgagctcaat	ctaggacgaa	gagaggagta	cgatgttttg	gacaagagac	gtggccggga	1260
ccctgagatg	gggggaaagc	cgcagagaag	gaagaaccct	caggaaggcc	tgtacaatga	1320
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cgacgccctt	cacatgcagg	ccctgcccc	tcgcggaagc	ggagccacca	acttcagcct	1500
gctgaagcag	gccggcgacg	tggaggagaa	ccccggcccc	atggccttac	cagtgaccgc	1560

cttgctcctg ccgctggcct tgctgctcca cgccgccagg ccgatatattc agatgaccca	1620
gagcccgagc agcctgagcg cgagcgtggg cgaccgcgtg accattacct gcaaagcgag	1680
ccaggatgtg ggcatcgcgg tggcgtggta tcagcagaaa ccgggcaaag tgccgaaact	1740
gctgatttat tgggcgagca cccgccatac cggcgtgccg gatcgcttta gcggcagcgg	1800
cagcggcacc gattttaccc tgaccattag cagcctgcag ccggaagatg tggcgacct	1860
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taaaggaggg gggggatccg ggggaggagg ctccggcgga ggcggaagcg aagtgcagct	1980
ggtggaaagc ggcggcggcc tggcgcagcc gggcggcagc ctgcgcctga gctgcgcggc	2040
gagcggcctt gattttagcc gctattggat gagctgggtg cgccaggcgc cgggcaaagg	2100
cctggaatgg attggcgaaa ttaaccgga tagcagcacc attaactatg cgccgagcct	2160
gaaagataaa tttattatta gccgcgataa cgcgaaaaac agcctgtatc tgcagatgaa	2220
cagcctgcgc gcggaagata ccgcggtgta ttattgcgcg cgcccggatg gcaactattg	2280
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gagaccagta caaactactc aagaggaaga tggctgtagc tgccgatttc cagaagaaga	2640
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ccctcaggaa ggcctgtaca atgaactgca gaaagataag atggcgagg cctacagtga	2880
gattgggatg aaaggcgagc gccggagggg caaggggcac gatggccttt accagggtct	2940
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agtttaaac	3009

<210> 23
 <211> 423
 <212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 23

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agctagctgc agtaacgcca ttttgcaagg catggaaaaa taccaaacca agaatagaga      60
agttcagatc aagggcgggt acatgaaaat agctaacgtt gggccaaaca ggatatctgc      120
ggtgagcagt ttcggccccc gcccgggggc aagaacagat ggtcaccgca gtttcggccc      180
cggcccagg ccaagaacag atggtcccca gatatggccc aaccctcagc agtttcttaa      240
gacccatcag atgtttccag gtcccccaa ggacctgaaa tgaccctgcg ctttatttga      300
attaaccaat cagcctgctt ctcgcttctg ttcgcgcgct tctgcttccc gagctctata      360
aaagagctca caaccctca ctcggcgcgc cagtcctccg acagactgag tcgcccgggt      420
acc                                                                 423
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<210> 24

<211> 165

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 24

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Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
1           5           10          15
```

```
Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
          20          25          30
```

```
Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
          35          40          45
```

```
Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
          50          55          60
```

```
Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
65          70          75          80
```

```
His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
```

85

90

95

Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
 100 105 110

Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
 115 120 125

Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
 130 135 140

Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
 145 150 155 160

Ala Leu Val Tyr Ser
 165

<210> 25
 <211> 54
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 25

Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
 1 5 10 15

Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
 20 25 30

Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
 35 40 45

Val Lys Gly Thr Asn Ala
 50

<210> 26
 <211> 204
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 26

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

Phe Pro Leu Lys Ser Lys Val Lys Gln Val Asp Ser Ile Val Trp Thr
20 25 30

Phe Asn Thr Thr Pro Leu Val Thr Ile Gln Pro Glu Gly Gly Thr Ile
35 40 45

Ile Val Thr Gln Asn Arg Asn Arg Glu Arg Val Asp Phe Pro Asp Gly
50 55 60

Gly Tyr Ser Leu Lys Leu Ser Lys Leu Lys Lys Asn Asp Ser Gly Ile
65 70 75 80

Tyr Tyr Val Gly Ile Tyr Ser Ser Ser Leu Gln Gln Pro Ser Thr Gln
85 90 95

Glu Tyr Val Leu His Val Tyr Glu His Leu Ser Lys Pro Lys Val Thr
100 105 110

Met Gly Leu Gln Ser Asn Lys Asn Gly Thr Cys Val Thr Asn Leu Thr
115 120 125

Cys Cys Met Glu His Gly Glu Glu Asp Val Ile Tyr Thr Trp Lys Ala
130 135 140

Leu Gly Gln Ala Ala Asn Glu Ser His Asn Gly Ser Ile Leu Pro Ile
145 150 155 160

Ser Trp Arg Trp Gly Glu Ser Asp Met Thr Phe Ile Cys Val Ala Arg
165 170 175

Asn Pro Val Ser Arg Asn Phe Ser Ser Pro Ile Leu Ala Arg Lys Leu
180 185 190

Cys Glu Gly Ala Ala Asp Asp Pro Asp Ser Ser Met

195

200

<210> 27
 <211> 46
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 27

Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
 1 5 10 15

Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
 20 25 30

Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys
 35 40 45

<210> 28
 <211> 242
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 28

Asp Pro Asn Phe Trp Leu Gln Val Gln Glu Ser Val Thr Val Gln Glu
 1 5 10 15

Gly Leu Cys Val Leu Val Pro Cys Thr Phe Phe His Pro Ile Pro Tyr
 20 25 30

Tyr Asp Lys Asn Ser Pro Val His Gly Tyr Trp Phe Arg Glu Gly Ala
 35 40 45

Ile Ile Ser Arg Asp Ser Pro Val Ala Thr Asn Lys Leu Asp Gln Glu
 50 55 60

Val Gln Glu Glu Thr Gln Gly Arg Phe Arg Leu Leu Gly Asp Pro Ser
 65 70 75 80

Arg Asn Asn Cys Ser Leu Ser Ile Val Asp Ala Arg Arg Arg Asp Asn
85 90 95

Gly Ser Tyr Phe Phe Arg Met Glu Arg Gly Ser Thr Lys Tyr Ser Tyr
100 105 110

Lys Ser Pro Gln Leu Ser Val His Val Thr Asp Leu Thr His Arg Pro
115 120 125

Lys Ile Leu Ile Pro Gly Thr Leu Glu Pro Gly His Ser Lys Asn Leu
130 135 140

Thr Cys Ser Val Ser Trp Ala Cys Glu Gln Gly Thr Pro Pro Ile Phe
145 150 155 160

Ser Trp Leu Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Thr His
165 170 175

Ser Ser Val Leu Ile Ile Thr Pro Arg Pro Gln Asp His Gly Thr Asn
180 185 190

Leu Thr Cys Gln Val Lys Phe Ala Gly Ala Gly Val Thr Thr Glu Arg
195 200 205

Thr Ile Gln Leu Asn Val Thr Tyr Val Pro Gln Asn Pro Thr Thr Gly
210 215 220

Ile Phe Pro Gly Asp Gly Ser Gly Lys Gln Glu Thr Arg Ala Gly Val
225 230 235 240

Val His

<210> 29
<211> 287
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 29

Thr Lys Glu Asp Pro Asn Pro Pro Ile Thr Asn Leu Arg Met Lys Ala
 1 5 10 15

Lys Ala Gln Gln Leu Thr Trp Asp Leu Asn Arg Asn Val Thr Asp Ile
 20 25 30

Glu Cys Val Lys Asp Ala Asp Tyr Ser Met Pro Ala Val Asn Asn Ser
 35 40 45

Tyr Cys Gln Phe Gly Ala Ile Ser Leu Cys Glu Val Thr Asn Tyr Thr
 50 55 60

Val Arg Val Ala Asn Pro Pro Phe Ser Thr Trp Ile Leu Phe Pro Glu
 65 70 75 80

Asn Ser Gly Lys Pro Trp Ala Gly Ala Glu Asn Leu Thr Cys Trp Ile
 85 90 95

His Asp Val Asp Phe Leu Ser Cys Ser Trp Ala Val Gly Pro Gly Ala
 100 105 110

Pro Ala Asp Val Gln Tyr Asp Leu Tyr Leu Asn Val Ala Asn Arg Arg
 115 120 125

Gln Gln Tyr Glu Cys Leu His Tyr Lys Thr Asp Ala Gln Gly Thr Arg
 130 135 140

Ile Gly Cys Arg Phe Asp Asp Ile Ser Arg Leu Ser Ser Gly Ser Gln
 145 150 155 160

Ser Ser His Ile Leu Val Arg Gly Arg Ser Ala Ala Phe Gly Ile Pro
 165 170 175

Cys Thr Asp Lys Phe Val Val Phe Ser Gln Ile Glu Ile Leu Thr Pro
 180 185 190

Pro Asn Met Thr Ala Lys Cys Asn Lys Thr His Ser Phe Met His Trp
 195 200 205

Lys Met Arg Ser His Phe Asn Arg Lys Phe Arg Tyr Glu Leu Gln Ile

210

215

220

Gln Lys Arg Met Gln Pro Val Ile Thr Glu Gln Val Arg Asp Arg Thr
 225 230 235 240

Ser Phe Gln Leu Leu Asn Pro Gly Thr Tyr Thr Val Gln Ile Arg Ala
 245 250 255

Arg Glu Arg Val Tyr Glu Phe Leu Ser Ala Trp Ser Thr Pro Gln Arg
 260 265 270

Phe Glu Cys Asp Gln Glu Glu Gly Ala Asn Thr Arg Ala Trp Arg
 275 280 285

<210> 30

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 30

Pro Glu Glu Pro Leu Val Val Lys Val Glu Glu Gly Asp Asn Ala Val
 1 5 10 15

Leu Gln Cys Leu Lys Gly Thr Ser Asp Gly Pro Thr Gln Gln Leu Thr
 20 25 30

Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu Ser Leu Gly
 35 40 45

Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ile Trp Leu Phe
 50 55 60

Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu Cys Gln Pro
 65 70 75 80

Gly Pro Pro Ser Glu Lys Ala Trp Gln Pro Gly Trp Thr Val Asn Val
 85 90 95

Glu Gly Ser Gly Glu Leu Phe Arg Trp Asn Val Ser Asp Leu Gly Gly

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

<210> 31
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 31

Pro Ile Cys Val Thr Val

1 5

<210> 32
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 32

Lys Ile Ser His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala
1 5 10 15

His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser
20 25 30

Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser
35 40 45

<210> 33
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 33

Asp Ser Ser Lys Trp Val Phe Glu His Pro Glu Thr Leu Tyr Ala Trp
1 5 10 15

Glu Gly Ala Cys Val Trp Ile Pro Cys Thr Tyr Arg Ala Leu Asp Gly
20 25 30

Asp Leu Glu Ser Phe Ile Leu Phe His Asn Pro Glu Tyr Asn Lys Asn
35 40 45

Thr Ser Lys Phe Asp Gly Thr Arg Leu Tyr Glu Ser Thr Lys Asp Gly
50 55 60

Lys Val Pro Ser Glu Gln Lys Arg Val Gln Phe Leu Gly Asp Lys Asn
65 70 75 80

Lys Asn Cys Thr Leu Ser Ile His Pro Val His Leu Asn Asp Ser Gly
85 90 95

Gln Leu Gly Leu Arg Met Glu Ser Lys Thr Glu Lys Trp Met Glu Arg
100 105 110

Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Leu
115 120 125

Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr Cys Leu Leu
130 135 140

Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp Leu Leu Glu
145 150 155 160

Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser Leu Thr Ile
165 170 175

Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro Gln Trp Ser
180 185 190

His His Gly Lys Ile Val Thr Cys Gln Leu Gln Asp Ala Asp Gly Lys
195 200 205

Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His Thr Pro Lys
210 215 220

Leu Glu Ile Lys Val Thr Pro Ser Asp Ala Ile Val Arg Glu Gly Asp
225 230 235 240

Ser Val Thr Met Thr Cys Glu Val Ser Ser Ser Asn Pro Glu Tyr Thr
245 250 255

Thr Val Ser Trp Leu Lys Asp Gly Thr Ser Leu Lys Lys Gln Asn Thr
260 265 270

Phe Thr Leu Asn Leu Arg Glu Val Thr Lys Asp Gln Ser Gly Lys Tyr
275 280 285

Cys Cys Gln Val Ser Asn Asp Val Gly Pro Gly Arg Ser Glu Glu Val

290

295

300

Phe Leu Gln Val Gln Tyr Ala Pro Glu Pro Ser Thr Val Gln Ile Leu
 305 310 315 320

His Ser Pro Ala Val Glu Gly Ser Gln Val Glu Phe Leu Cys Met Ser
 325 330 335

Leu Ala Asn Pro Leu Pro Thr Asn Tyr Thr Trp Tyr His Asn Gly Lys
 340 345 350

Glu Met Gln Gly Arg Thr Glu Glu Lys Val His Ile Pro Lys Ile Leu
 355 360 365

Pro Trp His Ala Gly Thr Tyr Ser Cys Val Ala Glu Asn Ile Leu Gly
 370 375 380

Thr Gly Gln Arg Gly Pro Gly Ala Glu Leu Asp Val Gln Tyr Pro Pro
 385 390 395 400

Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile Arg Glu Gly
 405 410 415

Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn Pro Ser Val
 420 425 430

Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu Pro Ser Leu
 435 440 445

Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr Thr Ile Ala
 450 455 460

Cys Ala Ala Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro Val Ala Leu
 465 470 475 480

<210> 34

<211> 480

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 34

Gln Ser Pro Thr Pro Ser Pro Thr Gly Leu Thr Thr Ala Lys Met Pro
1 5 10 15

Ser Val Pro Leu Ser Ser Asp Pro Leu Pro Thr His Thr Thr Ala Phe
20 25 30

Ser Pro Ala Ser Thr Phe Glu Arg Glu Asn Asp Phe Ser Glu Thr Thr
35 40 45

Thr Ser Leu Ser Pro Asp Asn Thr Ser Thr Gln Val Ser Pro Asp Ser
50 55 60

Leu Asp Asn Ala Ser Ala Phe Asn Thr Thr Gly Val Ser Ser Val Gln
65 70 75 80

Thr Pro His Leu Pro Thr His Ala Asp Ser Gln Thr Pro Ser Ala Gly
85 90 95

Thr Asp Thr Gln Thr Phe Ser Gly Ser Ala Ala Asn Ala Lys Leu Asn
100 105 110

Pro Thr Pro Gly Ser Asn Ala Ile Ser Asp Val Pro Gly Glu Arg Ser
115 120 125

Thr Ala Ser Thr Phe Pro Thr Asp Pro Val Ser Pro Leu Thr Thr Thr
130 135 140

Leu Ser Leu Ala His His Ser Ser Ala Ala Leu Pro Ala Arg Thr Ser
145 150 155 160

Asn Thr Thr Ile Thr Ala Asn Thr Ser Asp Ala Tyr Leu Asn Ala Ser
165 170 175

Glu Thr Thr Thr Leu Ser Pro Ser Gly Ser Ala Val Ile Ser Thr Thr
180 185 190

Thr Ile Ala Thr Thr Pro Ser Lys Pro Thr Cys Asp Glu Lys Tyr Ala
195 200 205

Asn Ile Thr Val Asp Tyr Leu Tyr Asn Lys Glu Thr Lys Leu Phe Thr
 210 215 220

Ala Lys Leu Asn Val Asn Glu Asn Val Glu Cys Gly Asn Asn Thr Cys
 225 230 235 240

Thr Asn Asn Glu Val His Asn Leu Thr Glu Cys Lys Asn Ala Ser Val
 245 250 255

Ser Ile Ser His Asn Ser Cys Thr Ala Pro Asp Lys Thr Leu Ile Leu
 260 265 270

Asp Val Pro Pro Gly Val Glu Lys Phe Gln Leu His Asp Cys Thr Gln
 275 280 285

Val Glu Lys Ala Asp Thr Thr Ile Cys Leu Lys Trp Lys Asn Ile Glu
 290 295 300

Thr Phe Thr Cys Asp Thr Gln Asn Ile Thr Tyr Arg Phe Gln Cys Gly
 305 310 315 320

Asn Met Ile Phe Asp Asn Lys Glu Ile Lys Leu Glu Asn Leu Glu Pro
 325 330 335

Glu His Glu Tyr Lys Cys Asp Ser Glu Ile Leu Tyr Asn Asn His Lys
 340 345 350

Phe Thr Asn Ala Ser Lys Ile Ile Lys Thr Asp Phe Gly Ser Pro Gly
 355 360 365

Glu Pro Gln Ile Ile Phe Cys Arg Ser Glu Ala Ala His Gln Gly Val
 370 375 380

Ile Thr Trp Asn Pro Pro Gln Arg Ser Phe His Asn Phe Thr Leu Cys
 385 390 395 400

Tyr Ile Lys Glu Thr Glu Lys Asp Cys Leu Asn Leu Asp Lys Asn Leu
 405 410 415

Ile Lys Tyr Asp Leu Gln Asn Leu Lys Pro Tyr Thr Lys Tyr Val Leu

420

425

430

Ser Leu His Ala Tyr Ile Ile Ala Lys Val Gln Arg Asn Gly Ser Ala
 435 440 445

Ala Met Cys His Phe Thr Thr Lys Ser Ala Pro Pro Ser Gln Val Trp
 450 455 460

Asn Met Thr Val Ser Met Thr Ser Asp Asn Ser Met His Val Lys Cys
 465 470 475 480

<210> 35

<211> 65

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 35

Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
 1 5 10 15

Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
 20 25 30

Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
 35 40 45

Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
 50 55 60

Arg

65

<210> 36

<211> 153

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 36

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
 1 5 10 15

Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala
 20 25 30

Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu
 35 40 45

Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu
 50 55 60

Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys
 65 70 75 80

Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala
 85 90 95

Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser
 100 105 110

Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu
 115 120 125

Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His
 130 135 140

Ile Val Gln Met Phe Ile Asn Thr Ser
 145 150