

SEQUENCE LISTING

<110> iCELL GENE THERAPEUTICS LLC
MA, Yupo

<120> COMPOUND CHIMERIC ANTIGEN RECEPTOR (cCAR) TARGETING MULTIPLE
ANTIGENS, COMPOSITIONS AND METHODS OF USE THEREOF

<130> 2541-10 PCT

<150> US 62/571,608

<151> 2017-10-12

<160> 61

<170> PatentIn version 3.5

<210> 1

<211> 734

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

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Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
35 40 45

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

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
65 70 75 80

Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser
85 90 95

Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser
100 105 110

Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val
 115 120 125

Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
 130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
 145 150 155 160

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

Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn
 180 185 190

Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu
 195 200 205

Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe
 210 215 220

Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val
 225 230 235 240

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr
 245 250 255

Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr
 260 265 270

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
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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

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Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu
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Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp
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Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Gln	Arg	Arg
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Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg	Gly	Ser	Gly
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Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr	Cys	Gly	Asp	Val	Glu	Glu	Asn	Pro
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Arg Gln Leu Ile Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp
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Leu Val Pro Glu Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys
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Glu Trp Ser Ala Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala
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Asn Thr Gly Asn Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu
 595 600 605

Lys Arg Lys Pro Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg
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Leu Thr Cys Pro Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu
 625 630 635 640

Phe Leu Glu Arg Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His
 645 650 655

Leu Ser Ser Arg Thr His Gly Ser Glu Asp Ser Thr Thr Thr Pro Ala
 660 665 670

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
 675 680 685

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
 690 695 700

Arg Gly Leu Asp Phe Ala Cys Asp Val Ala Ile Ser Thr Ser Thr Val
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Leu Leu Cys Gly Leu Ser Ala Val Ser Leu Leu Ala Cys Tyr
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<212> DNA

<213> Artificial Sequence

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<223> Synthetic Sequence

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gcacagccta catggagctc agcagcctga cctctgagga ctctgcggtc tattactgtg	360
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<213> Artificial Sequence

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<220>
<223> Synthetic Sequence

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<400> 3

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

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

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Asp Val Asn Thr Ala Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser
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Pro Lys Leu Leu Ile Phe Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro

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Tyr	Ser	Thr	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Asp	Ile	Lys
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Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln
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Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Asp	Leu	Lys	Lys	Pro	Gly	Glu	Thr
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Val	Lys	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Phe	Gly
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Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Ser	Tyr	Phe	Ala	Asp	Asp	Phe	Lys
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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
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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 Arg Ser
 325 330 335

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

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

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

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

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

Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu
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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

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Thr	Ile	Leu	Gly	Ser	His	Leu	Ile	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly
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Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe	Thr	Leu
		595					600					605			
Thr	Ile	Asp	Pro	Val	Glu	Glu	Asp	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Leu
	610					615					620				
Gln	Ser	Arg	Thr	Ile	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu
625						630					635				640
Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
				645					650					655	
Ser	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Leu	Lys	Lys	Pro	Gly
			660					665					670		
Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp
		675					680					685			
Tyr	Ser	Ile	Asn	Trp	Val	Lys	Arg	Ala	Pro	Gly	Lys	Gly	Leu	Lys	Trp
	690					695					700				
Met	Gly	Trp	Ile	Asn	Thr	Glu	Thr	Arg	Glu	Pro	Ala	Tyr	Ala	Tyr	Asp
705						710					715				720

Phe Arg Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala
 725 730 735

Tyr Leu Gln Ile Asn Asn Leu Lys Tyr Glu Asp Thr Ala Thr Tyr Phe
 740 745 750

Cys Ala Leu Asp Tyr Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
 755 760 765

Ser 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
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Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
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Ala Leu Pro Pro Arg
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

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

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

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

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

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Asp Arg Phe Thr Gly Ser Gly Ser Gly Ala Asp Phe Thr Leu Thr Ile

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85

90

95

Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His
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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 Arg Ser
 325 330 335

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

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

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

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

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

Asp Pro Glu Met Gly Gly Lys Pro Gln 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	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val
	530					535					540				
Thr	Pro	Gly	Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu
545					550				555						560
Leu	Phe	Ile	Asp	Gly	Asn	Asn	Tyr	Leu	Asn	Trp	Tyr	Leu	Gln	Lys	Pro
				565					570					575	
Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Gly	Ser	Asn	Arg	Ala	Ser
			580					585					590		
Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr
		595					600					605			
Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys
	610					615					620				
Gln	Gln	Tyr	Ser	Ser	Lys	Ser	Ala	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val
625					630					635					640
Glu	Ile	Lys	Arg	Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly
				645					650					655	
Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys
			660					665					670		
Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr
		675					680					685			
Phe	Thr	Ser	Tyr	Ser	Ile	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly
	690					695					700				
Leu	Glu	Trp	Met	Gly	Tyr	Ile	Asp	Pro	Asn	Arg	Gly	Asn	Thr	Asn	Tyr
705					710					715					720
Ala	Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Ile
				725					730					735	

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

Val Tyr Tyr Cys Ala Arg Glu Tyr Ile Tyr Phe Ile His Gly Met Leu
 755 760 765

Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr
 770 775 780

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
 785 790 795 800

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
 805 810 815

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

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
 835 840 845

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

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

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

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
 900 905 910

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

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

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met

945		950		955		960									
Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly
				965					970					975	
Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp
			980					985					990		
Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg			
		995					1000					1005			

<210> 6
 <211> 2966
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 6
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 agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag 180
 cccggccaga gcccgaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc 240
 gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag 300
 gccgaggacc tggccgtgta ctactgccag cagcactaca gcacccctg gaccttcggc 360
 ggcgggacca agctggacat caagggaggg gggggatccg ggggaggagg ctccggcgga 420
 ggcggaagcc agatccagct ggtgcagagc ggccccgacc tgaagaagcc cggcgagacc 480
 gtgaagctga gctgcaaggc cagcggctac accttcacca acttcggcat gaactgggtg 540
 aagcaggccc ccggcaaggg cttcaagtgg atggcctgga tcaacaccta caccggcgag 600
 agctacttcg ccgacgactt caagggcagg ttgccttca gcgtggagac cagcgccacc 660
 accgcctacc tgcagatcaa caacctgaag accgaggaca ccgccaccta cttctgcgcc 720
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 gtgaccgtga gcgccaccac gacgccagcg ccgcgaccac caacaccggc gccaccatc 840
 gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgcagtg 900

cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact	960
tgtgggggtcc ttctcctgtc actggttatc accctttact gcaggagtaa gaggagcagg	1020
ctcctgcaca gtgactacat gaacatgact ccccgccgcc ccgggcccac ccgcaagcat	1080
taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc	1140
aggagcgag acgccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat	1200
ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg	1260
gggggaaagc cgagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa	1320
gataagatgg cggaggccta cagtgaatt gggatgaaag gcgagcgccg gaggggcaag	1380
gggcacgatg gcctttacca gggctctcagt acagccacca aggacaccta cgacgccctt	1440
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gccggcgacg tggaggagaa ccccgcccc atggccctgc ccgtgaccgc cctgctgctg	1560
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agcctgcccc tgacccccgg cgagcccgcc agctacctgc agaagcccgg ccagagcccc	1680
cagctgctga tctacctggg cagcaacagg gccagcggcg tgcccgacag gttcagcggc	1740
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gtgtactact gccagcagta cagcagcaag agcgccacct tcggccaggg caccaagggtg	1860
gagatcaaga ggaccggcgg cggcggcagc ggcgccggcg gcagcggcgg cggcggcagc	1920
caggtgcagc tgggtgcagag cggcgccgag gtgaagaagc ccggcgccag cgtgaagggtg	1980
agctgcaagg ccagcggcta caccttcacc agctacagca tcaactgggt gaggcaggcc	2040
cccggccagg gcctggagtg gatgggctac atcgaccca acaggggcaa caccaactac	2100
gcccagaagt tccagggcag ggtgaccatg accagggaca ccagcatcag caccgcctac	2160
atggagctga gcagcctgag gagcgaggac accgccgtgt actactgcgc cagggagtac	2220
atctacttca tccacggcat gctggacttc tggggccagg gcaccctggt gaccgtgagc	2280
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ctgagcctga ggcccaggc ctgcaggccc gccgccggcg gcgccgtgca caccaggggc	2400
ctggacttcg cctgcgacat ctacatctgg gccccctgg ccggcacctg cggcgtgctg	2460
ctgctgagcc tggatgacac cctgtactgc aaacggggca gaaagaaact cctgtatata	2520

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ttcaaacaac catttatgag accagtacaa actactcaag aggaagatgg ctgtagctgc      2580
cgatttccag aagaagaaga aggaggatgt gaactgaggg tgaagttcag caggagcgcc      2640
gacgcccccg cctaccagca gggccagaac cagctgtaca acgagctgaa cctgggcagg      2700
agggaggagt acgacgtgct ggacaagagg aggggcaggg accccgagat gggcggcaag      2760
ccccagagga ggaagaaccc ccaggagggc ctgtacaacg agctgcagaa ggacaagatg      2820
gccgaggcct acagcgagat cggcatgaag ggcgagagga ggaggggcaa gggccacgac      2880
ggcctgtacc agggcctgag caccgccacc aaggacacct acgacgccct gcacatgcag      2940
gccctgcccc ccaggtaatg ttaaac                                          2966

```

```

<210> 7
<211> 1001
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Sequence

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<400> 7

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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

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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 Arg Ser

				325						330						335
Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	
			340					345					350			
Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	
		355					360					365				
Asp	Phe	Ala	Ala	Tyr	Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	
	370					375					380					
Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	
385					390					395					400	
Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	
				405					410					415		
Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Gln	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 Ala Ser Gln Asp Ile
 545 550 555 560

Ser Ala Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 565 570 575

Leu Leu Ile Thr Lys Val Ser Asn Leu Gln Ser Gly Val Pro Ser Arg
 580 585 590

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

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

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

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
 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 Thr Phe Ser Asn Tyr Gly
 675 680 685

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

Asn Ile Arg Ser Asp Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val Lys
 705 710 715 720

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Arg Tyr Trp Ser Lys Ser His Ala Ser Val Thr Asp Tyr Trp Gly

755					760					765					
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Thr	Thr	Thr	Pro	Ala	Pro	Arg
	770					775					780				
Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg
785					790					795					800
Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly
				805					810					815	
Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr
			820					825					830		
Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Lys	Arg
		835					840					845			
Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met	Arg	Pro
	850					855					860				
Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe	Pro	Glu
865					870					875					880
Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala
				885					890					895	
Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu
			900					905					910		
Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly
		915					920					925			
Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Gln	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> 8
 <211> 3014
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequences

<400> 8
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 agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag 180
 cccggccaga gcccgaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc 240
 gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag 300
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taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc	1140
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gaagaagaag gaggatgtga actgagggtg aagttcagca ggagcgccga cgccccgcc	2700

taccagcagg gccagaacca gctgtacaac gagctgaacc tgggcaggag ggaggagtac 2760
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<210> 9
<211> 1004
<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
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 Arg Ser
 325 330 335

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg

340	345	350
Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg		
355	360	365
Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp		
370	375	380
Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn		
385	390	395
Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg		
	405	410
Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu		
	420	425
Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser		
	435	440
Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly		
	450	455
Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu		
465	470	475
His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser		
	485	490
Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala		
	500	505
Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala		
	515	520
Ala Arg Pro Ala Gln Pro Ala Met Ala Lys Val Gln Leu Gln Glu Ser		
	530	535
Gly Pro Ser Leu Val Gln Pro Ser Gln Arg Leu Ser Ile Thr Cys Thr		
545	550	555
		560

Val Ser Gly Phe Ser Leu Ile Ser Tyr Gly Val His Trp Val Arg Gln
565 570 575

Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Arg Gly Gly
580 585 590

Ser Thr Asp Tyr Asn Ala Ala Phe Met Ser Arg Leu Ser Ile Thr Lys
595 600 605

Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ala
610 615 620

Asp Asp Thr Ala Ile Tyr Phe Cys Ala Lys Thr Leu Ile Thr Thr Gly
625 630 635 640

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
645 650 655

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
660 665 670

Ile Glu Leu Thr Gln Ser Pro Ser Ser Phe Ser Val Ser Leu Gly Asp
675 680 685

Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg Leu
690 695 700

Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Arg Leu Leu Ile Ser
705 710 715 720

Gly Ala Thr Ser Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser
725 730 735

Gly Ser Gly Lys Asp Tyr Thr Leu Ser Ile Thr Ser Leu Gln Thr Glu
740 745 750

Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ser Thr Pro Thr Phe
755 760 765

Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Thr Thr Thr Pro

770

775

780

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

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
 805 810 815

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

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

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

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

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

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
 900 905 910

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

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

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

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
 965 970 975

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

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 995 1000

<210> 10
 <211> 3023
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 10
 atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
 ccggacgtgg tgatgaccga gagccacagg ttcatgagca ccagcgtggg cgacagggtg 120
 agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag 180
 cccggccaga gcccgaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc 240
 gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag 300
 gccgaggacc tggccgtgta ctactgccag cagcactaca gcaccccctg gaccttcggc 360
 ggccggcacca agctggacat caagggaggg gggggatccg ggggaggagg ctccggcgga 420
 ggccggaagcc agatccagct ggtgcagagc ggccccgacc tgaagaagcc cggcgagacc 480
 gtgaagctga gctgcaaggc cagcggctac accttcacca acttcggcat gaactgggtg 540
 aagcaggccc ccggcaaggg cttcaagtgg atggcctgga tcaacaccta caccggcgag 600
 agctacttcg ccgacgactt caagggcagg ttgccttca gcgtggagac cagcgccacc 660
 accgcctacc tgcatgcaa caacctgaag accgaggaca ccgccaccta cttctgcgcc 720
 aggggcgaga tctactacgg ctacgacggc ggcttcgcct actggggcca gggcaccttg 780
 gtgaccgtga gcgccaccac gacgccagcg ccgcgaccac caacaccggc gccaccatc 840
 gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgagtg 900
 cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact 960
 tgtgggggtcc ttctcctgtc actggttatc accctttact gcaggagtaa gaggagcagg 1020
 ctctgcaca gtgactacat gaacatgact ccccgccgcc ccgggcccac ccgcaagcat 1080
 taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc 1140
 aggagcgag acgccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat 1200

ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg	1260
gggggaaagc cgagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa	1320
gataagatgg cggaggccta cagttagatt gggatgaaag gcgagcgccg gaggggcaag	1380
gggcacgatg gcctttacca ggggtctcagt acagccacca aggacaccta cgacgccctt	1440
cacatgcagg ccctgcccc tcgcggaagc ggagccacca acttcagcct gctgaagcag	1500
gccggcgacg tggaggagaa ccccgcccc atggccctgc ccgtgaccgc cctgctgctg	1560
cccctggccc tgctgctgca cgccgccagg cccgccagc ccgcatggc caaggtgcag	1620
ctgcaggaga gcggccccag cctggtgcag ccagccaga ggctgagcat cacctgcacc	1680
gtgagcggct tcagcctgat cagctacggc gtgactggg tgaggcagag ccccgcaag	1740
ggcctggagt ggctgggct gatctggagg ggcggcagca ccgactaca cgccgccttc	1800
atgagcaggc tgagcatcac caaggacaac agcaagagcc aggtgttctt caagatgaac	1860
agcctgcagg ccgacgacac cgccatctac ttctgcgcca agaccctgat caccaccggc	1920
tacgcatgg actactgggg ccagggcacc accgtgaccg tgagcagcgg cggcggcggc	1980
agcggcggcg gcggcagcgg cggcggcggc agcgacatcg agctgacca gagccccagc	2040
agcttcagcg tgagcctggg cgacagggtg accatcacct gcaaggccag cgaggacatc	2100
tacaacaggc tggcctggta ccagcagaag cccggcaacg ccccaggct gctgatcagc	2160
ggcgccacca gcctggagac cggcgtgccc agcaggttca gcggcagcgg cagcggcaag	2220
gactacacc tgagcatcac cagcctgcag accgaggacg tggccaccta ctactgccag	2280
cagtactgga gcacccccac cttcggcggc ggcaccaagc tggagatcaa gagggccgcc	2340
accaccacc ccgccccag gccccacc cccgccccca ccatcgccag ccagcccctg	2400
agcctgaggc ccgaggcctg caggcccgcc gccggcggcg ccgtgcacac caggggcctg	2460
gacttcgcct gcgacatcta catctgggcc cccctggccg gcacctgcgg cgtgctgctg	2520
ctgagcctgg tgatcacct gtactgcaaa cggggcagaa agaaactcct gtatatattc	2580
aaacaacat ttatgagacc agtacaact actcaagagg aagatggctg tagctgccga	2640
tttccagaag aagaagaagg aggatgtgaa ctgagggtga agttcagcag gagcgccgac	2700
gccccgcct accagcaggg ccagaaccag ctgtacaacg agctgaacct gggcaggagg	2760
gaggagtacg acgtgctgga caagaggagg ggcagggacc ccgagatggg cggcaagccc	2820

cagaggagga agaacccccca ggagggcctg tacaacgagc tgcagaagga caagatggcc 2880
 gaggcctaca gcgagatcgg catgaagggc gagaggagga ggggcaaggg ccacgacggc 2940
 ctgtaccagg gcctgagcac cgccaccaag gacacctacg acgccctgca catgcaggcc 3000
 ctgcccccca ggtaagttaa aac 3023

<210> 11
 <211> 687
 <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 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 Arg Ser
 325 330 335

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

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg

355	360	365
Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp 370 375 380		
Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn 385 390 395 400		
Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg 405 410 415		
Asp Pro Glu Met Gly Gly Lys Pro Gln 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 Tyr 500 505 510		
Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr 515 520 525		
Asn Ser Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn 530 535 540		
Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe 545 550 555 560		
Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile 565 570 575		

Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val
 580 585 590

Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn
 595 600 605

Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp
 610 615 620

Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp
 625 630 635 640

Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala
 645 650 655

Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp
 660 665 670

Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
 675 680 685

<210> 12
 <211> 2061
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 12
 atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
 ccggacgtgg tgatgaccga gagccacagg ttcattgagca ccagcgtggg cgacagggtg 120
 agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag 180
 cccggccaga gcccgaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc 240
 gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag 300
 gccgaggacc tggccgtgta ctactgccag cagcactaca gcacccctg gaccttcggc 360
 ggcggcacca agctggacat caagggaggg gggggatccg ggggaggagg ctccggcgga 420
 ggcggaagcc agatccagct ggtgcagagc ggccccgacc tgaagaagcc cggcgagacc 480

gtgaagctga gctgcaaggc cagcggctac accttcacca acttcggcat gaactgggtg	540
aagcaggccc ccggcaaggg cttcaagtgg atggcctgga tcaacaccta caccggcgag	600
agctacttcg ccgacgactt caagggcagg ttgccttca gcgtggagac cagcgccacc	660
accgcctacc tgcagatcaa caacctgaag accgaggaca ccgccaccta cttctgcgcc	720
aggggcgaga tctactacgg ctacgacggc ggcttcgcct actggggcca gggcaccctg	780
gtgacctga gcgccaccac gacgccagcg ccgcgaccac caacaccggc gcccaccatc	840
gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgagtg	900
cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact	960
tgtgggggtcc ttctcctgtc actggttatc accctttact gcaggagtaa gaggagcagg	1020
ctcctgcaca gtgactacat gaacatgact ccccgccgcc ccgggcccac ccgcaagcat	1080
taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc	1140
aggagcgag acgccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat	1200
ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg	1260
gggggaaagc cgagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa	1320
gataagatgg cggaggccta cagtgaatt gggatgaaag gcgagcgccg gaggggcaag	1380
gggcacgatg gcctttacca gggctctcagt acagccacca aggacaccta cgacgccctt	1440
cacatgcagg ccctgcccc tcgcggaagc ggagccacca acttcagcct gctgaagcag	1500
gccggcgacg tggaggagaa ccccgcccc atgtacagaa tgcagctgct gagctgcatc	1560
gccctgagcc tggccctggt gaccaacagc tacttcggca agctggagag caagctgagc	1620
gtgatcagga acctgaacga ccaggtgctg ttcatcgacc agggcaacag gccctgttc	1680
gaggacatga ccgacagcga ctgcaggac aacgccccca ggaccatctt catcatcagc	1740
atgtacaagg acagccagcc caggggcatg gccgtgacca tcagcgtgaa gtgcgagaag	1800
atcagcacc tgagctgcga gaacaagatc atcagcttca aggagatgaa ccccccgac	1860
aacatcaagg acaccaagag cgacatcatc ttcttccaga ggagcgtgcc cggccacgac	1920
aacaagatgc agttcgagag cagcagctac gagggtact tcctggcctg cgagaaggag	1980
agggacctgt tcaagctgat cctgaagaag gaggacgagc tgggcgacag gagcatcatg	2040
ttcaccgtgc agaacgagga c	2061

<210> 13
 <211> 754
 <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
 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 Arg Ser
 325 330 335

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

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

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

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

385		390		395		400
Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg						
		405		410		415
Asp Pro Glu Met Gly Gly Lys Pro Gln 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
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 Tyr						
		500		505		510
Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr						
		515		520		525
Asn Ser Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn						
		530		535		540
Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe						
		545		550		555
Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile						
		565		570		575
Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val						
		580		585		590
Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn						
		595		600		605

Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp
 610 615 620

Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp
 625 630 635 640

Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala
 645 650 655

Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp
 660 665 670

Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp Thr
 675 680 685

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
 690 695 700

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
 705 710 715 720

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Val Ala Ile Ser
 725 730 735

Thr Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val Ser Leu Leu Ala
 740 745 750

Cys Tyr

<210> 14
 <211> 2273
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 14
 atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
 ccggacgtgg tgatgacca gagccacagg ttcattagca ccagcgtggg cgacagggtg 120

agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag	180
cccggccaga gcccgaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc	240
gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag	300
gccgaggacc tggccgtgta ctactgccag cagcactaca gcacccctg gaccttcggc	360
ggcggcacca agctggacat caaggaggagg gggggatccg ggggaggagg ctccggcgga	420
ggcgggaagcc agatccagct ggtgcagagc ggccccgacc tgaagaagcc cggcgagacc	480
gtgaagctga gctgcaaggc cagcggctac accttcacca acttcggcat gaactgggtg	540
aagcaggccc ccggcaaggg cttcaagtgg atggcctgga tcaacaccta caccggcgag	600
agctacttcg ccgacgactt caagggcagg ttgccttca gcgtggagac cagcgccacc	660
accgcctacc tgcagatcaa caacctgaag accgaggaca ccgccaccta cttctgcgcc	720
aggggcgaga tctactacgg ctacgacggc ggcttcgcct actggggcca gggcacctg	780
gtgaccgtga gcgccaccac gacgccagcg ccgcgaccac caacaccggc gccaccatc	840
gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgagtg	900
cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact	960
tgtgggggtcc ttctcctgtc actggttatc accctttact gcaggagtaa gaggagcagg	1020
ctcctgcaca gtgactacat gaacatgact ccccgccgcc ccggggccac ccgcaagcat	1080
taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc	1140
aggagcgcag acgccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat	1200
ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg	1260
gggggaaagc cgagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa	1320
gataagatgg cggaggccta cagtgaattt gggatgaaag gcgagcgccg gaggggcaag	1380
gggcacgatg gcctttacca gggctctcagt acagccacca aggacaccta cgacgccctt	1440
cacatgcagg ccctgcccc tcgcggaagc ggagccacca acttcagcct gctgaagcag	1500
gccggcgacg tggaggagaa ccccgggccc atgtacagaa tgcagctgct gagctgcatc	1560
gccctgagcc tggccctggt gaccaacagc tacttcggca agctggagag caagctgagc	1620
gtgatcagga acctgaacga ccagggtctg ttcacgacc agggcaacag gccctgttc	1680
gaggacatga ccgacagcga ctgcagggac aacgccccca ggaccatctt catcatcagc	1740

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atgtacaagg acagccagcc caggggcatg gccgtgacca tcagcgtgaa gtgcgagaag      1800
atcagcaccc tgagctgcga gaacaagatc atcagcttca aggagatgaa cccccccgac      1860
aacatcaagg acaccaagag cgacatcatc ttcttccaga ggagcgtgcc cggccacgac      1920
aacaagatgc agttcgagag cagcagctac gagggtact tcctggcctg cgagaaggag      1980
agggacctgt tcaagctgat cctgaagaag gaggacgagc tgggcgacag gagcatcatg      2040
ttcaccgtgc agaacgagga caccaccacc cccgccccca ggccccccac ccccgcccccc      2100
accatcgcca gccagcccct gaggcctgagg cccgaggcct gcaggcccgc cgccggcggc      2160
gccgtgcaca ccaggggcct ggacttcgcc tgcgacgtgg ctatctccac gtccactgtc      2220
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<210> 15
 <211> 258
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 15

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Val Pro Arg Trp Arg Gln Gln Trp Ser Gly Pro Gly Thr Thr Lys Arg
1           5           10           15

```

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Phe Pro Glu Thr Val Leu Ala Arg Cys Val Lys Tyr Thr Glu Ile His
          20           25           30

```

```

Pro Glu Met Arg His Val Asp Cys Gln Ser Val Trp Asp Ala Phe Lys
          35           40           45

```

```

Gly Ala Phe Ile Ser Lys His Pro Cys Asn Ile Thr Glu Glu Asp Tyr
50           55           60

```

```

Gln Pro Leu Met Lys Leu Gly Thr Gln Thr Val Pro Cys Asn Lys Ile
65           70           75           80

```

```

Leu Leu Trp Ser Arg Ile Lys Asp Leu Ala His Gln Phe Thr Gln Val
          85           90           95

```

```

Gln Arg Asp Met Phe Thr Leu Glu Asp Thr Leu Leu Gly Tyr Leu Ala

```

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

Glu Ile

<210> 16
 <211> 667
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 16

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

Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val
 225 230 235 240

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr
 245 250 255

Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Thr
 260 265 270

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 Arg Val Lys Phe
 370 375 380

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

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

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

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met

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

Leu Ser Ser Arg Thr His Gly Ser Glu Asp Ser
 660 665

<210> 17
 <211> 2012
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 17
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 atgtcctgca aggcttctgg atacacattc actagctatg ttatgcactg ggtgaagcag 180
 aagcctgggc agggccttga gtggattgga tatattaatc cttacaatga tggtactaag 240
 tacaatgaga agttcaaagg caaggccaca ctgacttcag acaaatcctc cagcacagcc 300
 tacatggagc tcagcagcct gacctctgag gactctgcgg tctattactg tgcaagaggg 360
 acttattact acggtagtag ggtatttgac tactggggcc aaggcaccac tctcacagtc 420
 tcctcaggtg gagggggctc aggcggaggt ggctctgggg gtggaggctc ggacattgtg 480
 atgactcagg ctgcaccctc tatacctgtc actcctggag agtcagtatc catctcctgc 540
 aggtctagta agagtctcct gaatagtaat ggcaacactt acttgtattg gttcctgcag 600
 aggccaggcc agtctcctca gctcctgata tatcgatgt ccaaccttgc ctcaggagtc 660
 ccagacaggt tcagtggcag tgggtcagga actgctttca cactgagaat cagtagagtg 720
 gaggctgagg atgtgggtgt ttattactgt atgcaacatc tagaatatcc gttcacgttc 780
 ggtgctggga ccaagctgga gctgaaacgg accacgacgc cagcgccgcg accaccaaca 840
 ccggcgccca ccatcgctc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg 900
 gcggggggcg cagtgcacac gagggggctg gacttcgcct gtgatatacta catctgggcg 960
 cccttggccg ggacttgtgg ggtccttctc ctgtcactgg ttatcacctt ttactgcagg 1020
 agtaagagga gcaggctcct gcacagtgaac tacatgaaca tgactccccg ccgccccggg 1080
 cccacccgca agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc 1140
 agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggccga gaaccagctc 1200

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 1260
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 aatgaactgc agaaagataa gatggcggag gcctacagtg agattgggat gaaaggcgag 1380
 cgccggaggg gcaaggggca cgatggcctt taccagggtc tcagtacagc caccaaggac 1440
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 agcctgctga cctgcggcga tgtggaagaa aaccggggcc ccatgtacag aatgcagctg 1560
 ctgagctgca tcgccctgag cctggccctg gtgaccaaca gccagggcca ggacaggcac 1620
 atgatcagga tgaggcagct gatcgacatc gtggaccagc tgaagaacta cgtgaacgac 1680
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 ttcagctgct tccagaaggc ccagctgaag agcgccaaca ccggcaacaa cgagaggatc 1800
 atcaacgtga gcatcaagaa gctgaagagg aagccccca gcaccaacgc cggcaggagg 1860
 cagaagcaca ggctgacctg ccccagctgc gacagctacg agaagaagcc cccaaggag 1920
 ttcctggaga ggttcaagag cctgctgcag aagatgatcc accagcacct gagcagcagg 1980
 acccacggca gcgaggacag ctaagtttaa ac 2012

<210> 18
 <211> 1055
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 18

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

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

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

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

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

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

Trp Ser Ser Asn Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Gln Ile
115 120 125

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

Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
145 150 155 160

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

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly
180 185 190

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Val Lys
195 200 205

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

Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala
225 230 235 240

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
245 250 255

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

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

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

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Tyr Ala Ser Asp
 500 505 510

Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro Pro Ala Pro Arg Ala Arg
 515 520 525

Ala Cys Arg Val Leu Pro Trp Ala Leu Val Ala Gly Leu Leu Leu Leu
 530 535 540

Leu Leu Leu Ala Ala Ala Cys Ala Val Phe Leu Ala Cys Pro Trp Ala
 545 550 555 560

Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu
 565 570 575

Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp
 580 585 590

Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu
 595 600 605

Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val
 610 615 620

Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val
 625 630 635 640

Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg
 645 650 655

Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His
 660 665 670

Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr
 675 680 685

Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly
 690 695 700

Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val

705		710		715		720									
His	Leu	His	Thr	Glu	Ala	Arg	Ala	Arg	His	Ala	Trp	Gln	Leu	Thr	Gln
				725					730					735	
Gly	Ala	Thr	Val	Leu	Gly	Leu	Phe	Arg	Val	Thr	Pro	Glu	Ile	Pro	Ala
			740					745					750		
Gly	Leu	Pro	Ser	Pro	Arg	Ser	Glu	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser
		755					760					765			
Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Tyr
	770					775					780				
Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu	Ser	Leu	Ala	Leu	Val	Thr
785					790					795					800
Asn	Ser	Gly	Ile	His	Val	Phe	Ile	Leu	Gly	Cys	Phe	Ser	Ala	Gly	Leu
				805					810					815	
Pro	Lys	Thr	Glu	Ala	Asn	Trp	Val	Asn	Val	Ile	Ser	Asp	Leu	Lys	Lys
			820					825					830		
Ile	Glu	Asp	Leu	Ile	Gln	Ser	Met	His	Ile	Asp	Ala	Thr	Leu	Tyr	Thr
		835					840					845			
Glu	Ser	Asp	Val	His	Pro	Ser	Cys	Lys	Val	Thr	Ala	Met	Lys	Cys	Phe
	850					855					860				
Leu	Leu	Glu	Leu	Gln	Val	Ile	Ser	Leu	Glu	Ser	Gly	Asp	Ala	Ser	Ile
865					870					875					880
His	Asp	Thr	Val	Glu	Asn	Leu	Ile	Ile	Leu	Ala	Asn	Asn	Ser	Leu	Ser
				885					890					895	
Ser	Asn	Gly	Asn	Val	Thr	Glu	Ser	Gly	Cys	Lys	Glu	Cys	Glu	Glu	Leu
			900					905					910		
Glu	Glu	Lys	Asn	Ile	Lys	Glu	Phe	Leu	Gln	Ser	Phe	Val	His	Ile	Val
		915					920					925			

Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
 930 935 940

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu
 945 950 955 960

Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala
 965 970 975

Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr
 980 985 990

Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser
 995 1000 1005

Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe
 1010 1015 1020

Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
 1025 1030 1035

Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys
 1040 1045 1050

Ile Arg
 1055

<210> 19
 <211> 3170
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 19
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 accatcacct gcagcgccag cagcagcgtg agctacatga actggtacca gcagaccccc 180
 ggcaaggccc ccaagagatg gatctacgac accagcaagc tggccagcgg cgtgcccagc 240

agattcagcg gcagcggcag cggcaccgac tacaccttca ccatcagcag cctgcagccc	300
gaggacatcg ccacctacta ctgccagcag tggagcagca accccttcac cttcggccag	360
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ctgagctgca aggccagcgg ctacaccttc accagataca ccatgcactg ggtgagacag	540
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tacaaccaga aggtgaagga cagattcacc atcagcagag acaacagcaa gaacaccgcc	660
ttcctgcaga tggacagcct gagacccgag gacaccggcg tgtactttctg cgccagatac	720
tacgacgacc actactgcct ggactactgg ggccagggca cccccgtgac cgtgagcagc	780
accacgacgc cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg	840
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ctgtcactgg ttatcacctt ttactgcagg agtaagagga gcaggctcct gcacagtgc	1020
tacatgaaca tgactccccg ccgccccggg cccaccgcga agcattacca gccctatgcc	1080
ccaccacgcg acttcgcagc ctatcgctcc agagtgaagt tcagcaggag cgcagacgcc	1140
cccgcgtaac agcagggccga gaaccagctc tataacgagc tcaatctagg acgaagagag	1200
gagtacgatg ttttggacaa gagacgtggc cgggaccctg agatgggggg aaagccgcag	1260
agaaggaaga accctcagga aggcctgtac aatgaactgc agaaagataa gatggcggag	1320
gcctacagtg agattgggat gaaaggcgag cgccggaggg gcaaggggca cgatggcctt	1380
taccagggtc tcagtacagc caccaaggac acctacgacg cccttcacat gcaggccctg	1440
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aaccggggcc ccatggaata cgcctctgac gcttcactgg accccgaagc cccgtggcct	1560
cccgcgcccc gcgctcgcg ctgccgcgta ctgccttggg ccctggtcgc ggggctgctg	1620
ctgctgctgc tgctcgctgc cgcctgcgcc gtcttcctcg cctgcccctg ggccgtgtcc	1680
ggggctcgcg cctcgcccgg ctccgcggcc agcccagac tccgcgaggg tcccagcctt	1740
tcgcccgcg atcccgcgg cctcttggac ctgcggcagg gcatgtttgc gcagctgggtg	1800
gccccaaatg ttctgctgat cgatggggcc ctgagctggt acagtgaccc aggcctggca	1860

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aaggctggag tctactatgt cttctttcaa ctagagctgc ggcgctggt ggccggcgag 1980
ggctcaggct ccgtttcact tgcgctgcac ctgcagccac tgcgctctgc tgctggggcc 2040
gccgccctgg ctttgaccgt ggacctgcca cccgcctcct ccgaggctcg gaactcggcc 2100
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cacactgagg ccagggcacg ccatgcctgg cagcttacct agggcgccac agtcttggga 2220
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ggcatccacg tgttcatcct gggctgcttc agcgccggcc tgcccaagac cgaggccaac 2460
tgggtgaacg tgatcagcga cctgaagaag atcaggagcc tgatccagag catgcacatc 2520
gacgccaccc tgtacaccga gagcgacgtg caccacagct gcaaggtgac cgccatgaag 2580
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gagagcggct gcaaggagtg cgaggagctg gaggagaaga acatcaagga gttcctgcag 2760
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ctgagacccc ccgccaccag aggcatacc tgccccccc ccatgagcgt ggagcacgcc 3000
gacatctggg tgaagagcta cagcctgtac agcagagaga gatacatctg caacagcggc 3060
ttcaagagaa aggccggcac cagcagcctg accgagtgcg tgctgaacaa ggccaccaac 3120
gtggcccact ggaccacccc cagcctgaag tgcatacat aagtttaaac 3170

```

```

<210> 20
<211> 1066
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Sequence

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<400> 20

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

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

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

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

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

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

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp
 100 105 110

Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Arg Thr Phe Gly
 115 120 125

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

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

Glu Val Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser
 165 170 175

Gly Tyr Thr Phe Thr Ser Tyr Val Ile His Trp Val Arg Gln Lys Pro
 180 185 190

Gly Gln Gly Leu Asp Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly
 195 200 205

Thr Asp Tyr Asp Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp

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

Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
 435 440 445

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

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

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 485 490 495

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
 500 505 510

Glu Asn Pro Gly Pro Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro
 515 520 525

Glu Ala Pro Trp Pro Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu
 530 535 540

Pro Trp Ala Leu Val Ala Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala
 545 550 555 560

Ala Cys Ala Val Phe Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg
 565 570 575

Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu
 580 585 590

Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met
 595 600 605

Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu
 610 615 620

Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly
 625 630 635 640

Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly

	645		650		655	
Val Tyr Tyr	Val Phe Phe Gln Leu	Glu Leu Arg Arg	Val Val Ala Gly			
	660	665	670			
Glu Gly Ser	Gly Ser Val Ser	Leu Ala Leu His Leu	Gln Pro Leu Arg			
	675	680	685			
Ser Ala Ala	Gly Ala Ala Ala	Leu Ala Leu Thr	Val Asp Leu Pro Pro			
	690	695	700			
Ala Ser Ser	Glu Ala Arg Asn Ser	Ala Phe Gly Phe	Gln Gly Arg Leu			
705	710	715	720			
Leu His Leu	Ser Ala Gly Gln Arg	Leu Gly Val His	Leu His Thr Glu			
	725	730	735			
Ala Arg Ala	Arg His Ala Trp	Gln Leu Thr Gln	Gly Ala Thr Val Leu			
	740	745	750			
Gly Leu Phe	Arg Val Thr Pro	Glu Ile Pro Ala	Gly Leu Pro Ser Pro			
	755	760	765			
Arg Ser Glu	Gly Ser Gly Ala Thr	Asn Phe Ser Leu	Leu Lys Gln Ala			
	770	775	780			
Gly Asp Val	Glu Glu Asn Pro	Gly Pro Met Tyr	Arg Met Gln Leu Leu			
785	790	795	800			
Ser Cys Ile	Ala Leu Ser Leu	Ala Leu Val Thr	Asn Ser Gly Ile His			
	805	810	815			
Val Phe Ile	Leu Gly Cys Phe	Ser Ala Gly Leu	Pro Lys Thr Glu Ala			
	820	825	830			
Asn Trp Val	Asn Val Ile Ser	Asp Leu Lys Lys	Ile Glu Asp Leu Ile			
	835	840	845			
Gln Ser Met	His Ile Asp Ala	Thr Leu Tyr Thr	Glu Ser Asp Val His			
	850	855	860			

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
865 870 875 880

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
885 890 895

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
900 905 910

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
915 920 925

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
930 935 940

Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
945 950 955 960

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Ala Pro Arg Arg
965 970 975

Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala Leu Leu Leu Leu Leu
980 985 990

Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr Cys Pro Pro Pro Met
995 1000 1005

Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr
1010 1015 1020

Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala
1025 1030 1035

Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn
1040 1045 1050

Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
1055 1060 1065

<210> 21

<211> 3200
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 21
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 cccgacatcg tgatgaccca aagccccgac agcctggccg tgagcctggg cgagagggtg 120
 accatgaact gcaaaagcag ccagtccctg ctgtactcca ccaaccagaa gaactacctg 180
 gcttggtatc aacagaagcc cggacagagc cccaagctgc tgatctattg ggccagcact 240
 agggaaagcg gcgtgcccga taggttcagc ggcagcggga gcggcacaga cttcactctg 300
 accattagca gcgtgcaggc tgaggatgtg gccgtctact actgccagca gtactacagc 360
 tacaggacct ttggggggcgg aactaagctg gagatcaagg gagggggggg atccggggga 420
 ggaggctccg gcggaggcgg aagccaagtg caactgcagc agagcggccc agaggtggtc 480
 aaacctgggg caagcgtgaa gatgagctgc aaggctagcg gctatacctt caccagctat 540
 gtgatccact gggtgaggca gaaaccagga cagggcctgg actggatcgg ctacatcaac 600
 ccctacaatg acggcaccga ttatgacgaa aaattcaagg ggaaggccac cctgaccagc 660
 gacaccagca caagcaccgc ctacatggag ctgtccagcc tgagggtccga ggacaccgcc 720
 gtgtattact gtgccaggga gaaggacaat tacgccaccg gcgcttggtt cgcctactgg 780
 ggccagggca cactggtgac agtgagcagc accacgacgc cagcgccgcg accaccaaca 840
 ccggcgccca ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg 900
 gcggggggcg cagtgcacac gagggggctg gacttcgcct gtgatatacta catctgggcc 960
 cccctggccg gcacctgcgg cgtgctgctg ctgagcctgg tgatcacctt gtactgcagg 1020
 agtaagagga gcaggctcct gcacagtgcac tacatgaaca tgactccccg ccgccccggg 1080
 cccacccgca agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc 1140
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 tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 1260
 cgggaccctg agatgggggg aaagccgcag agaaggaaga accctcagga aggcctgtac 1320
 aatgaactgc agaaagataa gatggcggag gcctacagtg agattgggat gaaaggcgag 1380

cgccggaggg gcaaggggca cgatggcctt taccagggtc tcagtacagc caccaaggac	1440
acctacgacg cccttcacat gcaggccctg cccctcgcg gcagcggcga aggccgcggc	1500
agcctgctga cctgcggcga tgtggaagaa aaccggggcc ccatggaata cgcctctgac	1560
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cagcttacct agggcgccac agtcttggga ctcttcggg tgacccccga aatcccagcc	2280
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aacagcctga gcagcaacgg caacgtgacc gagagcggct gcaaggagtg cgaggagctg	2760
gaggagaaga acatcaagga gttcctgcag agcttcgtgc acatcgtgca gatgttcac	2820
aacaccagct ccggcggcgg ctccggcggc ggcggctccg gcggcggcgg ctccggcggc	2880
ggcggctccg gcggcggctc cctgcaggcc ccagaagag ccagaggctg cagaaccctg	2940
ggcctgcccc ccctgctgct gctgctgctg ctgagacccc ccgccaccag aggcattacc	3000

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tgcccccccc ccatgagcgt ggagcacgcc gacatctggg tgaagagcta cagcctgtac      3060
agcagagaga gatacatctg caacagcggc ttcaagagaa aggccggcac cagcagcctg      3120
accgagtgcg tgctgaacaa ggccaccaac gtggcccact ggaccacccc cagcctgaag      3180
tgcacacgat aagtttaaac                                          3200

```

```

<210> 22
<211> 832
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Sequence

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<400> 22

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```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Val
          100          105          110

```

```

Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Arg Thr Phe Gly Gly
          115          120          125

```

```

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

```

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

Val Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
165 170 175

Tyr Thr Phe Thr Ser Tyr Val Ile His Trp Val Arg Gln Lys Pro Gly
180 185 190

Gln Gly Leu Asp Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr
195 200 205

Asp Tyr Asp Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Thr
210 215 220

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

Thr Ala Val Tyr Tyr Cys Ala Arg Glu Lys Asp Asn Tyr Ala Thr Gly
245 250 255

Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
260 265 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
275 280 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
290 295 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
305 310 315 320

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

Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
340 345 350

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr

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

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

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

Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr
 610 615 620

Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys
 625 630 635 640

Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser
 645 650 655

Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu
 660 665 670

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
 725 730 735

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

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

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

Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe

785		790		795		800									
Lys	Arg	Lys	Ala	Gly	Thr	Ser	Ser	Leu	Thr	Glu	Cys	Val	Leu	Asn	Lys
			805						810					815	

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

<210> 23
 <211> 2501
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 23

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accatgaact gcaaaagcag ccagtccctg ctgtactcca ccaaccagaa gaactacctg	180
gcttggtatc aacagaagcc cggacagagc cccaagctgc tgatctattg ggccagcact	240
agggaaagcg gcgtgcccga taggttcagc ggcagcgga gcggcacaga cttcactctg	300
accattagca gcgtgcaggc tgaggatgtg gccgtctact actgccagca gtactacagc	360
tacaggacct ttggggggcg aactaagctg gagatcaagg gagggggggg atccggggga	420
ggagggtccg gcggaggcgg aagccaagtg caactgcagc agagcggccc agaggtggtc	480
aaacctgggg caagcgtgaa gatgagctgc aaggctagcg gctatacctt caccagctat	540
gtgatccact gggtaggca gaaaccagga cagggcctgg actggatcgg ctacatcaac	600
ccctacaatg acggcaccga ttatgacgaa aaattcaagg ggaaggccac cctgaccagc	660
gacaccagca caagcaccgc ctacatggag ctgtccagcc tgaggtccga ggacaccgcc	720
gtgtattact gtgccaggga gaaggacaat tacgccaccg gcgcttggtt cgcctactgg	780
ggccagggca cactggtgac agtgagcagc accacgacgc cagcgccgcg accaccaaca	840
ccggcgccca ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg	900
gcggggggcg cagtgcacac gagggggctg gacttcgcct gtgatattcta catctgggcg	960
cccttggccg ggacttgtgg ggtccttctc ctgtcactgg ttatcacctt ttactgcagg	1020

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agtaagagga gcaggctcct gcacagtgc tacatgaaca tgactccccg ccgccccggg      1080
cccacccgca agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc      1140
aaacgggggca gaaagaaact cctgtatata ttcaaacaac catttatgag accagtacaa      1200
actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt      1260
gaactgagag tgaagttcag caggagcgca gacgcccccg cgtaccagca gggccagaac      1320
cagctctata acgagctcaa tctaggacga agagaggagt acgatgtttt ggacaagaga      1380
cgtggccggg accctgagat ggggggaaag ccgcagagaa ggaagaaccc tcaggaaggc      1440
ctgtacaatg aactgcagaa agataagatg gcggaggcct acagtgagat tgggatgaaa      1500
ggcgagcgcc ggagggggcaa ggggcacgat ggcctttacc aggggtctcag tacagccacc      1560
aaggacacct acgacgccct tcacatgcag gccctgcccc ctcgcggaag cggagccacc      1620
aacttcagcc tgctgaagca ggccggcgac gtggaggaga accccggccc catgtacaga      1680
atgcagctgc tgagctgcat cgccctgagc ctggccctgg tgaccaacag cggcatccac      1740
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gtgatcagcg acctgaagaa gatcaggagc ctgatccaga gcatgcacat cgacgccacc      1860
ctgtacaccg agagcgacgt gcaccccgagc tgcaaggatga ccgccatgaa gtgcttcctg      1920
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aacctgatca tcctggccaa caacagcctg agcagcaacg gcaacgtgac cgagagcggc      2040
tgcaaggagt gcgaggagct ggaggagaag aacatcaagg agttcctgca gagcttcgtg      2100
cacatcgtgc agatgttcat caacaccagc tccggcgggc gctccggcgg cggcggctcc      2160
ggcggcggcg gctccggcgg cggcggctcc ggcggcggct ccctgcaggc cccagaaga      2220
gccagaggct gcagaaccct gggcctgccc gccctgctgc tgctgctgct gctgagaccc      2280
cccgccacca gaggcacac ctgccccccc cccatgagcg tggagcacgc cgacatctgg      2340
gtgaagagct acagcctgta cagcagagag agatacatct gcaacagcgg cttcaagaga      2400
aaggccggca ccagcagcct gaccgagtgc gtgctgaaca aggccaccaa cgtggcccac      2460
tggaccaccc ccagcctgaa gtgcatcaga taagtttaaa c      2501

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<210> 24
<211> 789
<212> PRT

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<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 24

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

Leu Leu His Ala Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly Pro
20 25 30

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

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

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly
65 70 75 80

Thr Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp
85 90 95

Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu
100 105 110

Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser
115 120 125

Arg Val Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
130 135 140

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

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

Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn
180 185 190

Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro
 195 200 205

Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp
 210 215 220

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser
 225 230 235 240

Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu
 245 250 255

Glu Tyr Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
 260 265 270

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
 275 280 285

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
 290 295 300

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
 305 310 315 320

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

Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
 340 345 350

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

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

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
 385 390 395 400

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

			405				410				415				
Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Gln
			420					425					430		
Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp
		435					440					445			
Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg
	450					455					460				
Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr
465					470					475					480
Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg	Gly
				485					490					495	
Ser	Gly	Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr	Cys	Gly	Asp	Val	Glu	Glu
			500					505					510		
Asn	Pro	Gly	Pro	Met	Tyr	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu
		515					520					525			
Ser	Leu	Ala	Leu	Val	Thr	Asn	Ser	Gly	Ile	His	Val	Phe	Ile	Leu	Gly
	530					535					540				
Cys	Phe	Ser	Ala	Gly	Leu	Pro	Lys	Thr	Glu	Ala	Asn	Trp	Val	Asn	Val
545					550					555					560
Ile	Ser	Asp	Leu	Lys	Lys	Ile	Glu	Asp	Leu	Ile	Gln	Ser	Met	His	Ile
				565					570					575	
Asp	Ala	Thr	Leu	Tyr	Thr	Glu	Ser	Asp	Val	His	Pro	Ser	Cys	Lys	Val
			580					585					590		
Thr	Ala	Met	Lys	Cys	Phe	Leu	Leu	Glu	Leu	Gln	Val	Ile	Ser	Leu	Glu
		595					600					605			
Ser	Gly	Asp	Ala	Ser	Ile	His	Asp	Thr	Val	Glu	Asn	Leu	Ile	Ile	Leu
	610					615					620				

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
 625 630 635 640

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
 645 650 655

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly
 660 665 670

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

Ser Gly Gly Gly Ser Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg
 690 695 700

Thr Leu Gly Leu Pro Ala Leu Leu Leu Leu Leu Leu Arg Pro Pro
 705 710 715 720

Ala Thr Arg Gly Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala
 725 730 735

Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile
 740 745 750

Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu
 755 760 765

Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser
 770 775 780

Leu Lys Cys Ile Arg
 785

<210> 25
 <211> 2372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 25

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atgtcctgca aggcttctgg atacacattc actagctatg ttatgcactg ggtgaagcag	180
aagcctgggc agggccttga gtggattgga tatattaatc cttacaatga tggactaag	240
tacaatgaga agttcaaagg caaggccaca ctgacttcag acaaatcctc cagcacagcc	300
tacatggagc tcagcagcct gacctctgag gactctgcgg tctattactg tgcaagaggg	360
acttattact acggtagtag ggtatttgac tactggggcc aaggcaccac tctcacagtc	420
tcctcaggtg gagggggctc aggcggaggt ggctctgggg gtggaggctc ggacattgtg	480
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aggtctagta agagtctcct gaatagtaat ggcaacactt acttgtattg gttcctgcag	600
aggccaggcc agtctcctca gctcctgata tatcggatgt ccaaccttgc ctcaggagtc	660
ccagacaggt tcagtggcag tgggtcagga actgctttca cactgagaat cagtagagtg	720
gaggctgagg atgtgggtgt ttattactgt atgcaacatc tagaatatcc gttcacgttc	780
ggtgctggga ccaagctgga gctgaaacgg accacgacgc cagcgccgcg accaccaaca	840
ccggcgccca ccatcgctc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg	900
gcggggggcg cagtgcacac gagggggctg gacttcgcct gtgatatcta catctgggcg	960
cccttggccg ggacttgtgg ggtccttctc ctgtcactgg ttatcacctt ttactgcagg	1020
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cccacccgca agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc	1140
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tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc	1260
cgggaccctg agatgggggg aaagccgcag agaaggaaga accctcagga aggcctgtac	1320
aatgaactgc agaaagataa gatggcggag gcctacagtg agattgggat gaaaggcgag	1380
cgccggaggg gcaaggggca cgatggcctt taccagggtc tcagtacagc caccaaggac	1440
acctacgacg cccttcacat gcaggccctg cccctcgcg gcagcggcga aggccgcggc	1500
agcctgctga cctgcggcga tgtggaagaa aaccggggcc ccatgtacag aatgcagctg	1560
ctgagctgca tcgccctgag cctggccctg gtgaccaaca gcggcatcca cgtgttcac	1620

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gacctgaaga agatcgagga cctgatccag agcatgcaca tcgacgccac cctgtacacc 1740
gagagcgacg tgcaccccag ctgcaaggtg accgccatga agtgcttcct gctggagctg 1800
caggtgatca gcctggagag cggcgacgcc agcatccacg acaccgtgga gaacctgatc 1860
atcctggcca acaacagcct gagcagcaac ggcaacgtga ccgagagcgg ctgcaaggag 1920
tgcgaggagc tggaggagaa gaacatcaag gagttcctgc agagcttcgt gcacatcgtg 1980
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tacagcctgt acagcagaga gagatacatc tgcaacagcg gcttcaagag aaaggccggc 2280
accagcagcc tgaccgagtg cgtgctgaac aaggccacca acgtggccca ctggaccacc 2340
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<210> 26
<211> 1066
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Sequence

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<400> 26

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

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Leu Leu Leu His Ala Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly
20           25           30

```

```

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

```

```

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

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Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp

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

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
 290 295 300

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
 305 310 315 320

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

Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser
 340 345 350

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

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
 370 375 380

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
 385 390 395 400

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
 405 410 415

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
 420 425 430

Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
 435 440 445

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

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

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 485 490 495

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu

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

Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu
725 730 735

Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu
740 745 750

Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro
755 760 765

Arg Ser Glu Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala
770 775 780

Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu
785 790 795 800

Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His
805 810 815

Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala
820 825 830

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
835 840 845

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
850 855 860

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
865 870 875 880

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
885 890 895

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
900 905 910

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
915 920 925

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn

930

935

940

Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 945 950 955 960

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Ala Pro Arg Arg
 965 970 975

Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala Leu Leu Leu Leu Leu
 980 985 990

Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr Cys Pro Pro Pro Met
 995 1000 1005

Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr
 1010 1015 1020

Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala
 1025 1030 1035

Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn
 1040 1045 1050

Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
 1055 1060 1065

<210> 27

<211> 3200

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 27

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atgtcctgca aggcttctgg atacacattc actagctatg ttatgcactg ggtgaagcag 180

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tacatggagc tcagcagcct gacctctgag gactctgcgg tctattactg tgcaagaggg	360
acttattact acggtagtag ggtatttgac tactggggcc aaggcaccac tctcacagtc	420
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accgagtgcg tgctgaacaa ggccaccaac gtggcccact ggaccacccc cagcctgaag 3180
tgcatcagat aagtttaaac 3200

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<210> 28
<211> 1300
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Sequence

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<400> 28

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

Ala Ser Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly
 50 55 60

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

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

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

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

Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 130 135 140

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

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

Ser Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
 180 185 190

Trp Met Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln
 195 200 205

Lys Phe Lys Gly Arg Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr

210		215		220
Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr				
225		230		235
Phe Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asp Val				
	245		250	255
Trp Gly Gln Gly Thr Thr Val Thr Val Ser 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 Gly Ser Gly Ala Thr Asn
 485 490 495

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

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

His Ala Ala Arg Pro Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu
 530 535 540

Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
 545 550 555 560

Thr Phe Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln
 565 570 575

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
 580 585 590

Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser
 595 600 605

Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser
 610 615 620

Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val
 625 630 635 640

Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly

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Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Val	
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Met	Thr	Gln	Ala	Ala	Pro	Ser	Ile	Pro	Val	Thr	Pro	Gly	Glu	Ser	Val	
		675					680					685				
Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser	Leu	Leu	Asn	Ser	Asn	Gly	Asn	
	690					695					700					
Thr	Tyr	Leu	Tyr	Trp	Phe	Leu	Gln	Arg	Pro	Gly	Gln	Ser	Pro	Gln	Leu	
705					710					715					720	
Leu	Ile	Tyr	Arg	Met	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Asp	Arg	Phe	
				725					730					735		
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ala	Phe	Thr	Leu	Arg	Ile	Ser	Arg	Val	
			740					745					750			
Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	His	Leu	Glu	Tyr	
		755					760					765				
Pro	Phe	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	Arg	Thr	Thr	
	770					775					780					
Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	
785					790					795					800	
Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	
				805					810					815		
Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	
			820					825					830			
Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	
		835					840					845				
Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	
	850					855					860					

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
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Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
885 890 895

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
900 905 910

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

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

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
945 950 955 960

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
965 970 975

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

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser
995 1000 1005

Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
1010 1015 1020

Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala
1025 1030 1035

Leu Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His Val Phe Ile
1040 1045 1050

Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp
1055 1060 1065

Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln

1070						1075						1080					
Ser	Met	His	Ile	Asp	Ala	Thr	Leu	Tyr	Thr	Glu	Ser	Asp	Val	His			
1085						1090					1095						
Pro	Ser	Cys	Lys	Val	Thr	Ala	Met	Lys	Cys	Phe	Leu	Leu	Glu	Leu			
1100						1105					1110						
Gln	Val	Ile	Ser	Leu	Glu	Ser	Gly	Asp	Ala	Ser	Ile	His	Asp	Thr			
1115						1120					1125						
Val	Glu	Asn	Leu	Ile	Ile	Leu	Ala	Asn	Asn	Ser	Leu	Ser	Ser	Asn			
1130						1135					1140						
Gly	Asn	Val	Thr	Glu	Ser	Gly	Cys	Lys	Glu	Cys	Glu	Glu	Leu	Glu			
1145						1150					1155						
Glu	Lys	Asn	Ile	Lys	Glu	Phe	Leu	Gln	Ser	Phe	Val	His	Ile	Val			
1160						1165					1170						
Gln	Met	Phe	Ile	Asn	Thr	Ser	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly			
1175						1180					1185						
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly			
1190						1195					1200						
Ser	Leu	Gln	Ala	Pro	Arg	Arg	Ala	Arg	Gly	Cys	Arg	Thr	Leu	Gly			
1205						1210					1215						
Leu	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	Pro	Pro	Ala	Thr			
1220						1225					1230						
Arg	Gly	Ile	Thr	Cys	Pro	Pro	Pro	Met	Ser	Val	Glu	His	Ala	Asp			
1235						1240					1245						
Ile	Trp	Val	Lys	Ser	Tyr	Ser	Leu	Tyr	Ser	Arg	Glu	Arg	Tyr	Ile			
1250						1255					1260						
Cys	Asn	Ser	Gly	Phe	Lys	Arg	Lys	Ala	Gly	Thr	Ser	Ser	Leu	Thr			
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Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr
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Pro Ser Leu Lys Cys Ile Arg
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<220>
 <223> Synthetic Sequence

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 aggttcagcg gcagcggcag cggcaccgac tacaccttca ccatcagcag cctgcagccc 300
 gaggacatcg ccacctacta ctgccagcag tggaccagca accccccac cttcggcggc 360
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caaccattta tgagaccagt acaaactact caagaggaag atggctgtag ctgccgattt	2640
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ccccctacc agcagggcca gaaccagctg tacaacgagc tgaacctggg caggagggag 2760
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tgcaacagcg gcttcaagag aaaggccggc accagcagcc tgaccgagtg cgtgctgaac 3840
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<210> 30
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<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Sequence

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<400> 30

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Asp Arg Thr Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala

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

Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Leu Asn
 225 230 235 240

Asn Leu Gln Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Asp Thr
 245 250 255

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

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

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

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
 305 310 315 320

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

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

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

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
 370 375 380

Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
 385 390 395 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
 405 410 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
 420 425 430

Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu

435

440

445

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
 450 455 460

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
 465 470 475 480

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
 485 490 495

Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
 500 505 510

Asp Val Glu Glu Asn Pro Gly Pro Met Glu Tyr Ala Ser Asp Ala Ser
 515 520 525

Leu Asp Pro Glu Ala Pro Trp Pro Pro Ala Pro Arg Ala Arg Ala Cys
 530 535 540

Arg Val Leu Pro Trp Ala Leu Val Ala Gly Leu Leu Leu Leu Leu Leu
 545 550 555 560

Leu Ala Ala Ala Cys Ala Val Phe Leu Ala Cys Pro Trp Ala Val Ser
 565 570 575

Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala Ser Pro Arg Leu Arg Glu
 580 585 590

Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala Gly Leu Leu Asp Leu Arg
 595 600 605

Gln Gly Met Phe Ala Gln Leu Val Ala Gln Asn Val Leu Leu Ile Asp
 610 615 620

Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly Leu Ala Gly Val Ser Leu
 625 630 635 640

Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr Lys Glu Leu Val Val Ala
 645 650 655

Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln Leu Glu Leu Arg Arg Val
 660 665 670

Val Ala Gly Glu Gly Ser Gly Ser Val Ser Leu Ala Leu His Leu Gln
 675 680 685

Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala Leu Ala Leu Thr Val Asp
 690 695 700

Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn Ser Ala Phe Gly Phe Gln
 705 710 715 720

Gly Arg Leu Leu His Leu Ser Ala Gly Gln Arg Leu Gly Val His Leu
 725 730 735

His Thr Glu Ala Arg Ala Arg His Ala Trp Gln Leu Thr Gln Gly Ala
 740 745 750

Thr Val Leu Gly Leu Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu
 755 760 765

Pro Ser Pro Arg Ser Glu Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu
 770 775 780

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg Met
 785 790 795 800

Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser
 805 810 815

Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys
 820 825 830

Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu
 835 840 845

Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser
 850 855 860

Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu

Arg

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

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 tacaccggcg tgcccagacag gttcatcggc agcggcagcg gcaccgactt caccctgacc 300
 atcagcagcg tgaggccga ggacctggcc gactacttct gccagcagca ctacagcacc 360
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 agacgtggcc gggaccctga gatgggggga aagccgcaga gaaggaagaa ccctcaggaa 1320

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aaaggcgagc gccggagggg caaggggcac gatggccttt accaggggtct cagtacagcc	1440
accaaggaca cctacgacgc ctttcacatg caggccctgc cccctcgcgg cagcggcgaa	1500
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tgccgcgtac tgccttgggc cctggctcgc gggctgctgc tgctgctgct gctcgtgcc	1680
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atgttcatca acaccagctc cggcggcggc tccggcggcg gcggctccgg cggcggcggc	2880
tccggcggcg gcggctccgg cggcggctcc ctgcaggccc ccagaagagc cagaggctgc	2940

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agaaccctgg gcctgcccgc cctgctgctg ctgctgctgc tgagaccccc cgccaccaga      3000
ggcatcacct gccccccccc catgagcgtg gagcacgccg acatctgggt gaagagctac      3060
agcctgtaca gcagagagag atacatctgc aacagcggct tcaagagaaa ggccggcacc      3120
agcagcctga ccgagtgcgt gctgaacaag gccaccaacg tggcccactg gaccaccccc      3180
agcctgaagt gcatcagata agtttaaac      3209

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<210> 32
 <211> 1081
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 32

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

```

```

Leu Leu Leu His Ala Ala Arg Pro Met Ala Asp Tyr Lys Asp Ile Val
          20           25           30

```

```

Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val
      35           40           45

```

```

Asn Ile Thr Cys Lys Ala Ser Gln Asn Val Asp Ser Ala Val Ala Trp
      50           55           60

```

```

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

```

```

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

```

```

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
      100           105           110

```

```

Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Trp Thr Phe Gly
      115           120           125

```

```

Gly Gly Thr Lys Leu Glu Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly

```

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

Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
 355 360 365

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
 370 375 380

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
 385 390 395 400

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
 405 410 415

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
 420 425 430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln
 435 440 445

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
 450 455 460

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
 465 470 475 480

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
 485 490 495

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly
 500 505 510

Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
 515 520 525

Asn Pro Gly Pro Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu
 530 535 540

Ala Pro Trp Pro Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro
 545 550 555 560

Trp Ala Leu Val Ala Gly Leu Leu Leu Leu Leu Leu Ala Ala Ala

565																570																575																						
Cys	Ala	Val	Phe	Leu	Ala	Cys	Pro	Trp	Ala	Val	Ser	Gly	Ala	Arg	Ala																																							
			580																	585																	590																	
Ser	Pro	Gly	Ser	Ala	Ala	Ser	Pro	Arg	Leu	Arg	Glu	Gly	Pro	Glu	Leu																																							
			595																	600																	605																	
Ser	Pro	Asp	Asp	Pro	Ala	Gly	Leu	Leu	Asp	Leu	Arg	Gln	Gly	Met	Phe																																							
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Ala	Gln	Leu	Val	Ala	Gln	Asn	Val	Leu	Leu	Ile	Asp	Gly	Pro	Leu	Ser																																							
			625																	630																	635																	
Trp	Tyr	Ser	Asp	Pro	Gly	Leu	Ala	Gly	Val	Ser	Leu	Thr	Gly	Gly	Leu																																							
							645																	650																	655													
Ser	Tyr	Lys	Glu	Asp	Thr	Lys	Glu	Leu	Val	Val	Ala	Lys	Ala	Gly	Val																																							
							660																	665																	670													
Tyr	Tyr	Val	Phe	Phe	Gln	Leu	Glu	Leu	Arg	Arg	Val	Val	Ala	Gly	Glu																																							
							675																	680																	685													
Gly	Ser	Gly	Ser	Val	Ser	Leu	Ala	Leu	His	Leu	Gln	Pro	Leu	Arg	Ser																																							
							690																	695																	700													
Ala	Ala	Gly	Ala	Ala	Ala	Leu	Ala	Leu	Thr	Val	Asp	Leu	Pro	Pro	Ala																																							
							705																	710																	715													
Ser	Ser	Glu	Ala	Arg	Asn	Ser	Ala	Phe	Gly	Phe	Gln	Gly	Arg	Leu	Leu																																							
							720																	725																	730													
His	Leu	Ser	Ala	Gly	Gln	Arg	Leu	Gly	Val	His	Leu	His	Thr	Glu	Ala																																							
							735																	740																	745													
Arg	Ala	Arg	His	Ala	Trp	Gln	Leu	Thr	Gln	Gly	Ala	Thr	Val	Leu	Gly																																							
							750																	755																	760													
Leu	Phe	Arg	Val	Thr	Pro	Glu	Ile	Pro	Ala	Gly	Leu	Pro	Ser	Pro	Arg																																							
							765																	770																	775													
							780																	785																	790													

Ser Glu Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
785 790 795 800

Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser
805 810 815

Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His Val
820 825 830

Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn
835 840 845

Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln
850 855 860

Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro
865 870 875 880

Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val
885 890 895

Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn
900 905 910

Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr
915 920 925

Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys
930 935 940

Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr
945 950 955 960

Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
965 970 975

Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Ala Pro Arg Arg Ala
980 985 990

Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala Leu Leu Leu Leu Leu Leu

995	1000	1005
Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr Cys Pro Pro Pro Met 1010 1015 1020		
Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr 1025 1030 1035		
Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala 1040 1045 1050		
Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn 1055 1060 1065		
Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg 1070 1075 1080		

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 <211> 3245
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 33
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 gtgggcgaca ggggtgaacat cacctgcaag gccagccaga acgtggacag cgccgtggcc 180
 tgggtaccagc agaagcccgg ccagagcccc aaggccctga tctacagcgc cagctacagg 240
 tacagcggcg tgcccgacag gttcaccggc aggggcagcg gcaccgactt caccctgacc 300
 atcagcagcg tgcaggccga ggacctggcc gtgtactact gccagcagta ctacagcacc 360
 ccctggacct tcggcggcgg caccaagctg gagatcaaga ggggcggcgg cggcagcggc 420
 ggccggcggca gcggcggcgg cggcagcggc ggccggcggca gcgaggtgaa gctggtggag 480
 agcggcggcg gcctggtgca gcccggcggc agcctgagcc tgagctgcgc cgccagcggc 540
 ttcaccttca ccgactacta catgagctgg gtgaggcagc cccccggcaa ggccctggag 600
 tggctggccc tgatcaggag caaggccgac ggctacacca ccgagtacag cgccagcgtg 660

aagggcaggt tcaccctgag cagggacgac agccagagca tcctgtacct gcagatgaac	720
gccctgaggc ccgaggacag cgccacctac tactgcgcca gggacgccgc ctactacagc	780
tactacagcc ccgagggcgc catggactac tggggccagg gcaccagcgt gaccgtgagc	840
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gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgcagtg	960
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ctcctgcaca gtgactacat gaacatgact ccccgccgcc ccgggcccac ccgcaagcat	1140
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gccacagtct tgggactctt ccgggtgacc cccgaaatcc cagccggact cccttcaccg      2340
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gagaaccctg gacctatgta cagaatgcag ctgctgagct gcatcgccct gagcctggcc      2460
ctggtgacca acagcggcat ccacgtgttc atcctgggct gcttcagcgc cggcctgccc      2520
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ctgctgctgc tgctgctgag accccccgcc accagaggca tcacctgccc ccccccatg      3060
agcgtggagc acgccgacat ctgggtgaag agctacagcc tgtacagcag agagagatac      3120
atctgcaaca gcggcttcaa gagaaaggcc ggcaccagca gcctgaccga gtgcgtgctg      3180
aacaaggcca ccaacgtggc ccactggacc acccccagcc tgaagtgcac cagataagtt      3240
taaac                                          3245

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<210> 34
<211> 1324
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Sequence

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<400> 34

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```

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

```

```

Leu Leu Leu His Ala Ala Arg Pro Met Ala Asp Tyr Lys Asp Ile Val
          20          25          30

```

```

Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val

```

35

40

45

Asn Ile Thr Cys Lys Ala Ser Gln Asn Val Asp Ser Ala Val Ala Trp
 50 55 60

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

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

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
 100 105 110

Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Trp Thr Phe Gly
 115 120 125

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys
 145 150 155 160

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

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asp Tyr Tyr Met Ser
 180 185 190

Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala Leu Ile
 195 200 205

Arg Ser Lys Ala Asp Gly Tyr Thr Thr Glu Tyr Ser Ala Ser Val Lys
 210 215 220

Gly Arg Phe Thr Leu Ser Arg Asp Asp Ser Gln Ser Ile Leu Tyr Leu
 225 230 235 240

Gln Met Asn Ala Leu Arg Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Ala
 245 250 255

Arg Asp Ala Ala Tyr Tyr Ser Tyr Tyr Ser Pro Glu Gly Ala Met Asp
 260 265 270

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Gly Ala
 275 280 285

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
 290 295 300

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
 305 310 315 320

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
 325 330 335

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
 340 345 350

Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
 355 360 365

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
 370 375 380

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
 385 390 395 400

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
 405 410 415

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
 420 425 430

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln
 435 440 445

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
 450 455 460

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg

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

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

Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Pro Leu Thr Ser Tyr Gly
705 710 715 720

Val Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly
725 730 735

Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr His Ser Ala Leu Ile Ser
740 745 750

Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
755 760 765

Leu Asn Asn Leu Gln Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
770 775 780

Asp Thr Tyr Tyr Pro Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
785 790 795 800

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

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

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

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

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys
865 870 875 880

Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr
885 890 895

Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu

	900		905		910	
Gly	Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro					
	915		920		925	
Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly						
	930		935		940	
Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro						
	945		950		955	960
Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu						
		965		970		975
Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile						
		980		985		990
Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr						
	995		1000		1005	
Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His						
	1010		1015		1020	
Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser						
	1025		1030		1035	
Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr						
	1040		1045		1050	
Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val						
	1055		1060		1065	
Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala						
	1070		1075		1080	
Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp						
	1085		1090		1095	
Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala						
	1100		1105		1110	

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1130						1135					1140			
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1145						1150					1155			
Leu	Ala	Asn	Asn	Ser	Leu	Ser	Ser	Asn	Gly	Asn	Val	Thr	Glu	Ser
1160						1165					1170			
Gly	Cys	Lys	Glu	Cys	Glu	Glu	Leu	Glu	Glu	Lys	Asn	Ile	Lys	Glu
1175						1180					1185			
Phe	Leu	Gln	Ser	Phe	Val	His	Ile	Val	Gln	Met	Phe	Ile	Asn	Thr
1190						1195					1200			
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1205						1210					1215			
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Leu	Gln	Ala	Pro	Arg
1220						1225					1230			
Arg	Ala	Arg	Gly	Cys	Arg	Thr	Leu	Gly	Leu	Pro	Ala	Leu	Leu	Leu
1235						1240					1245			
Leu	Leu	Leu	Leu	Arg	Pro	Pro	Ala	Thr	Arg	Gly	Ile	Thr	Cys	Pro
1250						1255					1260			
Pro	Pro	Met	Ser	Val	Glu	His	Ala	Asp	Ile	Trp	Val	Lys	Ser	Tyr
1265						1270					1275			
Ser	Leu	Tyr	Ser	Arg	Glu	Arg	Tyr	Ile	Cys	Asn	Ser	Gly	Phe	Lys
1280						1285					1290			
Arg	Lys	Ala	Gly	Thr	Ser	Ser	Leu	Thr	Glu	Cys	Val	Leu	Asn	Lys
1295						1300					1305			
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1310

1315

1320

Arg

<210> 35

<211> 3985

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 35

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actacagcac cccctggacc ttcggcggcg gcaccaagct ggagatcaag aggggcggcg	420
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<210> 36
<211> 1313
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Sequence

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<400> 36

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

Gly Arg Phe Thr Leu Ser Arg Asp Asp Ser Gln Ser Ile Leu Tyr Leu
225 230 235 240

Gln Met Asn Ala Leu Arg Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Ala
245 250 255

Arg Asp Ala Ala Tyr Tyr Ser Tyr Tyr Ser Pro Glu Gly Ala Met Asp
260 265 270

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Gly Ala
275 280 285

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
290 295 300

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
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Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
325 330 335

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
340 345 350

Ile Thr Leu Tyr Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
355 360 365

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
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Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
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Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
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Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
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Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln

435

440

445

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
 450 455 460

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
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Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
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Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly
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Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu
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Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro
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Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln
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Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr
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Cys Lys Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Phe Gln Gln
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Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Ser Pro Ser Tyr Arg
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Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
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Phe Thr Phe Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
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Tyr Cys Gln Gln Leu Tyr Ser Thr Pro Tyr Thr Phe Gly Gly Gly Thr
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Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
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Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val
675 680 685

Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr
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Phe Thr Asp Tyr Tyr Leu Asp Trp Val Lys Gln Ser His Gly Glu Ser
705 710 715 720

Phe Glu Trp Ile Gly Arg Val Asn Pro Tyr Asn Gly Gly Thr Ile Tyr
725 730 735

Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
740 745 750

Ser Thr Ala Tyr Met Asp Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala
755 760 765

Val Tyr Tyr Cys Ala Arg Asp His Tyr Arg Tyr Asp Pro Leu Leu Asp
770 775 780

Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Thr Thr Thr Pro
785 790 795 800

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
805 810 815

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
820 825 830

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
835 840 845

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

Cys Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met

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Cys	Lys	Val	Thr	Ala	Met	Lys	Cys	Phe	Leu	Leu	Glu	Leu	Gln	Val
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1145						1150					1155			
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1285

1290

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<220>
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<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Sequence

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<400> 38

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Leu Leu Leu His Ala Ala Arg Pro Asp Val Val Met Thr Gln Ser His
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Arg Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Arg
 35 40 45

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

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

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

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

Gln Gln His Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
 115 120 125

Asp Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 130 135 140

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

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

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

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

Asp Phe Lys Gly Arg Phe Ala Phe Ser Val Glu Thr Ser Ala Thr Thr

210	215	220
Ala Tyr Leu Gln Ile 225	Asn Asn Leu Lys Thr 230	Glu Asp Thr Ala Thr Tyr 235 240
Phe Cys Ala Arg Gly 245	Glu Ile Tyr Tyr Gly 250	Tyr Asp Gly Gly Phe Ala 255
Tyr Trp Gly Gln Gly 260	Thr Leu Val Thr Val 265	Ser Ala Thr Thr Thr Pro 270
Ala Pro Arg Pro Pro 275	Thr Pro Ala Pro Thr 280	Ile Ala Ser Gln Pro Leu 285
Ser Leu Arg Pro Glu 290	Ala Cys Arg Pro Ala 295	Ala Gly Gly Ala Val His 300
Thr Arg Gly Leu Asp 305	Phe Ala Cys Asp Ile 310 315	Tyr Ile Trp Ala Pro Leu 320
Ala Gly Thr Cys Gly 325	Val Leu Leu Leu Ser 330	Leu Val Ile Thr Leu Tyr 335
Cys Arg Ser Lys Arg 340	Ser Arg Leu Leu His 345	Ser Asp Tyr Met Asn Met 350
Thr Pro Arg Arg Pro 355	Gly Pro Thr Arg Lys 360	His Tyr Gln Pro Tyr Ala 365
Pro Pro Arg Asp Phe 370	Ala Ala Tyr Arg Ser 375	Arg Val Lys Phe Ser Arg 380
Ser Ala Asp Ala Pro 385	Ala Tyr Gln Gln Gly 390 395	Gln Asn Gln Leu Tyr Asn 400
Glu Leu Asn Leu Gly 405	Arg Arg Glu Glu Tyr 410	Asp Val Leu Asp Lys Arg 415
Arg Gly Arg Asp Pro 420	Glu Met Gly Gly Lys 425	Pro Gln Arg Arg Lys Asn 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 Glu Gly
 485 490 495

Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro
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Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro
 515 520 525

Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val
 530 535 540

Ala Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe
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Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser
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Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
 580 585 590

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
 595 600 605

Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
 610 615 620

Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu
 625 630 635 640

Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe

645							650							655						
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Val	Ser	Leu 675	Ala	Leu	His	Leu	Gln 680	Pro	Leu	Arg	Ser	Ala 685	Ala	Gly	Ala					
Ala	Ala 690	Leu	Ala	Leu	Thr	Val 695	Asp	Leu	Pro	Pro	Ala 700	Ser	Ser	Glu	Ala					
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Gly	Gln	Arg	Leu	Gly 725	Val	His	Leu	His 730	Thr	Glu	Ala	Arg	Ala 735	Arg	His					
Ala	Trp	Gln 740	Leu	Thr	Gln	Gly	Ala 745	Thr	Val	Leu	Gly	Leu 750	Phe	Arg	Val					
Thr	Pro	Glu 755	Ile	Pro	Ala	Gly	Leu 760	Pro	Ser	Pro	Arg	Ser 765	Glu	Gly	Ser					
Gly 770	Ala	Thr	Asn	Phe	Ser	Leu 775	Leu	Lys	Gln	Ala	Gly 780	Asp	Val	Glu	Glu					
Asn 785	Pro	Gly	Pro	Met	Tyr 790	Arg	Met	Gln	Leu 795	Leu	Ser	Cys	Ile	Ala	Leu 800					
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Cys	Phe	Ser	Ala 820	Gly	Leu	Pro	Lys	Thr 825	Glu	Ala	Asn	Trp	Val 830	Asn	Val					
Ile	Ser	Asp 835	Leu	Lys	Lys	Ile	Glu 840	Asp	Leu	Ile	Gln	Ser 845	Met	His	Ile					
Asp 850	Ala	Thr	Leu	Tyr	Thr	Glu 855	Ser	Asp	Val	His	Pro 860	Ser	Cys	Lys	Val					

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
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Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
885 890 895

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
900 905 910

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
915 920 925

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly
930 935 940

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
945 950 955 960

Ser Gly Gly Gly Ser Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg
965 970 975

Thr Leu Gly Leu Pro Ala Leu Leu Leu Leu Leu Leu Arg Pro Pro
980 985 990

Ala Thr Arg Gly Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala
995 1000 1005

Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr
1010 1015 1020

Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu
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Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr
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Thr Pro Ser Leu Lys Cys Ile Arg
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 <212> DNA
 <213> Artificial Sequence

<220>
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 <211> 1301
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 40

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Arg Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Arg
 35 40 45

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

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

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

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

Gln Gln His Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
 115 120 125

Asp Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 130 135 140

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

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

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

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

Asp Phe Lys Gly Arg Phe Ala Phe Ser Val Glu Thr Ser Ala Thr Thr
 210 215 220

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

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

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

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

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

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

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

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

Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala

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

Ala Pro Arg Leu Leu Ile Ser Gly Ala Thr Ser Leu Glu Thr Gly Val
 580 585 590

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Lys Asp Tyr Thr Leu Ser
 595 600 605

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

Tyr Trp Ser Thr Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 625 630 635 640

Arg Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 645 650 655

Gly Ser Ala Gln Pro Ala Met Ala Lys Val Gln Leu Gln Glu Ser Gly
 660 665 670

Pro Ser Leu Val Gln Pro Ser Gln Arg Leu Ser Ile Thr Cys Thr Val
 675 680 685

Ser Gly Phe Ser Leu Ile Ser Tyr Gly Val His Trp Val Arg Gln Ser
 690 695 700

Pro Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Arg Gly Gly Ser
 705 710 715 720

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

Asn Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ala Asp
 740 745 750

Asp Thr Ala Ile Tyr Phe Cys Ala Lys Thr Leu Ile Thr Thr Gly Tyr
 755 760 765

Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Thr
 770 775 780

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser

785		790		795		800									
Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly
				805					810					815	
Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp
			820					825					830		
Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile
		835					840					845			
Thr	Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys
	850					855					860				
Gln	Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys
865					870					875					880
Ser	Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val
				885					890					895	
Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn
			900					905					910		
Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val
		915					920					925			
Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Gln
	930					935					940				
Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp
945					950					955					960
Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg
				965					970					975	
Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr
			980					985					990		
Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg	Gly
		995					1000					1005			

Ser	Gly	Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr	Cys	Gly	Asp	Val	Glu
1010						1015					1020			
Glu	Asn	Pro	Gly	Pro	Met	Tyr	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile
1025						1030					1035			
Ala	Leu	Ser	Leu	Ala	Leu	Val	Thr	Asn	Ser	Gly	Ile	His	Val	Phe
1040						1045					1050			
Ile	Leu	Gly	Cys	Phe	Ser	Ala	Gly	Leu	Pro	Lys	Thr	Glu	Ala	Asn
1055						1060					1065			
Trp	Val	Asn	Val	Ile	Ser	Asp	Leu	Lys	Lys	Ile	Glu	Asp	Leu	Ile
1070						1075					1080			
Gln	Ser	Met	His	Ile	Asp	Ala	Thr	Leu	Tyr	Thr	Glu	Ser	Asp	Val
1085						1090					1095			
His	Pro	Ser	Cys	Lys	Val	Thr	Ala	Met	Lys	Cys	Phe	Leu	Leu	Glu
1100						1105					1110			
Leu	Gln	Val	Ile	Ser	Leu	Glu	Ser	Gly	Asp	Ala	Ser	Ile	His	Asp
1115						1120					1125			
Thr	Val	Glu	Asn	Leu	Ile	Ile	Leu	Ala	Asn	Asn	Ser	Leu	Ser	Ser
1130						1135					1140			
Asn	Gly	Asn	Val	Thr	Glu	Ser	Gly	Cys	Lys	Glu	Cys	Glu	Glu	Leu
1145						1150					1155			
Glu	Glu	Lys	Asn	Ile	Lys	Glu	Phe	Leu	Gln	Ser	Phe	Val	His	Ile
1160						1165					1170			
Val	Gln	Met	Phe	Ile	Asn	Thr	Ser	Ser	Gly	Gly	Gly	Ser	Gly	Gly
1175						1180					1185			
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
1190						1195					1200			
Gly	Ser	Leu	Gln	Ala	Pro	Arg	Arg	Ala	Arg	Gly	Cys	Arg	Thr	Leu

1205

1210

1215

Gly Leu Pro Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala
 1220 1225 1230

Thr Arg Gly Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala
 1235 1240 1245

Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr
 1250 1255 1260

Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu
 1265 1270 1275

Thr Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr
 1280 1285 1290

Thr Pro Ser Leu Lys Cys Ile Arg
 1295 1300

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 <211> 3905
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

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 agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag 180
 cccggccaga gcccgaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc 240
 gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag 300
 gccgaggacc tggccgtgta ctactgccag cagcactaca gcaccccctg gaccttcggc 360
 ggcggcacca agctggacat caagggaggg gggggatccg ggggaggagg ctccggcgga 420
 ggcggaagcc agatccagct ggtgcagagc ggccccgacc tgaagaagcc cggcgagacc 480
 gtgaagctga gctgcaaggc cagcggctac accttcacca acttcggcat gaactgggtg 540

aagcaggccc ccggcaaggg cttcaagtgg atggcctgga tcaacaccta caccggcgag	600
agctacttcg ccgacgactt caagggcagg ttgccttca gcgtggagac cagcgccacc	660
accgcctacc tgcagatcaa caacctgaag accgaggaca ccgccaccta cttctgcgcc	720
agggggcgaga tctactacgg ctacgacggc ggcttcgcct actggggcca gggcaccctg	780
gtgaccgtga gcgccaccac gacgccagcg ccgcgaccac caacaccggc gcccaccatc	840
gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgcagtg	900
cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact	960
tgtgggggtcc ttctcctgtc actggttatc accctttact gcaggagtaa gaggagcagg	1020
ctcctgcaca gtgactacat gaacatgact ccccgccgcc ccggggcccac ccgcaagcat	1080
taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc	1140
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gataagatgg cggaggccta cagtgcagatt gggatgaaag gcgagcgccg gaggggcaag	1380
gggcacgatg gcctttacca gggctctcagt acagccacca aggacaccta cgacgccctt	1440
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gccggcgacg tggaggagaa ccccggcccc atggccctgc ccgtgaccgc cctgctgctg	1560
cccctggccc tgctgctgca cgccgccagg ccgacatcg agctgacca gagccccagc	1620
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cagtactgga gcacccccac cttcggcggc ggcaccaagc tggagatcaa gagggccgcc	1920
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gccaaggtgc agctgcagga gagcggcccc agcctggtgc agcccagcca gaggctgagc	2040
atcacctgca ccgtgagcgg cttcagcctg atcagctacg gcgtgcactg ggtgaggcag	2100
agccccggca agggcctgga gtggctgggc gtgatctgga ggggcggcag caccgactac	2160

aacgccgcct tcatgagcag gctgagcatc accaaggaca acagcaagag ccaggtgttc	2220
ttcaagatga acagcctgca ggccgacgac accgccatct acttctgcgc caagaccctg	2280
atcaccaccg gctacgccat ggactactgg ggccagggca ccaccgtgac cgtgagcagc	2340
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gacttcgcct gcgacatcta catctgggcc cccctggccg gcacctgcgg cgtgctgctg	2520
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gccccgcct accagcaggg ccagaaccag ctgtacaacg agctgaacct gggcaggagg	2760
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cagaggagga agaaccccc ggagggcctg tacaacgagc tgcagaagga caagatggcc	2880
gaggcctaca gcgagatcgg catgaagggc gagaggagga ggggcaaggg ccacgacggc	2940
ctgtaccagg gcctgagcac cgccaccaag gacacctacg acgccctgca catgcaggcc	3000
ctgccccca ggggcagcgg cgaaggccgc ggcagcctgc tgacctgcgg cgatgtggaa	3060
gaaaaccgg gccccatgta cagaatgcag ctgctgagct gcatcgccct gagcctggcc	3120
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aagaccgagg ccaactgggt gaacgtgatc agcgacctga agaagatcga ggacctgatc	3240
cagagcatgc acatcgacgc caccctgtac accgagagcg acgtgcaccc cagctgcaag	3300
gtgaccgcca tgaagtgctt cctgctggag ctgcaggtga tcagcctgga gagcggcgac	3360
gccagcatcc acgacaccgt ggagaacctg atcatcctgg ccaacaacag cctgagcagc	3420
aacggcaacg tgaccgagag cggctgcaag gagtgcgagg agctggagga gaagaacatc	3480
aaggagtcc tgacagagctt cgtgcacatc gtgcagatgt tcatcaacac cagctccggc	3540
ggcggctccg gcggcggcgg ctccggcggc ggcggctccg gcggcggcgg ctccggcggc	3600
ggctccctgc aggccccag aagagccaga ggctgcagaa ccctgggcct gcccgccctg	3660
ctgctgctgc tgctgctgag accccccgcc accagaggca tcacctgccc ccccccatg	3720
agcgtggagc acgccgacat ctgggtgaag agctacagcc tgtacagcag agagagatac	3780

atctgcaaca gcggcttcaa gagaaaggcc ggcaccagca gcctgaccga gtgcgtgctg 3840
 aacaaggcca ccaacgtggc ccactggacc acccccagcc tgaagtgcac cagataagtt 3900
 taaac 3905

<210> 42
 <211> 1291
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 42

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

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

Arg Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Arg
 35 40 45

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

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

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

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

Gln Gln His Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
 115 120 125

Asp Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 130 135 140

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

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

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser 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 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu
 515 520 525

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

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

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

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

580	585	590
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr		
595	600	605
Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln		
610	615	620
Tyr Ser Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile		
625	630	635
Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser		
645	650	655
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly		
660	665	670
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe 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 Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
995 1000 1005

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Tyr Arg Met Gln

1010						1015						1020					
Leu	Leu	Ser	Cys	Ile	Ala	Leu	Ser	Leu	Ala	Leu	Val	Thr	Asn	Ser			
1025						1030					1035						
Gly	Ile	His	Val	Phe	Ile	Leu	Gly	Cys	Phe	Ser	Ala	Gly	Leu	Pro			
1040						1045					1050						
Lys	Thr	Glu	Ala	Asn	Trp	Val	Asn	Val	Ile	Ser	Asp	Leu	Lys	Lys			
1055						1060					1065						
Ile	Glu	Asp	Leu	Ile	Gln	Ser	Met	His	Ile	Asp	Ala	Thr	Leu	Tyr			
1070						1075					1080						
Thr	Glu	Ser	Asp	Val	His	Pro	Ser	Cys	Lys	Val	Thr	Ala	Met	Lys			
1085						1090					1095						
Cys	Phe	Leu	Leu	Glu	Leu	Gln	Val	Ile	Ser	Leu	Glu	Ser	Gly	Asp			
1100						1105					1110						
Ala	Ser	Ile	His	Asp	Thr	Val	Glu	Asn	Leu	Ile	Ile	Leu	Ala	Asn			
1115						1120					1125						
Asn	Ser	Leu	Ser	Ser	Asn	Gly	Asn	Val	Thr	Glu	Ser	Gly	Cys	Lys			
1130						1135					1140						
Glu	Cys	Glu	Glu	Leu	Glu	Glu	Lys	Asn	Ile	Lys	Glu	Phe	Leu	Gln			
1145						1150					1155						
Ser	Phe	Val	His	Ile	Val	Gln	Met	Phe	Ile	Asn	Thr	Ser	Ser	Gly			
1160						1165					1170						
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly			
1175						1180					1185						
Gly	Gly	Ser	Gly	Gly	Gly	Ser	Leu	Gln	Ala	Pro	Arg	Arg	Ala	Arg			
1190						1195					1200						
Gly	Cys	Arg	Thr	Leu	Gly	Leu	Pro	Ala	Leu	Leu	Leu	Leu	Leu	Leu			
1205						1210					1215						

Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr Cys Pro Pro Pro Met
 1220 1225 1230

Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser Leu Tyr
 1235 1240 1245

Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys Ala
 1250 1255 1260

Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn
 1265 1270 1275

Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
 1280 1285 1290

<210> 43
 <211> 3875
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 43
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 agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag 180
 cccggccaga gcccgaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc 240
 gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag 300
 gccgaggacc tggccgtgta ctactgccag cagcactaca gcaccccctg gaccttcggc 360
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 ggcggaagcc agatccagct ggtgcagagc ggccccgacc tgaagaagcc cggcgagacc 480
 gtgaagctga gctgcaaggc cagcggctac accttcacca acttcggcat gaactgggtg 540
 aagcaggccc ccggcaaggg cttcaagtgg atggcctgga tcaacaccta caccggcgag 600
 agctacttcg ccgacgactt caagggcagg ttgccttca gcgtggagac cagcgccacc 660
 accgcctacc tgcagatcaa caacctgaag accgaggaca ccgccaccta cttctgcgcc 720

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gcgtcgagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgagtg	900
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ctgcaggtga tcagcctgga gagcggcgac gccagcatcc acgacaccgt ggagaacctg	3360
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accagaggca tcacctgccc ccccccatg agcgtggagc acgccgacat ctgggtgaag	3720
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acccccagcc tgaagtgcac cagataagtt taaac	3875

<211> 1059
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 44

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

Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys
 35 40 45

Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Phe Gln Gln Lys Pro
 50 55 60

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

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

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

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

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

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

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

Asp Tyr Tyr Leu Asp Trp Val Lys Gln Ser His Gly Glu Ser Phe Glu

			180					185						190			
Trp	Ile	Gly	Arg	Val	Asn	Pro	Tyr	Asn	Gly	Gly	Thr	Ile	Tyr	Asn	Gln		
		195					200					205					
Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr		
	210					215					220						
Ala	Tyr	Met	Asp	Leu	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr		
225					230					235					240		
Tyr	Cys	Ala	Arg	Asp	His	Tyr	Arg	Tyr	Asp	Pro	Leu	Leu	Asp	Tyr	Trp		
				245					250					255			
Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Thr	Thr	Thr	Pro	Ala	Pro		
			260					265					270				
Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu		
		275					280					285					
Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg		
	290					295					300						
Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly		
305					310					315					320		
Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Arg		
				325					330					335			
Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro		
			340					345					350				
Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro		
		355					360					365					
Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	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 Glu Gly Arg Gly
 485 490 495

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

Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro Pro Ala
 515 520 525

Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val Ala Gly
 530 535 540

Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe Leu Ala
 545 550 555 560

Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala
 565 570 575

Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala
 580 585 590

Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln
 595 600 605

Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly

610		615		620											
Leu 625	Ala	Gly	Val	Ser	Leu 630	Thr	Gly	Gly	Leu	Ser 635	Tyr	Lys	Glu	Asp	Thr 640
Lys	Glu	Leu	Val	Val 645	Ala	Lys	Ala	Gly	Val 650	Tyr	Tyr	Val	Phe	Phe 655	Gln
Leu	Glu	Leu	Arg 660	Arg	Val	Val	Ala	Gly 665	Glu	Gly	Ser	Gly	Ser 670	Val	Ser
Leu	Ala	Leu	His 675	Leu	Gln	Pro	Leu	Arg 680	Ser	Ala	Ala	Gly 685	Ala	Ala	Ala
Leu 690	Ala	Leu	Thr	Val	Asp	Leu 695	Pro	Pro	Ala	Ser	Ser 700	Glu	Ala	Arg	Asn
Ser 705	Ala	Phe	Gly	Phe	Gln 710	Gly	Arg	Leu	Leu	His 715	Leu	Ser	Ala	Gly	Gln 720
Arg	Leu	Gly	Val	His 725	Leu	His	Thr	Glu	Ala 730	Arg	Ala	Arg	His	Ala 735	Trp
Gln	Leu	Thr	Gln 740	Gly	Ala	Thr	Val	Leu	Gly 745	Leu	Phe	Arg	Val 750	Thr	Pro
Glu	Ile	Pro	Ala	Gly 755	Leu	Pro	Ser	Pro	Arg	Ser	Glu	Gly 765	Ser	Gly	Ala
Thr 770	Asn	Phe	Ser	Leu	Leu	Lys 775	Gln	Ala	Gly	Asp	Val 780	Glu	Glu	Asn	Pro
Gly 785	Pro	Met	Tyr	Arg	Met	Gln 790	Leu	Leu	Ser	Cys 795	Ile	Ala	Leu	Ser	Leu 800
Ala	Leu	Val	Thr	Asn 805	Ser	Gly	Ile	His	Val 810	Phe	Ile	Leu	Gly	Cys 815	Phe
Ser	Ala	Gly	Leu 820	Pro	Lys	Thr	Glu	Ala 825	Asn	Trp	Val	Asn	Val 830	Ile	Ser

Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala
 835 840 845

Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala
 850 855 860

Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly
 865 870 875 880

Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn
 885 890 895

Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu
 900 905 910

Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe
 915 920 925

Val His Ile Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser
 930 935 940

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 945 950 955 960

Gly Gly Ser Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu
 965 970 975

Gly Leu Pro Ala Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr
 980 985 990

Arg Gly Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile
 995 1000 1005

Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys
 1010 1015 1020

Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu
 1025 1030 1035

Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro

1040

1045

1050

Ser Leu Lys Cys Ile Arg
1055

<210> 45
<211> 3190
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Sequence

<400> 45
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gcgacagggt gagcatcacc tgcaaggcca gccaggacgt gagcaccgcc gtggcctggt 180
tccagcagaa gcccggccag agccccaagc tgctgatcta cagccccagc tacaggtaca 240
ccggcgtgcc cgacaggttc accggcagcg gcagcggcac cgacttcacc ttcacatca 300
gcagcgtgca ggccgaggac ctggccgtgt actactgcca gcagctgtac agcaccacct 360
acaccttcgg cggcggcacc aagctggaga tcaaggaggagg ggggggatcc gggggaggag 420
gctccggcgg aggcggaagc gaggtgcagc tgcagcagag cggccccgag ctggtgaagc 480
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tggactgggt gaagcagagc cacggcgaga gcttcgagt gatcggcagg gtgaacctt 600
acaacggcgg caccatctac aaccagaagt tcaagggcaa ggccacctg accgtggaca 660
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ccgtgcacac caggggcctg gacttcgcct gcgacatcta catctgggcc cccctggccg 960
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gcagcaacgg caacgtgacc gagagcggct gcaaggagtg cgaggagctg gaggagaaga	2760

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acatcaagga gttcctgcag agcttcgtgc acatcgtgca gatgttcac aacaccagct      2820
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gcggcggctc cctgcaggcc ccagaagag ccagaggctg cagaaccctg ggcctgcccg      2940
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ccatgagcgt ggagcacgcc gacatctggg tgaagagcta cagcctgtac agcagagaga      3060
gatacatctg caacagcggc ttcaagagaa aggccggcac cagcagcctg accgagtgcg      3120
tgctgaacaa ggccaccaac gtggcccact ggaccacccc cagcctgaag tgcacagat      3180
aagtttaaac                                     3190

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<210> 46
<211> 1060
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Sequence

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<400> 46

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

```

```

Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
35           40           45

```

```

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

```

```

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

```

```

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
85           90           95

```

```

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
100          105          110

```

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

Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Gly Gly Gly Gly Ser Gly
 130 135 140

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

Gly Pro Glu Leu Glu Lys Pro Gly Ala Ser Val Met Ile Ser Cys Lys
 165 170 175

Ala Ser Gly Ser Ser Phe Thr Gly Tyr Asn Met Asn Trp Val Arg Gln
 180 185 190

Asn Ile Gly Lys Ser Leu Glu Trp Ile Gly Ala Ile Asp Pro Tyr Tyr
 195 200 205

Gly Gly Thr Ser Tyr Asn Gln Lys Phe Lys Gly Arg Ala Thr Leu Thr
 210 215 220

Val Asp Lys Ser Ser Ser Thr Ala Tyr Met His Leu Lys Ser Leu Thr
 225 230 235 240

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Ser Gly Met Glu Tyr Trp
 245 250 255

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

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

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

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

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg

			325					330						335	
Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro
			340					345					350		
Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro
		355					360					365			
Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	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	Glu	Gly	Arg	Gly
				485					490					495	
Ser	Leu	Leu	Thr	Cys	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu
			500					505					510		
Tyr	Ala	Ser	Asp	Ala	Ser	Leu	Asp	Pro	Glu	Ala	Pro	Trp	Pro	Pro	Ala
		515					520					525			
Pro	Arg	Ala	Arg	Ala	Cys	Arg	Val	Leu	Pro	Trp	Ala	Leu	Val	Ala	Gly
	530					535					540				

Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe Leu Ala
545 550 555 560

Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala
565 570 575

Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala
580 585 590

Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln
595 600 605

Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly
610 615 620

Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr
625 630 635 640

Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln
645 650 655

Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser
660 665 670

Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala
675 680 685

Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn
690 695 700

Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln
705 710 715 720

Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp
725 730 735

Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro
740 745 750

Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly Ser Gly Ala

755					760					765					
Thr	Asn	Phe	Leu	Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn
	770					775					780				
Pro	Gly	Pro	Met	Tyr	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu	Ser
	785					790					795				800
Leu	Ala	Leu	Val	Thr	Asn	Ser	Gly	Ile	His	Val	Phe	Ile	Leu	Gly	Cys
				805					810					815	
Phe	Ser	Ala	Gly	Leu	Pro	Lys	Thr	Glu	Ala	Asn	Trp	Val	Asn	Val	Ile
			820					825					830		
Ser	Asp	Leu	Lys	Lys	Ile	Glu	Asp	Leu	Ile	Gln	Ser	Met	His	Ile	Asp
		835					840					845			
Ala	Thr	Leu	Tyr	Thr	Glu	Ser	Asp	Val	His	Pro	Ser	Cys	Lys	Val	Thr
	850					855					860				
Ala	Met	Lys	Cys	Phe	Leu	Leu	Glu	Leu	Gln	Val	Ile	Ser	Leu	Glu	Ser
	865					870			875					880	
Gly	Asp	Ala	Ser	Ile	His	Asp	Thr	Val	Glu	Asn	Leu	Ile	Ile	Leu	Ala
				885					890					895	
Asn	Asn	Ser	Leu	Ser	Ser	Asn	Gly	Asn	Val	Thr	Glu	Ser	Gly	Cys	Lys
			900					905					910		
Glu	Cys	Glu	Glu	Leu	Glu	Glu	Lys	Asn	Ile	Lys	Glu	Phe	Leu	Gln	Ser
		915					920				925				
Phe	Val	His	Ile	Val	Gln	Met	Phe	Ile	Asn	Thr	Ser	Ser	Gly	Gly	Gly
	930					935					940				
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	945					950					955				960
Gly	Gly	Gly	Ser	Leu	Gln	Ala	Pro	Arg	Arg	Ala	Arg	Gly	Cys	Arg	Thr
				965				970						975	

Leu Gly Leu Pro Ala Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala
 980 985 990

Thr Arg Gly Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp
 995 1000 1005

Ile Trp Val Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile
 1010 1015 1020

Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr
 1025 1030 1035

Glu Cys Val Leu Asn Lys Ala Thr Asn Val Ala His Trp Thr Thr
 1040 1045 1050

Pro Ser Leu Lys Cys Ile Arg
 1055 1060

<210> 47
 <211> 3182
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 47
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 ccggagatcg tgatgacca gagccccgcc accctgagcg tgagccccgg cgagagggcc 120
 accctgagct gcaggagcag ccagagcctg gtgcacagga acggcaacac ctacctgcac 180
 tgggtacctgc agaagcccgg ccagagcccc aagctgctga tccacaaggt gagcaacagg 240
 ttcagcggcg tgcccacag gttcagcggc agcggcagcg gcaccgactt caccctgaag 300
 atcagcaggg tggaggccga ggacctgggc gtgtacttct gcagccagag caccacgtg 360
 cccccctga ctttcggcgc cggcaccaag ctggagctga agaggggagg cggcggcagc 420
 ggccggcggcg gcagcggcgg cggcggcagc gaggtgcagc tgctgcagag cggccccgag 480
 ctggagaagc ccggcgccag cgtgatgatc agctgcaagg ccagcggcag cagcttcacc 540
 ggctacaaca tgaactgggt gaggcagaac atcggcaaga gcctggagtg gatcggcgcc 600

atcgaccctt actacggcgg caccagctac aaccagaagt tcaagggcag ggccaccctg	660
accgtggaca agagcagcag caccgcctac atgcacctga agagcctgac cagcgaggac	720
agcgccgtgt actactgcgt gagcggcatg gactactggg gccagggcac cagcgtgacc	780
gtgagcagca ccacgacgcc agcgccgcga ccaccaacac cggcgcccac catcgcgctc	840
cagccccctgt ccctgcgccc agaggcgtgc cggccagcgg cggggggcgc agtgcacacg	900
agggggctgg acttcgcctg tgatatctac atctgggcgc ccttggccgg gacttgtggg	960
gtccttctcc tgtcactggg tatcaccctt tactgcagga gtaagaggag caggctcctg	1020
cacagtgact acatgaacat gactccccgc cggccgggc ccaccgcaa gcattaccag	1080
ccctatgccc caccacgcga cttcgcagcc tatcgctcca gactgaagtt cagcaggagc	1140
gcagacgccc ccggtacca gcagggccag aaccagctct ataacgagct caatctagga	1200
cgaagagagg agtacgatgt tttggacaag agacgtggcc gggaccctga gatgggggga	1260
aagccgcaga gaaggaagaa ccctcaggaa ggcctgtaca atgaactgca gaaagataag	1320
atggcggagg cctacagtga gattgggatg aaaggcgagc gccggagggg caaggggcac	1380
gatggccttt accagggtct cagtacagcc accaaggaca cctacgacgc cttcacatg	1440
caggccctgc cccctcgcgg cagcggcgaa ggccgcggca gcctgctgac ctgcggcgat	1500
gtggaagaaa acccgggccc catggaatac gcctctgacg cttcactgga cccgaagcc	1560
ccgtggcctc ccgcgccccg cgctcgcgcc tgccgcgtac tgccttgggc cctggtcgcg	1620
gggctgctgc tgctgctgct gctcgtgcc gcctgcgccg tcttcctcgc ctgcccctgg	1680
gccgtgtccg gggctcgcgc ctcgcccggc tccgcggcca gcccagagact ccgcgagggt	1740
cccagacttt cgcccacga tcccgccggc ctcttggacc tgcggcaggg catgtttgcg	1800
cagctggtgg cccaaaatgt tctgctgac gatgggcccc tgagctggta cagtgaccca	1860
ggcctggcag gcgtgtccct gacggggggc ctgagctaca aagaggacac gaaggagctg	1920
gtggtggcca aggctggagt ctactatgtc ttctttcaac tagagctgcg gcgctggtg	1980
gccggcgagg gctcaggctc cgtttcactt gcgctgcacc tgcagccact gcgctctgct	2040
gctggggccg ccgccctggc tttgaccgtg gacctgccac ccgcctctc cgaggctcgg	2100
aactcggcct tcggtttcca gggccgcttg ctgcacctga gtgccggcca gcgcctgggc	2160
gtccatcttc aactgaggc cagggcacgc catgcctggc agcttaccga gggcgccaca	2220

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gtcttgggac tcttccgggt gacccccgaa atcccagccg gactcccttc accgaggtcg      2280
gaaggaagcg gagtactaa cttcttgagc ctgctgaagc aggctggaga cgtggaggag      2340
aaccctggac ctatgtacag aatgcagctg ctgagctgca tcgccctgag cctggccctg      2400
gtgaccaaca gcggcatcca cgtgttcatc ctgggctgct tcagcgccgg cctgccccag      2460
accgaggcca actgggtgaa cgtgatcagc gacctgaaga agatcgagga cctgatccag      2520
agcatgcaca tcgacgccac cctgtacacc gagagcgacg tgcaccccag ctgcaagggtg      2580
accgccatga agtgcttcct gctggagctg caggtgatca gcctggagag cggcgacgcc      2640
agcatccacg acaccgtgga gaacctgatc atcctggcca acaacagcct gagcagcaac      2700
ggcaacgtga ccgagagcgg ctgcaaggag tgcgaggagc tggaggagaa gaacatcaag      2760
gagttcctgc agagcttcgt gcacatcgtg cagatgttca tcaacaccag ctccggcggc      2820
ggctccggcg gcggcggctc cggcggcggc ggctccggcg gcggcggctc cggcggcggc      2880
tccctgcagg cccccagaag agccagaggc tgcagaacct tgggcctgcc cgccctgctg      2940
ctgctgctgc tgctgagacc ccccgccacc agaggcatca cctgcccccc ccccatgagc      3000
gtggagcacg ccgacatctg ggtgaagagc tacagcctgt acagcagaga gagatacatc      3060
tgcaacagcg gcttcaagag aaaggccggc accagcagcc tgaccgagtg cgtgctgaac      3120
aaggccacca acgtggccca ctggaccacc cccagcctga agtgcatacag ataagtttaa      3180
ac                                                                 3182

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<210> 48
 <211> 880
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 48

```

Arg Ser Leu Thr Ser Arg Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe
1           5           10           15

```

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Gly Phe Ala Phe Leu Asp Thr Glu Val Phe Val Thr Gly Asp Ile Gln
          20           25           30

```

```

Val Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly Glu Arg Ile

```

35

40

45

Ser Leu Thr Cys Arg Thr Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp
 50 55 60

Phe Gln Gln Lys Pro Asp Gly Thr Phe Lys Arg Leu Ile Tyr Ala Thr
 65 70 75 80

Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly Ser Gly Ser
 85 90 95

Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser Glu Asp Phe
 100 105 110

Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Tyr Pro Phe Thr Phe Gly
 115 120 125

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

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

Gly Leu Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Val Thr
 165 170 175

Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr Trp His Trp Ile Arg Gln Phe
 180 185 190

Pro Gly Asn Lys Leu Gln Trp Met Gly Tyr Ile Ser Tyr Ser Gly Phe
 195 200 205

Thr Asn Tyr Lys Thr Ser Leu Ile Asn Arg Ile Ser Ile Thr His Asp
 210 215 220

Thr Ser Glu Asn Gln Phe Phe Leu Asn Leu Asn Ser Val Thr Thr Glu
 225 230 235 240

Asp Thr Ala Thr Tyr Tyr Cys Ala Gly Asp Arg Thr Gly Ser Trp Phe
 245 250 255

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

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

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
 290 295 300

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

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

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

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

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

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

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

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

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

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

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr

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

Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser
 690 695 700

Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu
 705 710 715 720

Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu
 725 730 735

Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile
 740 745 750

Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly
 755 760 765

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
 770 775 780

Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro
 785 790 795 800

Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile
 805 810 815

Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys
 820 825 830

Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe
 835 840 845

Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys
 850 855 860

Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
 865 870 875 880

<210> 49

<211> 2633

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 49

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gtgacagggg acatccaggt gaccagagc cccagcagcc tgagcgccag cctgggagcag	120
agaatcagcc tgacctgcag aaccagccag gacatcagca actacctgaa ctggttccag	180
cagaagcccc acggcacctt caagagactg atctacgcca ccagcagcct ggacagcggc	240
gtgccaaga gattcagcgg cagcggcagc ggcagcgact acagcctgac catcagcagc	300
ctggagagcg aggacttcgc cgactactac tgcctgcagt acgccagcta ccccttcacc	360
ttcggcagcg gcaccaagct ggagatcaag ggaggggggg gatccggggg aggaggctcc	420
ggcggaggcg gaagcgaggt gcagctgcag gagagcggcc ccggcctggt gaagcccagc	480
cagaccctga gcctgacctg cagcgtgacc ggctacagca tcaccagcgg ctactactgg	540
cactggatca gacagttccc cggcaacaag ctgcagtgga tgggctacat cagctacagc	600
ggcttcacca actacaagac cagcctgata aacagaatca gcatcaccca cgacaccagc	660
gagaaccagt tcttcctgaa cctgaacagc gtgaccaccg aggacaccgc cacctactac	720
tgcgccggcg acagaaccgg cagctggttc gcctactggg gccagggcac cctggtgacc	780
gtgagcgcca ccacgacgcc agcgccgca ccaccaacac cggcgccac catcgcgctc	840
cagcccctgt ccctgcgccc agaggcgtgc cggccagcgg cggggggcgc agtgcacacg	900
agggggctgg acttcgcctg tgatatctac atctgggcgc ccttggccgg gacttgtggg	960
gtccttctcc tgtcactggt tatcaccctt tactgcagga gtaagaggag caggctcctg	1020
cacagtgact acatgaacat gactccccgc cggccgggc ccaccgcaa gcattaccag	1080
ccctatgccc caccacgca cttcgcagcc tatcgctcca gagggaagtt cagcaggagc	1140
gcagacgccc ccgcgtacca gcagggccag aaccagctct ataacgagct caatctagga	1200
cgaagagagg agtacgatgt tttggacaag agacgtggcc gggaccctga gatgggggga	1260
aagccgcaga gaaggaagaa ccctcaggaa ggcctgtaca atgaactgca gaaagataag	1320
atggcggagg cctacagtga gattgggatg aaaggcgagc gccggagggg caaggggcac	1380
gatggccttt accagggtct cagtacagcc accaaggaca cctacgacgc ctttcacatg	1440
caggccctgc cccctcgcgg cagcggcgaa ggccgcggca gcctgctgac ctgcggcgat	1500

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gtggaagaaa acccgggccc catgtacctg tggctgaagc tgctggcctt cggcttcgcc      1560
ttcctggaca ccgaggtggt cgtgaccggc ggccagaacg acaccagcca gaccagcagc      1620
cccagcagcc cgctgtttcc gggcccagc aaaccgtttt gggtgctggt ggtggtgggc      1680
ggcgtgctgg cgtgctatag cctgctggtg accgtggcgt ttattatattt ttgggtggga      1740
agcggagcta ctaacttcag cctgctgaag caggctggag acgtggagga gaaccctgga      1800
cctatgtaca gaatgcagct gctgagctgc atcgccctga gcctggccct ggtgaccaac      1860
agcggcatcc acgtgttcac cctgggctgc ttcagcgccg gcctgcccac gaccgaggcc      1920
aactgggtga acgtgatcag cgacctgaag aagatcgagg acctgatcca gagcatgcac      1980
atcgacgcca ccctgtacac cgagagcgac gtgcacccca gctgcaaggt gaccgccatg      2040
aagtgccttc tgctggagct gcaggtgatc agcctggaga gcggcgacgc cagcatccac      2100
gacaccgtgg agaacctgat catcctggcc aacaacagcc tgagcagcaa cggcaacgtg      2160
accgagagcg gctgcaagga gtgcgaggag ctggaggaga agaacaatcaa ggagttcctg      2220
cagagcttcg tgcacatcgt gcagatgttc atcaacacca gctccggcgg cggctccggc      2280
ggcggcggct ccggcggcgg cggctccggc ggcggcggct ccggcggcgg ctccctgcag      2340
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ctgctgagac cccccgccac cagaggcatc acctgcccc ccccatgag cgtggagcac      2460
gccgacatct ggggtgaagag ctacagcctg tacagcagag agagatacat ctgcaacagc      2520
ggcttcaaga gaaaggccgg caccagcagc ctgaccgagt gcgtgctgaa caaggccacc      2580
aacgtggccc actggaccac cccagcctg aagtgcata gataagtta aac                2633

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<210> 50
<211> 1099
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Sequence

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<400> 50

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

```

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Leu Leu Leu His Ala Ala Arg Pro Asp Val Val Met Thr Gln Ser His

```

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

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

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

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

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

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

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

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

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

Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser 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	Met	Glu	Tyr	Ala	Ser	Asp	Ala	Ser	Leu	Asp	Pro	Glu	Ala	Pro	Trp	
		515					520					525				
Pro	Pro	Ala	Pro	Arg	Ala	Arg	Ala	Cys	Arg	Val	Leu	Pro	Trp	Ala	Leu	
	530					535					540					
Val	Ala	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ala	Ala	Cys	Ala	Val	
545					550					555					560	
Phe	Leu	Ala	Cys	Pro	Trp	Ala	Val	Ser	Gly	Ala	Arg	Ala	Ser	Pro	Gly	
				565					570					575		
Ser	Ala	Ala	Ser	Pro	Arg	Leu	Arg	Glu	Gly	Pro	Glu	Leu	Ser	Pro	Asp	
			580					585					590			
Asp	Pro	Ala	Gly	Leu	Leu	Asp	Leu	Arg	Gln	Gly	Met	Phe	Ala	Gln	Leu	
		595					600					605				
Val	Ala	Gln	Asn	Val	Leu	Leu	Ile	Asp	Gly	Pro	Leu	Ser	Trp	Tyr	Ser	
	610					615					620					
Asp	Pro	Gly	Leu	Ala	Gly	Val	Ser	Leu	Thr	Gly	Gly	Leu	Ser	Tyr	Lys	
625					630					635					640	
Glu	Asp	Thr	Lys	Glu	Leu	Val	Val	Ala	Lys	Ala	Gly	Val	Tyr	Tyr	Val	
				645					650					655		
Phe	Phe	Gln	Leu	Glu	Leu	Arg	Arg	Val	Val	Ala	Gly	Glu	Gly	Ser	Gly	
			660					665					670			

Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
 675 680 685

Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
 690 695 700

Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
 705 710 715 720

Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
 725 730 735

His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
 740 745 750

Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu Gly
 755 760 765

Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
 770 775 780

Asn Pro Gly Pro Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 785 790 795 800

Ser Leu Ala Leu Val Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly
 805 810 815

Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val
 820 825 830

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
 835 840 845

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
 850 855 860

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
 865 870 875 880

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu

				885						890						895
Ala	Asn	Asn	Ser	Leu	Ser	Ser	Asn	Gly	Asn	Val	Thr	Glu	Ser	Gly	Cys	
			900					905					910			
Lys	Glu	Cys	Glu	Glu	Leu	Glu	Glu	Lys	Asn	Ile	Lys	Glu	Phe	Leu	Gln	
		915					920					925				
Ser	Phe	Val	His	Ile	Val	Gln	Met	Phe	Ile	Asn	Thr	Ser	Ser	Gly	Gly	
	930					935					940					
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
945					950					955					960	
Ser	Gly	Gly	Gly	Ser	Leu	Gln	Ile	Thr	Cys	Pro	Pro	Pro	Met	Ser	Val	
				965					970					975		
Glu	His	Ala	Asp	Ile	Trp	Val	Lys	Ser	Tyr	Ser	Leu	Tyr	Ser	Arg	Glu	
			980					985					990			
Arg	Tyr	Ile	Cys	Asn	Ser	Gly	Phe	Lys	Arg	Lys	Ala	Gly	Thr	Ser	Ser	
		995					1000					1005				
Leu	Thr	Glu	Cys	Val	Leu	Asn	Lys	Ala	Thr	Asn	Val	Ala	His	Trp		
	1010					1015					1020					
Thr	Thr	Pro	Ser	Leu	Lys	Cys	Ile	Arg	Thr	Thr	Thr	Pro	Ala	Pro		
	1025					1030					1035					
Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser		
	1040					1045					1050					
Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His		
	1055					1060					1065					
Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Val	Ala	Ile	Ser	Thr	Ser		
	1070					1075					1080					
Thr	Val	Leu	Leu	Cys	Gly	Leu	Ser	Ala	Val	Ser	Leu	Leu	Ala	Cys		
	1085					1090					1095					

Tyr

<210> 51
 <211> 3299
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 51
 atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
 ccggacgtgg tgatgaccca gagccacagg ttcatgagca ccagcgtggg cgacagggtg 120
 agcatcacct gcagggccag ccaggacgtg aacaccgccg tgagctggta ccagcagaag 180
 cccggccaga gcccgaagct gctgatcttc agcgccagct acaggtacac cggcgtgccc 240
 gacaggttca ccggcagcgg cagcggcgcc gacttcaccc tgaccatcag cagcgtgcag 300
 gccgaggacc tggccgtgta ctactgccag cagcactaca gcaccccctg gaccttcggc 360
 ggccggcacca agctggacat caagggaggg gggggatccg ggggaggagg ctccggcgga 420
 ggccggaagcc agatccagct ggtgcagagc ggccccgacc tgaagaagcc cggcgagacc 480
 gtgaagctga gctgcaaggc cagcggctac accttcacca acttcggcat gaactgggtg 540
 aagcaggccc ccggcaaggg cttcaagtgg atggcctgga tcaacaccta caccggcgag 600
 agctacttcg ccgacgactt caagggcagg ttgccttca gcgtggagac cagcgccacc 660
 accgcctacc tgcatgcaa caacctgaag accgaggaca ccgccaccta cttctgcgcc 720
 aggggcgaga tctactacgg ctacgacggc ggcttcgcct actggggcca gggcaccctg 780
 gtgaccgtga gcgccaccac gacgccagcg ccgcgaccac caacaccggc gccaccatc 840
 gcgtcgcagc ccctgtccct gcgcccagag gcgtgccggc cagcggcggg gggcgagtg 900
 cacacgaggg ggctggactt cgcctgtgat atctacatct gggcgccctt ggccgggact 960
 tgtgggggtc ttctcctgtc actggttatc accctttact gcaggagtaa gaggagcagg 1020
 ctctgcaca gtgactacat gaacatgact ccccgccgcc ccgggcccac ccgcaagcat 1080
 taccagccct atgccccacc acgcgacttc gcagcctatc gctccagagt gaagttcagc 1140
 aggagcgag acgccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat 1200

ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg	1260
gggggaaagc cgagagaag gaagaaccct caggaaggcc tgtacaatga actgcagaaa	1320
gataagatgg cggaggccta cagttagatt gggatgaaag gcgagcgccg gaggggcaag	1380
gggcacgatg gcctttacca ggggtctcagt acagccacca aggacaccta cgacgccctt	1440
cacatgcagg ccctgcccc tcgcggaagc ggagccacca acttcagcct gctgaagcag	1500
gccggcgacg tggaggagaa ccccgccccc atggaatacg cctctgacgc ttcactggac	1560
cccgaagccc cgtggcctcc cgcgccccgc gctcgcgcct gccgcgtact gccttgggcc	1620
ctggtcgcgg ggctgctgct gctgctgctg ctcgctgccg cctgcgccgt cttcctcgcc	1680
tgtccctggg ccgtgtccgg ggctcgcgc tcgcccggct ccgcggccag cccgagactc	1740
cgcgagggtc ccgagctttc gcccagcat cccgccggcc tcttggacct gcggcagggc	1800
atgtttgcgc agctgggtggc ccaaaatgtt ctgctgatcg atgggcccct gagctggtac	1860
agtgaccag gcctggcagg cgtgtccctg acggggggcc tgagctacaa agaggacacg	1920
aaggagctgg tgggtggcaa ggctggagtc tactatgtct tctttcaact agagctgcgg	1980
cgcgtgggtg ccggcgaggg ctcaggctcc gtttcacttg cgctgcacct gcagccactg	2040
cgctctgctg ctggggccgc cgccctggct ttgaccgtgg acctgccacc cgcctcctcc	2100
gaggctcgga actcggcctt cggtttccag ggccgcttgc tgcacctgag tgccggccag	2160
cgcctgggcg tccatcttca cactgaggcc agggcacgcc atgcctggca gcttaccag	2220
ggcgccacag tcttgggact cttccgggtg acccccgaag tcccagccgg actcccttca	2280
ccgaggtcgg aaggcagcgg cgaaggccgc ggcagcctgc tgacctgcgg cgatgtggaa	2340
gaaaacccgg gcccacatga cagaatgcag ctgctgagct gcatcgccct gagcctggcc	2400
ctggtgacca acagcggcat ccacgtgttc atcctgggct gcttcagcgc cggcctgccc	2460
aagaccgagg ccaactgggt gaacgtgatc agcgacctga agaagatcga ggacctgatc	2520
cagagcatgc acatcgacgc caccctgtac accgagagcg acgtgcaccc cagctgcaag	2580
gtgaccgcca tgaagtgctt cctgctggag ctgcaggtga tcagcctgga gagcggcgac	2640
gccagcatcc acgacaccgt ggagaacctg atcatcctgg ccaacaacag cctgagcagc	2700
aacggcaacg tgaccgagag cggctgcaag gagtgcgagg agctggagga gaagaacatc	2760
aaggagtcc tgacagagctt cgtgcacatc gtgcagatgt tcatcaacac cagctccggc	2820

```

ggcggctccg gcggcggcgg ctccggcggc ggcggctccg gcggcggcgg ctccggcggc      2880
ggctccctgc agatcacctg ccccccccc atgagcgtgg agcacgccga catctgggtg      2940
aagagctaca gcctgtacag cagagagaga tacatctgca acagcggctt caagagaaag      3000
gccggcacca gcagcctgac cgagtgcgtg ctgaacaagg ccaccaacgt ggcccactgg      3060
accacccccca gcctgaagtg catcagaacc accacccccg ccccaggcc cccaccccc      3120
gcccccacca tcgccagcca gcccctgagc ctgaggcccc aggcctgcag gcccgccgcc      3180
ggcggcgccg tgcacaccag gggcctggac ttcgcctgcg acgtggctat ctccacgtcc      3240
actgtcctgc tgtgtgggct gagcgctgtg tctctcctgg catgctacta agtttaaac      3299

```

```

<210> 52
<211> 1006
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic Sequence

```

```

<400> 52

```

```

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

```

```

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

```

```

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

```

```

Ala Ser Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly
50           55           60

```

```

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

```

```

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

```

```

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

```

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

Ile Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 130 135 140

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

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

Ser Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
 180 185 190

Trp Met Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln
 195 200 205

Lys Phe Lys Gly Arg Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr
 210 215 220

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

Phe Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asp Val
 245 250 255

Trp Gly Gln Gly Thr Thr Val Thr Val Ser 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	Gly	Ser	Gly	Ala	Thr	Asn
				485					490					495	
Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro
			500					505					510		
Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
		515					520					525			
His	Ala	Ala	Arg	Pro	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu
	530					535					540				

Ile Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
 545 550 555 560

Thr Phe Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln
 565 570 575

Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys
 580 585 590

Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser
 595 600 605

Ser Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser
 610 615 620

Ala Val Tyr Tyr Cys Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val
 625 630 635 640

Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly
 645 650 655

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
 660 665 670

Met Thr Gln Ala Ala Pro Ser Ile Pro Val Thr Pro Gly Glu Ser Val
 675 680 685

Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser Asn Gly Asn
 690 695 700

Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Leu
 705 710 715 720

Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe
 725 730 735

Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile Ser Arg Val
 740 745 750

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His Leu Glu Tyr

755					760					765					
Pro	Phe	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	Arg	Thr	Thr
	770					775					780				
Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln
785						790					795				800
Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala
				805					810					815	
Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala
			820					825					830		
Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr
		835					840					845			
Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln
	850					855					860				
Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser
865						870					875				880
Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys
				885					890					895	
Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln
			900					905					910		
Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu
		915					920					925			
Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Gln	Arg
	930					935					940				
Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys
945						950					955				960
Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg
				965					970					975	

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

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 995 1000 1005

<210> 53
 <211> 3020
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 53
 atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
 ccggacatcc agctgaccga gagccccagc agcctgagcg ccagcgtggg cgacagggtg 120
 accatgacct gcagggccag cagcagcgtg agctacatcc actggttcca gcagaagccc 180
 ggcaaggccc ccaagccctg gatctacgcc accagcaacc tggccagcgg cgtgcccgtg 240
 aggttcagcg gcagcggcag cggcaccgac tacaccttca ccatcagcag cctgcagccc 300
 gaggacatcg ccacctacta ctgccagcag tggaccagca accccccac cttcggcggc 360
 ggaccaagc tggagatcaa gaggggcggc ggcggcagcg gcggcggcgg cagcggcggc 420
 ggcggcagcc aggtgcagct gcagcagagc ggcgccgagg tgaagaagcc cggcagcagc 480
 gtgaagggtga gctgcaaggc cagcggctac accttcagca gctacaacat gcaactgggtg 540
 aggcaggccc ccggccaggg cctggagtgg atgggcgccca tctaccccgg caacggcgac 600
 accagctaca accagaagtt caagggcagg gccaccatca ccgccgacga gagcaccaac 660
 accgcctaca tggagctgag cagcctgagg agcgaggaca ccgccttcta cttctgcgcc 720
 aggagcacct actacggcgg cgactgggtac ttcgacgtgt ggggccaggg caccaccgtg 780
 accgtgagca gcaccacgac gccagcgccg cgaccaccaa caccggcgcc caccatcgcg 840
 tcgcagcccc tgtccctgcg ccagaggcg tgccggccag cggcgggggg cgcagtgcac 900
 acgagggggc tggacttcgc ctgtgatatc tacatctggg cgcccttggc cgggacttgt 960
 ggggtccttc tcctgtcact gggtatcacc ctttactgca ggagtaagag gagcaggctc 1020
 ctgcacagtg actacatgaa catgactccc cgccgccccg ggcccacccg caagcattac 1080

cagccctatg cccaccacg cgacttcgca gcctatcgct ccagagtga gttcagcagg	1140
agcgagacg ccccgcgta ccagcagggc cagaaccagc tctataacga gctcaatcta	1200
ggacgaagag aggagtacga tgttttggac aagagacgtg gccgggaccc tgagatgggg	1260
ggaaagccgc agagaaggaa gaaccctcag gaaggcctgt acaatgaact gcagaaagat	1320
aagatggcgg aggcctacag tgagattggg atgaaaggcg agcgccggag gggcaagggg	1380
cacgatggcc tttaccaggg tctcagtaca gccaccaagg acacctacga cgcccttcac	1440
atgcaggccc tgccccctcg cggaagcgga gccaccaact tcagcctgct gaagcaggcc	1500
ggcgacgtgg aggagaaccc cggcccatg gccctgccc tgaccgccct gctgctgccc	1560
ctggccctgc tgctgcacgc cgccaggccc gaggtccagc tgcagcagtc tggacctgag	1620
ctgataaagc ctggggcttc agtgaagatg tcctgcaagg cttctggata cacattcact	1680
agctatgtta tgcactgggt gaagcagaag cctgggcagg gccttgagtg gattggatat	1740
attaatcctt acaatgatgg tactaagtac aatgagaagt tcaaaggcaa ggccacactg	1800
acttcagaca aatcctccag cacagcctac atggagctca gcagcctgac ctctgaggac	1860
tctgcggtct attactgtgc aagagggact tattactacg gtagtagggt atttgactac	1920
tggggccaag gcaccactct cacagtctcc tcaggtggag ggggctcagg cggaggtggc	1980
tctgggggtg gaggtcggga catttgtatg actcaggctg caccctctat acctgtcact	2040
cctggagagt cagtatccat ctctgcagg tctagtaaga gtctcctgaa tagtaatggc	2100
aacacttact tgtattgggt cctgcagagg ccaggccagt ctctcagct cctgatatat	2160
cggatgtcca accttgcctc aggagtcca gacaggttca gtggcagtgg gtcaggaact	2220
gctttcacac tgagaatcag tagagtggag gctgaggatg tgggtgttta ttactgtatg	2280
caacatctag aatatccgtt cacgttcggt gctgggacca agctggagct gaaacggacc	2340
accacccccg ccccaggcc cccaccccc gcccccacca tcgccagcca gccctgagc	2400
ctgaggcccc aggctgcag gcccgccgc ggcggcgcgc tgacaccag gggcctggac	2460
ttgcctgcg acatctacat ctgggcccc ctggccggca cctgcggcgt gctgctgctg	2520
agcctggtga tcaccctgta ctgcaaacgg ggcagaaaga aactcctgta tatattcaaa	2580
caaccattta tgagaccagt acaaactact caagaggaag atggctgtag ctgccgattt	2640
ccagaagaag aagaaggagg atgtgaactg agggatgaagt tcagcaggag cgccgacgcc	2700

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cccgctacc agcagggcca gaaccagctg tacaacgagc tgaacctggg caggagggag      2760
gagtacgacg tgctggacaa gaggaggggc agggaccccg agatgggcgg caagccccag      2820
aggaggaaga acccccagga gggcctgtac aacgagctgc agaaggacaa gatggccgag      2880
gcctacagcg agatcggcat gaagggcgag aggaggaggg gcaagggcca cgacggcctg      2940
taccagggcc tgagcaccgc caccaaggac acctacgacg ccctgcacat gcaggccctg      3000
ccccccaggt aagtttaaac                                                    3020

```

```

<210> 54
<211> 784
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic Sequence

```

```

<400> 54

```

```

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

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	400
Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg		
	405	410
Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro		
	420	425
Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala		
	435	440
Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His		
	450	455
Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp		
465	470	475
Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg		
	485	490
Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met		
	500	505
Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val		
	515	520
Thr Asn Ser Gly Ile His Val Phe Ile Leu Gly Cys Phe Ser Ala Gly		
	530	535
Leu Pro Lys Thr Glu Ala Asn Trp Val Asn Val Ile Ser Asp Leu Lys		
545	550	555
		560

Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr
 565 570 575

Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys
 580 585 590

Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser
 595 600 605

Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu
 610 615 620

Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu
 625 630 635 640

Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile
 645 650 655

Val Gln Met Phe Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly
 660 665 670

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

Leu Gln Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro
 690 695 700

Ala Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile
 705 710 715 720

Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys
 725 730 735

Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe
 740 745 750

Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys
 755 760 765

Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg

770

775

780

<210> 55
 <211> 2363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 55
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 accatcagct gcagggccag caagagcgtg agcaccagcg gctacagcta cctgcactgg 180
 taccagcaga agcccggcca gcccccaag ctgctgatct acctggccag caacctggag 240
 agcggcgtgc ccgccagggt cagcggcagc ggcagcggca ccgacttcac cctgaacatc 300
 caccctgtgg aggaggagga cgccgccacc tactactgcc agcacagcag ggagctgccc 360
 ttacacttcg gcagcggcac caagctggag atcaaggag gggggggatc cgggggagga 420
 ggctccggcg gaggcggaag ccaggtgcag ctggtggaga gcggcggcgg cctggtgcag 480
 cccggcggca gcctgaagct gagctgcgcc gccagcggct tcgacttcag caggtactgg 540
 atgagctggg tgaggcaggc ccccggcaag ggcctggagt ggatcggcga gatcaacccc 600
 accagcagca ccatcaactt cacccccagc ctgaaggaca aggtgttcat cagcagggac 660
 aacgccaaga acaccctgta cctgcagatg agcaaggtga ggagcgagga caccgccctg 720
 tactactgcg ccaggggcaa ctactacagg tacggcgacg ccatggacta ctggggccag 780
 ggcaccagcg tgaccgtgag caccacgacg ccagcggcgc gaccaccaac accggcgccc 840
 accatcgctg cgagcccct gtccctgcgc ccagaggcgt gccggccagc ggcggggggc 900
 gcagtgcaca cgagggggct ggacttcgcc tgtgatatct acatctgggc gcccttggcc 960
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 agcaggctcc tgcacagtga ctacatgaac atgactcccc gccgccccgg gccacccgc 1080
 aagcattacc agccctatgc cccaccacgc gacttcgcag cctatcgctc cagagtgaag 1140
 ttcagcagga gcgcagacgc ccccgctac cagcagggcc agaaccagct ctataacgag 1200
 ctcaatctag gacgaagaga ggagtacgat gttttggaca agagacgtgg ccgggaccct 1260

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gagatggggg gaaagccgca gagaaggaag aaccctcagg aaggcctgta caatgaactg      1320
cagaaagata agatggcgga ggcctacagt gagattggga tgaaaggcga gcgccggagg      1380
ggcaaggggc acgatggcct ttaccagggt ctcagtacag ccaccaagga cacctacgac      1440
gcccttcaca tgcaggccct gccccctcgc ggcagcggcg aaggccgcgg cagcctgctg      1500
acctgcggcg atgtggaaga aaacccgggc cccatgtaca gaatgcagct gctgagctgc      1560
atcgccctga gcctggccct ggtgaccaac agcggcatcc acgtgttcat cctgggctgc      1620
ttcagcgccg gcctgcccga gaccgaggcc aactgggtga acgtgatcag cgacctgaag      1680
aagatcgagg acctgatcca gagcatgcac atcgacgcca ccctgtacac cgagagcgac      1740
gtgcacccca gctgcaaggt gaccgcatg aagtgttcc tgctggagct gcaggtgatc      1800
agcctggaga gcggcgacgc cagcatccac gacaccgtgg agaacctgat catcctggcc      1860
aacaacagcc tgagcagcaa cggcaacgtg accgagagcg gctgcaagga gtgcgaggag      1920
ctggaggaga agaacatcaa ggagtccctg cagagcttcg tgcacatcgt gcagatgttc      1980
atcaacacca gtcggcgagg cggctccggc ggcggcggct ccggcgggcg cggctccggc      2040
ggcggcggct ccggcgggcg ctccctgcag gccccagaa gagccagagg ctgcagaacc      2100
ctgggcctgc ccgccctgct gctgctgctg ctgctgagac ccccgccac cagaggcatc      2160
acctgcccc ccccatgag cgtggagcac gccgacatct gggatgaagag ctacagcctg      2220
tacagcagag agagatacat ctgcaacagc ggcttcaaga gaaaggccgg caccagcagc      2280
ctgaccgagt gcgtgctgaa caaggccacc aacgtggccc actggaccac cccagcctg      2340
aagtgcata gataagtta aac                                          2363

```

```

<210> 56
<211> 489
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> Synthetic Sequence

```

```

<400> 56

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```

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

```

```

Leu Leu Leu His Ala Ala Arg Pro Glu Ile Val Met Thr Gln Ser Pro

```

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

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Ser Gly Met Glu Tyr Trp
 245 250 255

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

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

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

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

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

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

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

Arg Asp Phe Ala Ala Tyr Arg Ser 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
 485

<210> 57
 <211> 1480
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 57
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 acgccgccag gccggagatc gtgatgaccc agagccccgc caccctgagc gtgagccccg 120
 gcgagagggc caccctgagc tgcaggagca gccagagcct ggtgcacagg aacggcaaca 180
 cctacctgca ctggtacctg cagaagcccc gccagagccc caagctgctg atccacaagg 240
 tgagcaacag gttcagcggc gtgcccagca ggttcagcgg cagcggcagc ggcaccgact 300
 tcaccctgaa gatcagcagg gtggaggccg aggacctggg cgtgtacttc tgcagccaga 360
 gcacccacgt gccccccctg accttcggcg ccggcaccaa gctggagctg aagaggggcg 420
 gcggcggcag cggcggcggc ggagcggcg gcggcggcag cgaggtgcag ctgctgcaga 480
 gcggccccga gctggagaag cccggcgcca gcgtgatgat cagctgcaag gccagcggca 540
 gcagcttcac cggctacaac atgaactggg tgaggcagaa catcggcaag agcctggagt 600
 ggatcggcgc catcgacccc tactacggcg gcaccagcta caaccagaag ttcaagggca 660
 gggccaccct gaccgtggac aagagcagca gcaccgccta catgcacctg aagagcctga 720
 ccagcgagga cagcgccgtg tactactgcg tgagcggcat ggagtactgg ggccagggca 780
 ccagcgtgac cgtgagcagc accacgacgc cagcgccgag accaccaaca ccggcgccca 840
 ccatcgcgtc gcagcccctg tccctgcgcc cagaggcgtg ccggccagcg gcggggggcg 900
 cagtgcacac gagggggctg gacttcgcct gtgatattcta catctgggag cccttggccg 960
 ggacttgtgg ggtccttctc ctgtcactgg ttatcacctt ttactgcagg agtaagagga 1020

```

gcaggctcct gcacagtac tacatgaaca tgactccccg ccgccccggg cccacccgca      1080
agcattacca gccctatgcc ccaccacgcg acttcgcagc ctatcgctcc agagtgaagt      1140
tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc tataacgagc      1200
tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc cgggaccctg      1260
agatgggggg aaagccgcag agaaggaaga accctcagga aggcctgtac aatgaactgc      1320
agaaagataa gatggcggag gcctacagtg agattgggat gaaaggcgag cgccggaggg      1380
gcaaggggca cgatggcctt taccagggtc tcagtacagc caccaaggac acctacgacg      1440
cccttcacat gcaggccctg cccctcgct aagtttaaac      1480

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```

<210> 58
<211> 764
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic Sequence

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```

<400> 58

```

```

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

```

```

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

```

```

Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
35           40           45

```

```

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

```

```

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

```

```

Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
85           90           95

```

```

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
100          105          110

```

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

Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Gly Gly Gly Gly Ser Gly
 130 135 140

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

Gly Pro Glu Leu Glu Lys Pro Gly Ala Ser Val Met Ile Ser Cys Lys
 165 170 175

Ala Ser Gly Ser Ser Phe Thr Gly Tyr Asn Met Asn Trp Val Arg Gln
 180 185 190

Asn Ile Gly Lys Ser Leu Glu Trp Ile Gly Ala Ile Asp Pro Tyr Tyr
 195 200 205

Gly Gly Thr Ser Tyr Asn Gln Lys Phe Lys Gly Arg Ala Thr Leu Thr
 210 215 220

Val Asp Lys Ser Ser Ser Thr Ala Tyr Met His Leu Lys Ser Leu Thr
 225 230 235 240

Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Ser Gly Met Glu Tyr Trp
 245 250 255

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

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

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

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

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg

			325						330						335
Ser	Lys	Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro
			340					345					350		
Arg	Arg	Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro
		355					360					365			
Arg	Asp	Phe	Ala	Ala	Tyr	Arg	Ser	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	Glu	Gly	Arg	Gly
				485					490					495	
Ser	Leu	Leu	Thr	Cys	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Glu
			500					505					510		
Tyr	Ala	Ser	Asp	Ala	Ser	Leu	Asp	Pro	Glu	Ala	Pro	Trp	Pro	Pro	Ala
		515					520					525			
Pro	Arg	Ala	Arg	Ala	Cys	Arg	Val	Leu	Pro	Trp	Ala	Leu	Val	Ala	Gly
	530					535					540				

Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe Leu Ala
545 550 555 560

Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser Ala Ala
565 570 575

Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp Pro Ala
580 585 590

Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val Ala Gln
595 600 605

Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp Pro Gly
610 615 620

Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu Asp Thr
625 630 635 640

Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe Phe Gln
645 650 655

Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser Val Ser
660 665 670

Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala Ala Ala
675 680 685

Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala Arg Asn
690 695 700

Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala Gly Gln
705 710 715 720

Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His Ala Trp
725 730 735

Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val Thr Pro
740 745 750

Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu

755

760

<210> 59
 <211> 2294
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Sequence

<400> 59
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 ccggagatcg tgatgaccca gagccccgcc accctgagcg tgagccccgg cgagagggcc 120
 accctgagct gcaggagcag ccagagcctg gtgcacagga acggcaacac ctacctgcac 180
 tggctacctgc agaagcccgg ccagagcccc aagctgctga tccacaaggt gagcaacagg 240
 ttcagcggcg tgcccgcag gttcagcggc agcggcagcg gcaccgactt caccctgaag 300
 atcagcaggg tggaggccga ggacctgggc gtgtacttct gcagccagag caccacgtg 360
 cccccctga ctttcggcg cggcaccaag ctggagctga agaggggagg cggcggcagc 420
 ggccggcggcg gcagcggcgg cggcggcagc gaggtgcagc tgctgcagag cggccccgag 480
 ctggagaagc ccggcgccag cgtgatgatc agctgcaagg ccagcggcag cagcttcacc 540
 ggctacaaca tgaactgggt gaggcagaac atcggcaaga gcctggagtg gatcggcgcc 600
 atcgaccctt actacggcgg caccagctac aaccagaagt tcaagggcag ggccaccctg 660
 accgtggaca agagcagcag caccgcctac atgcacctga agagcctgac cagcaggac 720
 agcgccgtgt actactgctg gagcggcatg gactactggg gccagggcac cagcgtgacc 780
 gtgagcagca ccacgacgcc agcgccgca ccaccaacac cggcgccac catcgctcg 840
 cagcccctgt ccctgcgccc agaggcgtgc cggccagcgg cggggggcg agtgacacag 900
 agggggctgg acttcgcctg tgatatctac atctggcgcg ccttggccgg gacttgtggg 960
 gtccttctcc tgtcactggt tatcaccctt tactgcagga gtaagaggag caggctcctg 1020
 cacagtgact acatgaacat gactccccgc cggccggggc ccaccgcaa gcattaccag 1080
 ccctatgccc caccacgcga cttcgagcc tatcgctcca gactgaagtt cagcaggagc 1140
 gcagacgccc ccgctacca gcagggccag aaccagctct ataacgagct caatctagga 1200
 cgaagagagg agtacgatgt tttggacaag agacgtggcc gggaccctga gatgggggga 1260

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aagccgcaga gaaggaagaa ccctcaggaa ggcctgtaca atgaactgca gaaagataag      1320
atggcggagg cctacagtga gattgggatg aaaggcgagc gccggagggg caagggggcac      1380
gatggccttt accagggtct cagtacagcc accaaggaca cctacgacgc ctttcacatg      1440
caggccctgc cccctcgcgg cagcggcgaa ggccgcggca gcctgctgac ctgcggcgat      1500
gtggaagaaa acccggggcc catggaatac gcctctgacg cttcactgga cccgaagcc      1560
ccgtggcctc ccgcgccccg cgctcgcgcc tgccgcgtac tgccttgggc cctggtcgcg      1620
gggctgctgc tgctgctgct gctcgtgcc gcctgcgccg tcttcctcgc ctgcccctgg      1680
gccgtgtccg gggctcgcgc ctgccccggc tccgcggcca gcccagact ccgcgagggt      1740
cccgagcttt cgccccacga tcccgccggc ctcttggacc tgcggcaggg catgtttgcg      1800
cagctggtgg cccaaaatgt tctgctgac gatgggcccc tgagctggta cagtgaccca      1860
ggcctggcag gcgtgtccct gacggggggc ctgagctaca aagaggacac gaaggagctg      1920
gtggtggcca aggctggagt ctactatgtc ttctttcaac tagagctgcg gcgcgtggtg      1980
gccggcgagg gctcaggctc cgtttcactt gcgctgcacc tgcagccact gcgctctgct      2040
gctggggccg ccgccctggc tttgaccgtg gacctgccac ccgcctcctc cgaggctcgg      2100
aactcggcct tcggtttcca gggccgcttg ctgcacctga gtgccggcca gcgcctgggc      2160
gtccatcttc acactgaggc cagggcacgc catgcctggc agcttaccca gggcgccaca      2220
gtcttgggac tcttcgggt gacccccgaa atcccagccg gactcccttc accgaggtcg      2280
gaataagttt aaac                                                                2294

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```

<210> 60
<211> 1302
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> Synthetic Sequence

```

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<400> 60

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```

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

```

```

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

```

Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys
 35 40 45

Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Phe Gln Gln Lys Pro
 50 55 60

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

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

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

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

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

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

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

Asp Tyr Tyr Leu Asp Trp Val Lys Gln Ser His Gly Glu Ser Phe Glu
 180 185 190

Trp Ile Gly Arg Val Asn Pro Tyr Asn Gly Gly Thr Ile Tyr Asn Gln
 195 200 205

Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr
 210 215 220

Ala Tyr Met Asp Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
 225 230 235 240

Tyr Cys Ala Arg Asp His Tyr Arg Tyr Asp Pro Leu Leu Asp Tyr Trp

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

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