

SEQUENCE LISTING

<110> CATALENT PHARMA SOLUTIONS, LLC

<120> MULTIFUNCTIONAL PROTEIN MOLECULES COMPRISING DECORIN AND USE THEREOF

<130> GALA-33890

<150> US 62/693,766

<151> 2018-07-03

<160> 67

<170> PatentIn version 3.5

<210> 1

<211> 2424

<212> DNA

<213> Artificial Sequence

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<223> synthetic

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Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe
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Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala
65 70 75 80

Ala Asp Phe Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser
85 90 95

Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Lys Tyr Pro His Tyr Tyr Gly Ser Ser His Trp Tyr
115 120 125

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

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
145 150 155 160

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

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
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His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
195 200 205

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

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
 225 230 235 240

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 245 250 255

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 260 265 270

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 275 280 285

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

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
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Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 355 360 365

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 370 375 380

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 385 390 395 400

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 405 410 415

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 420 425 430

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 435 440 445

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

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

Glu Leu His Leu Asp Gly Asn Lys Ile Ser Arg Val Asp Ala Ala Ser
675 680 685

Leu Lys Gly Leu Asn Asn Leu Ala Lys Leu Gly Leu Ser Phe Asn Ser
690 695 700

Ile Ser Ala Val Asp Asn Gly Ser Leu Ala Asn Thr Pro His Leu Arg
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Glu Leu His Leu Asp Asn Asn Lys Leu Thr Arg Val Pro Gly Gly Leu
725 730 735

Ala Glu His Lys Tyr Ile Gln Val Val Tyr Leu His Asn Asn Asn Ile
740 745 750

Ser Val Val Gly Ser Ser Asp Phe Cys Pro Pro Gly His Asn Thr Lys
755 760 765

Lys Ala Ser Tyr Ser Gly Val Ser Leu Phe Ser Asn Pro Val Gln Tyr
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Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile
 35 40 45

Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 50 55 60

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

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

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

Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
 130 135 140

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
 145 150 155 160

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
195 200 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
210 215 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 5
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<212> PRT
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<220>
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<400> 5

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
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Thr Gln Ala

<210> 6
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<400> 6

Ser Gly Gly Gly Gly Ser
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Glu Pro Ser Leu Gly Pro Val Cys Pro Phe Arg Cys Gln Cys His Leu
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Arg Val Val Gln Cys Ser Asp Leu Gly Leu Asp Lys Val Pro Lys Asp
35 40 45

Leu Pro Pro Asp Thr Thr Leu Leu Asp Leu Gln Asn Asn Lys Ile Thr
50 55 60

Glu Ile Lys Asp Gly Asp Phe Lys Asn Leu Lys Asn Leu His Ala Leu
65 70 75 80

Ile Leu Val Asn Asn Lys Ile Ser Lys Val Ser Pro Gly Ala Phe Thr
85 90 95

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

Glu Leu Pro Glu Lys Met Pro Lys Thr Leu Gln Glu Leu Arg Ala His
115 120 125

Glu Asn Glu Ile Thr Lys Val Arg Lys Val Thr Phe Asn Gly Leu Asn
130 135 140

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

Ile Glu Asn Gly Ala Phe Gln Gly Met Lys Lys Leu Ser Tyr Ile Arg
165 170 175

Ile Ala Asp Thr Asn Ile Thr Ser Ile Pro Gln Gly Leu Pro Pro Ser
180 185 190

Leu Thr Glu Leu His Leu Asp Gly Asn Lys Ile Ser Arg Val Asp Ala
195 200 205

Ala Ser Leu Lys Gly Leu Asn Asn Leu Ala Lys Leu Gly Leu Ser Phe
210 215 220

Asn Ser Ile Ser Ala Val Asp Asn Gly Ser Leu Ala Asn Thr Pro His
 225 230 235 240

Leu Arg Glu Leu His Leu Asp Asn Asn Lys Leu Thr Arg Val Pro Gly
 245 250 255

Gly Leu Ala Glu His Lys Tyr Ile Gln Val Val Tyr Leu His Asn Asn
 260 265 270

Asn Ile Ser Val Val Gly Ser Ser Asp Phe Cys Pro Pro Gly His Asn
 275 280 285

Thr Lys Lys Ala Ser Tyr Ser Gly Val Ser Leu Phe Ser Asn Pro Val
 290 295 300

Gln Tyr Trp Glu Ile Gln Pro Ser Thr Phe Arg Cys Val Tyr Val Arg
 305 310 315 320

Ser Ala Ile Gln Leu Gly Asn Tyr Lys
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<220>
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Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe
 50 55 60

Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
 65 70 75 80

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Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	
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Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	
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Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
 355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
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Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
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Leu Ser Pro Gly Lys
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<220>
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Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
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Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
 35 40 45

Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Thr Val Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

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

Ser Ser Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

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

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 355 360 365

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 450 455 460

Pro Gly Lys Ser Gly Gly Gly Gly Ser Asp Glu Ala Ala Gly Ile Gly
 465 470 475 480

Pro Glu Val Pro Asp Asp Arg Asp Phe Glu Pro Ser Leu Gly Pro Val
 485 490 495

Cys Pro Phe Arg Cys Gln Cys His Leu Arg Val Val Gln Cys Ser Asp
 500 505 510

Leu Gly Leu Asp Lys Val Pro Lys Asp Leu Pro Pro Asp Thr Thr Leu
 515 520 525

Leu Asp Leu Gln Asn Asn Lys Ile Thr Glu Ile Lys Asp Gly Asp Phe
 530 535 540

Lys Asn Leu Lys Asn Leu His Ala Leu Ile Leu Val Asn Asn Lys Ile
 545 550 555 560

Ser Lys Val Ser Pro Gly Ala Phe Thr Pro Leu Val Lys Leu Glu Arg
 565 570 575

Leu Tyr Leu Ser Lys Asn Gln Leu Lys Glu Leu Pro Glu Lys Met Pro
 580 585 590

Lys Thr Leu Gln Glu Leu Arg Ala His Glu Asn Glu Ile Thr Lys Val
 595 600 605

Arg Lys Val Thr Phe Asn Gly Leu Asn Gln Met Ile Val Ile Glu Leu
 610 615 620

Gly Thr Asn Pro Leu Lys Ser Ser Gly Ile Glu Asn Gly Ala Phe Gln
 625 630 635 640

Gly Met Lys Lys Leu Ser Tyr Ile Arg Ile Ala Asp Thr Asn Ile Thr
 645 650 655

Ser Ile Pro Gln Gly Leu Pro Pro Ser Leu Thr Glu Leu His Leu Asp
 660 665 670

Gly Asn Lys Ile Ser Arg Val Asp Ala Ala Ser Leu Lys Gly Leu Asn
 675 680 685

Asn Leu Ala Lys Leu Gly Leu Ser Phe Asn Ser Ile Ser Ala Val Asp
 690 695 700

Asn Gly Ser Leu Ala Asn Thr Pro His Leu Arg Glu Leu His Leu Asp
 705 710 715 720

Asn Asn Lys Leu Thr Arg Val Pro Gly Gly Leu Ala Glu His Lys Tyr
 725 730 735

Ile Gln Val Val Tyr Leu His Asn Asn Asn Ile Ser Val Val Gly Ser
 740 745 750

Ser Asp Phe Cys Pro Pro Gly His Asn Thr Lys Lys Ala Ser Tyr Ser
 755 760 765

Gly Val Ser Leu Phe Ser Asn Pro Val Gln Tyr Trp Glu Ile Gln Pro
 770 775 780

Ser Thr Phe Arg Cys Val Tyr Val Arg Ser Ala Ile Gln Leu Gly Asn
 785 790 795 800

Tyr Lys

<210> 12
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 12
atgatgtcct ttgtctctct gtccttggtt ggcatacctat tccatgccac ccaggccgag 60
atcgtgctga cccagtcctcc cggcaccctg tccctgtccc ccggcgagcg ggccaccctg 120
tcctgcccggg cctcccagtc cgtgggctcc tcctacctgg cctgggtacca gcagaagccc 180
ggccaggccc cccggctgct gatctacggc gccttctccc gcgccaccgg catccccgac 240
cggttctccg gctccggctc cggcaccgac ttcaccctga ccatctcccg gctggagccc 300
gaggacttcg ccgtgtacta ctgccagcag tacggctcct cccctgggac cttcggccag 360
ggcaccaagg tggagatcaa gcgaactgtg gctgcaccat ctgtcttcat cttcccgcga 420
tctgatgagc agcttaagtc cggaactgct agcgttgtgt gcctgctgaa taacttctat 480
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 540
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 600
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 660
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gtttag 705

<210> 13
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 13

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
1 5 10 15

Thr Gln Ala Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
20 25 30

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

Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

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

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

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly
100 105 110

Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 14

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 14

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 15
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 15

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
 100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 16
<211> 2409
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 16
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gtacaactcg tggaatccgg cgggggactc gtccaaccgg gtggtagtct cagggttgagc 120
tgcgctgcca gcggtttcac tttctcagac tcatggattc attgggtgcg ccaagcacct 180
ggaaaagggg tggaatgggt tgcctggatc tctccttacg gaggttctac ctactacgct 240
gattcagtaa aggggcggtt cacaatttca gccgatactt caaaaaatac ggcttacctg 300
caaatgaact ctttgagggc ggaggatacg gcggtctact actgtgcacg caggcactgg 360
cctggagggg tcgattattg gggtaaggc actttggtta ccgtatcctc cgcttctacc 420
aaaggcccat cagtatttcc tttggctccc agctctaagt ccacttccgg tggaactgcc 480
gcacttggat gtctcgtcaa agactacttt cctgagccgg taactgtgtc atggaactcc 540
ggcgccctca ctageggcgt ccatacattt ccagcggttc tccagtcaag tggcctctac 600
agcctgtcca gtgtagttac tgtcccgctt tctagtctgg gaacgcaaac atatatttgc 660
aatgtgaatc ataagcctag taacacaaaa gtcgataaaa aagtggagcc gaaaagttgt 720
gacaaaacgc atacctgtcc gccttgtccg gccccgaac tcttggggcg cccatcagtc 780
tttctcttcc cgcccaaacc taaggacacg ttgatgataa gtcgcacgcc cgaggttaca 840
tgcgtcgtag tcgatgtcag ccacgaggat ccggaggtaa agtttaactg gtatgtagac 900
ggagttgaag tacacaacgc caaaactaaa ccgagagagg agcagtacgc atcaacctat 960
cgcgtagtat ctgtattgac ggtccttcac caagactggc tcaatgggaa agaatacaag 1020
tgcaaagttt ctaataaagc cctccctgca ccaatcgaaa agactatttc aaaagccaaa 1080
ggacaaccaa gagaaccaca agtttataca ttgccaccta gtcgcgagga gatgactaaa 1140
aaccaagtgt cccttacttg tctcgtaaag ggtttctatc caagcgacat agcagttgag 1200
tgggaaagta atggccagcc ggaaaacaac tacaagacga ccccccggt tctcgactcc 1260

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gatggatcat tctttttgta tagtaaactc acagttgata agagtcgatg gcagcagggg 1320
aatgtttttt cttgctctgt gatgcacgag gcgctccaca accactatac gcaaaagtcc 1380
ctcagcctga gccccgggaa atccgggggt ggcggatccg atgaggctgc agggataggc 1440
ccagaagttc ctgatgaccg cgacttcgag ccctccctag gcccagtgtg ccccttcgcg 1500
tgtcaatgcc atcttcgagt ggtccagtgt tctgatttgg gtctggacaa agtgccaaag 1560
gatcttcccc ctgacacaac tctgctagac ctgcaaaaca acaaaataac cgaaatcaaa 1620
gatggagact ttaagaacct gaagaacctt cacgcattga ttcttgtcaa caataaaatt 1680
agcaaagtta gtcctggagc atttacacct ttggtgaagt tggaacgact ttatctgtcc 1740
aagaatcagc tgaaggaatt gccagaaaaa atgccccaaa ctcttcagga gctgcgtgcc 1800
catgagaatg agatcaccaa agtgcgaaaa gttactttca atggactgaa ccagatgatt 1860
gtcatagaac tgggcaccaa tccgctgaag agctcaggaa ttgaaaatgg ggctttccag 1920
ggaatgaaga agctctccta catccgcatt gctgatacca atatcaccag cattcctcaa 1980
ggctcttctc cttcccttac ggaattacat cttgatggca acaaaatcag cagagttgat 2040
gcagctagcc tgaaaggact gaataatttg gctaagttgg gattgagttt caacagcatc 2100
tctgctgttg acaatggctc tctggccaac acgcctcatc tgaggagct tcacttgga 2160
aacaacaagc ttaccagagt acctggtggg ctggcagagc ataagtacat ccaggttgtc 2220
taccttcata acaacaatat ctctgtagtt ggatcaagtg acttctgccc acctggacac 2280
aacacaaaaa aggtcttcta ttcgggtgtg agtcttttca gcaaccgggt ccagtactgg 2340
gagatacagc catccacctt cagatgtgtc tacgtgcgct ctgccattca actcggaaac 2400
tataagtga 2409

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<210> 17
<211> 802
<212> PRT
<213> Artificial Sequence

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<220>
<223> synthetic

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<400> 17

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Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
1           5           10          15

```

```

Thr Gln Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
          20          25          30

```

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45

Ser Asp Ser Trp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60

Glu Trp Val Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala
 65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn
 85 90 95

Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 195 200 205

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

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr
 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 450 455 460

Pro Gly Lys Ser Gly Gly Gly Gly Ser Asp Glu Ala Ala Gly Ile Gly
 465 470 475 480

Pro Glu Val Pro Asp Asp Arg Asp Phe Glu Pro Ser Leu Gly Pro Val
 485 490 495

Cys Pro Phe Arg Cys Gln Cys His Leu Arg Val Val Gln Cys Ser Asp
500 505 510

Leu Gly Leu Asp Lys Val Pro Lys Asp Leu Pro Pro Asp Thr Thr Leu
515 520 525

Leu Asp Leu Gln Asn Asn Lys Ile Thr Glu Ile Lys Asp Gly Asp Phe
530 535 540

Lys Asn Leu Lys Asn Leu His Ala Leu Ile Leu Val Asn Asn Lys Ile
545 550 555 560

Ser Lys Val Ser Pro Gly Ala Phe Thr Pro Leu Val Lys Leu Glu Arg
565 570 575

Leu Tyr Leu Ser Lys Asn Gln Leu Lys Glu Leu Pro Glu Lys Met Pro
580 585 590

Lys Thr Leu Gln Glu Leu Arg Ala His Glu Asn Glu Ile Thr Lys Val
595 600 605

Arg Lys Val Thr Phe Asn Gly Leu Asn Gln Met Ile Val Ile Glu Leu
610 615 620

Gly Thr Asn Pro Leu Lys Ser Ser Gly Ile Glu Asn Gly Ala Phe Gln
625 630 635 640

Gly Met Lys Lys Leu Ser Tyr Ile Arg Ile Ala Asp Thr Asn Ile Thr
645 650 655

Ser Ile Pro Gln Gly Leu Pro Pro Ser Leu Thr Glu Leu His Leu Asp
660 665 670

Gly Asn Lys Ile Ser Arg Val Asp Ala Ala Ser Leu Lys Gly Leu Asn
675 680 685

Asn Leu Ala Lys Leu Gly Leu Ser Phe Asn Ser Ile Ser Ala Val Asp
690 695 700

Asn Gly Ser Leu Ala Asn Thr Pro His Leu Arg Glu Leu His Leu Asp
705 710 715 720

Asn Asn Lys Leu Thr Arg Val Pro Gly Gly Leu Ala Glu His Lys Tyr
725 730 735

Ile Gln Val Val Tyr Leu His Asn Asn Asn Ile Ser Val Val Gly Ser
740 745 750

Ser Asp Phe Cys Pro Pro Gly His Asn Thr Lys Lys Ala Ser Tyr Ser
755 760 765

Gly Val Ser Leu Phe Ser Asn Pro Val Gln Tyr Trp Glu Ile Gln Pro
770 775 780

Ser Thr Phe Arg Cys Val Tyr Val Arg Ser Ala Ile Gln Leu Gly Asn
785 790 795 800

Tyr Lys

<210> 18
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 18
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attcagatga cacaatcacc tagcagtctg agtgcgagcg taggtgatcg cgtaacgatt 120
acctgcaggg cctctcaaga cgtgtcaacg gcagtggcgt ggtaccagca gaagcctggt 180
aaagctccta agctcctcat ctattcagct tccttcttgt atagtggagt accgtcaaga 240
ttttccggaa gcggatcagg tacagatttt actttgacta tcagtagttt gcagccagag 300
gatttcgcta catattactg tcaacaatat ctctatcacc ctgccacttt tggacaaggg 360
actaaagtcg aaataaaacg aacagtggcc gcaccaagcg tttttatctt tcccccatcc 420
gacgagcagt tgaagagcgg caccgcgtcc gtggtctgcc tgttgaataa tttctatcca 480
agggaggcaa aagtgcaatg gaaagttgat aatgcgcttc aatccggaaa ctcaagaaga 540
tcagtaacag aacaagactc taaagacagt acatattctc ttagtagcac actcactctt 600
tcaaaggctg actatgagaa acataaagtg tacgcttggt aagtgcacac tcaaggtctt 660
agctccccag taactaagag cttaaatagg ggcgagtgct ga 702

<210> 19
 <211> 233
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 19

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
 1 5 10 15

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

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

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

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

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

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

His Pro Ala Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
 130 135 140

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
 145 150 155 160

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
 165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
 180 185 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
195 200 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
210 215 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 20
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 20

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ser
20 25 30

Trp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val
 290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 21
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 21

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Ser Thr Ala
 20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Leu Tyr His Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
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<210> 22
 <211> 2415
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 22
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 tgtgctgcca gtggcttcac attctcatct tacattatga tgtgggttcg acaggcccct 180
 gggaaggggc tggagtgggt ttctccatc taccctccg ggggaattac cttctatgcc 240
 gacacggtaa agggtcgctt cactataagt cgagataaca gcaaaaatac gctgtatctc 300
 cagatgaact ctctcagggc tgaggacaca gctgtatatt actgcgcgcg gattaagttg 360
 gggaccgtca caacagtgga ttactgggggt caaggcactc tggttaaccgt atcctcagca 420
 tccaccaagg gcccaagtgt attcccgtg gcccttcaa gttaaaccac gtctggcggc 480
 acagccgctc tcggttgctt ggtaaggac tacttcccag aacctgtcac tgtcagttgg 540
 aactcaggcg cattgacatc tgggtgcat acattccccg cagtcctgca aagctctgga 600
 ctttacagtc ttagtagcgt agtgacagtc ccatcttcaa gtcttggggac ccaaacttat 660
 atttgcaacg taaatcataa accctccaac actaaagtag acaaaaaagt agagccgaaa 720

tcttgcgaca aaacgcatac atgcccacca tgtcccgtctc cggaactcct gggcgggccc	780
tccgtttttt tctttccccc aaagcccaag gatacgctta tgatcagcag aacaccggaa	840
gttacttgtg tagtcgttga cgtgtctcac gaagatcccc aagtcaaatt taattggtat	900
gtggatggcg tcgaagtgca caacgcaaaa accaaaccca gagaggaaca gtataacagc	960
acgtatcgag tggctctccgt acttacggctc ctccaccagg actgggtgaa tggcaaggag	1020
tacaagtgca aagtgagcaa taaagcgttg ccagccccga tcgaaaaaac catcagcaag	1080
gccaagggac agcctagaga gccgcagggtt tacaccttgc cgccatcaag ggatgaactg	1140
actaaaaacc aggtatccct gacctgcctg gttaagggtt ttacccccag tgatatagcg	1200
gttgaatggg agtctaacgg gcagccagag aacaactaca aaacgacacc tcccgttctg	1260
gattccgatg gcagcttttt cttgtattct aaactcaccg tggataaatc ccgatggcag	1320
caaggcaacg tcttctcctg cagcgtgatg catgaagcct tgcacaacca ctatacccaa	1380
aagagtctca gcctgtcacc cgaggaaatcc gggggtggcg gatccgatga ggctgcaggg	1440
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cctcaaggctc ttctctcttc ctttacggaa ttacatcttg atggcaacaa aatcagcaga	2040
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gttgtctacc ttcataacaa caatatctct gtagttggat caagtgactt ctgccacct	2280
ggacacaaca caaaaaggc ttcttattcg ggtgtgagtc ttttcagcaa cccggtccag	2340
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ggaaactata agtga	2415

<210> 23
 <211> 804
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 23

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
 1 5 10 15

Thr Gln Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45

Ser Ser Tyr Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60

Glu Trp Val Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala
 65 70 75 80

Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr
 115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 145 150 155 160

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

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
195 200 205

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

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
225 230 235 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
245 250 255

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
260 265 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
275 280 285

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
290 295 300

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
305 310 315 320

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
325 330 335

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
340 345 350

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
355 360 365

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
370 375 380

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385 390 395 400

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
405 410 415

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 420 425 430
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 435 440 445
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 450 455 460
 Leu Ser Pro Gly Lys Ser Gly Gly Gly Gly Gly Ser Asp Glu Ala Ala Gly
 465 470 475 480
 Ile Gly Pro Glu Val Pro Asp Asp Arg Asp Phe Glu Pro Ser Leu Gly
 485 490 495
 Pro Val Cys Pro Phe Arg Cys Gln Cys His Leu Arg Val Val Gln Cys
 500 505 510
 Ser Asp Leu Gly Leu Asp Lys Val Pro Lys Asp Leu Pro Pro Asp Thr
 515 520 525
 Thr Leu Leu Asp Leu Gln Asn Asn Lys Ile Thr Glu Ile Lys Asp Gly
 530 535 540
 Asp Phe Lys Asn Leu Lys Asn Leu His Ala Leu Ile Leu Val Asn Asn
 545 550 555 560
 Lys Ile Ser Lys Val Ser Pro Gly Ala Phe Thr Pro Leu Val Lys Leu
 565 570 575
 Glu Arg Leu Tyr Leu Ser Lys Asn Gln Leu Lys Glu Leu Pro Glu Lys
 580 585 590
 Met Pro Lys Thr Leu Gln Glu Leu Arg Ala His Glu Asn Glu Ile Thr
 595 600 605
 Lys Val Arg Lys Val Thr Phe Asn Gly Leu Asn Gln Met Ile Val Ile
 610 615 620
 Glu Leu Gly Thr Asn Pro Leu Lys Ser Ser Gly Ile Glu Asn Gly Ala
 625 630 635 640
 Phe Gln Gly Met Lys Lys Leu Ser Tyr Ile Arg Ile Ala Asp Thr Asn
 645 650 655

Ile Thr Ser Ile Pro Gln Gly Leu Pro Pro Ser Leu Thr Glu Leu His
660 665 670

Leu Asp Gly Asn Lys Ile Ser Arg Val Asp Ala Ala Ser Leu Lys Gly
675 680 685

Leu Asn Asn Leu Ala Lys Leu Gly Leu Ser Phe Asn Ser Ile Ser Ala
690 695 700

Val Asp Asn Gly Ser Leu Ala Asn Thr Pro His Leu Arg Glu Leu His
705 710 715 720

Leu Asp Asn Asn Lys Leu Thr Arg Val Pro Gly Gly Leu Ala Glu His
725 730 735

Lys Tyr Ile Gln Val Val Tyr Leu His Asn Asn Asn Ile Ser Val Val
740 745 750

Gly Ser Ser Asp Phe Cys Pro Pro Gly His Asn Thr Lys Lys Ala Ser
755 760 765

Tyr Ser Gly Val Ser Leu Phe Ser Asn Pro Val Gln Tyr Trp Glu Ile
770 775 780

Gln Pro Ser Thr Phe Arg Cys Val Tyr Val Arg Ser Ala Ile Gln Leu
785 790 795 800

Gly Asn Tyr Lys

<210> 24
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 24
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tctgcactta cacaaccggc gtccgtttcc ggatctccag gacagagcat tactatcagt 120
tgcacgggaa cctcctcaga cgtagggggg tataattatg tgtcttggtta tcaacagcat 180
cccgggaaag cccccaaact gatgatctac gatgtcagca atagaccaag cggtgtgagt 240

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aatcgattta gcgggtctaa atctggtaac acagcatccc tcactattag tggactgcaa      300
gcagaagatg aggcagacta ttattgcagt agctatacgt ctagttccac ccgcgttttt      360
ggcactggga cgaaagtcac cgttctcgga caaccaaag caaacccac cgtgactctg      420
tttccgccta gcagcgaaga attgcaggcc aataaggcga cactcgtatg ccttatctcc      480
gacttctacc cgggcgctgt gacagtcgcg tggaaagccg acggcagccc tgtaaagct      540
ggagtcgaga ccacgaagcc gtccaagcag agtaacaata agtatgctgc atccagttat      600
ctctctctca ctccggaaca gtggaagtcc catcggtcct atagttgcca agtgacccat      660
gaggggtcca ccgtagagaa aacggtagca cctaccgaat gtagttga                      708

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<210> 25
<211> 235
<212> PRT
<213> Artificial Sequence

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<220>
<223> synthetic

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```

<400> 25

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```

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
1              5              10              15

```

```

Thr Gln Ala Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser
              20              25              30

```

```

Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val
              35              40              45

```

```

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

```

```

Pro Lys Leu Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser
65              70              75              80

```

```

Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
              85              90              95

```

```

Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr
100              105              110

```

```

Thr Ser Ser Ser Thr Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val
115              120              125

```

Leu Gly Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser
 130 135 140

Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser
 145 150 155 160

Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser
 165 170 175

Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn
 180 185 190

Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp
 195 200 205

Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr
 210 215 220

Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
 225 230 235

<210> 26
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 26

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala Asp Thr Val
 50 55 60

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys
 450

<210> 27
 <211> 216
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 27

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

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

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
85 90 95

Ser Thr Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
130 135 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 28
<211> 2418
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 28
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tgcgagcta	gtggttttac	cttctccaga	tactggatgt	catgggtccg	acaggcccct	180
ggcaaggggc	ttgaatgggt	tgcaaata	aagcaggacg	gttctgaaaa	gtactatgta	240
gactccgtca	aaggaagatt	tactattagt	cgagacaacg	ccaagaatag	cctctacctt	300
cagatgaatt	ctttgcgagc	ggaggacaca	gccgtatatt	actgcgcacg	agaagggggg	360
tggttcggtg	aactggcttt	tgactactgg	gggcaaggta	cgcttgtcac	ggtgagctct	420
gcctctacaa	aggggccgtc	tgtgtttcca	cttgctccat	ctagtaagtc	aacttctgga	480
ggtactgcgg	cattgggatg	ccttgттааg	gattattttc	ccgaacctgt	aactgtgagc	540
tggaattcag	gtgccctcac	ctctgggtga	catacctttc	cagcagtttt	gcaatcttcc	600
ggtttgtact	ctcttagttc	agttgтааct	gtccccctctt	cctctcttgg	tacccaaaca	660
tacatttgta	atgtcaatca	caaaccaagc	aataccaagg	tagacaagcg	ggtggaaccc	720
aaatcttgta	acaaaactca	tacctgccca	ccatgtcccg	ccccggagtt	tgaaggaggt	780
ccaagtgtat	ttcttttccc	gcctaagcct	aaggataccc	tcatgataag	tcggacacca	840
gaggtgacgt	gtgttggtgg	agacgtgagt	cacgaagatc	ccgaagttaa	atttaattgg	900
tatgtggacg	gggtggaagt	ccataacgcg	aagacaaaagc	cacgcgaaga	gcagtacaat	960
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gaatacaaat	gcaaagtatc	caacaaggcg	ttgcctgcga	gtatcgagaa	aacgatttct	1080
aaagctaaag	gacaaccccg	ggaacccag	gtctatacac	tgccgcccag	cagagaagag	1140
atgacgaaaa	atcaagtatc	ccttacgtgt	ctcgtcaaag	gcttctaccc	ttccgatatt	1200
gctgtagagt	gggaatctaa	cgggcagccg	gaaaataact	acaagactac	tccgccagta	1260
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caacaaggta	atgttttttag	ctgtagcgta	atgcacgaag	cgttgcataa	ccattataca	1380
cagaaatcac	tcagcctgtc	ccccgggaaa	tccgggggtg	gcggatccga	tgaggctgca	1440
gggataggcc	cagaagttcc	tgatgaccgc	gacttcgagc	cctccctagg	cccagtgtgc	1500
cccttccgct	gtcaatgcca	tcttcgagtg	gtccagtgtt	ctgatttggg	tctggacaaa	1560
gtgccaaagg	atcttcccc	tgacacaact	ctgctagacc	tgcaaaaaca	caaaataacc	1620
gaaatcaaag	atggagactt	taagaacctg	aagaaccttc	acgcattgat	tcttgtcaac	1680
aataaaatta	gcaaagttag	tcctggagca	tttacacctt	tggtgaagtt	ggaacgactt	1740
tatctgtcca	agaatcagct	gaaggaattg	ccagaaaaaa	tgcccaaaac	tcttcaggag	1800

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ctgcgtgccc atgagaatga gatcaccaaa gtgcgaaaag ttactttcaa tggactgaac 1860
cagatgattg tcatagaact gggcaccaat ccgctgaaga gctcaggaat tgaaaatggg 1920
gctttccagg gaatgaagaa gctctcctac atccgcattg ctgataccaa tatcaccagc 1980
attcctcaag gtcttctctc ttcccttacg gaattacatc ttgatggcaa caaaatcagc 2040
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aacagcatct ctgctgttga caatggctct ctggccaaca cgcctcatct gagggagctt 2160
cacttggaaca acaacaagct taccagagta cctggtgggc tggcagagca taagtacatc 2220
caggttgtct accttcataa caacaatatc tctgtagttg gatcaagtga cttctgcca 2280
cctggacaca acaccaaaaa ggcttcttat tcgggtgtga gtcttttcag caaccgggtc 2340
cagtactggg agatacagcc atccaccttc agatgtgtct acgtgcgctc tgccattcaa 2400
ctcggaaact ataagtga 2418

```

```

<210> 29
<211> 805
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> synthetic

```

```

<400> 29

```

```

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
1           5           10           15

```

```

Thr Gln Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
          20           25           30

```

```

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
          35           40           45

```

```

Ser Arg Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
          50           55           60

```

```

Glu Trp Val Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val
65           70           75           80

```

```

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
          85           90           95

```

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Glu Gly Gly Trp Phe Gly Glu Leu Ala Phe Asp
 115 120 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
 130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 145 150 155 160

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

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
 180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 195 200 205

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

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
 225 230 235 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 245 250 255

Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 275 280 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 305 310 315 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
340 345 350

Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
405 410 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
450 455 460

Ser Leu Ser Pro Gly Lys Ser Gly Gly Gly Gly Ser Asp Glu Ala Ala
465 470 475 480

Gly Ile Gly Pro Glu Val Pro Asp Asp Arg Asp Phe Glu Pro Ser Leu
485 490 495

Gly Pro Val Cys Pro Phe Arg Cys Gln Cys His Leu Arg Val Val Gln
500 505 510

Cys Ser Asp Leu Gly Leu Asp Lys Val Pro Lys Asp Leu Pro Pro Asp
515 520 525

Thr Thr Leu Leu Asp Leu Gln Asn Asn Lys Ile Thr Glu Ile Lys Asp
530 535 540

Gly Asp Phe Lys Asn Leu Lys Asn Leu His Ala Leu Ile Leu Val Asn
545 550 555 560

Asn Lys Ile Ser Lys Val Ser Pro Gly Ala Phe Thr Pro Leu Val Lys
 565 570 575

Leu Glu Arg Leu Tyr Leu Ser Lys Asn Gln Leu Lys Glu Leu Pro Glu
 580 585 590

Lys Met Pro Lys Thr Leu Gln Glu Leu Arg Ala His Glu Asn Glu Ile
 595 600 605

Thr Lys Val Arg Lys Val Thr Phe Asn Gly Leu Asn Gln Met Ile Val
 610 615 620

Ile Glu Leu Gly Thr Asn Pro Leu Lys Ser Ser Gly Ile Glu Asn Gly
 625 630 635 640

Ala Phe Gln Gly Met Lys Lys Leu Ser Tyr Ile Arg Ile Ala Asp Thr
 645 650 655

Asn Ile Thr Ser Ile Pro Gln Gly Leu Pro Pro Ser Leu Thr Glu Leu
 660 665 670

His Leu Asp Gly Asn Lys Ile Ser Arg Val Asp Ala Ala Ser Leu Lys
 675 680 685

Gly Leu Asn Asn Leu Ala Lys Leu Gly Leu Ser Phe Asn Ser Ile Ser
 690 695 700

Ala Val Asp Asn Gly Ser Leu Ala Asn Thr Pro His Leu Arg Glu Leu
 705 710 715 720

His Leu Asp Asn Asn Lys Leu Thr Arg Val Pro Gly Gly Leu Ala Glu
 725 730 735

His Lys Tyr Ile Gln Val Val Tyr Leu His Asn Asn Asn Ile Ser Val
 740 745 750

Val Gly Ser Ser Asp Phe Cys Pro Pro Gly His Asn Thr Lys Lys Ala
 755 760 765

Ser Tyr Ser Gly Val Ser Leu Phe Ser Asn Pro Val Gln Tyr Trp Glu
 770 775 780

Ile Gln Pro Ser Thr Phe Arg Cys Val Tyr Val Arg Ser Ala Ile Gln
 785 790 795 800

Leu Gly Asn Tyr Lys
805

<210> 30
<211> 705
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 30
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tcctgtaggg ctagccagag ggtatcttcc tcttacctgg catggtacca gcaaagccc 180
ggacaagccc cccgacttct gatttatgac gcctcatccc gggcgacagg catccctgac 240
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gaggatttcg cagtgtatta ctgtcaacaa tacggcagct tgccctggac ctttggacaa 360
ggaaccaagg tagagatcaa aaggaccgtt gccgccccgt ccgtgttcat cttccctccg 420
agcgatgagc aacttaaaag tggaactgca agcgttgtat gtcttctgaa caatttctat 480
ccccgagaag ccaaggtaca gtggaaagtg gataatgcc tccaatctgg caatagccaa 540
gagtctgtca cagagcagga cagcaaggac tcaacttatt cacttagctc caccctgacg 600
ctgagtaaag cagactacga gaagcataag gtgtatgctt gtgaggttac acaccaaggc 660
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<210> 31
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 31

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
1 5 10 15

Thr Gln Ala Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
20 25 30

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

Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

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

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

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly
100 105 110

Ser Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 32

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 32

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Gly Trp Phe Gly Glu Leu Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
 225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445

Pro Gly Lys
450

<210> 33
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 33

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

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

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 34
<211> 2385
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 34
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gtccagctcg tggaatcagg agggggtgta gtccaaccag ggcgagacct ccgacttgat 120
tgtaaagcat caggaattac attttctaata agcgggaatgc attgggtccg acaagcgcca 180
ggcaagggac tggaatgggt cgcggtgata tggatatgat gatcaaaacg ctattatgcg 240
gactctgtga agggctcgatt cactattagc agagataaca gcaagaatac tctcttcctt 300
cagatgaatt cacttagggc agaggacaca gcggtgtact attgcgcgac gaacgacgat 360
tattggggcc aaggacatt ggtaacggtg agttctgcta gtactaaagg gccttcgctc 420
ttcccactcg ccccttggtc tagaagtact agtgagtcaa cagctgcttt gggttgcttg 480
gttaaagact actttcctga acccgtgact gtgtcttgga attccggtgc tcttacttca 540
gggtgtcata cattcccagc agtattgcag agctctggct tgtattctct ctctcagtg 600
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ccatcaaaca cgaaagttga caagagagta gaaagcaagt atgggcctcc atgtcccccg 720
tgcccggcgc ccgagttcct gggtggtccg tcagtgttct tgttccctcc caagccaaaa 780
gatacattga tgataagtcg gacgccggag gtcacatgtg tagtagttga tgtctctcag 840
gaggatcctg aggtgcagtt taactggtac gtcgatggtg ttgaggtaca caacgccaaa 900
actaagccga gggaagagca gttcaattca acatatcggg tcgtgtccgt attgacagtt 960
ctgcaccaag attggttgaa cggaagagag tataagtga aagttagcaa taagggactt 1020
ccgtcctcaa ttgaaaaaac catttccaaa gcgaaaggcc aacctcgga acctcaggtg 1080
tataccttgc caccagcca agaagaaatg actaaaaacc aggttagttt gacatgtttg 1140

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gttaaaggct tttacccgct cgacattgcc gtcgagtggg aaagcaatgg gcagcctgaa 1200
aataactaca agacaacccc accagtattg gattccgacg gttccttctt tctttacagc 1260
cgcctcaccg tcgataagag tcggtggcaa gaggggaatg tcttttctct tagtgtcatg 1320
cacgaagcac ttcacaacca ttacacccaa aaatcattgt ccctgtcact ggggaaatcc 1380
gggggtggcg gatccgatga ggctgcaggg ataggcccag aagttcctga tgaccgagc 1440
ttcgagccct ccctaggccc agtgtgcccc ttccgctgtc aatgccatct tcgagtggtc 1500
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ctagacctgc aaaacaacaa aataaccgaa atcaaagatg gagactttaa gaacctgaag 1620
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ttacatcttg atggcaacaa aatcagcaga gttgatgcag ctagcctgaa aggactgaat 2040
aatttggtta agttgggatt gagtttcaac agcatctctg ctggtgacaa tggctctctg 2100
gccaacacgc ctcatctgag ggagcttcac ttggacaaca acaagcttac cagagtacct 2160
gggtgggctgg cagagcataa gtacatccag gttgtctacc ttcataacaa caatatctct 2220
gtagttggat caagtgactt ctgcccacct ggacacaaca caaaaaggc ttcttattcg 2280
gggtgtgagtc ttttcagcaa cccggtccag tactgggaga tacagccatc caccttcaga 2340
tgtgtctacg tgcgctctgc cattcaactc ggaaactata agtga 2385

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<210> 35
<211> 794
<212> PRT
<213> Artificial Sequence

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<220>
<223> synthetic

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<400> 35

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Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
1           5           10          15

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Thr Gln Ala Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe
35 40 45

Ser Asn Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Thr Asn Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val
115 120 125

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
130 135 140

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
145 150 155 160

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
165 170 175

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
180 185 190

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
195 200 205

Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
210 215 220

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
225 230 235 240

Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
245 250 255

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 260 265 270

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
 275 280 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 290 295 300

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 305 310 315 320

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 325 330 335

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
 340 345 350

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
 355 360 365

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 370 375 380

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 385 390 395 400

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 405 410 415

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
 420 425 430

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 435 440 445

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Ser Gly Gly Gly Gly
 450 455 460

Ser Asp Glu Ala Ala Gly Ile Gly Pro Glu Val Pro Asp Asp Arg Asp
 465 470 475 480

Phe Glu Pro Ser Leu Gly Pro Val Cys Pro Phe Arg Cys Gln Cys His
485 490 495

Leu Arg Val Val Gln Cys Ser Asp Leu Gly Leu Asp Lys Val Pro Lys
500 505 510

Asp Leu Pro Pro Asp Thr Thr Leu Leu Asp Leu Gln Asn Asn Lys Ile
515 520 525

Thr Glu Ile Lys Asp Gly Asp Phe Lys Asn Leu Lys Asn Leu His Ala
530 535 540

Leu Ile Leu Val Asn Asn Lys Ile Ser Lys Val Ser Pro Gly Ala Phe
545 550 555 560

Thr Pro Leu Val Lys Leu Glu Arg Leu Tyr Leu Ser Lys Asn Gln Leu
565 570 575

Lys Glu Leu Pro Glu Lys Met Pro Lys Thr Leu Gln Glu Leu Arg Ala
580 585 590

His Glu Asn Glu Ile Thr Lys Val Arg Lys Val Thr Phe Asn Gly Leu
595 600 605

Asn Gln Met Ile Val Ile Glu Leu Gly Thr Asn Pro Leu Lys Ser Ser
610 615 620

Gly Ile Glu Asn Gly Ala Phe Gln Gly Met Lys Lys Leu Ser Tyr Ile
625 630 635 640

Arg Ile Ala Asp Thr Asn Ile Thr Ser Ile Pro Gln Gly Leu Pro Pro
645 650 655

Ser Leu Thr Glu Leu His Leu Asp Gly Asn Lys Ile Ser Arg Val Asp
660 665 670

Ala Ala Ser Leu Lys Gly Leu Asn Asn Leu Ala Lys Leu Gly Leu Ser
675 680 685

Phe Asn Ser Ile Ser Ala Val Asp Asn Gly Ser Leu Ala Asn Thr Pro
690 695 700

His Leu Arg Glu Leu His Leu Asp Asn Asn Lys Leu Thr Arg Val Pro
705 710 715 720

Gly Gly Leu Ala Glu His Lys Tyr Ile Gln Val Val Tyr Leu His Asn
725 730 735

Asn Asn Ile Ser Val Val Gly Ser Ser Asp Phe Cys Pro Pro Gly His
740 745 750

Asn Thr Lys Lys Ala Ser Tyr Ser Gly Val Ser Leu Phe Ser Asn Pro
755 760 765

Val Gln Tyr Trp Glu Ile Gln Pro Ser Thr Phe Arg Cys Val Tyr Val
770 775 780

Arg Ser Ala Ile Gln Leu Gly Asn Tyr Lys
785 790

<210> 36
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 36
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atcgtattga ctacgtcccc tgctacactt tcaactgagtc cgggtgagcg ggcgactttg 120
tcatgtcggg catcacagag tgtaagtagt tatctggcct ggtatcaaca gaaaccggga 180
caggctcttc gcctgctgat ttatgacgca agcaatcgcg cgaccggcat cccggcgagg 240
ttctcagggt ctggatcagg tactgacttt acccttacga tctcttctct cgaacctgag 300
gatttcgctg tctattactg ccagcagtct tctaactggc cgagaacatt tgggtcaaggg 360
acaaaagtcg agattaagcg aactgtcgca ggcacatctg tctttatctt ccctccaagc 420
gacgaacagc ttaagagtgg caccgccagt gttgtctgcc ttctgaataa cttctatcca 480
agggaagcga aagttcagtg gaaggtggat aacgctctgc agtctgggaa ctctcaggaa 540
agtgtaacag aacaagactc caaagactca acctactctc ttagttccac gttgaccctc 600
tccaaagcgg actatgagaa gcataaggtc tacgcttgcg aggtaacaca ccaggggctg 660
agtagtccgg ttacgaagag cttcaacaga ggggaatgct ga 702

<210> 37
<211> 233

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 37

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
1 5 10 15

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

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

Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
50 55 60

Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg
65 70 75 80

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

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

Trp Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
130 135 140

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
145 150 155 160

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
195 200 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
 210 215 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230

<210> 38
 <211> 440
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 38

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

Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe Ser Asn Ser
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Thr Asn Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 100 105 110

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser
 115 120 125

Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
165 170 175

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys
180 185 190

Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp
195 200 205

Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala
210 215 220

Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
225 230 235 240

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
245 250 255

Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
260 265 270

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
275 280 285

Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
290 295 300

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
305 310 315 320

Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
325 330 335

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr
340 345 350

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
355 360 365

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
370 375 380

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 385 390 395 400

Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe
 405 410 415

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 420 425 430

Ser Leu Ser Leu Ser Leu Gly Lys
 435 440

<210> 39
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 39

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Ser Asn Trp Pro Arg
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 40
 <211> 2406
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 40
 atgatgtcct ttgtctctct gtccttggtt ggcattcctat tccatgccac ccaggcccag 60
 gtgcaattgg tccaaagtgg ggtcgaggtc aagaagccag gagcttctgt aaaagtttca 120
 tgtaaggcat ctgggtatac cttcacgaac tactatatgt attgggtgcg ccaagcgcca 180
 gggcagggcc tcgaatggat ggggtggcatc aatccgagca acggggggcac caactttaac 240
 gaaaagttta aaaaccgggt caccttgaca acggacagta gcacgactac cgcttatatg 300
 gagctgaaga gtttgcagtt tgatgatact gcggtttatt attgtgcacg cagagattat 360
 aggttcgaca tgggcttcga ctactggggt caaggacta cggtaactgt atcatctgct 420
 agtacaaagg gcccttccgt tttccccctc gccccgtgca gccgctcaac gtccgaaagc 480
 accgctgcac ttgggtgcct tgtaaaagac tattttccag agccagttac cgtgtcttgg 540
 aatagtggcg cacttacgtc cggggtgcac acttttccgg ctgtcttgca atcctctgga 600
 ctctattcct tgagtagcgt cgtaacagta ccaagtagta gtctcggcac caaaacgtat 660
 acgtgcaatg ttgatcataa gcctagcaac acgaaagttg acaaaagagt tgagagtaaa 720
 tatggacccc cctgtccgcc atgcccggcc cctgaattcc ttggggggccc gtctgtatatt 780

cttttcccgc ccaagccgaa ggatacactg atgataagca gaacgcctga ggttacctgc	840
gtcgtggtcg acgtaagcca ggaagatcct gaggtgcaat ttaattggta tgtggacggg	900
gtcgaggttc ataatgcaaa aacaaaaccc cgagaggagc aatttaattc aacgtacaga	960
gtcgttagcg tacttacagt gctgcaccag gattggctca acgggaagga gtataagtgc	1020
aaggtgtcta ataaaggttt gccctccagt atagaaaaaa ccatctcaaa ggcgaaagga	1080
cagcctagag aacctcaagt atataccctc ccaccctccc aagaagagat gacaaagaac	1140
caagtgagtc tcacatgcct cgtcaagggc ttctacccaa gcgatatagc cgtagagtgg	1200
gaatcaaatg gtcagccgga gaataactac aaaactactc cgccagtctt ggatagcgac	1260
gggtcttttt tcctgtactc taggctgacg gtggacaagt caagatggca ggaaggaaat	1320
gttttttagct gctccgttat gcatgaggct ctccacaatc attatacaca aaaaagtttg	1380
tctctgtcat tggggaaatc cgggggtggc ggatccgatg aggctgcagg gataggccca	1440
gaagttcctg atgaccgcga cttcgagccc tccctaggcc cagtgtgccc cttccgctgt	1500
caatgccatc ttcgagtggc ccagtgttct gatttgggtc tggacaaagt gccaaaggat	1560
cttccccctg acacaactct gctagacctg caaaacaaca aaataaccga aatcaaagat	1620
ggagacttta agaacctgaa gaaccttcac gcattgattc ttgtcaacaa taaaattagc	1680
aaagttagtc ctggagcatt tacacctttg gtgaagttgg aacgacttta tctgtccaag	1740
aatcagctga aggaattgcc agaaaaaatg cccaaaactc ttcaggagct gcgtgcccac	1800
gagaatgaga tcaccaaagt gcgaaaagtt actttcaatg gactgaacca gatgattgtc	1860
atagaactgg gcaccaatcc gctgaagagc tcaggaattg aaaatggggc tttccaggga	1920
atgaagaagc tctcctacat ccgcattgct gataccaata tcaccagcat tcctcaaggt	1980
cttcctcctt cccttacgga attacatctt gatggcaaca aaatcagcag agttgatgca	2040
gctagcctga aaggactgaa taatttggct aagttgggat tgagtttcaa cagcatctct	2100
gctgttgaca atggctctct ggccaacacg cctcatctga gggagcttca cttggacaac	2160
aacaagctta ccagagtacc tgggtgggctg gcagagcata agtacatcca ggttgtctac	2220
cttcataaca acaatatctc tgtagttgga tcaagtgact tctgcccacc tggacacaac	2280
acaaaaaagg cttcttattc ggggtgtgagt cttttcagca acccgggtcca gtactgggag	2340
atacagccat ccaccttcag atgtgtctac gtgcgctctg ccattcaact cggaactat	2400
aagtga	2406

<210> 41
 <211> 801
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 41

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
 1 5 10 15

Thr Gln Ala Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Asn Tyr Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Met Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn
 65 70 75 80

Glu Lys Phe Lys Asn Arg Val Thr Leu Thr Thr Asp Ser Ser Thr Thr
 85 90 95

Thr Ala Tyr Met Glu Leu Lys Ser Leu Gln Phe Asp Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr
 115 120 125

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
 145 150 155 160

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

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
195 200 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val
210 215 220

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
225 230 235 240

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
275 280 285

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
290 295 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
305 310 315 320

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
325 330 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
340 345 350

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385 390 395 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
405 410 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
420 425 430

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

Ile Pro Gln Gly Leu Pro Pro Ser Leu Thr Glu Leu His Leu Asp Gly
660 665 670

Asn Lys Ile Ser Arg Val Asp Ala Ala Ser Leu Lys Gly Leu Asn Asn
675 680 685

Leu Ala Lys Leu Gly Leu Ser Phe Asn Ser Ile Ser Ala Val Asp Asn
690 695 700

Gly Ser Leu Ala Asn Thr Pro His Leu Arg Glu Leu His Leu Asp Asn
705 710 715 720

Asn Lys Leu Thr Arg Val Pro Gly Gly Leu Ala Glu His Lys Tyr Ile
725 730 735

Gln Val Val Tyr Leu His Asn Asn Asn Ile Ser Val Val Gly Ser Ser
740 745 750

Asp Phe Cys Pro Pro Gly His Asn Thr Lys Lys Ala Ser Tyr Ser Gly
755 760 765

Val Ser Leu Phe Ser Asn Pro Val Gln Tyr Trp Glu Ile Gln Pro Ser
770 775 780

Thr Phe Arg Cys Val Tyr Val Arg Ser Ala Ile Gln Leu Gly Asn Tyr
785 790 795 800

Lys

<210> 42
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 42
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attgttctta cgcagagtcc agcaactttg tcaactctctc ccggcgaacg agcgacattg 120
tctgtcgcg cgagtaaggg tgtctcaaca tctggatact catatctgca ttggtaccag 180
caaaaaccgg gacaagcgcc gcgattgctg atttatctcg cctcctacct tgaaagtggg 240
gtgcctgcga ggttctccgg tagtggatca ggcaccgatt tcactttgac catcagcagc 300

ctcgaaccag aagattttgc cgtctactac tgccaacata gcagggattt gccactgaca 360
 ttcggcgggg gtacgaaagt tgagattaaa cggactgtag cggcaccttc tgtcttcac 420
 ttcccaccaa gcgatgagca gcttaaaagc ggtacagctt cagtgggtgtg ccttttgaac 480
 aacttttatc cgcgagaagc caaggtccaa tggaagggtg ataacgcttt gcaatccggt 540
 aactcacagg agtcagtaac agagcaagat agtaaagata gcacgtattc acttagcagt 600
 acccttactc ttagcaaggc tgattatgaa aacataagg tatatgcgtg cgaggtaacg 660
 caccaaggac ttagctcccc agtgacgaag tcatttaacc ggggggagtg ctga 714

<210> 43
 <211> 237
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 43

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
 1 5 10 15

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

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

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

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

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

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

His Ser Arg Asp Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
 115 120 125

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
 130 135 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
 145 150 155 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
 165 170 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
 180 185 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
 195 200 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
 210 215 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 44
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 44

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu Lys Phe
 50 55 60

Lys Asn Arg Val Thr Leu Thr Thr Asp Ser Ser Thr Thr Thr Ala Tyr
 65 70 75 80

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

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 45
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 45

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Gly Val Ser Thr Ser
20 25 30

Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Arg
85 90 95

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 46
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 46

Asp Glu Ala Ala Gly Ile Gly Pro Glu Val Pro Asp Asp Arg Asp Phe
1 5 10 15

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

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

Gly Leu Ala Glu His Lys Tyr Ile Gln Val Val Tyr Leu His Asn Asn
260 265 270

Asn Ile Ser Val Val Gly Ser Ser Asp Phe Cys Pro Pro Gly His Asn
275 280 285

Thr Lys Lys Ala Ser Tyr Ser Gly Val Ser Leu Phe Ser Asn Pro Val
290 295 300

Gln Tyr Trp Glu Ile Gln Pro Ser Thr Phe Arg Cys Val Tyr Val Arg
305 310 315 320

Ser Ala Ile Gln Leu Gly Asn Tyr Lys
325

<210> 47
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 47

Gly Pro Phe Gln Gln Arg Gly Leu Phe Asp Phe Met Leu Glu
1 5 10

<210> 48
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 48
ggcccgtttc aacagagagg cttatttgac tttatgctag aa 42

<210> 49
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 49
gatgaggctg cagggatagg cccagaagtt cctgatgacc gcgacttcga gccctcccta 60
ggcccagtgt gcccttccg ctgtcaatgc catcttcgag tgggtccagtg ttctgatttg 120

ggctctggaca aagtgccaaa ggatcttccc cctgacacaa ctctgctaga cctgcaaaac	180
aacaaaataa ccgaaatcaa agatggagac tttaagaacc tgaagaacct tcacgcattg	240
attcttgtca acaataaaat tagcaaagtt agtcctggag catttacacc tttggtgaag	300
ttggaacgac tttatctgtc caagaatcag ctgaaggaat tgccagaaaa aatgcccaaa	360
actcttcagg agctgcgtgc ccatgagaat gagatcacca aagtgcgaaa agttactttc	420
aatggactga accagatgat tgtcatagaa ctgggcacca atccgctgaa gagctcagga	480
attgaaaatg gggctttcca gggaatgaag aagctctcct acatccgcat tgctgatacc	540
aatatcacca gcattcctca aggtcttcct ccttccctta cggaattaca tcttgatggc	600
aacaaaatca gcagagttga tgcagctagc ctgaaaggac tgaataatth ggctaagttg	660
ggattgagtt tcaacagcat ctctgctggt gacaatggct ctctggccaa cacgcctcat	720
ctgagggagc ttcacttgga caacaacaag cttaccagag tacctgggtgg gctggcagag	780
cataagtaca tccaggttgt ctaccttcat aacaacaata tctctgtagt tggatcaagt	840
gacttctgcc cacctggaca caacaccaaa aaggcttctt attcgggtgt gactcttttc	900
agcaaccggg tccagtactg ggagatacag ccatccacct tcagatgtgt ctacgtgcgc	960
tctgccattc aactcggaaa ctataagtga	990

<210> 50
 <211> 2415
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 50	
atgatgtcct ttgtctctct gtccttggtt ggcacacctat tccatgccac ccaggccgag	60
gtacagcttt tggagtcagg cgggggggctc gtccaacctg ggggggtcact ccggttgtca	120
tgtgctgcca gtggcttcac attctcatct tacattatga tgtgggttcg acaggcccct	180
gggaaggggc tggagtgggt ttctccatc taccctccg ggggaattac cttctatgcc	240
gacacggtaa agggctcgctt cactataagt cgagataaca gcaaaaatac gctgtatctc	300
cagatgaact ctctcagggc tgaggacaca gctgtatatt actgcgcgcg gattaagttg	360
gggaccgtca caacagtgga ttactggggg caaggcactc tggtaacctg atcctcagca	420
tccaccaagg gcccaagtgt attcccgtg gcccttcaa gtaaattcac gtctggcggc	480
acagccgctc tcggttgctt ggtaaggac tacttcccag aacctgtcac tgtcagttgg	540

aactcaggcg cattgacatc tgggtgtccat acattccccg cagtcctgca aagctctgga	600
ctttacagtc ttagtagcgt agtgacagtc ccatcttcaa gtcttggggac ccaaacttat	660
atttgcaacg taaatcataa accctccaac actaaagtag acaaaaaagt agagccgaaa	720
tcttgcgaca aaacgcatac atgcccacca tgtcccgctc cggaactcct gggcggcccg	780
tccgtttttc tctttccccc aaagcccaag gatacgctta tgatcagcag aacaccggaa	840
gttacttgtg tagtcgttga cgtgtctcac gaagatcccc aagtcaaatt taattggtat	900
gtggatggcg tcgaagtgca caacgcaaaa accaaacca gagaggaaca gtataacagc	960
acgtatcgag tggctctccgt acttacggtc ctccaccagg actggttgaa tggcaaggag	1020
tacaagtgca aagtgagcaa taaagcgttg ccagccccga tcgaaaaaac catcagcaag	1080
gccaagggac agcctagaga gccgcagggt tacaccttgc cgccatcaag ggatgaactg	1140
actaaaaacc aggtatccct gacctgcctg gttaagggtt ttaccccag tgatatagcg	1200
gttgaatggg agtctaacgg gcagccagag aacaactaca aaacgacacc tcccgttctg	1260
gattccgatg gcagcttttt cttgtattct aaactcaccg tggataaatc ccgatggcag	1320
caaggcaacg tcttctcctg cagcgtgatg catgaagcct tgcacaacca ctatacccaa	1380
aagagtctca gcctgtcacc cgggaaatcc ggggggtggcg gatccgatga ggctgcaggg	1440
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cgtgcccattg agaatgagat caccaaagtg cgaaaagtta ctttcaatgg actgaaccag	1860
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ttccaggga tgaagaagct ctctacatc cgcattgctg ataccaatat caccagcatt	1980
cctcaaggtc ttctctcttc cttacggaa ttacatcttg atggcaacaa aatcagcaga	2040
gttgatgcag ctagcctgaa aggactgaat aatttggcta agttgggatt gagtttcaac	2100
agcatctctg ctgttgacaa tggctctctg gccaacacgc ctcatctgag ggagcttcac	2160
ttggacaaca acaagcttac cagagtacct ggtgggctgg cagagcataa gtacatccag	2220
gttgtctacc ttcataacaa caatatctct gtagttggat caagtgactt ctgcccacct	2280

ggacacaaca ccaaaaaggc ttcttattcg ggtgtgagtc ttttcagcaa cccggtccag 2340
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ggaaactata agtga 2415

<210> 51
<211> 804
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 51

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
1 5 10 15

Thr Gln Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala
65 70 75 80

Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr
115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
145 150 155 160

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

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 195 200 205

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

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
 225 230 235 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
 245 250 255

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 260 265 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 275 280 285

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 290 295 300

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 305 310 315 320

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 325 330 335

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 340 345 350

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 355 360 365

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
 370 375 380

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 385 390 395 400

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

Glu Leu Gly Thr Asn Pro Leu Lys Ser Ser Gly Ile Glu Asn Gly Ala
 625 630 635 640

Phe Gln Gly Met Lys Lys Leu Ser Tyr Ile Arg Ile Ala Asp Thr Asn
 645 650 655

Ile Thr Ser Ile Pro Gln Gly Leu Pro Pro Ser Leu Thr Glu Leu His
 660 665 670

Leu Asp Gly Asn Lys Ile Ser Arg Val Asp Ala Ala Ser Leu Lys Gly
 675 680 685

Leu Asn Asn Leu Ala Lys Leu Gly Leu Ser Phe Asn Ser Ile Ser Ala
 690 695 700

Val Asp Asn Gly Ser Leu Ala Asn Thr Pro His Leu Arg Glu Leu His
 705 710 715 720

Leu Asp Asn Asn Lys Leu Thr Arg Val Pro Gly Gly Leu Ala Glu His
 725 730 735

Lys Tyr Ile Gln Val Val Tyr Leu His Asn Asn Asn Ile Ser Val Val
 740 745 750

Gly Ser Ser Asp Phe Cys Pro Pro Gly His Asn Thr Lys Lys Ala Ser
 755 760 765

Tyr Ser Gly Val Ser Leu Phe Ser Asn Pro Val Gln Tyr Trp Glu Ile
 770 775 780

Gln Pro Ser Thr Phe Arg Cys Val Tyr Val Arg Ser Ala Ile Gln Leu
 785 790 795 800

Gly Asn Tyr Lys

<210> 52
 <211> 708
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 52
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60

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tgcacgggaa cctcctcaga cgtagggggg tataattatg tgtcttggtta tcaacagcat 180
cccgggaaag cccccaact gatgatctac gatgtcagca atagaccaag cgggtgtgagt 240
aatcgattta gcgggtctaa atctggtaac acagcatccc tcactattag tggactgcaa 300
gcagaagatg aggcagacta ttattgcagt agctatacgt ctagttccac ccgcgttttt 360
ggcactggga cgaaagtcac cgttctcgga caaccaaag caaacccac cgtgactctg 420
tttccgccta gcagcgaaga attgcaggcc aataaggcga cactcgtatg ccttatctcc 480
gacttctacc cgggcgctgt gacagtcgcg tggaaagccg acggcagccc tgttaaagct 540
ggagtcgaga ccacgaagcc gtccaagcag agtaacaata agtatgctgc atccagttat 600
ctctctctca ctccggaaca gtggaagtcc catcggtcct atagttgcca agtgacccat 660
gaggggtcca ccgtagagaa aacggtagca cctaccgaat gtagttga 708

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<210> 53
<211> 235
<212> PRT
<213> Artificial Sequence

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<220>
<223> synthetic

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<400> 53

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Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
1           5           10           15

```

```

Thr Gln Ala Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser
          20           25           30

```

```

Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val
          35           40           45

```

```

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

```

```

Pro Lys Leu Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser
65           70           75           80

```

```

Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
          85           90           95

```

Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr
100 105 110

Thr Ser Ser Ser Thr Arg Val Phe Gly Thr Gly Thr Lys Val Thr Val
115 120 125

Leu Gly Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser
130 135 140

Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser
145 150 155 160

Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser
165 170 175

Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn
180 185 190

Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp
195 200 205

Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr
210 215 220

Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225 230 235

<210> 54
<211> 3420
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 54
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tgtgctgcca gtggcttcac attctcatct tacattatga tgtgggttcg acaggcccct 180
gggaaggggc tggagtgggt ttctccatc taccctccg ggggaattac cttctatgcc 240
gacacggtaa agggtcgctt cactataagt cgagataaca gcaaaaatac gctgtatctc 300
cagatgaact ctctcagggc tgaggacaca gctgtatatt actgcgcgcg gattaagttg 360
gggaccgtca caacagtgga ttactggggt caaggcactc tggtaacctg atcctcagca 420

tccaccaagg gcccaagtgt attcccgtg gcccttcaa gtaaateccac gtctggcggc	480
acagccgctc tcggttgctt ggtaaggac tacttcccag aacctgtcac tgtcagttgg	540
aactcaggcg cattgacatc tgggtgtccat acattccccg cagtccctgca aagctctgga	600
ctttacagtc ttagtagcgt agtgacagtc ccatcttcaa gtcttggggac ccaaacttat	660
atttgcaacg taaatcataa accctccaac actaaagtag aaaaaaagt agagccgaaa	720
tcttgcgaca aaacgcatac atgcccacca tgtcccgctc cggaactcct gggcgggccg	780
tccgtttttc tctttcccc aaagcccaag gatacgctta tgatcagcag aacaccggaa	840
gttacttgtg tagtcgttga cgtgtctcac gaagatcccg aagtcaaatt taattggtat	900
gtggatggcg tcgaagtgca caacgcaaaa accaaacca gagaggaaca gtataacagc	960
acgtatcgag tggctctcgt acttacggtc ctccaccagg actggttgaa tggcaaggag	1020
tacaagtgca aagtgagcaa taaagcgttg ccagccccga tcgaaaaaac catcagcaag	1080
gccaaaggac agcctagaga gccgcagggt tacaccttgc cgccatcaag ggatgaactg	1140
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aagagtctca gcctgtcacc cgggaaatcc gggggtggcg gatccgatga ggctgcaggg	1440
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ttccgctgtc aatgccatct tcgagtggtc cagtgttctg atttgggtct ggacaaagtg	1560
ccaaaggatc tttcccctga cacaactctg ctagacctgc aaaacaaca aataaccgaa	1620
atcaaagatg gagactttaa gaacctgaag aaccttcacg cattgattct tgtcaacaat	1680
aaaattagca aagttagtcc tggagcattt acacctttgg tgaagttgga acgactttat	1740
ctgtccaaga atcagctgaa ggaattgcca gaaaaaatgc caaaactct tcaggagctg	1800
cgtgcccattg agaatgagat caccaaagtg cgaaaagtta ctttcaatgg actgaaccag	1860
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cctcaaggtc ttcctccttc cttacggaa ttacatcttg atggcaaca aatcagcaga	2040
gttgatgcag ctagcctgaa aggactgaat aatttggcta agttgggatt gagtttcaac	2100
agcatctctg ctgttgacaa tggctctctg gccaacacgc ctcatctgag ggagcttcac	2160

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gttgtctacc ttcataacaa caatatctct gtagttggat caagtgactt ctgcccacct 2280
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cttaccagag tacctgggtg gctggcagag cataagtaca tccaggthgt ctaccttcat 3240
aacaacaata tctctgtagt tggatcaagt gacttctgcc cacctggaca caacacaaa 3300
aaggcttctt attcgggtgt gagtcttttc agcaaccgg tccagtactg ggagatacag 3360
ccatccacct tcagatgtgt ctacgtgcgc tctgccattc aactcggaaa ctataagtga 3420

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<210> 55
<211> 1139
<212> PRT
<213> Artificial Sequence

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<220>
<223> synthetic

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<400> 55

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Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
1           5           10          15

```

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

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
260 265 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
275 280 285

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
290 295 300

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
305 310 315 320

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
325 330 335

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
340 345 350

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
355 360 365

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
370 375 380

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385 390 395 400

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
405 410 415

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
420 425 430

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
435 440 445

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
450 455 460

Leu Ser Pro Gly Lys Ser Gly Gly Gly Gly Ser Asp Glu Ala Ala Gly
465 470 475 480

Ile Gly Pro Glu Val Pro Asp Asp Arg Asp Phe Glu Pro Ser Leu Gly
485 490 495

Pro Val Cys Pro Phe Arg Cys Gln Cys His Leu Arg Val Val Gln Cys
500 505 510

Ser Asp Leu Gly Leu Asp Lys Val Pro Lys Asp Leu Pro Pro Asp Thr
515 520 525

Thr Leu Leu Asp Leu Gln Asn Asn Lys Ile Thr Glu Ile Lys Asp Gly
530 535 540

Asp Phe Lys Asn Leu Lys Asn Leu His Ala Leu Ile Leu Val Asn Asn
545 550 555 560

Lys Ile Ser Lys Val Ser Pro Gly Ala Phe Thr Pro Leu Val Lys Leu
565 570 575

Glu Arg Leu Tyr Leu Ser Lys Asn Gln Leu Lys Glu Leu Pro Glu Lys
580 585 590

Met Pro Lys Thr Leu Gln Glu Leu Arg Ala His Glu Asn Glu Ile Thr
595 600 605

Lys Val Arg Lys Val Thr Phe Asn Gly Leu Asn Gln Met Ile Val Ile
610 615 620

Glu Leu Gly Thr Asn Pro Leu Lys Ser Ser Gly Ile Glu Asn Gly Ala
625 630 635 640

Phe Gln Gly Met Lys Lys Leu Ser Tyr Ile Arg Ile Ala Asp Thr Asn
645 650 655

Ile Thr Ser Ile Pro Gln Gly Leu Pro Pro Ser Leu Thr Glu Leu His
660 665 670

Leu Asp Gly Asn Lys Ile Ser Arg Val Asp Ala Ala Ser Leu Lys Gly
675 680 685

Leu Asn Asn Leu Ala Lys Leu Gly Leu Ser Phe Asn Ser Ile Ser Ala
690 695 700

Val Asp Asn Gly Ser Leu Ala Asn Thr Pro His Leu Arg Glu Leu His
705 710 715 720

Leu Asp Asn Asn Lys Leu Thr Arg Val Pro Gly Gly Leu Ala Glu His
 725 730 735

Lys Tyr Ile Gln Val Val Tyr Leu His Asn Asn Asn Ile Ser Val Val
 740 745 750

Gly Ser Ser Asp Phe Cys Pro Pro Gly His Asn Thr Lys Lys Ala Ser
 755 760 765

Tyr Ser Gly Val Ser Leu Phe Ser Asn Pro Val Gln Tyr Trp Glu Ile
 770 775 780

Gln Pro Ser Thr Phe Arg Cys Val Tyr Val Arg Ser Ala Ile Gln Leu
 785 790 795 800

Gly Asn Tyr Lys Ser Gly Gly Gly Gly Ser Asp Glu Ala Ala Gly Ile
 805 810 815

Gly Pro Glu Val Pro Asp Asp Arg Asp Phe Glu Pro Ser Leu Gly Pro
 820 825 830

Val Cys Pro Phe Arg Cys Gln Cys His Leu Arg Val Val Gln Cys Ser
 835 840 845

Asp Leu Gly Leu Asp Lys Val Pro Lys Asp Leu Pro Pro Asp Thr Thr
 850 855 860

Leu Leu Asp Leu Gln Asn Asn Lys Ile Thr Glu Ile Lys Asp Gly Asp
 865 870 875 880

Phe Lys Asn Leu Lys Asn Leu His Ala Leu Ile Leu Val Asn Asn Lys
 885 890 895

Ile Ser Lys Val Ser Pro Gly Ala Phe Thr Pro Leu Val Lys Leu Glu
 900 905 910

Arg Leu Tyr Leu Ser Lys Asn Gln Leu Lys Glu Leu Pro Glu Lys Met
 915 920 925

Pro Lys Thr Leu Gln Glu Leu Arg Ala His Glu Asn Glu Ile Thr Lys
 930 935 940

Val	Arg	Lys	Val	Thr	Phe	Asn	Gly	Leu	Asn	Gln	Met	Ile	Val	Ile	Glu
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Leu	Gly	Thr	Asn	Pro	Leu	Lys	Ser	Ser	Gly	Ile	Glu	Asn	Gly	Ala	Phe
				965					970					975	
Gln	Gly	Met	Lys	Lys	Leu	Ser	Tyr	Ile	Arg	Ile	Ala	Asp	Thr	Asn	Ile
			980					985					990		
Thr	Ser	Ile	Pro	Gln	Gly	Leu	Pro	Pro	Ser	Leu	Thr	Glu	Leu	His	Leu
		995					1000					1005			
Asp	Gly	Asn	Lys	Ile	Ser	Arg	Val	Asp	Ala	Ala	Ser	Leu	Lys	Gly	
	1010					1015					1020				
Leu	Asn	Asn	Leu	Ala	Lys	Leu	Gly	Leu	Ser	Phe	Asn	Ser	Ile	Ser	
	1025					1030					1035				
Ala	Val	Asp	Asn	Gly	Ser	Leu	Ala	Asn	Thr	Pro	His	Leu	Arg	Glu	
	1040					1045					1050				
Leu	His	Leu	Asp	Asn	Asn	Lys	Leu	Thr	Arg	Val	Pro	Gly	Gly	Leu	
	1055					1060					1065				
Ala	Glu	His	Lys	Tyr	Ile	Gln	Val	Val	Tyr	Leu	His	Asn	Asn	Asn	
	1070					1075					1080				
Ile	Ser	Val	Val	Gly	Ser	Ser	Asp	Phe	Cys	Pro	Pro	Gly	His	Asn	
	1085					1090					1095				
Thr	Lys	Lys	Ala	Ser	Tyr	Ser	Gly	Val	Ser	Leu	Phe	Ser	Asn	Pro	
	1100					1105					1110				
Val	Gln	Tyr	Trp	Glu	Ile	Gln	Pro	Ser	Thr	Phe	Arg	Cys	Val	Tyr	
	1115					1120					1125				
Val	Arg	Ser	Ala	Ile	Gln	Leu	Gly	Asn	Tyr	Lys					
	1130					1135									

<210> 56
 <211> 2373
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 56

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aacaacaaaa taaccgaaat caaagatgga gactttaaga acctgaagaa ccttcacgca	1620
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ggcaacaaaa tcagcagagt tgatgcagct agcctgaaag gactgaataa tttggctaag 2040
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cgctctgcca ttcaactcgg aaactataag tga 2373

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<210> 57
<211> 790
<212> PRT
<213> Artificial Sequence

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<220>
<223> synthetic

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<400> 57

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Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
1           5           10           15

```

```

Thr Gln Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
          20           25           30

```

```

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
          35           40           45

```

```

Ser Ser Tyr Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50           55           60

```

```

Glu Trp Val Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala
65           70           75           80

```

```

Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
          85           90           95

```

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
325 330 335

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
340 345 350

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
355 360 365

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
370 375 380

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385 390 395 400

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
405 410 415

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
420 425 430

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
435 440 445

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
450 455 460

Leu Ser Pro Gly Lys Ser Gly Gly Gly Gly Ser Asp Phe Glu Pro Ser
465 470 475 480

Leu Gly Pro Val Cys Pro Phe Arg Cys Gln Cys His Leu Arg Val Val
485 490 495

Gln Cys Ser Asp Leu Gly Leu Asp Lys Val Pro Lys Asp Leu Pro Pro
500 505 510

Asp Thr Thr Leu Leu Asp Leu Gln Asn Asn Lys Ile Thr Glu Ile Lys
515 520 525

Asp Gly Asp Phe Lys Asn Leu Lys Asn Leu His Ala Leu Ile Leu Val
530 535 540

Asn Asn Lys Ile Ser Lys Val Ser Pro Gly Ala Phe Thr Pro Leu Val
545 550 555 560

Lys Leu Glu Arg Leu Tyr Leu Ser Lys Asn Gln Leu Lys Glu Leu Pro
565 570 575

Glu Lys Met Pro Lys Thr Leu Gln Glu Leu Arg Ala His Glu Asn Glu
580 585 590

Ile Thr Lys Val Arg Lys Val Thr Phe Asn Gly Leu Asn Gln Met Ile
595 600 605

Val Ile Glu Leu Gly Thr Asn Pro Leu Lys Ser Ser Gly Ile Glu Asn
610 615 620

Gly Ala Phe Gln Gly Met Lys Lys Leu Ser Tyr Ile Arg Ile Ala Asp
625 630 635 640

Thr Asn Ile Thr Ser Ile Pro Gln Gly Leu Pro Pro Ser Leu Thr Glu
645 650 655

Leu His Leu Asp Gly Asn Lys Ile Ser Arg Val Asp Ala Ala Ser Leu
660 665 670

Lys Gly Leu Asn Asn Leu Ala Lys Leu Gly Leu Ser Phe Asn Ser Ile
675 680 685

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

Leu His Leu Asp Asn Asn Lys Leu Thr Arg Val Pro Gly Gly Leu Ala
705 710 715 720

Glu His Lys Tyr Ile Gln Val Val Tyr Leu His Asn Asn Asn Ile Ser
725 730 735

Val Val Gly Ser Ser Asp Phe Cys Pro Pro Gly His Asn Thr Lys Lys
740 745 750

Ala Ser Tyr Ser Gly Val Ser Leu Phe Ser Asn Pro Val Gln Tyr Trp
755 760 765

Glu Ile Gln Pro Ser Thr Phe Arg Cys Val Tyr Val Arg Ser Ala Ile
770 775 780

Gln Leu Gly Asn Tyr Lys
785 790

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<211> 3336
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

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<210> 59
<211> 1111
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 59

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

Ser Ser Tyr Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala
65 70 75 80

Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr
115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
145 150 155 160

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

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
195 200 205

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

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
225 230 235 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
245 250 255

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
260 265 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
275 280 285

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
290 295 300

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
305 310 315 320

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
325 330 335

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
340 345 350

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
355 360 365

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
370 375 380

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 385 390 395 400

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 405 410 415

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 420 425 430

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 435 440 445

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 450 455 460

Leu Ser Pro Gly Lys Ser Gly Gly Gly Gly Ser Asp Phe Glu Pro Ser
 465 470 475 480

Leu Gly Pro Val Cys Pro Phe Arg Cys Gln Cys His Leu Arg Val Val
 485 490 495

Gln Cys Ser Asp Leu Gly Leu Asp Lys Val Pro Lys Asp Leu Pro Pro
 500 505 510

Asp Thr Thr Leu Leu Asp Leu Gln Asn Asn Lys Ile Thr Glu Ile Lys
 515 520 525

Asp Gly Asp Phe Lys Asn Leu Lys Asn Leu His Ala Leu Ile Leu Val
 530 535 540

Asn Asn Lys Ile Ser Lys Val Ser Pro Gly Ala Phe Thr Pro Leu Val
 545 550 555 560

Lys Leu Glu Arg Leu Tyr Leu Ser Lys Asn Gln Leu Lys Glu Leu Pro
 565 570 575

Glu Lys Met Pro Lys Thr Leu Gln Glu Leu Arg Ala His Glu Asn Glu
 580 585 590

Ile Thr Lys Val Arg Lys Val Thr Phe Asn Gly Leu Asn Gln Met Ile
 595 600 605

Val Ile Glu Leu Gly Thr Asn Pro Leu Lys Ser Ser Gly Ile Glu Asn
 610 615 620

Gly Ala Phe Gln Gly Met Lys Lys Leu Ser Tyr Ile Arg Ile Ala Asp
625 630 635 640

Thr Asn Ile Thr Ser Ile Pro Gln Gly Leu Pro Pro Ser Leu Thr Glu
645 650 655

Leu His Leu Asp Gly Asn Lys Ile Ser Arg Val Asp Ala Ala Ser Leu
660 665 670

Lys Gly Leu Asn Asn Leu Ala Lys Leu Gly Leu Ser Phe Asn Ser Ile
675 680 685

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

Leu His Leu Asp Asn Asn Lys Leu Thr Arg Val Pro Gly Gly Leu Ala
705 710 715 720

Glu His Lys Tyr Ile Gln Val Val Tyr Leu His Asn Asn Asn Ile Ser
725 730 735

Val Val Gly Ser Ser Asp Phe Cys Pro Pro Gly His Asn Thr Lys Lys
740 745 750

Ala Ser Tyr Ser Gly Val Ser Leu Phe Ser Asn Pro Val Gln Tyr Trp
755 760 765

Glu Ile Gln Pro Ser Thr Phe Arg Cys Val Tyr Val Arg Ser Ala Ile
770 775 780

Gln Leu Gly Asn Tyr Lys Ser Gly Gly Gly Gly Ser Asp Phe Glu Pro
785 790 795 800

Ser Leu Gly Pro Val Cys Pro Phe Arg Cys Gln Cys His Leu Arg Val
805 810 815

Val Gln Cys Ser Asp Leu Gly Leu Asp Lys Val Pro Lys Asp Leu Pro
820 825 830

Pro Asp Thr Thr Leu Leu Asp Leu Gln Asn Asn Lys Ile Thr Glu Ile
835 840 845

Lys Asp Gly Asp Phe Lys Asn Leu Lys Asn Leu His Ala Leu Ile Leu
850 855 860

Val Asn Asn Lys Ile Ser Lys Val Ser Pro Gly Ala Phe Thr Pro Leu
865 870 875 880

Val Lys Leu Glu Arg Leu Tyr Leu Ser Lys Asn Gln Leu Lys Glu Leu
885 890 895

Pro Glu Lys Met Pro Lys Thr Leu Gln Glu Leu Arg Ala His Glu Asn
900 905 910

Glu Ile Thr Lys Val Arg Lys Val Thr Phe Asn Gly Leu Asn Gln Met
915 920 925

Ile Val Ile Glu Leu Gly Thr Asn Pro Leu Lys Ser Ser Gly Ile Glu
930 935 940

Asn Gly Ala Phe Gln Gly Met Lys Lys Leu Ser Tyr Ile Arg Ile Ala
945 950 955 960

Asp Thr Asn Ile Thr Ser Ile Pro Gln Gly Leu Pro Pro Ser Leu Thr
965 970 975

Glu Leu His Leu Asp Gly Asn Lys Ile Ser Arg Val Asp Ala Ala Ser
980 985 990

Leu Lys Gly Leu Asn Asn Leu Ala Lys Leu Gly Leu Ser Phe Asn Ser
995 1000 1005

Ile Ser Ala Val Asp Asn Gly Ser Leu Ala Asn Thr Pro His Leu
1010 1015 1020

Arg Glu Leu His Leu Asp Asn Asn Lys Leu Thr Arg Val Pro Gly
1025 1030 1035

Gly Leu Ala Glu His Lys Tyr Ile Gln Val Val Tyr Leu His Asn
1040 1045 1050

Asn Asn Ile Ser Val Val Gly Ser Ser Asp Phe Cys Pro Pro Gly
1055 1060 1065

His Asn Thr Lys Lys Ala Ser Tyr Ser Gly Val Ser Leu Phe Ser
1070 1075 1080

Asn Pro Val Gln Tyr Trp Glu Ile Gln Pro Ser Thr Phe Arg Cys
 1085 1090 1095

Val Tyr Val Arg Ser Ala Ile Gln Leu Gly Asn Tyr Lys
 1100 1105 1110

<210> 60
 <211> 1746
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 60
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 tgtgctgcca gtggcttcac attctcatct tacattatga tgtgggttcg acaggcccct 180
 gggaaggggc tggagtgggt ttctccatc taccctccg gggaattac cttctatgcc 240
 gacacggtaa agggtcgctt cactataagt cgagataaca gcaaaaatac gctgtatctc 300
 cagatgaact ctctcagggc tgaggacaca gctgtatatt actgcgcgcg gattaagttg 360
 gggaccgtca caacagtgga ttactgggggt caaggcactc tggttaaccgt atcctcagca 420
 tccaccaagg gcccaagtgt attcccgctg gcccttcaa gtaaattccac gtctggcggc 480
 acagccgctc tcggttgctt ggtaaggac tacttcccag aacctgtcac tgtcagttgg 540
 aactcaggcg cattgacatc tgggtgtccat acattccccg cagtcttgca aagctctgga 600
 ctttacagtc ttagtagcgt agtgacagtc ccatcttcaa gtcttgggac ccaaacttat 660
 atttgcaacg taaatcataa accctccaac actaaagtag acaaaaaagt agagccgaaa 720
 tcttgcgaca aaacgcatac atgcccacca tgtcccgtc cggaactcct gggcggcccg 780
 tccgtttttc tctttccccc aaagcccaag gatacgctta tgatcagcag aacaccggaa 840
 gttacttggt tagtcgttga cgtgtctcac gaagatcccg aagtcaaatt taattggtat 900
 gtggatggcg tcgaagtgca caacgcaaaa accaaacca gagaggaaca gtataacagc 960
 acgtatcgag tggctctcgt acttacggtc ctccaccagg actggttgaa tggcaaggag 1020
 tacaagtgca aagtgagcaa taaagcgttg ccagccccga tcgaaaaaac catcagcaag 1080
 gccaaaggac agcctagaga gccgcagggt tacaccttgc cgccatcaag ggatgaactg 1140
 actaaaaacc aggtatccct gacctgcctg gttaagggtt ttaccccag tgatatagcg 1200

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gttgaatggg agtctaacgg gcagccagag aacaactaca aaacgacacc tcccgttctg 1260
gattccgatg gcagcttttt cttgtattct aaactcaccg tggataaatc cccgatggcag 1320
caaggcaacg tcttctcctg cagcgtgatg catgaagcct tgcacaacca ctatacccaa 1380
aagagtctca gcctgtcacc cgggaaatcc ggggggtggcg gatccctgcg tgcccatgag 1440
aatgagatca ccaaagtgcg aaaagttact ttcaatggac tgaaccagat gattgtcata 1500
gaactgggca ccaatccgct gaagagctca ggaattgaaa atgggggcttt ccagggaatg 1560
aagaagctct cctacatccg cattgctgat accaatatca ccagcattcc tcaaggtctt 1620
cctccttccc ttacggaatt acatcttgat ggcaacaaaa tcagcagagt tgatgcagct 1680
agcctgaaag gactgaataa tttggctaag ttgggattga gtttcaacag catctctgct 1740
gtttga 1746

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<210> 61
<211> 581
<212> PRT
<213> Artificial Sequence

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<220>
<223> synthetic

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<400> 61

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Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
1           5           10           15

```

```

Thr Gln Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
          20           25           30

```

```

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
          35           40           45

```

```

Ser Ser Tyr Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
          50           55           60

```

```

Glu Trp Val Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala
65           70           75           80

```

```

Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
          85           90           95

```

```

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
          100          105          110

```

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

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
340 345 350

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
355 360 365

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
370 375 380

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385 390 395 400

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
405 410 415

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
420 425 430

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
435 440 445

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
450 455 460

Leu Ser Pro Gly Lys Ser Gly Gly Gly Gly Ser Leu Arg Ala His Glu
465 470 475 480

Asn Glu Ile Thr Lys Val Arg Lys Val Thr Phe Asn Gly Leu Asn Gln
485 490 495

Met Ile Val Ile Glu Leu Gly Thr Asn Pro Leu Lys Ser Ser Gly Ile
500 505 510

Glu Asn Gly Ala Phe Gln Gly Met Lys Lys Leu Ser Tyr Ile Arg Ile
515 520 525

Ala Asp Thr Asn Ile Thr Ser Ile Pro Gln Gly Leu Pro Pro Ser Leu
530 535 540

Thr Glu Leu His Leu Asp Gly Asn Lys Ile Ser Arg Val Asp Ala Ala
545 550 555 560

Ser Leu Lys Gly Leu Asn Asn Leu Ala Lys Leu Gly Leu Ser Phe Asn
565 570 575

Ser Ile Ser Ala Val
580

<210> 62
<211> 2082
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 62
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tgtgctgcca gtggcttcac attctcatct tacattatga tgtgggttcg acaggcccct 180
gggaaggggc tggagtgggt ttctccatc taccctccg ggggaattac cttctatgcc 240
gacacggtaa agggtcgctt cactataagt cgagataaca gcaaaaatac gctgtatctc 300
cagatgaact ctctcagggc tgaggacaca gctgtatatt actgcgcgcg gattaagttg 360
gggaccgtca caacagtgga ttactggggc caaggcactc tggtaaccgt atcctcagca 420
tccaccaagg gcccaagtgt attcccgctg gccccttcaa gtaaataccac gtctggcggc 480
acagccgctc tcggttgctt ggttaaggac tacttcccag aacctgtcac tgtcagttgg 540
aactcaggcg cattgacatc tgggtgtccat acattccccg cagtccctgca aagctctgga 600
ctttacagtc ttagtagcgt agtgacagtc ccatcttcaa gtcttggggac ccaaacttat 660
atttgcaacg taaatcataa accctccaac actaaagtag acaaaaaagt agagccgaaa 720
tcttgcgaca aaacgcatac atgcccacca tgtcccgtc cggaactcct gggcggcccg 780
tccgtttttc tctttccccc aaagcccaag gatacgctta tgatcagcag aacaccggaa 840
gttacttggt tagtcgttga cgtgtctcac gaagatcccc aagtcaaatt taattggtat 900
gtggatggcg tcgaagtgca caacgcaaaa accaaaccca gagaggaaca gtataacagc 960
acgtatcgag tggctctcgt acttacggtc ctccaccagg actgggttgaa tggcaaggag 1020
tacaagtgca aagtgagcaa taaagcgttg ccagccccga tcgaaaaaac catcagcaag 1080
gccaagggac agcctagaga gccgcagggt tacaccttgc cgccatcaag ggatgaactg 1140
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gttgaatggg agtctaacgg gcagccagag aacaactaca aaacgacacc tcccgttctg 1260
gattccgatg gcagcttttt cttgtattct aaactcaccg tggataaatc ccgatggcag 1320

caaggcaacg tcttctcctg cagcgtgatg catgaagcct tgcacaacca ctatacccaa 1380
 aagagtctca gcctgtcacc cgggaaatcc gggggtggcg gatccctgcg tgcccatgag 1440
 aatgagatca ccaaagtgcg aaaagttact ttcaatggac tgaaccagat gattgtcata 1500
 gaactgggca ccaatccgct gaagagctca ggaattgaaa atgggggcttt ccagggaatg 1560
 aagaagctct cctacatccg cattgctgat accaatatca ccagcattcc tcaaggtctt 1620
 cctccttccc ttacggaatt acatcttgat ggcaacaaaa tcagcagagt tgatgcagct 1680
 agcctgaaag gactgaataa ttgggctaag ttgggattga gtttcaacag catctctgct 1740
 gtttccgggg gtggcggatc cctgcgtgcc catgagaatg agatcaccaa agtgcgaaaa 1800
 gttactttca atggactgaa ccagatgatt gtcatagaac tgggcaccaa tccgctgaag 1860
 agctcaggaa ttgaaaatgg ggctttccag ggaatgaaga agctctccta catccgcatt 1920
 gctgatacca atatcaccag cattcctcaa ggtcttcctc cttcccttac ggaattacat 1980
 cttgatggca acaaaatcag cagagttgat gcagctagcc tgaaaggact gaataatttg 2040
 gctaagttgg gattgagttt caacagcatc tctgctgttt ga 2082

<210> 63
 <211> 693
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 63

Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His Ala
 1 5 10 15

Thr Gln Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45

Ser Ser Tyr Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60

Glu Trp Val Ser Ser Ile Tyr Pro Ser Gly Gly Ile Thr Phe Tyr Ala
 65 70 75 80

Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Ile Lys Leu Gly Thr Val Thr Thr Val Asp Tyr
 115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 145 150 155 160

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

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 195 200 205

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

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
 225 230 235 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
 245 250 255

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 260 265 270

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 275 280 285

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 290 295 300

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 305 310 315 320

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

Thr Glu Leu His Leu Asp Gly Asn Lys Ile Ser Arg Val Asp Ala Ala
 545 550 555 560

Ser Leu Lys Gly Leu Asn Asn Leu Ala Lys Leu Gly Leu Ser Phe Asn
 565 570 575

Ser Ile Ser Ala Val Ser Gly Gly Gly Gly Ser Leu Arg Ala His Glu
 580 585 590

Asn Glu Ile Thr Lys Val Arg Lys Val Thr Phe Asn Gly Leu Asn Gln
 595 600 605

Met Ile Val Ile Glu Leu Gly Thr Asn Pro Leu Lys Ser Ser Gly Ile
 610 615 620

Glu Asn Gly Ala Phe Gln Gly Met Lys Lys Leu Ser Tyr Ile Arg Ile
 625 630 635 640

Ala Asp Thr Asn Ile Thr Ser Ile Pro Gln Gly Leu Pro Pro Ser Leu
 645 650 655

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

Ser Leu Lys Gly Leu Asn Asn Leu Ala Lys Leu Gly Leu Ser Phe Asn
 675 680 685

Ser Ile Ser Ala Val
 690

<210> 64
 <211> 315
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 64

Asp Phe Glu Pro Ser Leu Gly Pro Val Cys Pro Phe Arg Cys Gln Cys
 1 5 10 15

His Leu Arg Val Val Gln Cys Ser Asp Leu Gly Leu Asp Lys Val Pro
 20 25 30

Lys Asp Leu Pro Pro Asp Thr Thr Leu Leu Asp Leu Gln Asn Asn Lys
 35 40 45

Ile Thr Glu Ile Lys Asp Gly Asp Phe Lys Asn Leu Lys Asn Leu His
 50 55 60

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

Phe Thr Pro Leu Val Lys Leu Glu Arg Leu Tyr Leu Ser Lys Asn Gln
 85 90 95

Leu Lys Glu Leu Pro Glu Lys Met Pro Lys Thr Leu Gln Glu Leu Arg
 100 105 110

Ala His Glu Asn Glu Ile Thr Lys Val Arg Lys Val Thr Phe Asn Gly
 115 120 125

Leu Asn Gln Met Ile Val Ile Glu Leu Gly Thr Asn Pro Leu Lys Ser
 130 135 140

Ser Gly Ile Glu Asn Gly Ala Phe Gln Gly Met Lys Lys Leu Ser Tyr
 145 150 155 160

Ile Arg Ile Ala Asp Thr Asn Ile Thr Ser Ile Pro Gln Gly Leu Pro
 165 170 175

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

Asp Ala Ala Ser Leu Lys Gly Leu Asn Asn Leu Ala Lys Leu Gly Leu
 195 200 205

Ser Phe Asn Ser Ile Ser Ala Val Asp Asn Gly Ser Leu Ala Asn Thr
 210 215 220

Pro His Leu Arg Glu Leu His Leu Asp Asn Asn Lys Leu Thr Arg Val
 225 230 235 240

Pro Gly Gly Leu Ala Glu His Lys Tyr Ile Gln Val Val Tyr Leu His
 245 250 255

Asn Asn Asn Ile Ser Val Val Gly Ser Ser Asp Phe Cys Pro Pro Gly
 260 265 270

His Asn Thr Lys Lys Ala Ser Tyr Ser Gly Val Ser Leu Phe Ser Asn
275 280 285

Pro Val Gln Tyr Trp Glu Ile Gln Pro Ser Thr Phe Arg Cys Val Tyr
290 295 300

Val Arg Ser Ala Ile Gln Leu Gly Asn Tyr Lys
305 310 315

<210> 65
<211> 636
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 65

Asp Phe Glu Pro Ser Leu Gly Pro Val Cys Pro Phe Arg Cys Gln Cys
1 5 10 15

His Leu Arg Val Val Gln Cys Ser Asp Leu Gly Leu Asp Lys Val Pro
20 25 30

Lys Asp Leu Pro Pro Asp Thr Thr Leu Leu Asp Leu Gln Asn Asn Lys
35 40 45

Ile Thr Glu Ile Lys Asp Gly Asp Phe Lys Asn Leu Lys Asn Leu His
50 55 60

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

Phe Thr Pro Leu Val Lys Leu Glu Arg Leu Tyr Leu Ser Lys Asn Gln
85 90 95

Leu Lys Glu Leu Pro Glu Lys Met Pro Lys Thr Leu Gln Glu Leu Arg
100 105 110

Ala His Glu Asn Glu Ile Thr Lys Val Arg Lys Val Thr Phe Asn Gly
115 120 125

Leu Asn Gln Met Ile Val Ile Glu Leu Gly Thr Asn Pro Leu Lys Ser
130 135 140

Ser Gly Ile Glu Asn Gly Ala Phe Gln Gly Met Lys Lys Leu Ser Tyr
 145 150 155 160

Ile Arg Ile Ala Asp Thr Asn Ile Thr Ser Ile Pro Gln Gly Leu Pro
 165 170 175

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

Asp Ala Ala Ser Leu Lys Gly Leu Asn Asn Leu Ala Lys Leu Gly Leu
 195 200 205

Ser Phe Asn Ser Ile Ser Ala Val Asp Asn Gly Ser Leu Ala Asn Thr
 210 215 220

Pro His Leu Arg Glu Leu His Leu Asp Asn Asn Lys Leu Thr Arg Val
 225 230 235 240

Pro Gly Gly Leu Ala Glu His Lys Tyr Ile Gln Val Val Tyr Leu His
 245 250 255

Asn Asn Asn Ile Ser Val Val Gly Ser Ser Asp Phe Cys Pro Pro Gly
 260 265 270

His Asn Thr Lys Lys Ala Ser Tyr Ser Gly Val Ser Leu Phe Ser Asn
 275 280 285

Pro Val Gln Tyr Trp Glu Ile Gln Pro Ser Thr Phe Arg Cys Val Tyr
 290 295 300

Val Arg Ser Ala Ile Gln Leu Gly Asn Tyr Lys Ser Gly Gly Gly Gly
 305 310 315 320

Ser Asp Phe Glu Pro Ser Leu Gly Pro Val Cys Pro Phe Arg Cys Gln
 325 330 335

Cys His Leu Arg Val Val Gln Cys Ser Asp Leu Gly Leu Asp Lys Val
 340 345 350

Pro Lys Asp Leu Pro Pro Asp Thr Thr Leu Leu Asp Leu Gln Asn Asn
 355 360 365

Lys Ile Thr Glu Ile Lys Asp Gly Asp Phe Lys Asn Leu Lys Asn Leu
 370 375 380

His Ala Leu Ile Leu Val Asn Asn Lys Ile Ser Lys Val Ser Pro Gly
 385 390 395 400

Ala Phe Thr Pro Leu Val Lys Leu Glu Arg Leu Tyr Leu Ser Lys Asn
 405 410 415

Gln Leu Lys Glu Leu Pro Glu Lys Met Pro Lys Thr Leu Gln Glu Leu
 420 425 430

Arg Ala His Glu Asn Glu Ile Thr Lys Val Arg Lys Val Thr Phe Asn
 435 440 445

Gly Leu Asn Gln Met Ile Val Ile Glu Leu Gly Thr Asn Pro Leu Lys
 450 455 460

Ser Ser Gly Ile Glu Asn Gly Ala Phe Gln Gly Met Lys Lys Leu Ser
 465 470 475 480

Tyr Ile Arg Ile Ala Asp Thr Asn Ile Thr Ser Ile Pro Gln Gly Leu
 485 490 495

Pro Pro Ser Leu Thr Glu Leu His Leu Asp Gly Asn Lys Ile Ser Arg
 500 505 510

Val Asp Ala Ala Ser Leu Lys Gly Leu Asn Asn Leu Ala Lys Leu Gly
 515 520 525

Leu Ser Phe Asn Ser Ile Ser Ala Val Asp Asn Gly Ser Leu Ala Asn
 530 535 540

Thr Pro His Leu Arg Glu Leu His Leu Asp Asn Asn Lys Leu Thr Arg
 545 550 555 560

Val Pro Gly Gly Leu Ala Glu His Lys Tyr Ile Gln Val Val Tyr Leu
 565 570 575

His Asn Asn Asn Ile Ser Val Val Gly Ser Ser Asp Phe Cys Pro Pro
 580 585 590

Gly His Asn Thr Lys Lys Ala Ser Tyr Ser Gly Val Ser Leu Phe Ser
 595 600 605

Asn Pro Val Gln Tyr Trp Glu Ile Gln Pro Ser Thr Phe Arg Cys Val
610 615 620

Tyr Val Arg Ser Ala Ile Gln Leu Gly Asn Tyr Lys
625 630 635

<210> 66
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 66

Leu Arg Ala His Glu Asn Glu Ile Thr Lys Val Arg Lys Val Thr Phe
1 5 10 15

Asn Gly Leu Asn Gln Met Ile Val Ile Glu Leu Gly Thr Asn Pro Leu
20 25 30

Lys Ser Ser Gly Ile Glu Asn Gly Ala Phe Gln Gly Met Lys Lys Leu
35 40 45

Ser Tyr Ile Arg Ile Ala Asp Thr Asn Ile Thr Ser Ile Pro Gln Gly
50 55 60

Leu Pro Pro Ser Leu Thr Glu Leu His Leu Asp Gly Asn Lys Ile Ser
65 70 75 80

Arg Val Asp Ala Ala Ser Leu Lys Gly Leu Asn Asn Leu Ala Lys Leu
85 90 95

Gly Leu Ser Phe Asn Ser Ile Ser Ala Val
100 105

<210> 67
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 67

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