

SEQUENCE LISTING

<110> PALLEON PHARMACEUTICALS INC.

<120> RECOMBINANT SIALIDASES WITH REDUCED PROTEASE SENSITIVITY,
SIALIDASE FUSION PROTEINS, AND METHODS OF USING THE SAME

<130> PAL-023W0

<140> PCT/US2021/040240

<141> 2021-07-02

<150> 63/134,411

<151> 2021-01-06

<150> 63/047,989

<151> 2020-07-03

<160> 349

<170> PatentIn version 3.5

<210> 1

<211> 380

<212> PRT

<213> Homo sapiens

<400> 1

Met	Ala	Ser	Leu	Pro	Val	Leu	Gln	Lys	Glu	Ser	Val	Phe	Gln	Ser	Gly
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Ala	His	Ala	Tyr	Arg	Ile	Pro	Ala	Leu	Leu	Tyr	Leu	Pro	Gly	Gln	Gln
			20					25					30		

Ser	Leu	Leu	Ala	Phe	Ala	Glu	Gln	Arg	Ala	Ser	Lys	Lys	Asp	Glu	His
			35				40					45			

Ala	Glu	Leu	Ile	Val	Leu	Arg	Arg	Gly	Asp	Tyr	Asp	Ala	Pro	Thr	His
	50					55					60				

Gln	Val	Gln	Trp	Gln	Ala	Gln	Glu	Val	Val	Ala	Gln	Ala	Arg	Leu	Asp
65					70					75				80	

Gly	His	Arg	Ser	Met	Asn	Pro	Cys	Pro	Leu	Tyr	Asp	Ala	Gln	Thr	Gly
				85					90					95	

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Ile Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

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

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

 $\langle 210 \rangle$ 2

<211> 385

<212> PRT

<213> Mus musculus

 $\langle 400 \rangle$ 2

Met Glu Asp Leu Arg Pro Met Ala Thr Cys Pro Val Leu Gln Lys Glu
1 5 10 15

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

Tyr Leu Lys Lys Gln Lys Thr Leu Leu Ala Phe Ala Glu Lys Arg Ala
35 40 45

Ser Lys Thr Asp Glu His Ala Glu Leu Ile Val Leu Arg Arg Gly Ser
50 55 60

Tyr Asn Glu Ala Thr Asn Arg Val Lys Trp Gln Pro Glu Glu Val Val
65 70 75 80

Thr Gln Ala Gln Leu Glu Gly His Arg Ser Met Asn Pro Cys Pro Leu
85 90 95

Tyr Asp Lys Gln Thr Lys Thr Leu Phe Leu Phe Phe Ile Ala Val Pro
100 105 110

Gly Arg Val Ser Glu His His Gln Leu His Thr Lys Val Asn Val Thr
115 120 125

Arg Leu Cys Cys Val Ser Ser Thr Asp His Gly Arg Thr Trp Ser Pro
 130 135 140

Ile Gln Asp Leu Thr Glu Thr Thr Ile Gly Ser Thr His Gln Glu Trp
 145 150 155 160

Ala Thr Phe Ala Val Gly Pro Gly His Cys Leu Gln Leu Arg Asn Pro
 165 170 175

Ala Gly Ser Leu Leu Val Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro
 180 185 190

Ala Gln Lys Pro Thr Pro Phe Ala Phe Cys Phe Ile Ser Leu Asp His
 195 200 205

Gly His Thr Trp Lys Leu Gly Asn Phe Val Ala Glu Asn Ser Leu Glu
 210 215 220

Cys Gln Val Ala Glu Val Gly Thr Gly Ala Gln Arg Met Val Tyr Leu
 225 230 235 240

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

Asp Gly Leu Asp Phe Gln Asp Asn Arg Val Val Ser Lys Leu Val Glu
 260 265 270

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

Ser Lys Pro His Ala Leu Asp Thr Trp Leu Leu Tyr Thr His Pro Thr
 290 295 300

Asp Ser Arg Asn Arg Thr Asn Leu Gly Val Tyr Leu Asn Gln Met Pro
 305 310 315 320

Leu Asp Pro Thr Ala Trp Ser Glu Pro Thr Leu Leu Ala Met Gly Ile
 325 330 335

Cys Ala Tyr Ser Asp Leu Gln Asn Met Gly Gln Gly Pro Asp Gly Ser
 340 345 350

Pro Gln Phe Gly Cys Leu Tyr Glu Ser Gly Asn Tyr Glu Glu Ile Ile
355 360 365

Phe Leu Ile Phe Thr Leu Lys Gln Ala Phe Pro Thr Val Phe Asp Ala
370 375 380

Gln
385

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<210> 3
<211> 5
<212> PRT
<213> Mus musculus
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<400> 3
Glu Asp Leu Arg Pro
1          5
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<210> 4
<211> 6
<212> PRT
<213> Mus musculus
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<400> 4
Met Glu Asp Leu Arg Pro
1 5

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<210> 5
<211> 227
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<213> Artificial Sequence
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<220>
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Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 100 105 110

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

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 130 135 140

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

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

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 210 215 220

Pro Gly Lys
 225

<210> 6

<211> 1143

<212> DNA

<213> Salmonella typhimurium

<400> 6

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tgcaccacca gcaagggcac cattgtggtg ttcgccgacg ccagacacaa caccgccagc     180
gatcagagct tcatcgatac cgctgccgcc agatctaccg atggcggcaa gacctggaac     240
aagaagatcg ccatctacaa cgaccgcgtg aacagcaagc tgagcagagt gatggaccct     300
acctgcatcg tggccaacat ccagggcaga gaaaccatcc tggatcatggt cggaaagtgg     360
aacaacaacg ataagacctg gggcgcctac agagacaagg cccctgatac cgattgggac     420
ctcgtgctgt acaagagcac cgatgacggc gtgaccttca gcaaggtgga aacaaacatc     480
cacgacatcg tgaccaagaa cggcaccatc tctgccatgc tcggcggcgt tggatctggc     540
ctgcaactga atgatggcaa gctggtgttc cccgtgcaga tgggtccgaac aaagaatatc     600
accaccgtgc tgaataccag cttcatctac agcaccgacg gcatcacatg gtccctgcct     660
agcgggtact gtgaaggctt tggcagcgag aacaacatca tcgagttcaa cgccagcctg     720
gtcaacaaca tccggaacag cggcctgcgg agaagcttcg agacaaagga cttcggaag     780
acgtggaccg agtttctcc aatggacaag aaggtggaca accggaacca cggcgtgcag     840
ggcagcacia tcacaatccc tagcggcaac aaactggtgg ccgctcactc tagcgcccag     900
aacaagaaca acgactacac cagaagcgac atcagcctgt acgcccacia cctgtacagc     960
ggcgaagtga agctgatcga cgacttctac cccaaagtgg gcaatgccag cggagccggc    1020
tacagctgtc tgagctaccg gaaaaatgtg gacaaagaaa ccctgtacgt ggtgtacgag    1080
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aac                                                                    1143

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<210> 7

<211> 364

<212> PRT

<213> Homo sapiens

<400> 7

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Glu Asn Asp Phe Gly Leu Val Gln Pro Leu Val Thr Met Glu Gln Leu
1           5           10          15

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Leu Trp Val Ser Gly Arg Gln Ile Gly Ser Val Asp Thr Phe Arg Ile

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

His Cys Arg Ile Val Leu Arg Ser Tyr Asp Ala Cys Asp Thr Leu Arg
245 250 255

Pro	Arg	Asp	Val	Thr	Phe	Asp	Pro	Glu	Leu	Val	Asp	Pro	Val	Val	Ala
			260					265					270		

Ala Gly Ala Val Val Thr Ser Ser Gly Ile Val Phe Phe Ser Asn Pro
275 280 285

Ala His Pro Glu Phe Arg Val Asn Leu Thr Leu Arg Trp Ser Phe Ser
290 295 300

Asn Gly Thr Ser Trp Arg Lys Glu Thr Val Gln Leu Trp Pro Gly Pro
305 310 315 320

Ser Gly Tyr Ser Ser Leu Ala Thr Leu Glu Gly Ser Met Asp Gly Glu
325 330 335

Glu Gln Ala Pro Gln Leu Tyr Val Leu Tyr Glu Lys Gly Arg Asn His
340 345 350

Tyr Thr Glu Ser Ile Ser Val Ala Lys Ile Ser Val
355 360

$\langle 210 \rangle$ 8

<211> 428

<212> PRT

<213> Homo sapiens

$\langle 400 \rangle$ 8

Met Glu Glu Val Thr Thr Cys Ser Phe Asn Ser Pro Leu Phe Arg Gln
1 5 10 15

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

Pro Pro Thr His Thr Phe Leu Ala Phe Ala Glu Lys Arg Ser Thr Arg
35 40 45

Arg Asp Glu Asp Ala Leu His Leu Val Leu Arg Arg Gly Leu Arg Ile
50 55 60

Gly Gln Leu Val Gln Trp Gly Pro Leu Lys Pro Leu Met Glu Ala Thr
 65 70 75 80

Leu Pro Gly His Arg Thr Met Asn Pro Cys Pro Val Trp Glu Gln Lys
 85 90 95

Ser Gly Cys Val Phe Leu Phe Phe Ile Cys Val Arg Gly His Val Thr
 100 105 110

Glu Arg Gln Gln Ile Val Ser Gly Arg Asn Ala Ala Arg Leu Cys Phe
 115 120 125

Ile Tyr Ser Gln Asp Ala Gly Cys Ser Trp Ser Glu Val Arg Asp Leu
 130 135 140

Thr Glu Glu Val Ile Gly Ser Glu Leu Lys His Trp Ala Thr Phe Ala
 145 150 155 160

Val Gly Pro Gly His Gly Ile Gln Leu Gln Ser Gly Arg Leu Val Ile
 165 170 175

Pro Ala Tyr Thr Tyr Tyr Ile Pro Ser Trp Phe Phe Cys Phe Gln Leu
 180 185 190

Pro Cys Lys Thr Arg Pro His Ser Leu Met Ile Tyr Ser Asp Asp Leu
 195 200 205

Gly Val Thr Trp His His Gly Arg Leu Ile Arg Pro Met Val Thr Val
 210 215 220

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

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

Thr Asp His Gly Glu Gly Phe Gln Arg Leu Ala Leu Ser Arg Gln Leu
 260 265 270

Cys Glu Pro Pro His Gly Cys Gln Gly Ser Val Val Ser Phe Arg Pro

275

280

285

Leu Glu Ile Pro His Arg Cys Gln Asp Ser Ser Ser Lys Asp Ala Pro
 290 295 300

Thr Ile Gln Gln Ser Ser Pro Gly Ser Ser Leu Arg Leu Glu Glu Glu
 305 310 315 320

Ala Gly Thr Pro Ser Glu Ser Trp Leu Leu Tyr Ser His Pro Thr Ser
 325 330 335

Arg Lys Gln Arg Val Asp Leu Gly Ile Tyr Leu Asn Gln Thr Pro Leu
 340 345 350

Glu Ala Ala Cys Trp Ser Arg Pro Trp Ile Leu His Cys Gly Pro Cys
 355 360 365

Gly Tyr Ser Asp Leu Ala Ala Leu Glu Glu Glu Gly Leu Phe Gly Cys
 370 375 380

Leu Phe Glu Cys Gly Thr Lys Gln Glu Cys Glu Gln Ile Ala Phe Arg
 385 390 395 400

Leu Phe Thr His Arg Glu Ile Leu Ser His Leu Gln Gly Asp Cys Thr
 405 410 415

Ser Pro Gly Arg Asn Pro Ser Gln Phe Lys Ser Asn
 420 425

<210> 9

<211> 461

<212> PRT

<213> Homo sapiens

<400> 9

Met Arg Pro Ala Asp Leu Pro Pro Arg Pro Met Glu Glu Ser Pro Ala
 1 5 10 15

Ser Ser Ser Ala Pro Thr Glu Thr Glu Glu Pro Gly Ser Ser Ala Glu
 20 25 30

Val Met Glu Glu Val Thr Thr Cys Ser Phe Asn Ser Pro Leu Phe Arg

35

40

45

Gln Glu Asp Asp Arg Gly Ile Thr Tyr Arg Ile Pro Ala Leu Leu Tyr
 50 55 60

Ile Pro Pro Thr His Thr Phe Leu Ala Phe Ala Glu Lys Arg Ser Thr
 65 70 75 80

Arg Arg Asp Glu Asp Ala Leu His Leu Val Leu Arg Arg Gly Leu Arg
 85 90 95

Ile Gly Gln Leu Val Gln Trp Gly Pro Leu Lys Pro Leu Met Glu Ala
 100 105 110

Thr Leu Pro Gly His Arg Thr Met Asn Pro Cys Pro Val Trp Glu Gln
 115 120 125

Lys Ser Gly Cys Val Phe Leu Phe Phe Ile Cys Val Arg Gly His Val
 130 135 140

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

Phe Ile Tyr Ser Gln Asp Ala Gly Cys Ser Trp Ser Glu Val Arg Asp
 165 170 175

Leu Thr Glu Glu Val Ile Gly Ser Glu Leu Lys His Trp Ala Thr Phe
 180 185 190

Ala Val Gly Pro Gly His Gly Ile Gln Leu Gln Ser Gly Arg Leu Val
 195 200 205

Ile Pro Ala Tyr Thr Tyr Tyr Ile Pro Ser Trp Phe Phe Cys Phe Gln
 210 215 220

Leu Pro Cys Lys Thr Arg Pro His Ser Leu Met Ile Tyr Ser Asp Asp
 225 230 235 240

Leu Gly Val Thr Trp His His Gly Arg Leu Ile Arg Pro Met Val Thr
 245 250 255

Val Glu Cys Glu Val Ala Glu Val Thr Gly Arg Ala Gly His Pro Val
 260 265 270

Leu Tyr Cys Ser Ala Arg Thr Pro Asn Arg Cys Arg Ala Glu Ala Leu
 275 280 285

Ser Thr Asp His Gly Glu Gly Phe Gln Arg Leu Ala Leu Ser Arg Gln
 290 295 300

Leu Cys Glu Pro Pro His Gly Cys Gln Gly Ser Val Val Ser Phe Arg
 305 310 315 320

Pro Leu Glu Ile Pro His Arg Cys Gln Asp Ser Ser Ser Lys Asp Ala
 325 330 335

Pro Thr Ile Gln Gln Ser Ser Pro Gly Ser Ser Leu Arg Leu Glu Glu
 340 345 350

Glu Ala Gly Thr Pro Ser Glu Ser Trp Leu Leu Tyr Ser His Pro Thr
 355 360 365

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

Leu Glu Ala Ala Cys Trp Ser Arg Pro Trp Ile Leu His Cys Gly Pro
 385 390 395 400

Cys Gly Tyr Ser Asp Leu Ala Ala Leu Glu Glu Gly Leu Phe Gly
 405 410 415

Cys Leu Phe Glu Cys Gly Thr Lys Gln Glu Cys Glu Gln Ile Ala Phe
 420 425 430

Arg Leu Phe Thr His Arg Glu Ile Leu Ser His Leu Gln Gly Asp Cys
 435 440 445

Thr Ser Pro Gly Arg Asn Pro Ser Gln Phe Lys Ser Asn
 450 455 460

<210> 10

<211> 484
 <212> PRT
 <213> Homo sapiens

<400> 10

Met Gly Val Pro Arg Thr Pro Ser Arg Thr Val Leu Phe Glu Arg Glu
 1 5 10 15

Arg Thr Gly Leu Thr Tyr Arg Val Pro Ser Leu Leu Pro Val Pro Pro
 20 25 30

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

Ser His Ala His Arg Leu Val Leu Arg Arg Gly Thr Leu Ala Gly Gly
 50 55 60

Ser Val Arg Trp Gly Ala Leu His Val Leu Gly Thr Ala Ala Leu Ala
 65 70 75 80

Glu His Arg Ser Met Asn Pro Cys Pro Val His Asp Ala Gly Thr Gly
 85 90 95

Thr Val Phe Leu Phe Phe Ile Ala Val Leu Gly His Thr Pro Glu Ala
 100 105 110

Val Gln Ile Ala Thr Gly Arg Asn Ala Ala Arg Leu Cys Cys Val Ala
 115 120 125

Ser Arg Asp Ala Gly Leu Ser Trp Gly Ser Ala Arg Asp Leu Thr Glu
 130 135 140

Glu Ala Ile Gly Gly Ala Val Gln Asp Trp Ala Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Gly Val Gln Leu Pro Ser Gly Arg Leu Leu Val Pro Ala
 165 170 175

Tyr Thr Tyr Arg Val Asp Arg Arg Glu Cys Phe Gly Lys Ile Cys Arg
 180 185 190

Thr Ser Pro His Ser Phe Ala Phe Tyr Ser Asp Asp His Gly Arg Thr

195					200					205					
Trp	Arg	Cys	Gly	Gly	Leu	Val	Pro	Asn	Leu	Arg	Ser	Gly	Glu	Cys	Gln
	210					215					220				
Leu	Ala	Ala	Val	Asp	Gly	Gly	Gln	Ala	Gly	Ser	Phe	Leu	Tyr	Cys	Asn
225					230					235					240
Ala	Arg	Ser	Pro	Leu	Gly	Ser	Arg	Val	Gln	Ala	Leu	Ser	Thr	Asp	Glu
				245					250					255	
Gly	Thr	Ser	Phe	Leu	Pro	Ala	Glu	Arg	Val	Ala	Ser	Leu	Pro	Glu	Thr
			260					265					270		
Ala	Trp	Gly	Cys	Gln	Gly	Ser	Ile	Val	Gly	Phe	Pro	Ala	Pro	Ala	Pro
		275					280					285			
Asn	Arg	Pro	Arg	Asp	Asp	Ser	Trp	Ser	Val	Gly	Pro	Gly	Ser	Pro	Leu
	290					295					300				
Gln	Pro	Pro	Leu	Leu	Gly	Pro	Gly	Val	His	Glu	Pro	Pro	Glu	Glu	Ala
305					310					315					320
Ala	Val	Asp	Pro	Arg	Gly	Gly	Gln	Val	Pro	Gly	Gly	Pro	Phe	Ser	Arg
				325					330					335	
Leu	Gln	Pro	Arg	Gly	Asp	Gly	Pro	Arg	Gln	Pro	Gly	Pro	Arg	Pro	Gly
			340					345					350		
Val	Ser	Gly	Asp	Val	Gly	Ser	Trp	Thr	Leu	Ala	Leu	Pro	Met	Pro	Phe
		355					360					365			
Ala	Ala	Pro	Pro	Gln	Ser	Pro	Thr	Trp	Leu	Leu	Tyr	Ser	His	Pro	Val
	370					375					380				
Gly	Arg	Arg	Ala	Arg	Leu	His	Met	Gly	Ile	Arg	Leu	Ser	Gln	Ser	Pro
385					390					395					400
Leu	Asp	Pro	Arg	Ser	Trp	Thr	Glu	Pro	Trp	Val	Ile	Tyr	Glu	Gly	Pro
				405					410					415	

Ser Gly Tyr Ser Asp Leu Ala Ser Ile Gly Pro Ala Pro Glu Gly Gly
 420 425 430

Leu Val Phe Ala Cys Leu Tyr Glu Ser Gly Ala Arg Thr Ser Tyr Asp
 435 440 445

Glu Ile Ser Phe Cys Thr Phe Ser Leu Arg Glu Val Leu Glu Asn Val
 450 455 460

Pro Ala Ser Pro Lys Pro Pro Asn Leu Gly Asp Lys Pro Arg Gly Cys
 465 470 475 480

Cys Trp Pro Ser

<210> 11

<211> 496

<212> PRT

<213> Homo sapiens

<400> 11

Met Met Ser Ser Ala Ala Phe Pro Arg Trp Leu Ser Met Gly Val Pro
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 20 25 30

Thr Tyr Arg Val Pro Ser Leu Leu Pro Val Pro Pro Gly Pro Thr Leu
 35 40 45

Leu Ala Phe Val Glu Gln Arg Leu Ser Pro Asp Asp Ser His Ala His
 50 55 60

Arg Leu Val Leu Arg Arg Gly Thr Leu Ala Gly Gly Ser Val Arg Trp
 65 70 75 80

Gly Ala Leu His Val Leu Gly Thr Ala Ala Leu Ala Glu His Arg Ser
 85 90 95

Met Asn Pro Cys Pro Val His Asp Ala Gly Thr Gly Thr Val Phe Leu
 100 105 110

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

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

Gly Leu Ser Trp Gly Ser Ala Arg Asp Leu Thr Glu Glu Ala Ile Gly
 145 150 155 160

Gly Ala Val Gln Asp Trp Ala Thr Phe Ala Val Gly Pro Gly His Gly
 165 170 175

Val Gln Leu Pro Ser Gly Arg Leu Leu Val Pro Ala Tyr Thr Tyr Arg
 180 185 190

Val Asp Arg Arg Glu Cys Phe Gly Lys Ile Cys Arg Thr Ser Pro His
 195 200 205

Ser Phe Ala Phe Tyr Ser Asp Asp His Gly Arg Thr Trp Arg Cys Gly
 210 215 220

Gly Leu Val Pro Asn Leu Arg Ser Gly Glu Cys Gln Leu Ala Ala Val
 225 230 235 240

Asp Gly Gly Gln Ala Gly Ser Phe Leu Tyr Cys Asn Ala Arg Ser Pro
 245 250 255

Leu Gly Ser Arg Val Gln Ala Leu Ser Thr Asp Glu Gly Thr Ser Phe
 260 265 270

Leu Pro Ala Glu Arg Val Ala Ser Leu Pro Glu Thr Ala Trp Gly Cys
 275 280 285

Gln Gly Ser Ile Val Gly Phe Pro Ala Pro Ala Pro Asn Arg Pro Arg
 290 295 300

Asp Asp Ser Trp Ser Val Gly Pro Gly Ser Pro Leu Gln Pro Pro Leu
 305 310 315 320

Leu Gly Pro Gly Val His Glu Pro Pro Glu Glu Ala Ala Val Asp Pro

325

330

335

Arg Gly Gly Gln Val Pro Gly Gly Pro Phe Ser Arg Leu Gln Pro Arg
 340 345 350

Gly Asp Gly Pro Arg Gln Pro Gly Pro Arg Pro Gly Val Ser Gly Asp
 355 360 365

Val Gly Ser Trp Thr Leu Ala Leu Pro Met Pro Phe Ala Ala Pro Pro
 370 375 380

Gln Ser Pro Thr Trp Leu Leu Tyr Ser His Pro Val Gly Arg Arg Ala
 385 390 395 400

Arg Leu His Met Gly Ile Arg Leu Ser Gln Ser Pro Leu Asp Pro Arg
 405 410 415

Ser Trp Thr Glu Pro Trp Val Ile Tyr Glu Gly Pro Ser Gly Tyr Ser
 420 425 430

Asp Leu Ala Ser Ile Gly Pro Ala Pro Glu Gly Gly Leu Val Phe Ala
 435 440 445

Cys Leu Tyr Glu Ser Gly Ala Arg Thr Ser Tyr Asp Glu Ile Ser Phe
 450 455 460

Cys Thr Phe Ser Leu Arg Glu Val Leu Glu Asn Val Pro Ala Ser Pro
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Lys Pro Pro Asn Leu Gly Asp Lys Pro Arg Gly Cys Cys Trp Pro Ser
 485 490 495

<210> 12

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<213> Homo sapiens

<400> 12

Met Ala Ser Leu Pro

1

5

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<400> 13
 Ala Ser Leu Pro
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<210> 14
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<210> 15
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 Ser Met Asp Gln Gly Ser Thr Trp
 1 5

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Pro Arg Pro Pro Ala Pro Glu Ala
1 5

<210> 19

<211> 8

<212> PRT

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Gln Thr Pro Leu Glu Ala Ala Cys
1 5

<210> 20

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<212> PRT

<213> Homo sapiens

<400> 20

Asn Pro Arg Pro Pro Ala Pro Glu Ala
1 5

<210> 21

<211> 7

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
recombinant mutant human sialidase sequence

<400> 21

Ser Gln Asn Asp Gly Glu Ser
1 5

<210> 22

<211> 7

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
recombinant mutant human sialidase sequence

<400> 22

Leu Ser His Ser Leu Ser Thr
1 5

<210> 23

<211> 1092
 <212> DNA
 <213> Homo sapiens

<400> 23
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 ggacacctgc tggcctttgc cgaggccaga aagatgagca gctctgacga gggcgccaag 180
 ttatttggcc tgaggcggct tatggaccag ggctctacat ggtcccctac cgccttcac 240
 gtgaacgatg gcgacgtgcc cgatggcctg aatctgggag ctgtggtgtc cgatgtggaa 300
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 agagagccca gaaagggcag actgatcgtg tgtggccacg gcacccttga gagagatggc 540
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 aagatcagcg tt 1092

<210> 24
 <211> 1140
 <212> DNA
 <213> Homo sapiens

<400> 24
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cgggccagca	agaaggatga	gcacgccgaa	ctgatcgtgc	tgcggagagg	cgattacgac	180
gcccctacac	atcaggtgca	gtggcaggct	caagaggtgg	tggctcaggc	tagactggac	240
ggccacagat	ctatgaaccc	ctgtcctctg	tacgatgccc	agaccggcac	actgtttctg	300
ttctttatcg	ctatccccgg	ccaagtgacc	gagcagcagc	agctgcagac	aagagccaac	360
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<210> 25

<211> 1284

<212> DNA

<213> Homo sapiens

<400> 25

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ttcgccgaga	agcggagcac	cagacgagat	gaagatgccc	tgacacctgg	gctgagaaga	180
ggcctgagaa	tcggacagct	ggtgcagtgg	ggacctctga	agcctctgat	ggaagccaca	240
ctgcccggcc	acagaacccat	gaatccttgt	cctgtgtggg	agcagaaaag	cggctgcgtg	300
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agaaacgccg	ccagactgtg	cttcatctac	agccaggatg	ccggctgctc	ttggagcgaa	420

gttcgggatc tgaccgaaga agtgatcggc agcgagctga agcactgggc cacatttgct	480
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tactatatcc ccagctgggtt cttctgcttc caactgcctt gcaagacccg gcctcacagc	600
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atggtcaccg tggaatgcga ggtggccgaa gtgacaggca gagctggaca ccctgtgctg	720
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aaggatgccc ctaccatcca gcagtctagc cctggcagca gcctgagact ggaagaggaa	960
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ctgttcaccc acagagagat cctgagccat ctgcagggcg actgcacaag cccaggcaga	1260
aatcccagcc agttcaagag caac	1284

<210> 26

<211> 1452

<212> DNA

<213> Homo sapiens

<400> 26

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acctacagag tgccttctct gctgcctgtg cctcctggac ctacactgct ggccttcgtg	120
gaacagagac tgagccccga tgattctcac gccacagac tgggtgctgag aagaggaaca	180
ctggctggcg gctctgttag atggggagca ctgcatgtgc tgggcacagc tgctcttgcc	240
gagcacagat ccatgaatcc ctgtcctgtg cagcagccg gaaccggcac agtgtttctg	300
ttctttatcg ccgtgctggg ccacacacct gaggccgttc aaattgccac cggcagaaat	360
gccgccagac tgtgttgtgt ggcctccaga gatgccggcc tgtcttgggg atctgccaga	420
gatctgaccg aggaagccat tggcggagcc gttcaggatt gggccacatt tgctgttgga	480

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cctggacacg gcgtgcagct gccaaagtgg agactgctgg tgcctgccta cacatacaga      540
gtggatcgga gagagtgctt cggaaagatc tgccggacaa gccctcacag cttcgccttc      600
tactccgacg atcacggccg gacttggaga tgtggtggcc tggcgcctaa tctgagaagc      660
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gccagatctc ctctgggctc tagagtgcag gccctgtcta ccgatgaggg caccagtttt      780
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aactggccc tgcctatgcc ttttgccgct cctcctcagt ctcctacctg gctgctgtac     1140
tctcaccctg ttggcagacg ggccagactg cacatgggca tcagactgtc tcagagccct     1200
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gatctggcct ctattggccc agctcctgaa ggcggactgg tgttcgcttg tctgtatgag     1320
agcggcgcca gaaccagcta cgacgagatc agcttctgca ccttcagcct gcgcgaggtg     1380
ctggaaaatg tgccgcctc tcctaagcct cctaacctgg gcgataagcc tagaggctgt     1440
tgctggccat ct                                                                1452

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<210> 27

<211> 47

<212> PRT

<213> Homo sapiens

<400> 27

```

Met Thr Gly Glu Arg Pro Ser Thr Ala Leu Pro Asp Arg Arg Trp Gly
1           5           10           15

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```

Pro Arg Ile Leu Gly Phe Trp Gly Gly Cys Arg Val Trp Val Phe Ala
          20          25          30

```

```

Ala Ile Phe Leu Leu Leu Ser Leu Ala Ala Ser Trp Ser Lys Ala
          35          40          45

```

<210> 28

<211> 22
 <212> PRT
 <213> Unknown

<220>

<223> Description of Unknown:
 recombinant mutant human sialidase sequence

<400> 28

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15

Leu Pro Gly Ala Arg Cys
 20

<210> 29

<211> 4

<212> PRT

<213> Homo sapiens

<400> 29

Tyr Gly Thr Leu
 1

<210> 30

<211> 382

<212> PRT

<213> Salmonella typhimurium

<400> 30

Met Thr Val Glu Lys Ser Val Val Phe Lys Ala Glu Gly Glu His Phe
 1 5 10 15

Thr Asp Gln Lys Gly Asn Thr Ile Val Gly Ser Gly Ser Gly Gly Thr
 20 25 30

Thr Lys Tyr Phe Arg Ile Pro Ala Met Cys Thr Thr Ser Lys Gly Thr
 35 40 45

Ile Val Val Phe Ala Asp Ala Arg His Asn Thr Ala Ser Asp Gln Ser
 50 55 60

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

Asn Lys Lys Ile Ala Ile Tyr Asn Asp Arg Val Asn Ser Lys Leu Ser

95

Arg Val Met Asp Pro Thr Cys Ile Val Ala Asn Ile Gln Gly Arg Glu
100 105 110

Thr Ile Leu Val Met Val Gly Lys Trp Asn Asn Asn Asp Lys Thr Trp
115 120 125

Gly Ala Tyr Arg Asp Lys Ala Pro Asp Thr Asp Trp Asp Leu Val Leu
130 135 140

Tyr Lys Ser Thr Asp Asp Gly Val Thr Phe Ser Lys Val Glu Thr Asn
145 150 155 160

Ile His Asp Ile Val Thr Lys Asn Gly Thr Ile Ser Ala Met Leu Gly
165 170 175

Gly Val Gly Ser Gly Leu Gln Leu Asn Asp Gly Lys Leu Val Phe Pro
180 185 190

Val	Gln	Met	Val	Arg	Thr	Lys	Asn	Ile	Thr	Thr	Val	Leu	Asn	Thr	Ser
		195					200					205			

Phe Ile Tyr Ser Thr Asp Gly Ile Thr Trp Ser Leu Pro Ser Gly Tyr
210 215 220

Cys Glu Gly Phe Gly Ser Glu Asn Asn Ile Ile Glu Phe Asn Ala Ser
225 230 235 240

Leu Val Asn Asn Ile Arg Asn Ser Gly Leu Arg Arg Ser Phe Glu Thr
245 250 255

Lys Asp Phe Gly Lys Thr Trp Thr Glu Phe Pro Pro Met Asp Lys Lys
260 265 270

Val	Asp	Asn	Arg	Asn	His	Gly	Val	Gln	Gly	Ser	Thr	Ile	Thr	Ile	Pro
		275					280					285			

Ser Gly Asn Lys Leu Val Ala Ala His Ser Ser Ala Gln Asn Lys Asn
290 295 300

Asn Asp Tyr Thr Arg Ser Asp Ile Ser Leu Tyr Ala His Asn Leu Tyr
 305 310 315 320

Ser Gly Glu Val Lys Leu Ile Asp Asp Phe Tyr Pro Lys Val Gly Asn
 325 330 335

Ala Ser Gly Ala Gly Tyr Ser Cys Leu Ser Tyr Arg Lys Asn Val Asp
 340 345 350

Lys Glu Thr Leu Tyr Val Val Tyr Glu Ala Asn Gly Ser Ile Glu Phe
 355 360 365

Gln Asp Leu Ser Arg His Leu Pro Val Ile Lys Ser Tyr Asn
 370 375 380

<210> 31

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 31

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 130 135 140

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 32

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 32

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 100 105 110

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

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 130 135 140

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

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

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr Val
 180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 210 215 220

Pro Gly Lys
 225

<210> 33

<211> 232
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 33

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 130 135 140

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr

180

185

190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 34

<211> 1383

<212> DNA

<213> Homo sapiens

<400> 34

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ccgacagaga cggaggagcc ggggtccagt gcagaggtca tggaagaagt gacaacatgc	120
tccttcaaca gccctctgtt ccggcaggaa gatgacagag ggattaccta ccggatccca	180
gccctgctct acataccccc caccacacc ttcttgacct ttgcagagaa gcgttctacg	240
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aat	1383

<210> 35

<211> 1488

<212> DNA

<213> Homo sapiens

<400> 35

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cggacagtgc tcttcgagcg ggagaggacg ggcctgacct accgcgtgcc ctcgctgctc	120
cccgtgcccc ccggggccac cctgctggcc tttgtggagc agcggctcag ccctgacgac	180
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cccaggcctg gggtcagtgg ggatgtgggg tcctggaccc tggcactccc catgcccttt      1140
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gagatttcct tttgtacatt ctccctgcgt gaggtcctgg agaacgtgcc cgccagcccc      1440
aaaccgcca accttgggga caagcctcgg gggtgctgct ggccctcc      1488

```

<210> 36

<211> 781

<212> PRT

<213> *Vibrio cholera*

<400> 36

```

Met Arg Phe Lys Asn Val Lys Lys Thr Ala Leu Met Leu Ala Met Phe
1              5              10              15

```

```

Gly Met Ala Thr Ser Ser Asn Ala Ala Leu Phe Asp Tyr Asn Ala Thr
              20              25              30

```

```

Gly Asp Thr Glu Phe Asp Ser Pro Ala Lys Gln Gly Trp Met Gln Asp
              35              40              45

```

```

Asn Thr Asn Asn Gly Ser Gly Val Leu Thr Asn Ala Asp Gly Met Pro
              50              55              60

```

```

Ala Trp Leu Val Gln Gly Ile Gly Gly Arg Ala Gln Trp Thr Tyr Ser
65              70              75              80

```

```

Leu Ser Thr Asn Gln His Ala Gln Ala Ser Ser Phe Gly Trp Arg Met
              85              90              95

```

```

Thr Thr Glu Met Lys Val Leu Ser Gly Gly Met Ile Thr Asn Tyr Tyr
              100              105              110

```

```

Ala Asn Gly Thr Gln Arg Val Leu Pro Ile Ile Ser Leu Asp Ser Ser

```

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

Val Ala Ser Gly Asn Trp Gln Ala Pro Ile Asp Val Thr Asp Gln Val
 340 345 350

Lys Glu Arg Ser Phe Gln Ile Ala Gly Trp Gly Gly Ser Glu Leu Tyr
 355 360 365

Arg Arg Asn Thr Ser Leu Asn Ser Gln Gln Asp Trp Gln Ser Asn Ala
 370 375 380

Lys Ile Arg Ile Val Asp Gly Ala Ala Asn Gln Ile Gln Val Ala Asp
 385 390 395 400

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

Leu Val Ala Asn Leu Asn Gly Val Ser Ala Pro Ile Ile Leu Gln Ser
 420 425 430

Glu His Ala Lys Val His Ser Phe His Asp Tyr Glu Leu Gln Tyr Ser
 435 440 445

Ala Leu Asn His Thr Thr Thr Leu Phe Val Asp Gly Gln Gln Ile Thr
 450 455 460

Thr Trp Ala Gly Glu Val Ser Gln Glu Asn Asn Ile Gln Phe Gly Asn
 465 470 475 480

Ala Asp Ala Gln Ile Asp Gly Arg Leu His Val Gln Lys Ile Val Leu
 485 490 495

Thr Gln Gln Gly His Asn Leu Val Glu Phe Asp Ala Phe Tyr Leu Ala
 500 505 510

Gln Gln Thr Pro Glu Val Glu Lys Asp Leu Glu Lys Leu Gly Trp Thr
 515 520 525

Lys Ile Lys Thr Gly Asn Thr Met Ser Leu Tyr Gly Asn Ala Ser Val
 530 535 540

Asn Pro Gly Pro Gly His Gly Ile Thr Leu Thr Arg Gln Gln Asn Ile

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Arg	Phe	Phe	Leu	Asn	Val	Met	Ser	Ile	Tyr	Ser	Asp	Asp	Gly	Gly	Ser
			580					585					590		
Asn	Trp	Gln	Thr	Gly	Ser	Thr	Leu	Pro	Ile	Pro	Phe	Arg	Trp	Lys	Ser
		595					600					605			
Ser	Ser	Ile	Leu	Glu	Thr	Leu	Glu	Pro	Ser	Glu	Ala	Asp	Met	Val	Glu
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Leu	Gln	Asn	Gly	Asp	Leu	Leu	Leu	Thr	Ala	Arg	Leu	Asp	Phe	Asn	Gln
625					630					635					640
Ile	Val	Asn	Gly	Val	Asn	Tyr	Ser	Pro	Arg	Gln	Gln	Phe	Leu	Ser	Lys
				645					650					655	
Asp	Gly	Gly	Ile	Thr	Trp	Ser	Leu	Leu	Glu	Ala	Asn	Asn	Ala	Asn	Val
			660					665					670		
Phe	Ser	Asn	Ile	Ser	Thr	Gly	Thr	Val	Asp	Ala	Ser	Ile	Thr	Arg	Phe
		675					680					685			
Glu	Gln	Ser	Asp	Gly	Ser	His	Phe	Leu	Leu	Phe	Thr	Asn	Pro	Gln	Gly
	690					695					700				
Asn	Pro	Ala	Gly	Thr	Asn	Gly	Arg	Gln	Asn	Leu	Gly	Leu	Trp	Phe	Ser
705					710					715					720
Phe	Asp	Glu	Gly	Val	Thr	Trp	Lys	Gly	Pro	Ile	Gln	Leu	Val	Asn	Gly
				725					730					735	
Ala	Ser	Ala	Tyr	Ser	Asp	Ile	Tyr	Gln	Leu	Asp	Ser	Glu	Asn	Ala	Ile
			740					745					750		
Val	Ile	Val	Glu	Thr	Asp	Asn	Ser	Asn	Met	Arg	Ile	Leu	Arg	Met	Pro
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Ile Thr Leu Leu Lys Gln Lys Leu Thr Leu Ser Gln Asn
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<210> 37

<211> 2424

<212> DNA

<213> *Vibrio cholera*

<400> 37

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gctcaatgga catattctct ctctactaat caacatgccc aagcatcaag tttcggttgg	360
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<210> 38

<211> 409

<212> PRT

<213> Mus musculus

<400> 38

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          20          25          30

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Ser Ala Ala Glu Ser Glu Ala Arg Ala Glu Asp Asp Phe Ser Leu Val
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Gln Pro Leu Val Thr Met Glu Gln Leu Leu Trp Val Ser Gly Lys Gln
 50 55 60

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

Arg Gly Thr Leu Leu Ala Phe Ala Glu Ala Arg Lys Lys Ser Ala Ser
 85 90 95

Asp Glu Gly Ala Lys Phe Ile Ala Met Arg Arg Ser Thr Asp Gln Gly
 100 105 110

Ser Thr Trp Ser Ser Thr Ala Phe Ile Val Asp Asp Gly Glu Ala Ser
 115 120 125

Asp Gly Leu Asn Leu Gly Ala Val Val Asn Asp Val Asp Thr Gly Ile
 130 135 140

Val Phe Leu Ile Tyr Thr Leu Cys Ala His Lys Val Asn Cys Gln Val
 145 150 155 160

Ala Ser Thr Met Leu Val Trp Ser Lys Asp Asp Gly Ile Ser Trp Ser
 165 170 175

Pro Pro Arg Asn Leu Ser Val Asp Ile Gly Thr Glu Met Phe Ala Pro
 180 185 190

Gly Pro Gly Ser Gly Ile Gln Lys Gln Arg Glu Pro Gly Lys Gly Arg
 195 200 205

Leu Ile Val Cys Gly His Gly Thr Leu Glu Arg Asp Gly Val Phe Cys
 210 215 220

Leu Leu Ser Asp Asp His Gly Ala Ser Trp His Tyr Gly Thr Gly Val
 225 230 235 240

Ser Gly Ile Pro Phe Gly Gln Pro Lys His Asp His Asp Phe Asn Pro
 245 250 255

Asp Glu Cys Gln Pro Tyr Glu Leu Pro Asp Gly Ser Val Ile Ile Asn
 260 265 270

Ala Arg Asn Gln Asn Asn Tyr His Cys Arg Cys Arg Ile Val Leu Arg
 275 280 285

Ser Tyr Asp Ala Cys Asp Thr Leu Arg Pro Arg Asp Val Thr Phe Asp
 290 295 300

Pro Glu Leu Val Asp Pro Val Val Ala Ala Gly Ala Leu Ala Thr Ser
 305 310 315 320

Ser Gly Ile Val Phe Phe Ser Asn Pro Ala His Pro Glu Phe Arg Val
 325 330 335

Asn Leu Thr Leu Arg Trp Ser Phe Ser Asn Gly Thr Ser Trp Leu Lys
 340 345 350

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

Ala Leu Glu Asn Ser Thr Asp Gly Lys Lys Gln Pro Pro Gln Leu Phe
 370 375 380

Val Leu Tyr Glu Lys Gly Leu Asn Arg Tyr Thr Glu Ser Ile Ser Met
 385 390 395 400

Val Lys Ile Ser Val Tyr Gly Thr Leu
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<210> 39

<211> 393

<212> PRT

<213> Mus musculus

<400> 39

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

Leu Ala Phe Ala Glu Lys Arg Ala Ser Lys Thr Asp Glu His Ala Glu
 50 55 60

Leu Ile Val Leu Arg Arg Gly Ser Tyr Asn Glu Ala Thr Asn Arg Val
 65 70 75 80

Lys Trp Gln Pro Glu Glu Val Val Thr Gln Ala Gln Leu Glu Gly His
 85 90 95

Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Lys Gln Thr Lys Thr Leu
 100 105 110

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

Leu His Thr Lys Val Asn Val Thr Arg Leu Cys Cys Val Ser Ser Thr
 130 135 140

Asp His Gly Arg Thr Trp Ser Pro Ile Gln Asp Leu Thr Glu Thr Thr
 145 150 155 160

Ile Gly Ser Thr His Gln Glu Trp Ala Thr Phe Ala Val Gly Pro Gly
 165 170 175

His Cys Leu Gln Leu Arg Asn Pro Ala Gly Ser Leu Leu Val Pro Ala
 180 185 190

Tyr Ala Tyr Arg Lys Leu His Pro Ala Gln Lys Pro Thr Pro Phe Ala
 195 200 205

Phe Cys Phe Ile Ser Leu Asp His Gly His Thr Trp Lys Leu Gly Asn
 210 215 220

Phe Val Ala Glu Asn Ser Leu Glu Cys Gln Val Ala Glu Val Gly Thr
 225 230 235 240

Gly Ala Gln Arg Met Val Tyr Leu Asn Ala Arg Ser Phe Leu Gly Ala
245 250 255

Arg Val Gln Ala Gln Ser Pro Asn Asp Gly Leu Asp Phe Gln Asp Asn
260 265 270

Arg Val Val Ser Lys Leu Val Glu Pro Pro His Gly Cys His Gly Ser
275 280 285

Val	Val	Ala	Phe	His	Asn	Pro	Ile	Ser	Lys	Pro	His	Ala	Leu	Asp	Thr
290						295					300				

Trp Leu Leu Tyr Thr His Pro Thr Asp Ser Arg Asn Arg Thr Asn Leu
305 310 315 320

Gly Val Tyr Leu Asn Gln Met Pro Leu Asp Pro Thr Ala Trp Ser Glu
325 330 335

Pro Thr Leu Leu Ala Met Gly Ile Cys Ala Tyr Ser Asp Leu Gln Asn
340 345 350

Met Gly Gln Gly Pro Asp Gly Ser Pro Gln Phe Gly Cys Leu Tyr Glu
355 360 365

Ser Gly Asn Tyr Glu Glu Ile Ile Phe Leu Ile Phe Thr Leu Lys Gln
370 375 380

Ala Phe Pro Thr Val Phe Asp Ala Gln
385 390

$\langle 210 \rangle$ 40

<211> 418

<212> PRT

<213> Mus musculus

<400> 40

Met Glu Glu Val Pro Pro Tyr Ser Leu Ser Ser Thr Leu Phe Gln Gln
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Glu Glu Gln Ser Gly Val Thr Tyr Arg Ile Pro Ala Leu Leu Tyr Leu
20 25 30

Pro Pro Thr His Thr Phe Leu Ala Phe Ala Glu Lys Arg Thr Ser Val
 35 40 45

Arg Asp Glu Asp Ala Ala Cys Leu Val Leu Arg Arg Gly Leu Met Lys
 50 55 60

Gly Arg Ser Val Gln Trp Gly Pro Gln Arg Leu Leu Met Glu Ala Thr
 65 70 75 80

Leu Pro Gly His Arg Thr Met Asn Pro Cys Pro Val Trp Glu Lys Asn
 85 90 95

Thr Gly Arg Val Tyr Leu Phe Phe Ile Cys Val Arg Gly His Val Thr
 100 105 110

Glu Arg Cys Gln Ile Val Trp Gly Lys Asn Ala Ala Arg Leu Cys Phe
 115 120 125

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

Thr Glu Glu Val Ile Gly Ser Glu Val Lys Arg Trp Ala Thr Phe Ala
 145 150 155 160

Val Gly Pro Gly His Gly Ile Gln Leu His Ser Gly Arg Leu Ile Ile
 165 170 175

Pro Ala Tyr Ala Tyr Tyr Val Ser Arg Trp Phe Leu Cys Phe Ala Cys
 180 185 190

Ser Val Lys Pro His Ser Leu Met Ile Tyr Ser Asp Asp Phe Gly Val
 195 200 205

Thr Trp His His Gly Lys Phe Ile Glu Pro Gln Val Thr Gly Glu Cys
 210 215 220

Gln Val Ala Glu Val Ala Gly Thr Ala Gly Asn Pro Val Leu Tyr Cys
 225 230 235 240

Ser Ala Arg Thr Pro Ser Arg Phe Arg Ala Glu Ala Phe Ser Thr Asp
 245 250 255

Ser Gly Gly Cys Phe Gln Lys Pro Thr Leu Asn Pro Gln Leu His Glu
 260 265 270

Pro Arg Thr Gly Cys Gln Gly Ser Val Val Ser Phe Arg Pro Leu Lys
 275 280 285

Met Pro Asn Thr Tyr Gln Asp Ser Ile Gly Lys Gly Ala Pro Ala Thr
 290 295 300

Gln Lys Cys Pro Leu Leu Asp Ser Pro Leu Glu Val Glu Lys Gly Ala
 305 310 315 320

Glu Thr Pro Ser Ala Thr Trp Leu Leu Tyr Ser His Pro Thr Ser Lys
 325 330 335

Arg Lys Arg Ile Asn Leu Gly Ile Tyr Tyr Asn Arg Asn Pro Leu Glu
 340 345 350

Val Asn Cys Trp Ser Arg Pro Trp Ile Leu Asn Arg Gly Pro Ser Gly
 355 360 365

Tyr Ser Asp Leu Ala Val Val Glu Glu Gln Asp Leu Val Ala Cys Leu
 370 375 380

Phe Glu Cys Gly Glu Lys Asn Glu Tyr Glu Arg Ile Asp Phe Cys Leu
 385 390 395 400

Phe Ser Asp His Glu Val Leu Ser Cys Glu Asp Cys Thr Ser Pro Ser
 405 410 415

Ser Asp

<210> 41

<211> 501

<212> PRT

<213> Mus musculus

<400> 41

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

Ala Leu Leu Cys Val Pro Pro Arg Pro Thr Leu Leu Ala Phe Ala Glu
 50 55 60

Gln Arg Leu Ser Pro Asp Asp Ser His Ala His Arg Leu Val Leu Arg
 65 70 75 80

Arg Gly Thr Leu Thr Arg Gly Ser Val Arg Trp Gly Thr Leu Ser Val
 85 90 95

Leu Glu Thr Ala Val Leu Glu Glu His Arg Ser Met Asn Pro Cys Pro
 100 105 110

Val Leu Asp Glu His Ser Gly Thr Ile Phe Leu Phe Phe Ile Ala Val
 115 120 125

Leu Gly His Thr Pro Glu Ala Val Gln Ile Ala Thr Gly Lys Asn Ala
 130 135 140

Ala Arg Leu Cys Cys Val Thr Ser Cys Asp Ala Gly Leu Thr Trp Gly
 145 150 155 160

Ser Val Arg Asp Leu Thr Glu Glu Ala Ile Gly Ala Ala Leu Gln Asp
 165 170 175

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

Gly Arg Leu Leu Val Pro Ala Tyr Thr Tyr His Val Asp Arg Arg Glu
 195 200 205

Cys Phe Gly Lys Ile Cys Trp Thr Ser Pro His Ser Leu Ala Phe Tyr
 210 215 220

Ser Asp Asp His Gly Ile Ser Trp His Cys Gly Gly Leu Val Pro Asn
 225 230 235 240

Leu Arg Ser Gly Glu Cys Gln Leu Ala Ala Val Asp Gly Asp Phe Leu
 245 250 255

Tyr Cys Asn Ala Arg Ser Pro Leu Gly Asn Arg Val Gln Ala Leu Ser
 260 265 270

Ala Asp Glu Gly Thr Ser Phe Leu Pro Gly Glu Leu Val Pro Thr Leu
 275 280 285

Ala Glu Thr Ala Arg Gly Cys Gln Gly Ser Ile Val Gly Phe Leu Ala
 290 295 300

Pro Pro Ser Ile Glu Pro Gln Asp Asp Arg Trp Thr Gly Ser Pro Arg
 305 310 315 320

Asn Thr Pro His Ser Pro Cys Phe Asn Leu Arg Val Gln Glu Ser Ser
 325 330 335

Gly Glu Gly Ala Arg Gly Leu Leu Glu Arg Trp Met Pro Arg Leu Pro
 340 345 350

Leu Cys Tyr Pro Gln Ser Arg Ser Pro Glu Asn His Gly Leu Glu Pro
 355 360 365

Gly Ser Asp Gly Asp Lys Thr Ser Trp Thr Pro Glu Cys Pro Met Ser
 370 375 380

Ser Asp Ser Met Leu Gln Ser Pro Thr Trp Leu Leu Tyr Ser His Pro
 385 390 395 400

Ala Gly Arg Arg Ala Arg Leu His Met Gly Ile Tyr Leu Ser Arg Ser
 405 410 415

Pro Leu Asp Pro His Ser Trp Thr Glu Pro Trp Val Ile Tyr Glu Gly
 420 425 430

Pro Ser Gly Tyr Ser Asp Leu Ala Phe Leu Gly Pro Met Pro Gly Ala
 435 440 445

Ser Leu Val Phe Ala Cys Leu Phe Glu Ser Gly Thr Arg Thr Ser Tyr
 450 455 460

Glu Asp Ile Ser Phe Cys Leu Phe Ser Leu Ala Asp Val Leu Glu Asn
 465 470 475 480

Val Pro Thr Gly Leu Glu Met Leu Ser Leu Arg Asp Lys Ala Gln Gly
 485 490 495

His Cys Trp Pro Ser
 500

<210> 42

<211> 3850

<212> DNA

<213> Mus musculus

<400> 42

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<213> Mus musculus

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<223> Phe, Trp, Tyr or Val

<220>

<221> MOD_RES

<222> (9)..(9)

<223> Lys or Asp

<220>

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<222> (62)..(62)

<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>

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<223> Arg, Ile, or Lys

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 <223> Val or Arg

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 <223> Leu, Gln, His, Ile, Lys, or Ser

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Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
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Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
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Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
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Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln
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Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
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Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
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Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
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Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
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Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
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Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
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Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
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Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
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Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
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Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
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Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
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<220>
 <221> MOD_RES
 <222> (164)..(164)
 <223> Cys or Gly

<220>
 <221> MOD_RES
 <222> (171)..(171)
 <223> Ala or Gly

<220>
 <221> MOD_RES
 <222> (187)..(187)
 <223> Arg, Ile, or Lys

<220>
 <221> MOD_RES
 <222> (196)..(196)
 <223> Ala, Cys, Leu, or Val

<220>
 <221> MOD_RES
 <222> (217)..(217)
 <223> Leu, Ala, or Val

<220>
 <221> MOD_RES
 <222> (249)..(249)
 <223> Thr or Ala

<220>
 <221> MOD_RES
 <222> (251)..(251)
 <223> Asp or Gly

<220>

<221> MOD_RES
<222> (257)..(257)
<223> Glu or Lys

<220>
<221> MOD_RES
<222> (270)..(270)
<223> Gln, Ala, His, Phe, or Pro

<220>
<221> MOD_RES
<222> (272)..(272)
<223> Cys or Val

<220>
<221> MOD_RES
<222> (292)..(292)
<223> Trp or Arg

<220>
<221> MOD_RES
<222> (301)..(301)
<223> Ser or Arg

<220>
<221> MOD_RES
<222> (302)..(302)
<223> Trp or Lys

<220>
<221> MOD_RES
<222> (325)..(325)
<223> Lys or Val

<220>
<221> MOD_RES
<222> (332)..(332)
<223> Ala, Cys, Ser, or Val

<220>
<221> MOD_RES
<222> (352)..(352)
<223> Cys, Leu, or Val

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Val or Arg

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Leu, Gln, His, Ile, Lys, or Ser

<400> 47

Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Xaa Xaa Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
 50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
 85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
 100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Xaa Leu Gln Leu His Asp Arg Xaa Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val

210

215

220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
 245 250 255

Xaa Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Xaa
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 48

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 48

Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly

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

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 49

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 49

Asp Ala Ser Leu Pro Tyr Leu Gln Asp Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu

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

 <210> 50
 <211> 380
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

 <400> 50
 Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

 Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln

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

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 51

<211> 380

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 51

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln

	245		250		255
Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys	260	265	270		
Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser	275	280	285		
Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg	290	295	300		
Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala	305	310	315	320	
Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp	325	330	335		
Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys	340	345	350		
Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr	355	360	365		
Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln	370	375	380		

<210> 52
 <211> 380
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 52
 Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His

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

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 53

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 53

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Thr Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

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

260

265

270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 54

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 54

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His

50

55

60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 55

<211> 379

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 55

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

His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln Ser
 20 25 30

Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His Ala
 35 40 45

Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His Gln
 50 55 60

Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp Gly
65 70 75 80

His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly Thr
85 90 95

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

Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr Ser
115 120 125

Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp Ala
130 135 140

Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly Pro
145 150 155 160

Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val Pro
165 170 175

Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro Ser
180 185 190

Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg Gly
195 200 205

His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val Glu
210 215 220

Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu Arg
225 230 235 240

Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln Glu
245 250 255

Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys Gln
260 265 270

Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser Pro

275

280

285

Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg Ala
 290 295 300

Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala Trp
 305 310 315 320

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

Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys Leu
 340 345 350

Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr Leu
 355 360 365

Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375

<210> 56

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 56

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp

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

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

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

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 57

<211> 379

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 57

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

His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln Ser
 20 25 30

Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His Ala
 35 40 45

Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His Gln
 50 55 60

Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp Gly
 65 70 75 80

His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly Thr
85 90 95

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

Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr Ser
115 120 125

Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp Ala
130 135 140

Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly Pro
145 150 155 160

Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val Pro
165 170 175

Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro Ser
180 185 190

Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg Gly
195 200 205

His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val Glu
210 215 220

Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu Arg
225 230 235 240

Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln Glu
245 250 255

Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys Gln
260 265 270

Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser Pro
275 280 285

Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg Ala

290

295

300

Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala Trp
 305 310 315 320

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

Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys Leu
 340 345 350

Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr Leu
 355 360 365

Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375

<210> 58

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 58

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 59

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 59

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

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

305 310 315 320
 Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Cys Ala Tyr Ser Asp
 325 330 335
 Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350
 Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365
 Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

 <210> 60
 <211> 380
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

 <400> 60
 Ala Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

 Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

 Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

 Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

 Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

 Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

 Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln

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

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

$\langle 210 \rangle$ 61

<211> 380

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 61

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp

325

330

335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 62

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 62

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr

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

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 63

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 63

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

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

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

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

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

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

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110

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

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

Tyr 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> 64

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 64

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

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

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

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
 210

<210> 65

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 65

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
 225 230 235 240

Ile Lys

<210> 66

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 66

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

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

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

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
 210

<210> 67

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 67

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

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

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

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

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

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

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110

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

Phe Pro Leu Ala Pro 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 Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365
 Tyr 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> 68
 <211> 617
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide
 <400> 68
 Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
 1 5 10 15
 Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln

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

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu

450

455

460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 69

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 69

Asp Ala Ser Leu Pro Tyr Leu Gln Asp Glu Ser Val Phe Gln Ser Gly

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

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Arg Phe Ile Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

435

440

445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 70

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 70

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

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

420

425

430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 71

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 71

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 72

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 72

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

Ala	His	Ala	Tyr	Arg	Ile	Pro	Ala	Leu	Leu	Tyr	Leu	Pro	Gly	Gln	Gln
		20						25					30		

Ser	Leu	Leu	Ala	Phe	Ala	Glu	Gln	Arg	Ala	Ser	Lys	Lys	Asp	Glu	His
		35					40					45			

Ala	Glu	Leu	Ile	Val	Leu	Arg	Arg	Gly	Asp	Tyr	Asp	Ala	Ser	Thr	His
	50					55					60				

Gln	Val	Gln	Trp	Gln	Ala	Gln	Glu	Val	Val	Ala	Gln	Ala	Arg	Leu	Asp
65					70					75					80

Gly	His	Arg	Ser	Met	Asn	Pro	Cys	Pro	Leu	Tyr	Asp	Ala	Gln	Thr	Gly
				85					90					95	

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

Gln	Gln	Leu	Gln	Thr	Arg	Ala	Asn	Val	Thr	Arg	Leu	Cys	Gln	Val	Thr
		115					120					125			

Ser	Thr	Asp	His	Gly	Arg	Thr	Trp	Ser	Ser	Pro	Arg	Asp	Leu	Thr	Asp
	130					135					140				

Ala	Ala	Ile	Gly	Pro	Ala	Tyr	Arg	Glu	Trp	Ser	Thr	Phe	Ala	Val	Gly
145					150					155					160

Pro	Gly	His	Cys	Leu	Gln	Leu	His	Asp	Arg	Ala	Arg	Ser	Leu	Val	Val
				165					170					175	

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 73

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 73

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Thr Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly

370

375

380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 74

<211> 617

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 74

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr

355

360

365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 75
 <211> 617
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<220>
 <221> MOD_RES
 <222> (1)..(1)
 <223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr,
 Val, or not present

<220>
 <221> MOD_RES
 <222> (6)..(6)
 <223> Phe, Trp, Tyr or Val

<220>
 <221> MOD_RES
 <222> (9)..(9)
 <223> Lys or Asp

<220>
 <221> MOD_RES
 <222> (62)..(62)
 <223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
 <221> MOD_RES
 <222> (93)..(93)
 <223> Ala, Glu, or Lys

<220>
 <221> MOD_RES
 <222> (187)..(187)
 <223> Arg, Ile, or Lys

<220>
 <221> MOD_RES
 <222> (270)..(270)
 <223> Gln, Ala, His, Phe, or Pro

<220>
 <221> MOD_RES
 <222> (301)..(301)
 <223> Ser or Arg

<220>
 <221> MOD_RES
 <222> (302)..(302)
 <223> Trp or Lys

<220>
 <221> MOD_RES
 <222> (332)..(332)
 <223> Ala, Cys, Ser, or Val

<220>
 <221> MOD_RES
 <222> (363)..(363)
 <223> Val or Arg

<220>
 <221> MOD_RES
 <222> (365)..(365)
 <223> Leu, Gln, His, Ile, Lys, or Ser

<400> 75
 Xaa Ala Ser Leu Pro Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
 290 295 300

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

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

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 76

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<221> MOD_RES

<222> (1)..(1)

<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr, Val, or not present

<220>

<221> MOD_RES

<222> (2)..(2)

<223> Ala or Lys

<220>

<221> MOD_RES

<222> (4)..(4)

<223> Asn or Leu

<220>

<221> MOD_RES

<222> (5)..(5)

<223> Pro or His

<220>

<221> MOD_RES

<222> (6)..(6)

<223> Phe, Trp, Tyr or Val

<220>

<221> MOD_RES

<222> (9)..(9)

<223> Lys or Asp

<220>

<221> MOD_RES

<222> (44)..(44)

<223> Lys, Arg, or Glu

<220>

<221> MOD_RES

<222> (45)..(45)

<223> Lys, Ala, Arg, or Glu

<220>

<221> MOD_RES

<222> (54)..(54)

<223> Leu or Met

<220>

<221> MOD_RES

<222> (62)..(62)

<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>

<221> MOD_RES

<222> (69)..(69)

<223> Gln or His

<220>

<221> MOD_RES

<222> (78)..(78)

<223> Arg or Lys

<220>

<221> MOD_RES

<222> (93)..(93)

<223> Ala, Glu or Lys

<220>

<221> MOD_RES

<222> (107)..(107)

<223> Gly or Asp

<220>

<221> MOD_RES

<222> (108)..(108)

<223> Gln or His

<220>

<221> MOD_RES

<222> (112)..(112)

<223> Gln, Arg, or Lys

<220>

<221> MOD_RES

<222> (125)..(125)

<223> Ala, Cys, Ile, Ser, Val, or Leu

<220>

<221> MOD_RES

<222> (126)..(126)

<223> Gln or Leu

<220>

<221> MOD_RES

<222> (150)..(150)

<223> Ala or Val

<220>

<221> MOD_RES

<222> (164)..(164)

<223> Cys or Gly

<220>

<221> MOD_RES

<222> (171)..(171)

<223> Ala or Gly

<220>

<221> MOD_RES

<222> (187)..(187)

<223> Arg, Ile, or Lys

<220>

<221> MOD_RES

<222> (196)..(196)

<223> Ala, Cys, Leu, or Val

<220>

<221> MOD_RES

<222> (217)..(217)

<223> Leu, Ala, or Val

<220>

<221> MOD_RES

<222> (249)..(249)

<223> Thr or Ala

<220>

<221> MOD_RES
<222> (251)..(251)
<223> Asp or Gly

<220>
<221> MOD_RES
<222> (257)..(257)
<223> Glu or Lys

<220>
<221> MOD_RES
<222> (270)..(270)
<223> Gln, Ala, His, Phe, or Pro

<220>
<221> MOD_RES
<222> (272)..(272)
<223> Cys or Val

<220>
<221> MOD_RES
<222> (292)..(292)
<223> Trp or Arg

<220>
<221> MOD_RES
<222> (301)..(301)
<223> Ser or Arg

<220>
<221> MOD_RES
<222> (302)..(302)
<223> Trp or Lys

<220>
<221> MOD_RES
<222> (325)..(325)
<223> Lys or Val

<220>
<221> MOD_RES
<222> (332)..(332)
<223> Ala, Cys, Ser, or Val

<220>
<221> MOD_RES
<222> (352)..(352)
<223> Cys, Leu, or Val

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Val or Arg

<220>

<221> MOD_RES

<222> (365)..(365)

<223> Leu, Gln, His, Ile, Lys, or Ser

<400> 76

Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Xaa Xaa Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
 50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
 85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
 100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Xaa Leu Gln Leu His Asp Arg Xaa Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
 245 250 255

Xaa Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Xaa
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 77
 <211> 874
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 77

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 625 630 635 640

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 645 650 655

Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala
 660 665 670

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly
 675 680 685

Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala
 690 695 700

Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
 705 710 715 720

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
 725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
 785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 805 810 815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 820 825 830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
850 855 860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
865 870

<210> 78

<211> 874

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 78

Asp Ala Ser Leu Pro Tyr Leu Gln Asp Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Arg Phe Ile Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
625 630 635 640

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
645 650 655

Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala
660 665 670

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly
675 680 685

Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala
690 695 700

Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
705 710 715 720

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
 785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 805 810 815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 820 825 830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
 850 855 860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 865 870

<210> 79

<211> 874

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 79

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 625 630 635 640

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 645 650 655

Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala
 660 665 670

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly
 675 680 685

Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala
 690 695 700

Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
 705 710 715 720

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
805 810 815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
820 825 830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
850 855 860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
865 870

<210> 80

<211> 874

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 80

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 625 630 635 640

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 645 650 655

Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala
 660 665 670

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly
 675 680 685

Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala
 690 695 700

Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
 705 710 715 720

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
 725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
 785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 805 810 815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 820 825 830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
 850 855 860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 865 870

<210> 81

<211> 874

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 81

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

Ala	His	Ala	Tyr	Arg	Ile	Pro	Ala	Leu	Leu	Tyr	Leu	Pro	Gly	Gln	Gln
			20					25					30		

Ser	Leu	Leu	Ala	Phe	Ala	Glu	Gln	Arg	Ala	Ser	Lys	Lys	Asp	Glu	His
		35					40					45			

Ala	Glu	Leu	Ile	Val	Leu	Arg	Arg	Gly	Asp	Tyr	Asp	Ala	Ser	Thr	His
	50					55					60				

Gln	Val	Gln	Trp	Gln	Ala	Gln	Glu	Val	Val	Ala	Gln	Ala	Arg	Leu	Asp
65					70					75				80	

Gly	His	Arg	Ser	Met	Asn	Pro	Cys	Pro	Leu	Tyr	Asp	Ala	Gln	Thr	Gly
				85					90					95	

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

Gln	Gln	Leu	Gln	Thr	Arg	Ala	Asn	Val	Thr	Arg	Leu	Cys	Gln	Val	Thr
		115					120					125			

Ser	Thr	Asp	His	Gly	Arg	Thr	Trp	Ser	Ser	Pro	Arg	Asp	Leu	Thr	Asp
	130					135					140				

Ala	Ala	Ile	Gly	Pro	Ala	Tyr	Arg	Glu	Trp	Ser	Thr	Phe	Ala	Val	Gly
145					150					155					160

Pro	Gly	His	Cys	Leu	Gln	Leu	His	Asp	Arg	Ala	Arg	Ser	Leu	Val	Val
				165					170					175	

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 625 630 635 640

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 645 650 655

Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala
 660 665 670

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly
 675 680 685

Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala
 690 695 700

Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
 705 710 715 720

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
 725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
 785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 805 810 815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 820 825 830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
 850 855 860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 865 870

<210> 82

<211> 874

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 82

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Thr Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 625 630 635 640

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 645 650 655

Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala
 660 665 670

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly
 675 680 685

Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala
 690 695 700

Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
 705 710 715 720

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
 725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
 785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 805 810 815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 820 825 830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
 850 855 860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 865 870

<210> 83

<211> 874

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 83

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 625 630 635 640

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 645 650 655

Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala
 660 665 670

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly
 675 680 685

Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala
 690 695 700

Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
705 710 715 720

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
805 810 815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
820 825 830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
850 855 860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
865 870

<210> 84

<211> 874

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
 <221> MOD_RES
 <222> (1)..(1)
 <223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr,
 Val, or not present

<220>
 <221> MOD_RES
 <222> (6)..(6)
 <223> Phe, Trp, Tyr or Val

<220>
 <221> MOD_RES
 <222> (9)..(9)
 <223> Lys or Asp

<220>
 <221> MOD_RES
 <222> (62)..(62)
 <223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
 <221> MOD_RES
 <222> (93)..(93)
 <223> Ala, Glu, or Lys

<220>
 <221> MOD_RES
 <222> (187)..(187)
 <223> Arg, Ile, or Lys

<220>
 <221> MOD_RES
 <222> (270)..(270)
 <223> Gln, Ala, His, Phe, or Pro

<220>
 <221> MOD_RES
 <222> (301)..(301)
 <223> Ser or Arg

<220>
 <221> MOD_RES
 <222> (302)..(302)
 <223> Trp or Lys

<220>
 <221> MOD_RES
 <222> (332)..(332)
 <223> Ala, Cys, Ser, or Val

<220>
 <221> MOD_RES
 <222> (363)..(363)

<223> Val or Arg

<220>

<221> MOD_RES

<222> (365)..(365)

<223> Leu, Gln, His, Ile, Lys, or Ser

<400> 84

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

Ala	His	Ala	Tyr	Arg	Ile	Pro	Ala	Leu	Leu	Tyr	Leu	Pro	Gly	Gln	Gln
			20					25					30		

Ser	Leu	Leu	Ala	Phe	Ala	Glu	Gln	Arg	Ala	Ser	Lys	Lys	Asp	Glu	His
		35					40					45			

Ala	Glu	Leu	Ile	Val	Leu	Arg	Arg	Gly	Asp	Tyr	Asp	Ala	Xaa	Thr	His
	50					55					60				

Gln	Val	Gln	Trp	Gln	Ala	Gln	Glu	Val	Val	Ala	Gln	Ala	Arg	Leu	Asp
65					70					75				80	

Gly	His	Arg	Ser	Met	Asn	Pro	Cys	Pro	Leu	Tyr	Asp	Xaa	Gln	Thr	Gly
				85					90					95	

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

Gln	Gln	Leu	Gln	Thr	Arg	Ala	Asn	Val	Thr	Arg	Leu	Cys	Gln	Val	Thr
		115					120					125			

Ser	Thr	Asp	His	Gly	Arg	Thr	Trp	Ser	Ser	Pro	Arg	Asp	Leu	Thr	Asp
	130					135					140				

Ala	Ala	Ile	Gly	Pro	Ala	Tyr	Arg	Glu	Trp	Ser	Thr	Phe	Ala	Val	Gly
145					150					155					160

Pro	Gly	His	Cys	Leu	Gln	Leu	His	Asp	Arg	Ala	Arg	Ser	Leu	Val	Val
				165					170					175	

Pro	Ala	Tyr	Ala	Tyr	Arg	Lys	Leu	His	Pro	Xaa	Gln	Arg	Pro	Ile	Pro
			180					185					190		

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
			420					425					430		

Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr
		435					440					445			

Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu
450						455						460			

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
625 630 635 640

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
645 650 655

Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala
660 665 670

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly
675 680 685

Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala
690 695 700

Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
705 710 715 720

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
805 810 815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
820 825 830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
 850 855 860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 865 870

<210> 85

<211> 874

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<220>

<221> MOD_RES

<222> (1)..(1)

<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr,
 Val, or not present

<220>

<221> MOD_RES

<222> (2)..(2)

<223> Ala or Lys

<220>

<221> MOD_RES

<222> (4)..(4)

<223> Asn or Leu

<220>

<221> MOD_RES

<222> (5)..(5)

<223> Pro or His

<220>

<221> MOD_RES

<222> (6)..(6)

<223> Phe, Trp, Tyr or Val

<220>

<221> MOD_RES

<222> (9)..(9)

<223> Lys or Asp

<220>

<221> MOD_RES
<222> (44)..(44)
<223> Lys, Arg, or Glu

<220>
<221> MOD_RES
<222> (45)..(45)
<223> Lys, Ala, Arg, or Glu

<220>
<221> MOD_RES
<222> (54)..(54)
<223> Leu or Met

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
<221> MOD_RES
<222> (69)..(69)
<223> Gln or His

<220>
<221> MOD_RES
<222> (78)..(78)
<223> Arg or Lys

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Ala, Glu or Lys

<220>
<221> MOD_RES
<222> (107)..(107)
<223> Gly or Asp

<220>
<221> MOD_RES
<222> (108)..(108)
<223> Gln or His

<220>
<221> MOD_RES
<222> (112)..(112)
<223> Gln, Arg, or Lys

<220>
<221> MOD_RES
<222> (125)..(125)
<223> Ala, Cys, Ile, Ser, Val, or Leu

<220>
<221> MOD_RES
<222> (126)..(126)
<223> Gln or Leu

<220>
<221> MOD_RES
<222> (150)..(150)
<223> Ala or Val

<220>
<221> MOD_RES
<222> (164)..(164)
<223> Cys or Gly

<220>
<221> MOD_RES
<222> (171)..(171)
<223> Ala or Gly

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Arg, Ile, or Lys

<220>
<221> MOD_RES
<222> (196)..(196)
<223> Ala, Cys, Leu, or Val

<220>
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<222> (217)..(217)
<223> Leu, Ala, or Val

<220>
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<222> (249)..(249)
<223> Thr or Ala

<220>
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<223> Asp or Gly

<220>
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<222> (257)..(257)
<223> Glu or Lys

<220>
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<222> (270)..(270)
<223> Gln, Ala, His, Phe, or Pro

<220>
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 <222> (272)..(272)
 <223> Cys or Val

<220>
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 <223> Trp or Arg

<220>
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 <223> Ser or Arg

<220>
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 <223> Trp or Lys

<220>
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 <223> Lys or Val

<220>
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 <222> (332)..(332)
 <223> Ala, Cys, Ser, or Val

<220>
 <221> MOD_RES
 <222> (352)..(352)
 <223> Cys, Leu, or Val

<220>
 <221> MOD_RES
 <222> (363)..(363)
 <223> Val or Arg

<220>
 <221> MOD_RES
 <222> (365)..(365)
 <223> Leu, Gln, His, Ile, Lys, or Ser

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Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Xaa Xaa Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
 50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
 85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
 100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Xaa Leu Gln Leu His Asp Arg Xaa Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln

			245					250						255	
Xaa	Ser	Gln	Leu	Val	Lys	Lys	Leu	Val	Glu	Pro	Pro	Pro	Xaa	Gly	Xaa
			260					265					270		
Gln	Gly	Ser	Val	Ile	Ser	Phe	Pro	Ser	Pro	Arg	Ser	Gly	Pro	Gly	Ser
		275					280					285			
Pro	Ala	Gln	Xaa	Leu	Leu	Tyr	Thr	His	Pro	Thr	His	Xaa	Xaa	Gln	Arg
	290					295					300				
Ala	Asp	Leu	Gly	Ala	Tyr	Leu	Asn	Pro	Arg	Pro	Pro	Ala	Pro	Glu	Ala
305					310					315					320
Trp	Ser	Glu	Pro	Xaa	Leu	Leu	Ala	Lys	Gly	Ser	Xaa	Ala	Tyr	Ser	Asp
				325					330					335	
Leu	Gln	Ser	Met	Gly	Thr	Gly	Pro	Asp	Gly	Ser	Pro	Leu	Phe	Gly	Xaa
			340					345					350		
Leu	Tyr	Glu	Ala	Asn	Asp	Tyr	Glu	Glu	Ile	Xaa	Phe	Xaa	Met	Phe	Thr
		355					360					365			
Leu	Lys	Gln	Ala	Phe	Pro	Ala	Glu	Tyr	Leu	Pro	Gln	Gly	Gly	Gly	Gly
	370					375					380				
Ser	Gly	Gly	Gly	Gly	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro
385					390					395					400
Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
				405					410					415	
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
			420					425					430		
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr
		435					440					445			
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu
	450					455					460				

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 625 630 635 640

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 645 650 655

Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala
 660 665 670

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly

675

680

685

Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala
 690 695 700

Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
 705 710 715 720

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
 725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
 785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 805 810 815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 820 825 830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
 850 855 860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 865 870

<210> 86

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 86

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ggcaaggccc ctaagctgct gatctacagc gccagctttc	tgtactccgg cgtgcccagc	180
agattcagcg gctctagaag cggcaccgac ttcaccctga	ccataagcag tctgcagccc	240
gaggacttcg ccacctacta ctgtcagcag cactacacca	cacctccaac ctttggccag	300
ggcaccaagg tggaaatcaa gcgtacggtg gctgcaccat	ctgtcttcat cttcccgcc	360
tctgatgagc agttgaaatc tggaaactgcc tctgttgtgt	gcctgctgaa taacttctat	420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc	tccaatcggg taactcccag	480
gagagtgtca cagagcagga cagcaaggac agcacctaca	gcctcagcag caccctgacg	540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct	gcgaagtcac ccatcagggc	600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt	gt	642

<210> 87

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 87

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tcttgtgccg ccagcggctt caacatcaag gacacctaca	tccactgggt ccgacaggcc	120
cctggcaaag gacttgaatg ggtcgccaga atctaccca	ccaacggcta caccagatac	180
gccgactctg tgaagggcag attcaccatc agcgccgaca	ccagcaagaa caccgcctac	240
ctgcagatga acagcctgag agccgaggac accgccgtgt	actactgttc tagatgggga	300
ggcgacggct tctacgcat ggattattgg ggccagggca	ccctgggtcac cgtttcttct	360
gctagcacca agggcccatc cgtcttcccc ctggcaccct	cctccaagag cacctctggg	420

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ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcc      480
tggaactcag gcgctctgac cagcggcgctg cacaccttcc cggctgtcct acagtcctca      540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc      600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc      660
aaatcttgtg aaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga      720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt      780
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg      840
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac      900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag      960
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc     1020
aaagccaaag ggcagccccg agaaccacag gtctacaccc tgccccatc ccgggaggag     1080
atgaccaaga accaggtcag cctgtactgc ctgggtcaaag gcttctatcc cagcgacatc     1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg     1200
ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg     1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     1320
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<210> 88

<211> 1851

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 88

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cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac     180
gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac     240
ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg     300
ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac     360

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gtgaccagac	tgtgtcaagt	gacctccacc	gaccacggca	gaacctggtc	tagccctaga	420
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cctggacact	gtctccagct	gcacgacagg	gctagatctc	tggtgggtgcc	tgacctagcc	540
tatagaaagc	tgcccccaa	acagcggcct	attcctagcg	ccttctgctt	tctgagccac	600
gatcacggca	ggacatgggc	cagaggacat	ttcgtggccc	aggacacact	ggaatgccag	660
gtggccgaag	tggaaccgg	cgagcagaga	gtcgtgacct	tgaacgccag	atctcacctg	720
agagccagag	tgaggccca	gagcacaac	gacggcctgg	atttccaaga	gagccagctg	780
gtcaagaaac	tggtggaacc	tcctccacag	ggctgtcagg	gaagcgtgat	cagctttcca	840
tctcctagaa	gcggccctgg	ctctcctgct	cagtggctgc	tgtatacaca	ccccacacac	900
agctggcaga	gagccgatct	gggcgcctac	ctgaatccta	gacctcctgc	tcctgaggct	960
tgagagcgaac	ctgttctgct	ggccaagggc	agcgtgcct	acagcgatct	gcagtctatg	1020
ggcacaggcc	ctgatggcag	ccctctgttt	ggctgtctgt	acgaggccaa	cgactacgaa	1080
gagatcgtgt	tcctgatgtt	caccctgaag	caggcctttc	cagccgagta	cctgcctcaa	1140
ggcggagggtg	gaagtggcgg	aggcggatcc	gacaaaactc	acacatgccc	accgtgcccc	1200
gcacctgaac	tcctgggggg	accgtcagtc	ttcctcttcc	ccccaaaacc	caaggacacc	1260
ctcatgatct	cccggacccc	tgaggtcaca	tgctgtgtgg	tggacgtgag	ccacgaagac	1320
cctgagggtca	agttcaactg	gtacgtggac	ggcgtggagg	tgcataatgc	caagacaaag	1380
ccgcgggagg	agcagtacaa	cagcacgtac	cgtgtgtgtca	gcgtcctcac	cgctcctgcac	1440
caggactggc	tgaatggcaa	ggagtacaag	tgcaaggtct	ccaacaaagc	cctcccagcc	1500
cccatcgaga	aaaccatctc	caaagccaaa	gggcagcccc	gagaaccaca	ggtctacacc	1560
ctgcccccat	cccgggagga	gatgaccaag	aaccagggtca	gcctgacctg	cctgggtcaaa	1620
ggcttctatc	ccagcgacat	cgccgtggag	tgggagagca	atgggcagcc	ggagaacaac	1680
tacaagacca	cgctcccggt	gctggactcc	gacggctcct	tcttctcac	tagcaagctc	1740
accgtggaca	agagcagggtg	gcagcagggg	aacgtcttct	catgctccgt	gatgcatgag	1800
gctctgcaca	accactacac	gcagaagagc	ctctccctgt	ctccgggtaa	a	1851

<210> 89

<211> 1140

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 89

gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac	60
agaattcccc ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag	120
cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac	180
gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac	240
ggccacagat ctatgaacct ctgtcctctg tacgatgaac agaccggcac actgtttctg	300
ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac	360
gtgaccagac tgtgtcaagt gacctcacc gaccacggca gaacctggtc tagccctaga	420
gatctgaccg acgccgcat cggacctgcc tatagagagt ggtccacctt cgccgttgga	480
cctggacact gtctccagct gcacgacagg gctagatctc tgggtggtgcc tgcctacgcc	540
tatagaaagc tgcaccccaa acagcggcct attcctagcg ctttctgctt tctgagccac	600
gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag	660
gtggccgaag tggaaaccgg cgagcagaga gtcgtgacct tgaacgccag atctcacctg	720
agagccagag tgcaggccca gagcacaac gacggcctgg atttccaaga gagccagctg	780
gtcaagaaac tgggtggaacc tcctccacag ggctgtcagg gaagcgtgat cagctttcca	840
tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca cccacacac	900
agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct	960
tggagcgaac ctgttctgct ggccaagggc agcgtgcct acagcgatct gcagtctatg	1020
ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa	1080
gagatcgtgt tcctgatggt caccctgaag caggcctttc cagccgagta cctgcctcaa	1140

<210> 90

<211> 618

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 90

Thr Val Glu Lys Ser Val Val Phe Lys Ala Glu Gly Glu His Phe Thr
 1 5 10 15

Asp Gln Lys Gly Asn Thr Ile Val Gly Ser Gly Ser Gly Gly Thr Thr
 20 25 30

Lys Tyr Phe Arg Ile Pro Ala Met Cys Thr Thr Ser Lys Gly Thr Ile
 35 40 45

Val Val Phe Ala Asp Ala Arg His Asn Thr Ala Ser Asp Gln Ser Phe
 50 55 60

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

Lys Lys Ile Ala Ile Tyr Asn Asp Arg Val Asn Ser Lys Leu Ser Arg
 85 90 95

Val Met Asp Pro Thr Cys Ile Val Ala Asn Ile Gln Gly Arg Glu Thr
 100 105 110

Ile Leu Val Met Val Gly Lys Trp Asn Asn Asn Asp Lys Thr Trp Gly
 115 120 125

Ala Tyr Arg Asp Lys Ala Pro Asp Thr Asp Trp Asp Leu Val Leu Tyr
 130 135 140

Lys Ser Thr Asp Asp Gly Val Thr Phe Ser Lys Val Glu Thr Asn Ile
 145 150 155 160

His Asp Ile Val Thr Lys Asn Gly Thr Ile Ser Ala Met Leu Gly Gly
 165 170 175

Val Gly Ser Gly Leu Gln Leu Asn Asp Gly Lys Leu Val Phe Pro Val
 180 185 190

Gln Met Val Arg Thr Lys Asn Ile Thr Thr Val Leu Asn Thr Ser Phe
 195 200 205

Ile Tyr Ser Thr Asp Gly Ile Thr Trp Ser Leu Pro Ser Gly Tyr Cys
 210 215 220

Glu Gly Phe Gly Ser Glu Asn Asn Ile Ile Glu Phe Asn Ala Ser Leu
 225 230 235 240

Val Asn Asn Ile Arg Asn Ser Gly Leu Arg Arg Ser Phe Glu Thr Lys
 245 250 255

Asp Phe Gly Lys Thr Trp Thr Glu Phe Pro Pro Met Asp Lys Lys Val
 260 265 270

Asp Asn Arg Asn His Gly Val Gln Gly Ser Thr Ile Thr Ile Pro Ser
 275 280 285

Gly Asn Lys Leu Val Ala Ala His Ser Ser Ala Gln Asn Lys Asn Asn
 290 295 300

Asp Tyr Thr Arg Ser Asp Ile Ser Leu Tyr Ala His Asn Leu Tyr Ser
 305 310 315 320

Gly Glu Val Lys Leu Ile Asp Asp Phe Tyr Pro Lys Val Gly Asn Ala
 325 330 335

Ser Gly Ala Gly Tyr Ser Cys Leu Ser Tyr Arg Lys Asn Val Asp Lys
 340 345 350

Glu Thr Leu Tyr Val Val Tyr Glu Ala Asn Gly Ser Ile Glu Phe Gln
 355 360 365

Asp Leu Ser Arg His Leu Pro Val Ile Lys Ser Tyr Asn Gly Gly Gly
 370 375 380

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
 385 390 395 400

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 405 410 415

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

420

425

430

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 435 440 445

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 450 455 460

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 465 470 475 480

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 485 490 495

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 500 505 510

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 515 520 525

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 530 535 540

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 545 550 555 560

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 565 570 575

Leu Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 580 585 590

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 595 600 605

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 91

<211> 1854

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 91

acagtggaaa agtccgtggt gttcaaggcc gagggcgagc acttcaccga ccagaaaggc	60
aataccatcg tcggctctgg cagcggcggc accaccaagt actttagaat ccccgccatg	120
tgcaccacca gcaagggcac cattgtggtg ttcgccgacg ccagacacaa caccgccagc	180
gatcagagct tcatcgatac cgctgccgcc agatctaccg atggcggcaa gacctggaac	240
aagaagatcg ccatctacaa cgaccgcgtg aacagcaagc tgagcagagt gatggaccct	300
acctgcatcg tggccaacat ccagggcaga gaaaccatcc tggatcatggt cggaaagtgg	360
aacaacaacg ataagacctg gggcgcctac agagacaagg cccctgatac cgattgggac	420
ctcgtgctgt acaagagcac cgatgacggc gtgaccttca gcaaggtgga aacaaacatc	480
cacgacatcg tgaccaagaa cggcaccatc tctgccatgc tcggcggcgt tggatctggc	540
ctgcaactga atgatggcaa gctggtgttc cccgtgcaga tgggtccgaac aaagaatatc	600
accaccgtgc tgaataccag cttcatctac agcaccgacg gcatcacatg gtccctgcct	660
agcggctact gtgaaggctt tggcagcgag aacaacatca tcgagttcaa cgccagcctg	720
gtcaacaaca tccggaacag cggcctgcgg agaagcttcg agacaaaagga cttcggaaag	780
acgtggaccg agtttctcc aatggacaag aaggtggaca accggaacca cggcgtgcag	840
ggcagcacia tcacaatccc tagcggcaac aaactggtgg ccgctcactc tagcgcccag	900
aacaagaaca acgactacac cagaagcgac atcagcctgt acgcccacia cctgtacagc	960
ggcgaagtga agctgatcga cgacttctac cccaaagtgg gcaatgccag cggagccggc	1020
tacagctgtc tgagctaccg gaaaaatgtg gacaaagaaa ccctgtacgt ggtgtacgag	1080
gccaacggca gcatcgagtt tcaggacctg agcagacatc tgcccgtgat caagagctac	1140
aacggcggag gtggaagtgg cggaggcggg tccgacaaaa ctacacatg cccaccgtgc	1200
ccagcacctg aactcctggg gggaccgtca gtcttctct tcccccaaa acccaaggac	1260
accctcatga tctcccggac ccctgaggtc acatgcgtgg tgggtggacgt gagccacgaa	1320
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca	1380
aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg	1440

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caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca      1500
gcccccatcg agaaaacccat ctccaaagcc aaagggcagc cccgagaacc acaggtctac      1560
accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc      1620
aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac      1680
aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttcct cactagcaag      1740
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat      1800
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaa          1854

```

<210> 92

<211> 846

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 92

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
          100             105             110

```

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

Phe Pro Leu Ala Pro 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 Glu Glu Met 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 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460

Ser Thr Val Glu Lys Ser Val Val Phe Lys Ala Glu Gly Glu His Phe
 465 470 475 480

Thr Asp Gln Lys Gly Asn Thr Ile Val Gly Ser Gly Ser Gly Gly Thr
 485 490 495

Thr Lys Tyr Phe Arg Ile Pro Ala Met Cys Thr Thr Ser Lys Gly Thr
 500 505 510

Ile Val Val Phe Ala Asp Ala Arg His Asn Thr Ala Ser Asp Gln Ser
 515 520 525

Phe Ile Asp Thr Ala Ala Ala Arg Ser Thr Asp Gly Gly Lys Thr Trp
 530 535 540

Asn Lys Lys Ile Ala Ile Tyr Asn Asp Arg Val Asn Ser Lys Leu Ser
 545 550 555 560

Arg Val Met Asp Pro Thr Cys Ile Val Ala Asn Ile Gln Gly Arg Glu
 565 570 575

Thr Ile Leu Val Met Val Gly Lys Trp Asn Asn Asn Asp Lys Thr Trp
 580 585 590

Gly Ala Tyr Arg Asp Lys Ala Pro Asp Thr Asp Trp Asp Leu Val Leu
 595 600 605

Tyr Lys Ser Thr Asp Asp Gly Val Thr Phe Ser Lys Val Glu Thr Asn
 610 615 620

Ile His Asp Ile Val Thr Lys Asn Gly Thr Ile Ser Ala Met Leu Gly
 625 630 635 640

Gly Val Gly Ser Gly Leu Gln Leu Asn Asp Gly Lys Leu Val Phe Pro
 645 650 655

Val Gln Met Val Arg Thr Lys Asn Ile Thr Thr Val Leu Asn Thr Ser
 660 665 670

Phe Ile Tyr Ser Thr Asp Gly Ile Thr Trp Ser Leu Pro Ser Gly Tyr
 675 680 685

Cys Glu Gly Phe Gly Ser Glu Asn Asn Ile Ile Glu Phe Asn Ala Ser
 690 695 700

Leu Val Asn Asn Ile Arg Asn Ser Gly Leu Arg Arg Ser Phe Glu Thr
 705 710 715 720

Lys Asp Phe Gly Lys Thr Trp Thr Glu Phe Pro Pro Met Asp Lys Lys
 725 730 735

Val Asp Asn Arg Asn His Gly Val Gln Gly Ser Thr Ile Thr Ile Pro
 740 745 750

Ser Gly Asn Lys Leu Val Ala Ala His Ser Ser Ala Gln Asn Lys Asn
 755 760 765

Asn Asp Tyr Thr Arg Ser Asp Ile Ser Leu Tyr Ala His Asn Leu Tyr
 770 775 780

Ser Gly Glu Val Lys Leu Ile Asp Asp Phe Tyr Pro Lys Val Gly Asn
 785 790 795 800

Ala Ser Gly Ala Gly Tyr Ser Cys Leu Ser Tyr Arg Lys Asn Val Asp
 805 810 815

Lys Glu Thr Leu Tyr Val Val Tyr Glu Ala Asn Gly Ser Ile Glu Phe
 820 825 830

Gln Asp Leu Ser Arg His Leu Pro Val Ile Lys Ser Tyr Asn
 835 840 845

<210> 93

<211> 2538

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 93

gaggtgcagc tggttgaatc tggcggagga ctggttcagc ctggcggatc tctgagactg	60
tcttgtgccg ccagcggcctt caacatcaag gacacctaca tccactgggt ccgacaggcc	120
cctggcaaag gacttgaatg ggtcgccaga atctaccca ccaacggcta caccagatac	180
gccgactctg tgaagggcag attcaccatc agcgccgaca ccagcaagaa caccgcctac	240
ctgcagatga acagcctgag agccgaggac accgccgtgt actactgttc tagatgggga	300
ggcgacggct tctacgcat ggattattgg ggccagggca ccctgggtcac cgtttcttct	360
gctagcacca agggcccatc cgtcttcccc ctggcaccct cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcc	480
tggaactcag gcgctctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660

aaatcttgtg	acaaaactca	cacatgccc	ccgtgcccag	cacctgaact	cctgggggga	720
ccgtcagtct	tcctcttccc	cccaaaaccc	aaggacaccc	tcattgatctc	ccggaccctt	780
gaggtcacat	gcgtgggtgt	ggacgtgagc	cacgaagacc	ctgaggtcaa	gttcaactgg	840
tacgtggacg	gcgtggaggt	gcataatgcc	aagacaaagc	cgcgaggagga	gcagtacaac	900
agcacgtacc	gtgtgggtcag	cgtcctcacc	gtcctgcacc	aggactggct	gaatggcaag	960
gagtacaagt	gcaaggtctc	caacaaagcc	ctcccagccc	ccatcgagaa	aaccatctcc	1020
aaagccaaag	ggcagccccg	agaaccacag	gtctacaccc	tgccccatc	ccgggaggag	1080
atgaccaaga	accaggtcag	cctgacctgc	ctgggtcaaag	gcttctatcc	cagcgacatc	1140
gccgtggagt	gggagagcaa	tgggcagccg	gagaacaact	acaagaccac	gcctcccgtg	1200
ctggactccg	acggctcctt	cttcctctat	agcaagctca	ccgtggacaa	gagcaggtgg	1260
cagcagggga	acgtcttctc	atgctccgtg	atgcatgagg	ctctgcacaa	ccactacacg	1320
cagaagagcc	tctccctgtc	tccgggtaaa	ggtggcggag	gatctggcgg	aggtggaagc	1380
ggcggaggcg	gatctacagt	ggaaaagtcc	gtggtgttca	aggccgaggg	cgagcacttc	1440
accgaccaga	aaggcaatac	catcgtcggc	tctggcagcg	gcggcaccac	caagtacttt	1500
agaatccccg	ccatgtgcac	caccagcaag	ggcaccattg	tggtgttcgc	cgacgccaga	1560
cacaacaccg	ccagcgatca	gagcttcatc	gataaccgtg	ccgccagaag	tacagacggc	1620
ggcaagacct	ggaacaagaa	gatcgccatc	tacaacgacc	gcgtgaacag	caagctgagc	1680
agagtgatgg	accctacctg	catcgtggcc	aacatccagg	gcagagaaac	catcctggtc	1740
atggtcggaa	agtggaacaa	caacgataag	acctggggcg	cctacagaga	caaggcccct	1800
gataccgatt	gggacctcgt	gctgtataag	agcaccgacg	acggcgtgac	cttcagcaag	1860
gtggaaacaa	acatccacga	catcgtgacc	aagaacggca	ccatctctgc	catgctcggc	1920
ggcgttggtg	ctggcctgca	actgaatgat	ggcaagctgg	tgttccccgt	gcagatggtc	1980
cgaacaaaga	acatcaccac	cgtgctgaat	accagcttca	tctactccac	cgacggcatc	2040
acatggtccc	tgcttagcgg	ctactgtgaa	ggctttggca	gcgagaacaa	catcatcgag	2100
ttcaacgcca	gcctgggtcaa	caacatccgg	aacagcggcc	tgcggagaag	cttcgagaca	2160
aaggacttcg	gaaagacgtg	gaccgagttt	cctccaatgg	acaagaaggt	ggacaaccgg	2220
aaccacggcg	tgcaaggcag	cacaatcaca	atccctagcg	gcaacaaact	ggtggccgct	2280

cactctagcg cccagaacaa gaacaacgat tacaccagaa gcgacatcag cctgtacgcc 2340
 cacaacctgt actccggcga agtgaagctg atcgacgact tctaccccaa agtgggcaat 2400
 gccagcggag ccggctacag ctgtctgagc taccggaaaa atgtggacaa agaaaccctg 2460
 tacgtggtgt acgaggccaa cggcagcatc gagtttcagg acctgagcag acatctgccc 2520
 gtgatcaaga gctacaat 2538

<210> 94

<211> 875

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 94

Thr Val Glu Lys Ser Val Val Phe Lys Ala Glu Gly Glu His Phe Thr
 1 5 10 15

Asp Gln Lys Gly Asn Thr Ile Val Gly Ser Gly Ser Gly Gly Thr Thr
 20 25 30

Lys Tyr Phe Arg Ile Pro Ala Met Cys Thr Thr Ser Lys Gly Thr Ile
 35 40 45

Val Val Phe Ala Asp Ala Arg His Asn Thr Ala Ser Asp Gln Ser Phe
 50 55 60

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

Lys Lys Ile Ala Ile Tyr Asn Asp Arg Val Asn Ser Lys Leu Ser Arg
 85 90 95

Val Met Asp Pro Thr Cys Ile Val Ala Asn Ile Gln Gly Arg Glu Thr
 100 105 110

Ile Leu Val Met Val Gly Lys Trp Asn Asn Asn Asp Lys Thr Trp Gly
 115 120 125

Ala Tyr Arg Asp Lys Ala Pro Asp Thr Asp Trp Asp Leu Val Leu Tyr

130

135

140

Lys Ser Thr Asp Asp Gly Val Thr Phe Ser Lys Val Glu Thr Asn Ile
 145 150 155 160

His Asp Ile Val Thr Lys Asn Gly Thr Ile Ser Ala Met Leu Gly Gly
 165 170 175

Val Gly Ser Gly Leu Gln Leu Asn Asp Gly Lys Leu Val Phe Pro Val
 180 185 190

Gln Met Val Arg Thr Lys Asn Ile Thr Thr Val Leu Asn Thr Ser Phe
 195 200 205

Ile Tyr Ser Thr Asp Gly Ile Thr Trp Ser Leu Pro Ser Gly Tyr Cys
 210 215 220

Glu Gly Phe Gly Ser Glu Asn Asn Ile Ile Glu Phe Asn Ala Ser Leu
 225 230 235 240

Val Asn Asn Ile Arg Asn Ser Gly Leu Arg Arg Ser Phe Glu Thr Lys
 245 250 255

Asp Phe Gly Lys Thr Trp Thr Glu Phe Pro Pro Met Asp Lys Lys Val
 260 265 270

Asp Asn Arg Asn His Gly Val Gln Gly Ser Thr Ile Thr Ile Pro Ser
 275 280 285

Gly Asn Lys Leu Val Ala Ala His Ser Ser Ala Gln Asn Lys Asn Asn
 290 295 300

Asp Tyr Thr Arg Ser Asp Ile Ser Leu Tyr Ala His Asn Leu Tyr Ser
 305 310 315 320

Gly Glu Val Lys Leu Ile Asp Asp Phe Tyr Pro Lys Val Gly Asn Ala
 325 330 335

Ser Gly Ala Gly Tyr Ser Cys Leu Ser Tyr Arg Lys Asn Val Asp Lys
 340 345 350

Glu Thr Leu Tyr Val Val Tyr Glu Ala Asn Gly Ser Ile Glu Phe Gln
 355 360 365

Asp Leu Ser Arg His Leu Pro Val Ile Lys Ser Tyr Asn Gly Gly Gly
 370 375 380

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
 385 390 395 400

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 405 410 415

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 420 425 430

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 435 440 445

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 450 455 460

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 465 470 475 480

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 485 490 495

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 500 505 510

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 515 520 525

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 530 535 540

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 545 550 555 560

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
770 775 780

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
785 790 795 800

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
805 810 815

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
820 825 830

Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
835 840 845

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
850 855 860

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
865 870 875

<210> 95

<211> 2625

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 95

```
acagtggaaa agtccgtggt gttcaaggcc gagggcgagc acttcaccga ccagaaaggc      60
aataccatcg tcggctctgg cagcggcggc accaccaagt actttagaat ccccgccatg      120
tgaccacca gcaagggcac cattgtggtg ttcgccgacg ccagacacaa caccgccagc      180
gatcagagct tcatcgatac cgctgccgcc agatctaccg atggcggcaa gacctggaac      240
aagaagatcg ccatctacaa cgaccgcgtg aacagcaagc tgagcagagt gatggaccct      300
acctgcatcg tggccaacat ccagggcaga gaaaccatcc tggatcatggt cggaagtgg      360
aacaacaacg ataagacctg gggcgcctac agagacaagg cccctgatac cgattgggac      420
ctcgtgctgt acaagagcac cgatgacggc gtgaccttca gcaaggtgga aacaacatc      480
cacgacatcg tgaccaagaa cggcaccatc tctgccatgc tcggcggcgt tggatctggc      540
ctgcaactga atgatggcaa gctggtgttc cccgtgcaga tgggtccgaac aaagaatatc      600
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accaccgtgc tgaataccag cttcatctac agcaccgacg gcatcacatg gtccctgcct	660
agcgggtact gtgaaggctt tggcagcgag aacaacatca tcgagttcaa cgccagcctg	720
gtcaacaaca tccggaacag cggcctgcgg agaagcttcg agacaaagga cttcggaaag	780
acgtggaccg agtttcctcc aatggacaag aaggtggaca accggaacca cggcgtgcag	840
ggcagcacia tcacaatccc tagcggcaac aaactggtgg ccgctcactc tagcgcccag	900
aacaagaaca acgactacac cagaagcgac atcagcctgt acgcccacia cctgtacagc	960
ggcgaagtga agctgatcga cgacttctac cccaaagtgg gcaatgccag cggagccggc	1020
tacagctgtc tgagctaccg gaaaaatgtg gacaaagaaa ccctgtacgt ggtgtacgag	1080
gccaacggca gcatcgagtt tcaggacctg agcagacatc tgcccgtgat caagagctac	1140
aacggcggag gtggaagtgg cggaggcgga tccgacaaaa ctacacatg cccaccgtgc	1200
ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac	1260
accctcatga tctcccgac ccctgaggtc acatgcgtgg tgggtggacgt gagccacgaa	1320
gacctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca	1380
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caccaggact ggctgaatgg caaggagtac aagtgcagg tctccaacia agccctccca	1500
gcccccatcg agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtctac	1560
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aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac	1680
aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttct ctatagcaag	1740
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat	1800
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaaggaggc	1860
ggaggatctg gcggaggtgg aagtggcgga ggcggatctg aggtgcagct ggttgaatct	1920
ggcggaggac tggttcagcc tggcggatct ctgagactgt cttgtgccgc cagcggcttc	1980
aacatcaagg acacctacat ccactgggtc cgacaggccc ctggcaaagg acttgaatgg	2040
gtcgccagaa tctacccac caacggctac accagatacg ccgactctgt gaagggcaga	2100
ttcaccatca gcgccgacac cagcaagaac accgcctacc tgcagatgaa cagcctgaga	2160
gccgaggaca ccgccgtgta ctactgttct agatggggag gcgacggctt ctacgccatg	2220

gattatttggg gccagggcac cctggtcacc gtttcttctg gcggaggagg atctggcgga 2280
 ggcggaagtg gcggaggcgg atctgacatc cagatgacac agagccctag cagcctgtct 2340
 gccagcgtgg gagacagagt gaccatcacc tgtagagcca gccaggacgt gaacacagcc 2400
 gtggcttggt atcagcagaa gcctggcaag gcccctaagc tgctgatcta cagcgccagc 2460
 tttctgtact ccggcgtgcc cagcagattc agcggctcta gaagcggcac cgacttcacc 2520
 ctgaccataa gcagtctgca gcccaggagac ttcgccacct actactgtca gcagcactac 2580
 accacacctc caacctttgg ccagggcacc aaggtggaaa tcaag 2625

<210> 96

<211> 618

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 96

Thr Val Glu Lys Ser Val Val Phe Lys Ala Glu Gly Glu His Phe Thr
 1 5 10 15

Asp Gln Lys Gly Asn Thr Ile Val Gly Ser Gly Ser Gly Gly Thr Thr
 20 25 30

Lys Tyr Phe Arg Ile Pro Ala Met Cys Thr Thr Ser Lys Gly Thr Ile
 35 40 45

Val Val Phe Ala Asp Ala Arg His Asn Thr Ala Ser Asp Gln Ser Phe
 50 55 60

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

Lys Lys Ile Ala Ile Tyr Asn Asp Arg Val Asn Ser Lys Leu Ser Arg
 85 90 95

Val Met Val Pro Thr Cys Ile Val Ala Asn Ile Gln Gly Arg Glu Thr
 100 105 110

Ile Leu Val Met Val Gly Lys Trp Asn Asn Asn Asp Lys Thr Trp Gly
 115 120 125

Ala Tyr Arg Asp Lys Ala Pro Asp Thr Asp Trp Asp Leu Val Leu Tyr
 130 135 140

Lys Ser Thr Asp Asp Gly Val Thr Phe Ser Lys Val Glu Thr Asn Ile
 145 150 155 160

His Asp Ile Val Thr Lys Asn Gly Thr Ile Ser Ala Met Leu Gly Gly
 165 170 175

Val Gly Ser Gly Leu Gln Leu Asn Asp Gly Lys Leu Val Phe Pro Val
 180 185 190

Gln Met Val Arg Thr Lys Asn Ile Thr Thr Val Leu Asn Thr Ser Phe
 195 200 205

Ile Tyr Ser Thr Asp Gly Ile Thr Trp Ser Leu Pro Ser Gly Tyr Cys
 210 215 220

Glu Gly Phe Gly Ser Val Asn Asn Ile Ile Glu Phe Asn Ala Ser Leu
 225 230 235 240

Val Asn Asn Ile Arg Asn Ser Gly Leu Arg Arg Ser Phe Glu Thr Lys
 245 250 255

Asp Phe Gly Lys Thr Trp Thr Glu Phe Pro Pro Met Asp Lys Lys Val
 260 265 270

Asp Asn Arg Asn His Gly Val Gln Gly Ser Thr Ile Thr Ile Pro Ser
 275 280 285

Gly Asn Lys Leu Val Ala Ala His Ser Ser Ala Gln Asn Lys Asn Asn
 290 295 300

Asp Tyr Thr Arg Ser Asp Ile Ser Leu Tyr Ala His Asn Leu Tyr Ser
 305 310 315 320

Gly Glu Val Lys Leu Ile Asp Asp Phe Tyr Pro Lys Val Gly Asn Ala
 325 330 335

Ser Gly Ala Gly Tyr Ser Cys Leu Ser Tyr Arg Lys Asn Val Asp Lys
 340 345 350

Glu Thr Leu Tyr Val Val Tyr Glu Ala Asn Gly Ser Ile Glu Phe Gln
 355 360 365

Asp Leu Ser Arg His Leu Pro Val Ile Lys Ser Tyr Asn Gly Gly Gly
 370 375 380

Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys
 385 390 395 400

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 405 410 415

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 420 425 430

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 435 440 445

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 450 455 460

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 465 470 475 480

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 485 490 495

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 500 505 510

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 515 520 525

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 530 535 540

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
545 550 555 560

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
565 570 575

Leu Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
580 585 590

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
595 600 605

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 97

<211> 1854

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 97

acagtggaaa agtccgtggt gttcaaggcc gagggcgagc acttcaccga ccagaaaggc	60
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tgcaccacca gcaagggcac cattgtggtg ttcgccgacg ccagacacaa caccgccagc	180
gatcagagct tcatcgatac cgctgccgcc agaagtacag acggcggcaa gacctggaac	240
aagaagatcg ccatctacaa cgaccgcgtg aacagcaagc tgagcagagt gatggtcctt	300
acctgcatcg tggccaacat ccagggcaga gaaaccatcc tggatcatggt cggaaagtgg	360
aacaacaacg ataagacctg gggcgcctac agagacaagg cccctgatac cgattgggac	420
ctcgtgctgt ataagagcac cgacgacggc gtgaccttca gcaaggtgga aacaaacatc	480
cacgacatcg tgaccaagaa cggcaccatc tctgccatgc tcggcggcgt tggatctggc	540
ctgcaactga atgatggcaa gctggtgttc cccgtgcaga tgggtccgaac aaagaacatc	600
accaccgtgc tgaataccag cttcatctac tccaccgacg gcatcacatg gtccctgcct	660
agcggctact gtgaaggctt tggcagcgtg aacaacatca tcgagttcaa cgccagcctg	720

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gtcaacaaca tccggaacag cggcctgcgg agaagcttcg agacaaagga cttcggaaag      780
acgtggaccg agtttcctcc aatggacaag aaggtggaca accggaacca cggcgtgcag      840
ggcagcacia tcacaatccc tagcggcaac aaactggtgg ccgctcactc tagcgcccag      900
aacaagaaca acgattacac cagaagcgac atcagcctgt acgcccacaa cctgtactcc      960
ggcgaagtga agctgatcga cgacttctac cccaaagtgg gcaatgccag cggagccggc     1020
tacagctgtc tgagctaccg gaaaaatgtg gacaaagaaa ccctgtacgt ggtgtacgag     1080
gccaacggca gcatcgagtt tcaggacctg agcagacatc tgcccgtgat caagagctac     1140
aatggcggag gtggaagtgg cggaggcgga tccgacaaaa ctacacatg cccaccgtgc     1200
ccagcacctg aactcctggg gggaccgtca gtcttctct tcccccaaa acccaaggac     1260
accctcatga tctcccggac ccctgaggtc acatgcgtgg tgggtggacgt gagccacgaa     1320
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca     1380
aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg     1440
caccaggact ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca     1500
gcccccatcg agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtctac     1560
accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc     1620
aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagAAC     1680
aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttct cactagcaag     1740
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat     1800
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaa          1854

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<210> 98

<211> 611

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 98

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

```

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His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln Ser

```

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

Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln Glu
 245 250 255

Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys Gln
 260 265 270

Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser Pro
 275 280 285

Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg Ala
 290 295 300

Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala Trp
 305 310 315 320

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

Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys Leu
 340 345 350

Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr Leu
 355 360 365

Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser Ser
 370 375 380

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 385 390 395 400

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

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 420 425 430

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 435 440 445

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

450

455

460

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 465 470 475 480

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 485 490 495

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 500 505 510

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 515 520 525

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 530 535 540

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 545 550 555 560

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr Val
 565 570 575

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 580 585 590

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 595 600 605

Pro Gly Lys
 610

<210> 99

<211> 611

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 99

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

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

Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu Arg
 225 230 235 240

Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln Glu
 245 250 255

Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys Gln
 260 265 270

Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser Pro
 275 280 285

Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg Ala
 290 295 300

Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala Trp
 305 310 315 320

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

Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys Leu
 340 345 350

Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr Leu
 355 360 365

Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser Ser
 370 375 380

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 385 390 395 400

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

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 420 425 430

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

435

440

445

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

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 465 470 475 480

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 485 490 495

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 500 505 510

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 515 520 525

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 530 535 540

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 545 550 555 560

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr Val
 565 570 575

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 580 585 590

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 595 600 605

Pro Gly Lys
 610

<210> 100

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 100

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser

420

425

430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 101

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 101

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu

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

<210> 102

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 102

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

Ala	His	Ala	Tyr	Arg	Ile	Pro	Ala	Leu	Leu	Tyr	Leu	Pro	Gly	Gln	Gln
			20					25					30		

Ser	Leu	Leu	Ala	Phe	Ala	Glu	Gln	Arg	Ala	Ser	Lys	Lys	Asp	Glu	His
		35					40					45			

Ala	Glu	Leu	Ile	Val	Leu	Arg	Arg	Gly	Asp	Tyr	Asp	Ala	Pro	Thr	His
	50					55					60				

Gln	Val	Gln	Trp	Gln	Ala	Gln	Glu	Val	Val	Ala	Gln	Ala	Arg	Leu	Asp
65					70					75					80

Gly	His	Arg	Ser	Met	Asn	Pro	Cys	Pro	Leu	Tyr	Asp	Ala	Gln	Thr	Gly
				85					90					95	

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

Gln	Gln	Leu	Gln	Thr	Arg	Ala	Asn	Val	Thr	Arg	Leu	Cys	Gln	Val	Thr
		115					120					125			

Ser	Thr	Asp	His	Gly	Arg	Thr	Trp	Ser	Ser	Pro	Arg	Asp	Leu	Thr	Asp
	130					135					140				

Ala	Ala	Ile	Gly	Pro	Ala	Tyr	Arg	Glu	Trp	Ser	Thr	Phe	Ala	Val	Gly
145					150					155					160

Pro	Gly	His	Cys	Leu	Gln	Leu	His	Asp	Arg	Ala	Arg	Ser	Leu	Val	Val
				165					170					175	

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

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

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu

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

Ser Pro Gly Lys
610

<210> 103

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 103

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

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

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser

370

375

380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

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<210> 104
<211> 612
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 104
Met Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

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

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 105

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 105

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys

340

345

350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 106

<211> 612

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 106

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 107

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 107

Asp Ala Ser Leu Pro Tyr Leu Gln Asp Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

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

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 108

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 108

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg

290

295

300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 109

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 109

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 110

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 110

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Ser Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

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

260	265	270
Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser		
275	280	285
Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg		
290	295	300
Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala		
305	310	315
Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp		
325	330	335
Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys		
340	345	350
Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr		
355	360	365
Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser		
370	375	380
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu		
385	390	395
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu		
405	410	415
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser		
420	425	430
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu		
435	440	445
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr		
450	455	460
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn		
465	470	475
		480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

 $\langle 210 \rangle$ 111

<211> 612

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic polypeptide

 $\langle 400 \rangle$ 111

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Thr Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln

Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
450						455					460				

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 112

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 112

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu

225					230					235					240	
Arg	Ala	Arg	Val	Gln	Ala	Gln	Ser	Thr	Asn	Asp	Gly	Leu	Asp	Phe	Gln	
				245					250					255		
Glu	Ser	Gln	Leu	Val	Lys	Lys	Leu	Val	Glu	Pro	Pro	Pro	Ala	Gly	Cys	
				260					265					270		
Gln	Gly	Ser	Val	Ile	Ser	Phe	Pro	Ser	Pro	Arg	Ser	Gly	Pro	Gly	Ser	
				275					280					285		
Pro	Ala	Gln	Trp	Leu	Leu	Tyr	Thr	His	Pro	Thr	His	Arg	Lys	Gln	Arg	
				290					295					300		
Ala	Asp	Leu	Gly	Ala	Tyr	Leu	Asn	Pro	Arg	Pro	Pro	Ala	Pro	Glu	Ala	
				305					310					315		
Trp	Ser	Glu	Pro	Val	Leu	Leu	Ala	Lys	Gly	Ser	Ala	Ala	Tyr	Ser	Asp	
				325					330					335		
Leu	Gln	Ser	Met	Gly	Thr	Gly	Pro	Asp	Gly	Ser	Pro	Leu	Phe	Gly	Cys	
				340					345					350		
Leu	Tyr	Glu	Ala	Asn	Asp	Tyr	Glu	Glu	Ile	Val	Phe	Leu	Met	Phe	Thr	
				355					360					365		
Leu	Lys	Gln	Ala	Phe	Pro	Ala	Glu	Tyr	Leu	Pro	Gln	Glu	Pro	Lys	Ser	
				370					375					380		
Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	
				385					390					395		
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	
				405					410					415		
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	
				420					425					430		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	
				435					440					445		

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 113

<211> 616

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 113

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

His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln Ser
 20 25 30

Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His Ala
 35 40 45

Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His Gln
 50 55 60

Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp Gly
 65 70 75 80

His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly Thr
 85 90 95

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

Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr Ser
 115 120 125

Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp Ala
 130 135 140

Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly Pro
 145 150 155 160

Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val Pro
 165 170 175

Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro Ser
 180 185 190

Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg Gly
 195 200 205

His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val Glu

210

215

220

Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu Arg
 225 230 235 240

Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln Glu
 245 250 255

Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys Gln
 260 265 270

Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser Pro
 275 280 285

Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg Ala
 290 295 300

Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala Trp
 305 310 315 320

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

Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys Leu
 340 345 350

Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr Leu
 355 360 365

Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly Ser
 370 375 380

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 385 390 395 400

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

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 420 425 430

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 435 440 445

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 450 455 460

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 465 470 475 480

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 485 490 495

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 500 505 510

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 515 520 525

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 530 535 540

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 545 550 555 560

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 565 570 575

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 580 585 590

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 595 600 605

Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 114

<211> 616

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 114

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

His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln Ser
 20 25 30

Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His Ala
 35 40 45

Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His Gln
 50 55 60

Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp Gly
 65 70 75 80

His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly Thr
 85 90 95

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

Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr Ser
 115 120 125

Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp Ala
 130 135 140

Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly Pro
 145 150 155 160

Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val Pro
 165 170 175

Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro Ser
 180 185 190

Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg Gly

195	200	205
His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val Glu 210 215 220		
Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu Arg 225 230 235 240		
Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln Glu 245 250 255		
Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys Gln 260 265 270		
Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser Pro 275 280 285		
Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg Ala 290 295 300		
Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala Trp 305 310 315 320		
Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp Leu 325 330 335		
Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys Leu 340 345 350		
Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr Leu 355 360 365		
Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly Ser 370 375 380		
Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala 385 390 395 400		
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro 405 410 415		

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 420 425 430

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 435 440 445

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 450 455 460

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 465 470 475 480

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 485 490 495

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 500 505 510

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 515 520 525

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 530 535 540

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 545 550 555 560

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 565 570 575

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 580 585 590

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 595 600 605

Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 115

<211> 617
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 115

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys

610

615

<210> 116

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 116

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val

165	170	175
Pro Ala Tyr 180	Ala Tyr Arg Lys Leu His 185	Pro Lys Gln Arg Pro Ile Pro 190
Ser Ala Phe 195	Cys Phe Leu Ser His Asp His 200	Gly Arg Thr Trp Ala Arg 205
Gly His Phe 210	Val Ala Gln Asp Thr Leu Glu Cys 215	Gln Val Ala Glu Val 220
Glu Thr Gly 225	Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu 230	235 240
Arg Ala Arg 245	Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln 250	255
Glu Ser Gln 260	Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys 265	270
Gln Gly Ser 275	Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser 280	285
Pro Ala Gln 290	Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg 295	300
Ala Asp Leu 305	Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala 310	315 320
Trp Ser Glu 325	Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp 330	335
Leu Gln Ser 340	Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys 345	350
Leu Tyr Glu 355	Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr 360	365
Leu Lys Gln 370	Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly 375	380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

595

600

605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 117

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 117

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly

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

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val

580

585

590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 118

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 118

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp

130

135

140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

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

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu

565

570

575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 119

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 119

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr

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

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

545 550 555 560
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615
 <210> 120
 <211> 617
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide
 <400> 120
 Met Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
 1 5 10 15
 Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30
 Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45
 Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60
 Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80
 Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95
 Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln

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

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

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

530

535

540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 121

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 121

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly

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

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

515 520 525
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615
 <210> 122
 <211> 617
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide
 <400> 122
 Asp Ala Ser Leu Pro Tyr Leu Gln Asp Glu Ser Val Phe Gln Ser Gly
 1 5 10 15
 Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30
 Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45
 Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60
 Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp

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

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Arg Phe Ile Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

500

505

510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 123

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 123

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His

50

55

60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

485

490

495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 124

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 124

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His

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

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His

465 470 475 480
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615
 <210> 125
 <211> 617
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide
 <400> 125
 Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
 1 5 10 15
 Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln

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

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu

450

455

460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 126

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 126

Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly

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

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

435

440

445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 127

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 127

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

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

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

<210> 128

<211> 611

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 128

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

His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln Ser
20 25 30

Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His Ala
35 40 45

Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His Gln
50 55 60

Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp Gly
65 70 75 80

His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly Thr
85 90 95

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

Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr Ser
115 120 125

Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp Ala
130 135 140

Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly Pro
145 150 155 160

Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val Pro
165 170 175

Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro Ser
180 185 190

Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg Gly
 195 200 205

His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val Glu
 210 215 220

Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu Arg
 225 230 235 240

Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln Glu
 245 250 255

Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys Gln
 260 265 270

Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser Pro
 275 280 285

Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg Ala
 290 295 300

Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala Trp
 305 310 315 320

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

Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys Leu
 340 345 350

Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr Leu
 355 360 365

Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser Ser
 370 375 380

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 385 390 395 400

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

415

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
420 425 430

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
435 440 445

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

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
465 470 475 480

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
485 490 495

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
500 505 510

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
515 520 525

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
530 535 540

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
545 550 555 560

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
565 570 575

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
580 585 590

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
595 600 605

Pro Gly Lys
610

<210> 129

<211> 611

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 129

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

His	Ala	Tyr	Arg	Ile	Pro	Ala	Leu	Leu	Tyr	Leu	Pro	Gly	Gln	Gln	Ser
			20					25					30		

Leu	Leu	Ala	Phe	Ala	Glu	Gln	Arg	Ala	Ser	Lys	Lys	Asp	Glu	His	Ala
		35					40					45			

Glu	Leu	Ile	Val	Leu	Arg	Arg	Gly	Asp	Tyr	Asp	Ala	Pro	Thr	His	Gln
	50					55					60				

Val	Gln	Trp	Gln	Ala	Gln	Glu	Val	Val	Ala	Gln	Ala	Arg	Leu	Asp	Gly
65					70					75					80

His	Arg	Ser	Met	Asn	Pro	Cys	Pro	Leu	Tyr	Asp	Ala	Gln	Thr	Gly	Thr
				85					90					95	

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

Gln	Leu	Gln	Thr	Arg	Ala	Asn	Val	Thr	Arg	Leu	Cys	Gln	Val	Thr	Ser
		115					120					125			

Thr	Asp	His	Gly	Arg	Thr	Trp	Ser	Ser	Pro	Arg	Asp	Leu	Thr	Asp	Ala
	130					135					140				

Ala	Ile	Gly	Pro	Ala	Tyr	Arg	Glu	Trp	Ser	Thr	Phe	Ala	Val	Gly	Pro
145					150					155					160

Gly	His	Cys	Leu	Gln	Leu	His	Asp	Arg	Ala	Arg	Ser	Leu	Val	Val	Pro
				165					170					175	

Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro Ser
 180 185 190

Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg Gly
 195 200 205

His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val Glu
 210 215 220

Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu Arg
 225 230 235 240

Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln Glu
 245 250 255

Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys Gln
 260 265 270

Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser Pro
 275 280 285

Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg Ala
 290 295 300

Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala Trp
 305 310 315 320

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

Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys Leu
 340 345 350

Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr Leu
 355 360 365

Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser Ser
 370 375 380

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

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

Pro Gly Lys
610

<210> 130

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 130

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser

370

375

380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

```
<210> 131
<211> 612
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 131
Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 132

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 132

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

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

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys

340

345

350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 133

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 133

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Cys Ala Tyr Ser Asp

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 134

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 134

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

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

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 135

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 135

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg

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

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 136

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 136

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 137

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 137

Asp Ala Ser Leu Pro Tyr Leu Gln Asp Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

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

260					265					270					
Gln	Gly	Ser	Val	Ile	Ser	Phe	Pro	Ser	Pro	Arg	Ser	Gly	Pro	Gly	Ser
		275					280					285			
Pro	Ala	Gln	Trp	Leu	Leu	Tyr	Thr	His	Pro	Thr	His	Ser	Trp	Gln	Arg
	290					295					300				
Ala	Asp	Leu	Gly	Ala	Tyr	Leu	Asn	Pro	Arg	Pro	Pro	Ala	Pro	Glu	Ala
305					310					315					320
Trp	Ser	Glu	Pro	Val	Leu	Leu	Ala	Lys	Gly	Ser	Ala	Ala	Tyr	Ser	Asp
				325					330					335	
Leu	Gln	Ser	Met	Gly	Thr	Gly	Pro	Asp	Gly	Ser	Pro	Leu	Phe	Gly	Cys
			340					345						350	
Leu	Tyr	Glu	Ala	Asn	Asp	Tyr	Glu	Glu	Ile	Arg	Phe	Ile	Met	Phe	Thr
		355					360						365		
Leu	Lys	Gln	Ala	Phe	Pro	Ala	Glu	Tyr	Leu	Pro	Gln	Glu	Pro	Lys	Ser
	370					375					380				
Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
385					390					395					400
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
				405					410					415	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
			420					425					430		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
		435					440					445			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
		450				455					460				
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
465					470					475					480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 138

<211> 612

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 138

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln

	245		250		255
Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys	260	265	270		
Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser	275	280	285		
Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg	290	295	300		
Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala	305	310	315		320
Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp	325	330	335		
Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys	340	345	350		
Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr	355	360	365		
Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser	370	375	380		
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu	385	390	395		400
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu	405	410	415		
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser	420	425	430		
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu	435	440	445		
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr	450	455	460		

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 139

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 139

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu

225					230					235					240	
Arg	Ala	Arg	Val	Gln	Ala	Gln	Ser	Thr	Asn	Asp	Gly	Leu	Asp	Phe	Gln	
				245					250					255		
Glu	Ser	Gln	Leu	Val	Lys	Lys	Leu	Val	Glu	Pro	Pro	Pro	Ala	Gly	Cys	
				260					265					270		
Gln	Gly	Ser	Val	Ile	Ser	Phe	Pro	Ser	Pro	Arg	Ser	Gly	Pro	Gly	Ser	
				275					280					285		
Pro	Ala	Gln	Trp	Leu	Leu	Tyr	Thr	His	Pro	Thr	His	Arg	Lys	Gln	Arg	
				290					295					300		
Ala	Asp	Leu	Gly	Ala	Tyr	Leu	Asn	Pro	Arg	Pro	Pro	Ala	Pro	Glu	Ala	
				305					310					315		
Trp	Ser	Glu	Pro	Val	Leu	Leu	Ala	Lys	Gly	Ser	Ala	Ala	Tyr	Ser	Asp	
				325					330					335		
Leu	Gln	Ser	Met	Gly	Thr	Gly	Pro	Asp	Gly	Ser	Pro	Leu	Phe	Gly	Cys	
				340					345					350		
Leu	Tyr	Glu	Ala	Asn	Asp	Tyr	Glu	Glu	Ile	Val	Phe	Leu	Met	Phe	Thr	
				355					360					365		
Leu	Lys	Gln	Ala	Phe	Pro	Ala	Glu	Tyr	Leu	Pro	Gln	Glu	Pro	Lys	Ser	
				370					375					380		
Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	
				385					390					395		
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	
				405					410					415		
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	
				420					425					430		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	
				435					440					445		

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 140

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 140

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Ser Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val

210	215	220
Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu 225 230 235 240		
Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln 245 250 255		
Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys 260 265 270		
Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser 275 280 285		
Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg 290 295 300		
Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala 305 310 315 320		
Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp 325 330 335		
Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys 340 345 350		
Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr 355 360 365		
Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser 370 375 380		
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 385 390 395 400		
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu 405 410 415		
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser 420 425 430		

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 141

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 141

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Thr Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg

195	200	205
Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val 210 215 220		
Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu 225 230 235 240		
Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln 245 250 255		
Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys 260 265 270		
Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser 275 280 285		
Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg 290 295 300		
Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala 305 310 315 320		
Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp 325 330 335		
Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys 340 345 350		
Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr 355 360 365		
Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser 370 375 380		
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 385 390 395 400		
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu 405 410 415		

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 142

<211> 612
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 142

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro

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

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys

610

<210> 143
 <211> 617
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<220>
 <221> MOD_RES
 <222> (1)..(1)
 <223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr, Val, or not present

<220>
 <221> MOD_RES
 <222> (6)..(6)
 <223> Phe, Trp, Tyr or Val

<220>
 <221> MOD_RES
 <222> (9)..(9)
 <223> Lys or Asp

<220>
 <221> MOD_RES
 <222> (62)..(62)
 <223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
 <221> MOD_RES
 <222> (93)..(93)
 <223> Ala, Glu, or Lys

<220>
 <221> MOD_RES
 <222> (187)..(187)
 <223> Arg, Ile, or Lys

<220>
 <221> MOD_RES
 <222> (270)..(270)
 <223> Gln, Ala, His, Phe, or Pro

<220>
 <221> MOD_RES
 <222> (301)..(301)
 <223> Ser or Arg

<220>
 <221> MOD_RES
 <222> (302)..(302)
 <223> Trp or Lys

<220>
 <221> MOD_RES
 <222> (332)..(332)
 <223> Ala, Cys, Ser, or Val

<220>
 <221> MOD_RES
 <222> (363)..(363)
 <223> Val or Arg

<220>
 <221> MOD_RES
 <222> (365)..(365)
 <223> Leu, Gln, His, Ile, Lys, or Ser

<220>
 <221> MOD_RES
 <222> (381)..(390)
 <223> This region may encompass one of the following sequences:
 "GGGGSGGGGS" or "EPKSS"

<400> 143
 Xaa Ala Ser Leu Pro Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 144

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<220>

<221> MOD_RES

<222> (1)..(1)

<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr,
 Val, or not present

<220>

<221> MOD_RES

<222> (2)..(2)

<223> Ala or Lys

<220>

<221> MOD_RES

<222> (4)..(4)

<223> Asn or Leu

<220>

<221> MOD_RES

<222> (5)..(5)

<223> Pro or His

<220>

<221> MOD_RES

<222> (6)..(6)
 <223> Phe, Trp, Tyr or Val

<220>
 <221> MOD_RES
 <222> (9)..(9)
 <223> Lys or Asp

<220>
 <221> MOD_RES
 <222> (44)..(44)
 <223> Lys, Arg, or Glu

<220>
 <221> MOD_RES
 <222> (45)..(45)
 <223> Lys, Ala, Arg, or Glu

<220>
 <221> MOD_RES
 <222> (54)..(54)
 <223> Leu or Met

<220>
 <221> MOD_RES
 <222> (62)..(62)
 <223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
 <221> MOD_RES
 <222> (69)..(69)
 <223> Gln or His

<220>
 <221> MOD_RES
 <222> (78)..(78)
 <223> Arg or Lys

<220>
 <221> MOD_RES
 <222> (93)..(93)
 <223> Ala, Glu or Lys

<220>
 <221> MOD_RES
 <222> (107)..(107)
 <223> Gly or Asp

<220>
 <221> MOD_RES
 <222> (108)..(108)
 <223> Gln or His

<220>

<221> MOD_RES
<222> (112)..(112)
<223> Gln, Arg, or Lys

<220>
<221> MOD_RES
<222> (125)..(125)
<223> Ala, Cys, Ile, Ser, Val, or Leu

<220>
<221> MOD_RES
<222> (126)..(126)
<223> Gln or Leu

<220>
<221> MOD_RES
<222> (150)..(150)
<223> Ala or Val

<220>
<221> MOD_RES
<222> (164)..(164)
<223> Cys or Gly

<220>
<221> MOD_RES
<222> (171)..(171)
<223> Ala or Gly

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Arg, Ile, or Lys

<220>
<221> MOD_RES
<222> (196)..(196)
<223> Ala, Cys, Leu, or Val

<220>
<221> MOD_RES
<222> (217)..(217)
<223> Leu, Ala, or Val

<220>
<221> MOD_RES
<222> (249)..(249)
<223> Thr or Ala

<220>
<221> MOD_RES
<222> (251)..(251)
<223> Asp or Gly

<220>
<221> MOD_RES
<222> (257)..(257)
<223> Glu or Lys

<220>
<221> MOD_RES
<222> (270)..(270)
<223> Gln, Ala, His, Phe, or Pro

<220>
<221> MOD_RES
<222> (272)..(272)
<223> Cys or Val

<220>
<221> MOD_RES
<222> (292)..(292)
<223> Trp or Arg

<220>
<221> MOD_RES
<222> (301)..(301)
<223> Ser or Arg

<220>
<221> MOD_RES
<222> (302)..(302)
<223> Trp or Lys

<220>
<221> MOD_RES
<222> (325)..(325)
<223> Lys or Val

<220>
<221> MOD_RES
<222> (332)..(332)
<223> Ala, Cys, Ser, or Val

<220>
<221> MOD_RES
<222> (352)..(352)
<223> Cys, Leu, or Val

<220>
<221> MOD_RES
<222> (363)..(363)
<223> Val or Arg

<220>
<221> MOD_RES
<222> (365)..(365)
<223> Leu, Gln, His, Ile, Lys, or Ser

<220>

<221> MOD_RES

<222> (381)..(390)

<223> This region may encompass one of the following sequences:
"GGGGSGGGGS" or "EPKSS"

<400> 144

Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Xaa Xaa Asp Glu His
35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Xaa Leu Gln Leu His Asp Arg Xaa Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
 245 250 255

Xaa Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Xaa
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Xaa Xaa Xaa
 370 375 380

Xaa Xaa Xaa Xaa Xaa Xaa Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 145
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 145
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10

<210> 146
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 146
 Glu Pro Lys Ser Ser
 1 5

<210> 147
 <211> 232
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 147
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
130 135 140

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

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

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 148

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 148

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 100 105 110

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

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 130 135 140

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

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

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 210 215 220

Pro Gly Lys
 225

<210> 149
 <211> 380
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 149
 Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ala Arg Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 150

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 150

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ala Arg Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 151

<211> 612

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 151

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ala Arg Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 152

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 152

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ala Arg Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 153

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 153

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ala Arg Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 154

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 154

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 155

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 155

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 156

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 156

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 157

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 157

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 158

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 158

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 159

<211> 380

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 159

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 160

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 160

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 161

<211> 612

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 161

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
435 440 445

Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
450						455					460				

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 162

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 162

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 163

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 163

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 164

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<221> MOD_RES

<222> (1)..(1)

<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr, Val, or not present

<220>

<221> MOD_RES

<222> (6)..(6)

<223> Phe, Trp, Tyr or Val

<220>

<221> MOD_RES

<222> (9)..(9)

<223> Lys or Asp

<220>

<221> MOD_RES

<222> (62)..(62)

<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>

<221> MOD_RES

<222> (93)..(93)

<223> Ala, Glu, or Lys

<220>

<221> MOD_RES

<222> (126)..(126)

<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>

<221> MOD_RES

<222> (187)..(187)

<223> Arg, Ile, or Lys

<220>

<221> MOD_RES

<222> (242)..(242)

<223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser, Val, Trp, or Tyr

<220>

<221> MOD_RES

<222> (270)..(270)

<223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>

<221> MOD_RES
 <222> (301)..(301)
 <223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
 Pro, Gln, Thr, Val, Trp, or Tyr

<220>
 <221> MOD_RES
 <222> (302)..(302)
 <223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
 Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>
 <221> MOD_RES
 <222> (332)..(332)
 <223> Ala, Cys, Ser, or Val

<220>
 <221> MOD_RES
 <222> (363)..(363)
 <223> Val or Arg

<220>
 <221> MOD_RES
 <222> (365)..(365)
 <223> Leu, Gln, His, Ile, Lys, or Ser

<220>
 <221> MOD_RES
 <222> (381)..(390)
 <223> This region may encompass one of the following sequences:
 "GGGGS" or "GGGSGGGGS" or "EPKSS"

<400> 164
 Xaa Ala Ser Leu Pro Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly

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

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Xaa Xaa Xaa
 370 375 380

Xaa Xaa Xaa Xaa Xaa Xaa Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

515

520

525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 165

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<221> MOD_RES

<222> (1)..(1)

<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr, Val, or not present

<220>

<221> MOD_RES

<222> (2)..(2)

<223> Ala or Lys

<220>

<221> MOD_RES

<222> (4)..(4)

<223> Asn or Leu

<220>

<221> MOD_RES
<222> (5)..(5)
<223> Pro or His

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe, Trp, Tyr or Val

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Lys or Asp

<220>
<221> MOD_RES
<222> (44)..(44)
<223> Lys, Arg, or Glu

<220>
<221> MOD_RES
<222> (45)..(45)
<223> Lys, Ala, Arg, or Glu

<220>
<221> MOD_RES
<222> (54)..(54)
<223> Leu or Met

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
<221> MOD_RES
<222> (69)..(69)
<223> Gln or His

<220>
<221> MOD_RES
<222> (78)..(78)
<223> Arg or Lys

<220>
<221> MOD_RES
<222> (80)..(80)
<223> Asp or Pro

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Ala, Glu or Lys

<220>
<221> MOD_RES
<222> (107)..(107)
<223> Gly or Asp

<220>
<221> MOD_RES
<222> (108)..(108)
<223> Gln or His

<220>
<221> MOD_RES
<222> (112)..(112)
<223> Gln, Arg, or Lys

<220>
<221> MOD_RES
<222> (125)..(125)
<223> Ala, Cys, Ile, Ser, Val, or Leu

<220>
<221> MOD_RES
<222> (126)..(126)
<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>
<221> MOD_RES
<222> (150)..(150)
<223> Ala or Val

<220>
<221> MOD_RES
<222> (164)..(164)
<223> Cys or Gly

<220>
<221> MOD_RES
<222> (170)..(170)
<223> Arg or Pro

<220>
<221> MOD_RES
<222> (171)..(171)
<223> Ala or Gly

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Arg, Ile, or Lys

<220>
<221> MOD_RES
<222> (188)..(188)
<223> Gln or Pro

<220>
 <221> MOD_RES
 <222> (189)..(189)
 <223> Arg or Pro

<220>
 <221> MOD_RES
 <222> (196)..(196)
 <223> Ala, Cys, Leu, or Val

<220>
 <221> MOD_RES
 <222> (213)..(213)
 <223> Ala, Cys, Asn, Ser, or Thr

<220>
 <221> MOD_RES
 <222> (217)..(217)
 <223> Leu, Ala, or Val

<220>
 <221> MOD_RES
 <222> (225)..(225)
 <223> Glu or Pro

<220>
 <221> MOD_RES
 <222> (239)..(239)
 <223> His or Pro

<220>
 <221> MOD_RES
 <222> (240)..(240)
 <223> Leu, Asp, Asn, or Tyr

<220>
 <221> MOD_RES
 <222> (241)..(241)
 <223> Arg, Ala, Asp, Leu, Gln, or Tyr

<220>
 <221> MOD_RES
 <222> (242)..(242)
 <223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser,
 Val, Trp, or Tyr

<220>
 <221> MOD_RES
 <222> (244)..(244)
 <223> Val, Ile, or Lys

<220>
 <221> MOD_RES

<222> (249)..(249)
 <223> Thr or Ala

<220>
 <221> MOD_RES
 <222> (251)..(251)
 <223> Asp or Gly

<220>
 <221> MOD_RES
 <222> (257)..(257)
 <223> Glu, Lys, or Pro

<220>
 <221> MOD_RES
 <222> (258)..(258)
 <223> Ser or Cys

<220>
 <221> MOD_RES
 <222> (260)..(260)
 <223> Leu, Asp, Phe, Gln, or Thr

<220>
 <221> MOD_RES
 <222> (265)..(265)
 <223> Val or Phe

<220>
 <221> MOD_RES
 <222> (270)..(270)
 <223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>
 <221> MOD_RES
 <222> (272)..(272)
 <223> Cys or Val

<220>
 <221> MOD_RES
 <222> (292)..(292)
 <223> Trp or Arg

<220>
 <221> MOD_RES
 <222> (301)..(301)
 <223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
 Pro, Gln, Thr, Val, Trp, or Tyr

<220>
 <221> MOD_RES
 <222> (302)..(302)
 <223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
 Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>
 <221> MOD_RES
 <222> (325)..(325)
 <223> Lys or Val

<220>
 <221> MOD_RES
 <222> (332)..(332)
 <223> Ala, Cys, Ser, or Val

<220>
 <221> MOD_RES
 <222> (352)..(352)
 <223> Cys, Leu, or Val

<220>
 <221> MOD_RES
 <222> (363)..(363)
 <223> Val or Arg

<220>
 <221> MOD_RES
 <222> (365)..(365)
 <223> Leu, Gln, His, Ile, Lys, or Ser

<220>
 <221> MOD_RES
 <222> (381)..(390)
 <223> This region may encompass one of the following sequences:
 "GGGGS" or "GGGGSGGGGS" or "EPKSS"

<400> 165
 Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Xaa Xaa Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
 50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Xaa
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly

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

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Xaa Xaa Xaa
 370 375 380

Xaa Xaa Xaa Xaa Xaa Xaa Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

515 520 525
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575
 Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615
 <210> 166
 <211> 874
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide
 <400> 166
 Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
 1 5 10 15
 Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30
 Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45
 Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60
 Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp

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

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ala Arg Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

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

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
 725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
 785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 805 810 815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 820 825 830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
 850 855 860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 865 870

<210> 167

<211> 874

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 167

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu

225					230					235					240
Arg	Ala	Arg	Val	Gln	Ala	Gln	Ser	Thr	Asn	Asp	Gly	Leu	Asp	Phe	Gln
				245					250					255	
Glu	Ser	Gln	Leu	Val	Lys	Lys	Leu	Val	Glu	Pro	Pro	Pro	Thr	Gly	Cys
			260					265					270		
Gln	Gly	Ser	Val	Ile	Ser	Phe	Pro	Ser	Pro	Arg	Ser	Gly	Pro	Gly	Ser
		275					280					285			
Pro	Ala	Gln	Trp	Leu	Leu	Tyr	Thr	His	Pro	Thr	His	Ser	Trp	Gln	Arg
	290					295					300				
Ala	Asp	Leu	Gly	Ala	Tyr	Leu	Asn	Pro	Arg	Pro	Pro	Ala	Pro	Glu	Ala
305					310					315					320
Trp	Ser	Glu	Pro	Val	Leu	Leu	Ala	Lys	Gly	Ser	Ala	Ala	Tyr	Ser	Asp
				325					330					335	
Leu	Gln	Ser	Met	Gly	Thr	Gly	Pro	Asp	Gly	Ser	Pro	Leu	Phe	Gly	Cys
			340					345					350		
Leu	Tyr	Glu	Ala	Asn	Asp	Tyr	Glu	Glu	Ile	Val	Phe	Leu	Met	Phe	Thr
		355					360					365			
Leu	Lys	Gln	Ala	Phe	Pro	Ala	Glu	Tyr	Leu	Pro	Gln	Gly	Gly	Gly	Gly
	370					375					380				
Ser	Gly	Gly	Gly	Gly	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro
385					390					395					400
Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
				405					410					415	
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
			420					425					430		
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr
		435					440					445			

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 625 630 635 640

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 645 650 655

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

660	665	670
Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly		
675	680	685
Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala		
690	695	700
Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala		
705	710	715
Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe		
725	730	735
Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser		
740	745	750
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp		
755	760	765
Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp		
770	775	780
Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val		
785	790	795
Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr		
805	810	815
Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser		
820	825	830
Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu		
835	840	845
Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr		
850	855	860
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys		
865	870	

<210> 168

<211> 874

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 168

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

Ala	His	Ala	Tyr	Arg	Ile	Pro	Ala	Leu	Leu	Tyr	Leu	Pro	Gly	Gln	Gln
			20					25					30		

Ser	Leu	Leu	Ala	Phe	Ala	Glu	Gln	Arg	Ala	Ser	Lys	Lys	Asp	Glu	His
		35					40					45			

Ala	Glu	Leu	Ile	Val	Leu	Arg	Arg	Gly	Asp	Tyr	Asp	Ala	Gly	Thr	His
	50					55					60				

Gln	Val	Gln	Trp	Gln	Ala	Gln	Glu	Val	Val	Ala	Gln	Ala	Arg	Leu	Asp
65					70					75					80

Gly	His	Arg	Ser	Met	Asn	Pro	Cys	Pro	Leu	Tyr	Asp	Glu	Gln	Thr	Gly
				85					90					95	

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

Gln	Gln	Leu	Gln	Thr	Arg	Ala	Asn	Val	Thr	Arg	Leu	Cys	Tyr	Val	Thr
		115					120					125			

Ser	Thr	Asp	His	Gly	Arg	Thr	Trp	Ser	Ser	Pro	Arg	Asp	Leu	Thr	Asp
	130					135					140				

Ala	Ala	Ile	Gly	Pro	Ala	Tyr	Arg	Glu	Trp	Ser	Thr	Phe	Ala	Val	Gly
145					150					155					160

Pro	Gly	His	Cys	Leu	Gln	Leu	His	Asp	Arg	Ala	Arg	Ser	Leu	Val	Val
				165					170					175	

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 625 630 635 640

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 645 650 655

Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala
 660 665 670

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly
 675 680 685

Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala
 690 695 700

Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
 705 710 715 720

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
 725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
 785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 805 810 815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser

820

825

830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
 850 855 860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 865 870

<210> 169

<211> 869

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 169

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr

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

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro

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

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
 770 775 780

Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
 785 790 795 800

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu
 805 810 815

Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp
 820 825 830

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
 835 840 845

Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr
 850 855 860

Lys Val Glu Ile Lys
 865

<210> 170

<211> 869

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 170

Asp Ala Ser Leu Pro Tyr Leu Gln Asp Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 625 630 635 640

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile
 645 650 655

Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 660 665 670

Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala
 675 680 685

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

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

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

<210> 171
 <211> 869
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

 <400> 171
 Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly

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

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu

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

Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 660 665 670

Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala
 675 680 685

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

Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 705 710 715 720

Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr
 725 730 735

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
 755 760 765

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
 770 775 780

Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
 785 790 795 800

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu
 805 810 815

Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp
 820 825 830

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
 835 840 845

Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr
 850 855 860

Lys Val Glu Ile Lys

865

<210> 172

<211> 869

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 172

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val

165

170

175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu

595					600					605					
Ser	Pro	Gly	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
	610					615					620				
Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln
625					630					635					640
Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asn	Ile
				645					650					655	
Lys	Asp	Thr	Tyr	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
			660					665					670		
Glu	Trp	Val	Ala	Arg	Ile	Tyr	Pro	Thr	Asn	Gly	Tyr	Thr	Arg	Tyr	Ala
		675					680					685			
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn
	690					695					700				
Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val
705					710					715					720
Tyr	Tyr	Cys	Ser	Arg	Trp	Gly	Gly	Asp	Gly	Phe	Tyr	Ala	Met	Asp	Tyr
				725					730					735	
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser
			740					745					750		
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Met	Thr	Gln
		755					760				765				
Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr
	770					775					780				
Cys	Arg	Ala	Ser	Gln	Asp	Val	Asn	Thr	Ala	Val	Ala	Trp	Tyr	Gln	Gln
785					790					795					800
Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ser	Ala	Ser	Phe	Leu
				805					810					815	

Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp
 820 825 830

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
 835 840 845

Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr
 850 855 860

Lys Val Glu Ile Lys
 865

<210> 173

<211> 869

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 173

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Ser Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 625 630 635 640

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile
 645 650 655

Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 660 665 670

Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala
 675 680 685

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

Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 705 710 715 720

Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr
 725 730 735

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln

755

760

765

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
 770 775 780

Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
 785 790 795 800

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu
 805 810 815

Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp
 820 825 830

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
 835 840 845

Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr
 850 855 860

Lys Val Glu Ile Lys
 865

<210> 174

<211> 869

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 174

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Thr Thr His

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

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro

				485					490						495
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
			500					505					510		
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val
		515					520					525			
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val
	530					535					540				
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro
545					550					555					560
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr
				565					570					575	
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val
			580					585					590		
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu
		595					600					605			
Ser	Pro	Gly	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
	610					615					620				
Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln
625					630					635					640
Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asn	Ile
				645					650					655	
Lys	Asp	Thr	Tyr	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
			660					665					670		
Glu	Trp	Val	Ala	Arg	Ile	Tyr	Pro	Thr	Asn	Gly	Tyr	Thr	Arg	Tyr	Ala
		675					680					685			
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn
	690					695					700				

Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
705 710 715 720

Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr
725 730 735

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
755 760 765

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
770 775 780

Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
785 790 795 800

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu
805 810 815

Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp
820 825 830

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
835 840 845

Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr
850 855 860

Lys Val Glu Ile Lys
865

<210> 175

<211> 869

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 175

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Asn Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val

210	215	220															
Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu																	
225					230					235							240
Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln																	
				245					250							255	
Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Ala Gly Cys																	
			260					265							270		
Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser																	
		275					280						285				
Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Arg Lys Gln Arg																	
	290					295						300					
Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala																	
305					310					315							320
Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp																	
				325					330								335
Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys																	
			340					345								350	
Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr																	
	355						360							365			
Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser																	
	370					375						380					
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu																	
385					390					395							400
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu																	
				405					410								415
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser																	
			420				425							430			

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 625 630 635 640

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile

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

Lys Val Glu Ile Lys
865

<210> 176

<211> 869

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 176

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ala Arg Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser

370

375

380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 625 630 635 640

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile
 645 650 655

Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 660 665 670

Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala
 675 680 685

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

Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 705 710 715 720

Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr
 725 730 735

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
 755 760 765

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
 770 775 780

Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
 785 790 795 800

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu

805

810

815

Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp
 820 825 830

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
 835 840 845

Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr
 850 855 860

Lys Val Glu Ile Lys
 865

<210> 177

<211> 869

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 177

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln

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

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

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

530		535		540
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro				
545		550		555
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr				
		565		570
				575
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val				
		580		585
				590
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu				
		595		600
				605
Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly				
		610		615
				620
Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln				
625		630		635
				640
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile				
		645		650
				655
Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu				
		660		665
				670
Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala				
		675		680
				685
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn				
		690		695
				700
Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val				
705		710		715
				720
Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr				
		725		730
				735
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser				
		740		745
				750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
 755 760 765

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
 770 775 780

Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
 785 790 795 800

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu
 805 810 815

Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp
 820 825 830

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
 835 840 845

Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr
 850 855 860

Lys Val Glu Ile Lys
 865

<210> 178

<211> 869

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 178

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys

260	265	270
Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser		
275	280	285
Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg		
290	295	300
Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala		
305	310	315
Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp		
325	330	335
Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys		
340	345	350
Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr		
355	360	365
Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser		
370	375	380
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu		
385	390	395
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu		
405	410	415
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser		
420	425	430
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu		
435	440	445
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr		
450	455	460
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn		
465	470	475
		480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 625 630 635 640

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile
 645 650 655

Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 660 665 670

Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala
 675 680 685

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

690

695

700

Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 705 710 715 720

Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr
 725 730 735

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
 755 760 765

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
 770 775 780

Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
 785 790 795 800

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu
 805 810 815

Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp
 820 825 830

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
 835 840 845

Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr
 850 855 860

Lys Val Glu Ile Lys
 865

<210> 179

<211> 874

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polypeptide

<220>

<221> MOD_RES

<222> (1)..(1)

<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr, Val, or not present

<220>

<221> MOD_RES

<222> (6)..(6)

<223> Phe, Trp, Tyr or Val

<220>

<221> MOD_RES

<222> (9)..(9)

<223> Lys or Asp

<220>

<221> MOD_RES

<222> (62)..(62)

<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>

<221> MOD_RES

<222> (93)..(93)

<223> Ala, Glu, or Lys

<220>

<221> MOD_RES

<222> (126)..(126)

<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>

<221> MOD_RES

<222> (187)..(187)

<223> Arg, Ile, or Lys

<220>

<221> MOD_RES

<222> (242)..(242)

<223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser, Val, Trp, or Tyr

<220>

<221> MOD_RES

<222> (270)..(270)

<223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>

<221> MOD_RES

<222> (301)..(301)

<223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,

Pro, Gln, Thr, Val, Trp, or Tyr

<220>

<221> MOD_RES

<222> (302)..(302)

<223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>

<221> MOD_RES

<222> (332)..(332)

<223> Ala, Cys, Ser, or Val

<220>

<221> MOD_RES

<222> (363)..(363)

<223> Val or Arg

<220>

<221> MOD_RES

<222> (365)..(365)

<223> Leu, Gln, His, Ile, Lys, or Ser

<220>

<221> MOD_RES

<222> (381)..(390)

<223> This region may encompass one of the following sequences:
"GGGGS" or "GGGGSGGGGS" or "EPKSS"

<400> 179

Xaa	Ala	Ser	Leu	Pro	Xaa	Leu	Gln	Xaa	Glu	Ser	Val	Phe	Gln	Ser	Gly
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Ala	His	Ala	Tyr	Arg	Ile	Pro	Ala	Leu	Leu	Tyr	Leu	Pro	Gly	Gln	Gln
			20					25					30		

Ser	Leu	Leu	Ala	Phe	Ala	Glu	Gln	Arg	Ala	Ser	Lys	Lys	Asp	Glu	His
		35					40					45			

Ala	Glu	Leu	Ile	Val	Leu	Arg	Arg	Gly	Asp	Tyr	Asp	Ala	Xaa	Thr	His
	50					55					60				

Gln	Val	Gln	Trp	Gln	Ala	Gln	Glu	Val	Val	Ala	Gln	Ala	Arg	Leu	Asp
65					70					75				80	

Gly	His	Arg	Ser	Met	Asn	Pro	Cys	Pro	Leu	Tyr	Asp	Xaa	Gln	Thr	Gly
				85					90					95	

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Xaa Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Xaa Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Xaa Xaa Xaa
 370 375 380

Xaa Xaa Xaa Xaa Xaa Xaa Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 625 630 635 640

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 645 650 655

Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala
 660 665 670

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly
 675 680 685

Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala
 690 695 700

Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
 705 710 715 720

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
 725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
 785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 805 810 815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 820 825 830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
 850 855 860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 865 870

<210> 180

<211> 874

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic polypeptide

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<222> (1)..(1)

<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr, Val, or not present

<220>

<221> MOD_RES

<222> (2)..(2)

<223> Ala or Lys

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Asn or Leu

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Pro or His

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe, Trp, Tyr or Val

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Lys or Asp

<220>
<221> MOD_RES
<222> (44)..(44)
<223> Lys, Arg, or Glu

<220>
<221> MOD_RES
<222> (45)..(45)
<223> Lys, Ala, Arg, or Glu

<220>
<221> MOD_RES
<222> (54)..(54)
<223> Leu or Met

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
<221> MOD_RES
<222> (69)..(69)
<223> Gln or His

<220>
<221> MOD_RES
<222> (78)..(78)
<223> Arg or Lys

<220>
<221> MOD_RES
<222> (80)..(80)

<223> Asp or Pro

<220>

<221> MOD_RES

<222> (93)..(93)

<223> Ala, Glu or Lys

<220>

<221> MOD_RES

<222> (107)..(107)

<223> Gly or Asp

<220>

<221> MOD_RES

<222> (108)..(108)

<223> Gln or His

<220>

<221> MOD_RES

<222> (112)..(112)

<223> Gln, Arg, or Lys

<220>

<221> MOD_RES

<222> (125)..(125)

<223> Ala, Cys, Ile, Ser, Val, or Leu

<220>

<221> MOD_RES

<222> (126)..(126)

<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>

<221> MOD_RES

<222> (150)..(150)

<223> Ala or Val

<220>

<221> MOD_RES

<222> (164)..(164)

<223> Cys or Gly

<220>

<221> MOD_RES

<222> (170)..(170)

<223> Arg or Pro

<220>

<221> MOD_RES

<222> (171)..(171)

<223> Ala or Gly

<220>

<221> MOD_RES

<222> (187)..(187)
 <223> Arg, Ile, or Lys

<220>
 <221> MOD_RES
 <222> (188)..(188)
 <223> Gln or Pro

<220>
 <221> MOD_RES
 <222> (189)..(189)
 <223> Arg or Pro

<220>
 <221> MOD_RES
 <222> (196)..(196)
 <223> Ala, Cys, Leu, or Val

<220>
 <221> MOD_RES
 <222> (213)..(213)
 <223> Ala, Cys, Asn, Ser, or Thr

<220>
 <221> MOD_RES
 <222> (217)..(217)
 <223> Leu, Ala, or Val

<220>
 <221> MOD_RES
 <222> (225)..(225)
 <223> Glu or Pro

<220>
 <221> MOD_RES
 <222> (239)..(239)
 <223> His or Pro

<220>
 <221> MOD_RES
 <222> (240)..(240)
 <223> Leu, Asp, Asn, or Tyr

<220>
 <221> MOD_RES
 <222> (241)..(241)
 <223> Arg, Ala, Asp, Leu, Gln, or Tyr

<220>
 <221> MOD_RES
 <222> (242)..(242)
 <223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser, Val, Trp, or Tyr

<220>
 <221> MOD_RES
 <222> (244)..(244)
 <223> Val, Ile, or Lys

<220>
 <221> MOD_RES
 <222> (249)..(249)
 <223> Thr or Ala

<220>
 <221> MOD_RES
 <222> (251)..(251)
 <223> Asp or Gly

<220>
 <221> MOD_RES
 <222> (257)..(257)
 <223> Glu, Lys, or Pro

<220>
 <221> MOD_RES
 <222> (258)..(258)
 <223> Ser or Cys

<220>
 <221> MOD_RES
 <222> (260)..(260)
 <223> Leu, Asp, Phe, Gln, or Thr

<220>
 <221> MOD_RES
 <222> (265)..(265)
 <223> Val or Phe

<220>
 <221> MOD_RES
 <222> (270)..(270)
 <223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>
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 <222> (272)..(272)
 <223> Cys or Val

<220>
 <221> MOD_RES
 <222> (292)..(292)
 <223> Trp or Arg

<220>
 <221> MOD_RES
 <222> (301)..(301)
 <223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met,

Asn, Pro, Gln, Thr, Val, Trp, or Tyr

<220>

<221> MOD_RES

<222> (302)..(302)

<223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met,
Asn, Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>

<221> MOD_RES

<222> (325)..(325)

<223> Lys or Val

<220>

<221> MOD_RES

<222> (332)..(332)

<223> Ala, Cys, Ser, or Val

<220>

<221> MOD_RES

<222> (352)..(352)

<223> Cys, Leu, or Val

<220>

<221> MOD_RES

<222> (363)..(363)

<223> Val or Arg

<220>

<221> MOD_RES

<222> (365)..(365)

<223> Leu, Gln, His, Ile, Lys, or Ser

<220>

<221> MOD_RES

<222> (381)..(390)

<223> This region may encompass one of the following sequences:
"GGGGS" or "GGGGSGGGGS" or "EPKSS"

<400> 180

Xaa	Xaa	Ser	Xaa	Xaa	Xaa	Leu	Gln	Xaa	Glu	Ser	Val	Phe	Gln	Ser	Gly
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Ala	His	Ala	Tyr	Arg	Ile	Pro	Ala	Leu	Leu	Tyr	Leu	Pro	Gly	Gln	Gln
			20					25					30		

Ser	Leu	Leu	Ala	Phe	Ala	Glu	Gln	Arg	Ala	Ser	Xaa	Xaa	Asp	Glu	His
			35				40					45			

Ala	Glu	Leu	Ile	Val	Xaa	Arg	Arg	Gly	Asp	Tyr	Asp	Ala	Xaa	Thr	His
						55					60				

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Xaa
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Xaa Leu Gln Leu His Asp Xaa Xaa Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Xaa Xaa Pro Ile Pro
180 185 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Xaa Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
210 215 220

Xaa Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser Xaa Xaa
225 230 235 240

Xaa Xaa Arg Xaa Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
245 250 255

Xaa Xaa Gln Xaa Val Lys Lys Leu Xaa Glu Pro Pro Pro Xaa Gly Xaa
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Xaa Xaa Xaa
 370 375 380

Xaa Xaa Xaa Xaa Xaa Xaa Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 625 630 635 640

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 645 650 655

Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala
 660 665 670

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly
 675 680 685

Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala
 690 695 700

Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
 705 710 715 720

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
 725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
 785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 805 810 815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 820 825 830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
 850 855 860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 865 870

<210> 181

<211> 1140

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 181


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agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag      120
cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac      180
gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac      240
ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg      300
ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac      360
gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga      420
gatctgaccg acgccgcat cggacctgcc tatagagagt ggtccacctt cgccgttgga      480
cctggacact gtctccagct gcacgacagg gctagatctc tgggtggtgcc tgcctacgcc      540
tatagaaagc tgcaccccaa acagcggcct attcctagcg ctttctgctt tctgagccac      600
gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag      660
gtggccgaag tggaaaccgg cgagcagaga gtcgtgacct tgaacgccag atctcacctg      720
agattcagag tgcaggccca gagcacaac gacggcctgg atttccaaga gagccagctg      780
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tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca cccacacac      900
agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct      960
tggagcgaac ctgttctgct ggccaagggc agcgtgcct acagcgatct gcagtctatg     1020
ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa     1080
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<210> 182

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>

<221> MOD_RES

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<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr,
Val, or not present

<220>
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<222> (2)..(2)
<223> Ala or Lys

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Asn or Leu

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Pro or His

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe, Trp, Tyr or Val

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Lys or Asp

<220>
<221> MOD_RES
<222> (44)..(44)
<223> Lys, Arg, or Glu

<220>
<221> MOD_RES
<222> (45)..(45)
<223> Lys, Ala, Arg, or Glu

<220>
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<222> (54)..(54)
<223> Leu or Met

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
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<222> (69)..(69)
<223> Gln or His

<220>
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<222> (78)..(78)

<223> Arg or Lys

<220>

<221> MOD_RES

<222> (80)..(80)

<223> Asp or Pro

<220>

<221> MOD_RES

<222> (93)..(93)

<223> Ala, Glu or Lys

<220>

<221> MOD_RES

<222> (107)..(107)

<223> Gly or Asp

<220>

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<222> (108)..(108)

<223> Gln or His

<220>

<221> MOD_RES

<222> (112)..(112)

<223> Gln, Arg, or Lys

<220>

<221> MOD_RES

<222> (125)..(125)

<223> Ala, Cys, Ile, Ser, Val, or Leu

<220>

<221> MOD_RES

<222> (126)..(126)

<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>

<221> MOD_RES

<222> (150)..(150)

<223> Ala or Val

<220>

<221> MOD_RES

<222> (164)..(164)

<223> Cys or Gly

<220>

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<222> (170)..(170)

<223> Arg or Pro

<220>

<221> MOD_RES

<222> (171)..(171)

<223> Ala or Gly

<220>

<221> MOD_RES

<222> (187)..(187)

<223> Arg, Ile, or Lys

<220>

<221> MOD_RES

<222> (188)..(188)

<223> Gln or Pro

<220>

<221> MOD_RES

<222> (189)..(189)

<223> Arg or Pro

<220>

<221> MOD_RES

<222> (196)..(196)

<223> Ala, Cys, Leu, or Val

<220>

<221> MOD_RES

<222> (213)..(213)

<223> Ala, Cys, Asn, Ser, or Thr

<220>

<221> MOD_RES

<222> (217)..(217)

<223> Leu, Ala, or Val

<220>

<221> MOD_RES

<222> (225)..(225)

<223> Glu or Pro

<220>

<221> MOD_RES

<222> (239)..(239)

<223> His or Pro

<220>

<221> MOD_RES

<222> (240)..(240)

<223> Leu, Asp, Asn, or Tyr

<220>

<221> MOD_RES

<222> (241)..(241)

<223> Arg, Ala, Asp, Leu, Gln, or Tyr

<220>

<221> MOD_RES
 <222> (242)..(242)
 <223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser,
 Val, Trp, or Tyr

<220>
 <221> MOD_RES
 <222> (244)..(244)
 <223> Val, Ile, or Lys

<220>
 <221> MOD_RES
 <222> (249)..(249)
 <223> Thr or Ala

<220>
 <221> MOD_RES
 <222> (251)..(251)
 <223> Asp or Gly

<220>
 <221> MOD_RES
 <222> (257)..(257)
 <223> Glu, Lys, or Pro

<220>
 <221> MOD_RES
 <222> (258)..(258)
 <223> Ser or Cys

<220>
 <221> MOD_RES
 <222> (260)..(260)
 <223> Leu, Asp, Phe, Gln, or Thr

<220>
 <221> MOD_RES
 <222> (265)..(265)
 <223> Val or Phe

<220>
 <221> MOD_RES
 <222> (270)..(270)
 <223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>
 <221> MOD_RES
 <222> (272)..(272)
 <223> Cys or Val

<220>
 <221> MOD_RES
 <222> (292)..(292)
 <223> Trp or Arg

<220>
 <221> MOD_RES
 <222> (301)..(301)
 <223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
 Pro, Gln, Thr, Val, Trp, or Tyr

<220>
 <221> MOD_RES
 <222> (302)..(302)
 <223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
 Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>
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 <222> (325)..(325)
 <223> Lys or Val

<220>
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 <223> Ala, Cys, Ser, or Val

<220>
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 <222> (352)..(352)
 <223> Cys, Leu, or Val

<220>
 <221> MOD_RES
 <222> (363)..(363)
 <223> Val or Arg

<220>
 <221> MOD_RES
 <222> (365)..(365)
 <223> Leu, Gln, His, Ile, Lys, or Ser

<400> 182
 Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Xaa Xaa Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
 50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Xaa
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Xaa Leu Gln Leu His Asp Xaa Xaa Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Xaa Xaa Pro Ile Pro
180 185 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Xaa Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
210 215 220

Xaa Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser Xaa Xaa
225 230 235 240

Xaa Xaa Arg Xaa Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
245 250 255

Xaa Xaa Gln Xaa Val Lys Lys Leu Xaa Glu Pro Pro Pro Xaa Gly Xaa
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser

275

280

285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 183

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<221> MOD_RES

<222> (1)..(1)

<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr, Val, or not present

<220>

<221> MOD_RES

<222> (6)..(6)

<223> Phe, Trp, Tyr or Val

<220>

<221> MOD_RES

<222> (9)..(9)

<223> Lys or Asp

<220>

<221> MOD_RES
 <222> (62)..(62)
 <223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
 <221> MOD_RES
 <222> (93)..(93)
 <223> Ala, Glu, or Lys

<220>
 <221> MOD_RES
 <222> (126)..(126)
 <223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>
 <221> MOD_RES
 <222> (187)..(187)
 <223> Arg, Ile, or Lys

<220>
 <221> MOD_RES
 <222> (242)..(242)
 <223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser, Val, Trp, or Tyr

<220>
 <221> MOD_RES
 <222> (270)..(270)
 <223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>
 <221> MOD_RES
 <222> (301)..(301)
 <223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Thr, Val, Trp, or Tyr

<220>
 <221> MOD_RES
 <222> (302)..(302)
 <223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>
 <221> MOD_RES
 <222> (332)..(332)
 <223> Ala, Cys, Ser, or Val

<220>
 <221> MOD_RES
 <222> (363)..(363)
 <223> Val or Arg

<220>
 <221> MOD_RES

<222> (365)..(365)

<223> Leu, Gln, His, Ile, Lys, or Ser

<400> 183

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

Ala	His	Ala	Tyr	Arg	Ile	Pro	Ala	Leu	Leu	Tyr	Leu	Pro	Gly	Gln	Gln
			20					25					30		

Ser	Leu	Leu	Ala	Phe	Ala	Glu	Gln	Arg	Ala	Ser	Lys	Lys	Asp	Glu	His
		35					40					45			

Ala	Glu	Leu	Ile	Val	Leu	Arg	Arg	Gly	Asp	Tyr	Asp	Ala	Xaa	Thr	His
	50					55					60				

Gln	Val	Gln	Trp	Gln	Ala	Gln	Glu	Val	Val	Ala	Gln	Ala	Arg	Leu	Asp
65					70					75					80

Gly	His	Arg	Ser	Met	Asn	Pro	Cys	Pro	Leu	Tyr	Asp	Xaa	Gln	Thr	Gly
				85					90					95	

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

Gln	Gln	Leu	Gln	Thr	Arg	Ala	Asn	Val	Thr	Arg	Leu	Cys	Xaa	Val	Thr
		115					120					125			

Ser	Thr	Asp	His	Gly	Arg	Thr	Trp	Ser	Ser	Pro	Arg	Asp	Leu	Thr	Asp
	130					135					140				

Ala	Ala	Ile	Gly	Pro	Ala	Tyr	Arg	Glu	Trp	Ser	Thr	Phe	Ala	Val	Gly
145					150					155					160

Pro	Gly	His	Cys	Leu	Gln	Leu	His	Asp	Arg	Ala	Arg	Ser	Leu	Val	Val
			165					170						175	

Pro	Ala	Tyr	Ala	Tyr	Arg	Lys	Leu	His	Pro	Xaa	Gln	Arg	Pro	Ile	Pro
			180					185					190		

Ser	Ala	Phe	Cys	Phe	Leu	Ser	His	Asp	His	Gly	Arg	Thr	Trp	Ala	Arg
		195					200					205			

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Xaa Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 184

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 peptide

<400> 184

Gly Gly Gly Gly Ser
1 5

<210> 185

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 185

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 186
 <211> 1836
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 186
 gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60
 agaattcccc ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120
 cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180
 gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240
 ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300
 ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360
 gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga 420
 gatctgaccg acgccgcat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480
 cctggacact gtctccagct gcacgacagg gctagatctc tgggtggtgcc tgcctacgcc 540
 tatagaaagc tgcaccccaa acagcggcct attcctagcg ctttctgctt tctgagccac 600
 gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660
 gtggccgaag tggaaaccgg cgagcagaga gtcgtgacct tgaacgccag atctcacctg 720
 agagccagag tgcaggccca gagcacaac gacggcctgg atttccaaga gagccagctg 780
 gtcaagaaac tgggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca 840
 tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca cccacacac 900
 agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960
 tggagcgaac ctgttctgct ggccaagggc agcgtgcct acagcgatct gcagtctatg 1020

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ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa      1080
gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa      1140
gagcccaaatt cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg      1200
gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg      1260
acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      1320
aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag      1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc      1500
atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg      1560
gaggagatga ccaagaacca ggtcagcctg tactgcctgg tcaaaggctt ctatcccagc      1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      1680
cccggtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc      1740
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      1800
tacacgcaga agagcctctc cctgtctccg ggtaaa                                1836

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<210> 187

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 187

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

```

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Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
          20           25           30

```

```

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
          35           40           45

```

```

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
          50           55           60

```


Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 188

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 188

gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cgggccagca agaaggatga gcacgccgaa ctgatactgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaacct ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac	tgtgttacgt	gacctccacc	gaccacggca	gaacctggtc	tagccctaga	420
gatctgaccg	acgccgccat	cggacctgcc	tatagagagt	ggtccacctt	cgccgttgga	480
cctggacact	gtctccagct	gcacgacagg	gctagatctc	tggtgggtgcc	tgccctacgcc	540
tatagaaagc	tgcccccaa	acagcggcct	attcctagcg	ccttctgctt	tctgagccac	600
gatcacggca	ggacatgggc	cagaggacat	ttcgtggccc	aggacacact	ggaatgccag	660
gtggccgaag	tggaaaccgg	cgagcagaga	gtcgtgacct	tgaacgccag	atctcacctg	720
agattcagag	tgaggccca	gagcacaac	gacggcctgg	atttccaaga	gagccagctg	780
gtcaagaaac	tggtggaacc	tcctccaacc	ggctgtcagg	gaagcgtgat	cagctttcca	840
tctcctagaa	gcggccctgg	ctctcctgct	cagtggctgc	tgtatacaca	ccccacacac	900
agctggcaga	gagccgatct	gggcgcctac	ctgaatccta	gacctcctgc	tcctgaggct	960
tggagcgaac	ctgttctgct	ggccaagggc	agcgtgcct	acagcgatct	gcagtctatg	1020
ggcacaggcc	ctgatggcag	ccctctgttt	ggctgtctgt	acgaggccaa	cgactacgaa	1080
gagatcgtgt	tcctgatgtt	caccctgaag	caggcctttc	cagccgagta	cctgcctcaa	1140
gagcccaaat	cttctgacaa	aactcacaca	tgcccaccgt	gccagcacc	tgaactcctg	1200
gggggaccgt	cagtcttcct	cttccccca	aaaccaagg	acaccctcat	gatctcccgg	1260
acccctgagg	tcacatgcgt	ggtgggtggac	gtgagccacg	aagaccctga	ggtcaagtcc	1320
aactgggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	1380
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgaccagga	ctggctgaat	1440
ggcaaggagt	acaagtgcaa	ggtctccaac	aaagccctcc	cagcccccat	cgagaaaacc	1500
atctccaaag	caaaggga	gccccgagaa	ccacaggtct	acaccctgcc	cccatcccgg	1560
gaggagatga	ccaagaacca	ggtcagcctg	tactgcctgg	tcaaaggctt	ctatcccagc	1620
gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	1680
cccgtgctgg	actccgacgg	ctccttcttc	ctctatagca	agctcaccgt	ggacaagagc	1740
aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	1800
tacacgcaga	agagcctctc	cctgtctccg	ggtaaa			1836

<210> 189

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 189

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

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

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

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

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

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

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110

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

Phe Pro Leu Ala Pro 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 Glu Glu Met 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 Thr 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> 190

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 190

gaggtgcagc tggttgaatc tggcggagga ctggttcagc ctggcggatc tctgagactg	60
tcttgtgccg ccagcggctt caacatcaag gacacctaca tccactgggt ccgacaggcc	120
cctggcaaag gacttgaatg ggtcgccaga atctaccca ccaacggcta caccagatac	180
gccgactctg tgaagggcag attcaccatc agcgccgaca ccagcaagaa caccgcctac	240
ctgcagatga acagcctgag agccgaggac accgccgtgt actactgttc tagatgggga	300
ggcgacggct tctacgcat ggattattgg ggccagggca ccctggtcac cgtttcttct	360
gctagcacca agggcccatc cgtcttcccc ctggcaccct cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcc	480
tggaactcag gcgctctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca	540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660
aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt	780
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	840

```

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac      900
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag      960
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc     1020
aaagccaaag ggcagccccg agaaccacag gtctacaccc tgcccccatc ccgggaggag     1080
atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc     1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg     1200
ctggactccg acggctcctt cttcctcact agcaagctca ccgtggacaa gagcaggtgg     1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     1320
cagaagagcc tctccctgtc tccgggtaaa     1350

```

<210> 191

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 191

```

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

```

```

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
          20          25          30

```

```

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
          35          40          45

```

```

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
          50          55          60

```

```

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65          70          75          80

```

```

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
          85          90          95

```

```

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln

```


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

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
370 375 380

<210> 192

<211> 612

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 192

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 193

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 193

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

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

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 194

<211> 869

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 194

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg

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

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 625 630 635 640

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile
 645 650 655

Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 660 665 670

Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala
 675 680 685

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

Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 705 710 715 720

Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr

725

730

735

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
 755 760 765

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
 770 775 780

Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
 785 790 795 800

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu
 805 810 815

Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp
 820 825 830

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
 835 840 845

Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr
 850 855 860

Lys Val Glu Ile Lys
 865

<210> 195

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 195

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln

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

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu

450

455

460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 196

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 196

Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly

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

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr

435

440

445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 197

<211> 874

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 197

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

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

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

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
645 650 655

Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala
660 665 670

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly
675 680 685

Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala
690 695 700

Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
705 710 715 720

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
805 810 815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
820 825 830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr

850

855

860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
865 870

<210> 198

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 198

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly

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

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 199
 <211> 380
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<220>
 <221> MOD_RES
 <222> (1)..(1)
 <223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr,
 Val, or not present

<220>
 <221> MOD_RES
 <222> (2)..(2)
 <223> Ala or Lys

<220>
 <221> MOD_RES
 <222> (4)..(4)
 <223> Asn or Leu

<220>
 <221> MOD_RES
 <222> (5)..(5)
 <223> Pro or His

<220>
 <221> MOD_RES
 <222> (6)..(6)
 <223> Phe, Trp, Tyr or Val

<220>
 <221> MOD_RES
 <222> (9)..(9)
 <223> Lys or Asp

<220>
 <221> MOD_RES
 <222> (42)..(42)
 <223> Ala or Arg

<220>
 <221> MOD_RES
 <222> (44)..(44)

<223> Lys, Arg, or Glu

<220>

<221> MOD_RES

<222> (45)..(45)

<223> Lys, Ala, Arg, or Glu

<220>

<221> MOD_RES

<222> (54)..(54)

<223> Leu or Met

<220>

<221> MOD_RES

<222> (62)..(62)

<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>

<221> MOD_RES

<222> (69)..(69)

<223> Gln or His

<220>

<221> MOD_RES

<222> (78)..(78)

<223> Arg or Lys

<220>

<221> MOD_RES

<222> (80)..(80)

<223> Asp or Pro

<220>

<221> MOD_RES

<222> (93)..(93)

<223> Ala, Glu or Lys

<220>

<221> MOD_RES

<222> (107)..(107)

<223> Gly or Asp

<220>

<221> MOD_RES

<222> (108)..(108)

<223> Gln or His

<220>

<221> MOD_RES

<222> (112)..(112)

<223> Gln, Arg, or Lys

<220>

<221> MOD_RES

<222> (125)..(125)
 <223> Ala, Cys, Ile, Ser, Val, or Leu

<220>
 <221> MOD_RES
 <222> (126)..(126)
 <223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>
 <221> MOD_RES
 <222> (150)..(150)
 <223> Ala or Val

<220>
 <221> MOD_RES
 <222> (164)..(164)
 <223> Cys or Gly

<220>
 <221> MOD_RES
 <222> (170)..(170)
 <223> Arg or Pro

<220>
 <221> MOD_RES
 <222> (171)..(171)
 <223> Ala or Gly

<220>
 <221> MOD_RES
 <222> (187)..(187)
 <223> Arg, Ile, or Lys

<220>
 <221> MOD_RES
 <222> (188)..(188)
 <223> Gln or Pro

<220>
 <221> MOD_RES
 <222> (189)..(189)
 <223> Arg or Pro

<220>
 <221> MOD_RES
 <222> (196)..(196)
 <223> Ala, Cys, Leu, or Val

<220>
 <221> MOD_RES
 <222> (213)..(213)
 <223> Ala, Cys, Asn, Ser, or Thr

<220>

<221> MOD_RES
 <222> (217)..(217)
 <223> Leu, Ala, or Val

<220>
 <221> MOD_RES
 <222> (225)..(225)
 <223> Glu or Pro

<220>
 <221> MOD_RES
 <222> (239)..(239)
 <223> His or Pro

<220>
 <221> MOD_RES
 <222> (240)..(240)
 <223> Leu, Asp, Asn, or Tyr

<220>
 <221> MOD_RES
 <222> (241)..(241)
 <223> Arg, Ala, Asp, Leu, Gln, or Tyr

<220>
 <221> MOD_RES
 <222> (242)..(242)
 <223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser,
 Val, Trp, or Tyr

<220>
 <221> MOD_RES
 <222> (244)..(244)
 <223> Val, Ile, or Lys

<220>
 <221> MOD_RES
 <222> (249)..(249)
 <223> Thr or Ala

<220>
 <221> MOD_RES
 <222> (251)..(251)
 <223> Asp or Gly

<220>
 <221> MOD_RES
 <222> (257)..(257)
 <223> Glu, Lys, or Pro

<220>
 <221> MOD_RES
 <222> (258)..(258)
 <223> Ser or Cys

<220>
 <221> MOD_RES
 <222> (260)..(260)
 <223> Leu, Asp, Phe, Gln, or Thr

<220>
 <221> MOD_RES
 <222> (265)..(265)
 <223> Val or Phe

<220>
 <221> MOD_RES
 <222> (270)..(270)
 <223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>
 <221> MOD_RES
 <222> (272)..(272)
 <223> Cys or Val

<220>
 <221> MOD_RES
 <222> (292)..(292)
 <223> Trp or Arg

<220>
 <221> MOD_RES
 <222> (301)..(301)
 <223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
 Pro, Gln, Thr, Val, Trp, or Tyr

<220>
 <221> MOD_RES
 <222> (302)..(302)
 <223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
 Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>
 <221> MOD_RES
 <222> (325)..(325)
 <223> Lys or Val

<220>
 <221> MOD_RES
 <222> (332)..(332)
 <223> Ala, Cys, Ser, or Val

<220>
 <221> MOD_RES
 <222> (352)..(352)
 <223> Cys, Leu, or Val

<220>

<221> MOD_RES
 <222> (363)..(363)
 <223> Val or Arg

<220>
 <221> MOD_RES
 <222> (365)..(365)
 <223> Leu, Gln, His, Ile, Lys, or Ser

<400> 199
 Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Xaa Ser Xaa Xaa Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
 50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Xaa
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
 85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
 100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Xaa Leu Gln Leu His Asp Xaa Xaa Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Xaa Xaa Pro Ile Pro
 180 185 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Xaa Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
 210 215 220

Xaa Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser Xaa Xaa
 225 230 235 240

Xaa Xaa Arg Xaa Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
 245 250 255

Xaa Xaa Gln Xaa Val Lys Lys Leu Xaa Glu Pro Pro Pro Xaa Gly Xaa
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 200

<211> 380

<212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<221> MOD_RES

<222> (1)..(1)

<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr, Val, or not present

<220>

<221> MOD_RES

<222> (6)..(6)

<223> Phe, Trp, Tyr or Val

<220>

<221> MOD_RES

<222> (9)..(9)

<223> Lys or Asp

<220>

<221> MOD_RES

<222> (42)..(42)

<223> Arg or Ala

<220>

<221> MOD_RES

<222> (62)..(62)

<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>

<221> MOD_RES

<222> (93)..(93)

<223> Ala, Glu, or Lys

<220>

<221> MOD_RES

<222> (126)..(126)

<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>

<221> MOD_RES

<222> (187)..(187)

<223> Arg, Ile, or Lys

<220>

<221> MOD_RES

<222> (242)..(242)

<223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser, Val, Trp, or Tyr

<220>

<221> MOD_RES

<222> (270)..(270)

<223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>

<221> MOD_RES

<222> (301)..(301)

<223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Thr, Val, Trp, or Tyr

<220>

<221> MOD_RES

<222> (302)..(302)

<223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>

<221> MOD_RES

<222> (332)..(332)

<223> Ala, Cys, Ser, or Val

<220>

<221> MOD_RES

<222> (363)..(363)

<223> Val or Arg

<220>

<221> MOD_RES

<222> (365)..(365)

<223> Leu, Gln, His, Ile, Lys, or Ser

<400> 200

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

Ala	His	Ala	Tyr	Arg	Ile	Pro	Ala	Leu	Leu	Tyr	Leu	Pro	Gly	Gln	Gln
			20					25					30		

Ser	Leu	Leu	Ala	Phe	Ala	Glu	Gln	Arg	Xaa	Ser	Lys	Lys	Asp	Glu	His
			35				40					45			

Ala	Glu	Leu	Ile	Val	Leu	Arg	Arg	Gly	Asp	Tyr	Asp	Ala	Xaa	Thr	His
	50					55					60				

Gln	Val	Gln	Trp	Gln	Ala	Gln	Glu	Val	Val	Ala	Gln	Ala	Arg	Leu	Asp
65					70					75				80	

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Xaa Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Xaa Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln
 370 375 380

<210> 201

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<220>

<221> MOD_RES

<222> (1)..(1)

<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr,
 Val, or not present

<220>

<221> MOD_RES

<222> (2)..(2)

<223> Ala or Lys

<220>

<221> MOD_RES

<222> (4)..(4)

<223> Asn or Leu

<220>

<221> MOD_RES

<222> (5)..(5)

<223> Pro or His

<220>

<221> MOD_RES
<222> (6)..(6)
<223> Phe, Trp, Tyr or Val

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Lys or Asp

<220>
<221> MOD_RES
<222> (42)..(42)
<223> Ala or Arg

<220>
<221> MOD_RES
<222> (44)..(44)
<223> Lys, Arg, or Glu

<220>
<221> MOD_RES
<222> (45)..(45)
<223> Lys, Ala, Arg, or Glu

<220>
<221> MOD_RES
<222> (54)..(54)
<223> Leu or Met

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
<221> MOD_RES
<222> (69)..(69)
<223> Gln or His

<220>
<221> MOD_RES
<222> (78)..(78)
<223> Arg or Lys

<220>
<221> MOD_RES
<222> (80)..(80)
<223> Asp or Pro

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Ala, Glu or Lys

<220>
<221> MOD_RES
<222> (107)..(107)
<223> Gly or Asp

<220>
<221> MOD_RES
<222> (108)..(108)
<223> Gln or His

<220>
<221> MOD_RES
<222> (112)..(112)
<223> Gln, Arg, or Lys

<220>
<221> MOD_RES
<222> (125)..(125)
<223> Ala, Cys, Ile, Ser, Val, or Leu

<220>
<221> MOD_RES
<222> (126)..(126)
<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>
<221> MOD_RES
<222> (150)..(150)
<223> Ala or Val

<220>
<221> MOD_RES
<222> (164)..(164)
<223> Cys or Gly

<220>
<221> MOD_RES
<222> (170)..(170)
<223> Arg or Pro

<220>
<221> MOD_RES
<222> (171)..(171)
<223> Ala or Gly

<220>
<221> MOD_RES
<222> (187)..(187)
<223> Arg, Ile, or Lys

<220>
<221> MOD_RES
<222> (188)..(188)
<223> Gln or Pro

<220>
 <221> MOD_RES
 <222> (189)..(189)
 <223> Arg or Pro

<220>
 <221> MOD_RES
 <222> (196)..(196)
 <223> Ala, Cys, Leu, or Val

<220>
 <221> MOD_RES
 <222> (213)..(213)
 <223> Ala, Cys, Asn, Ser, or Thr

<220>
 <221> MOD_RES
 <222> (217)..(217)
 <223> Leu, Ala, or Val

<220>
 <221> MOD_RES
 <222> (225)..(225)
 <223> Glu or Pro

<220>
 <221> MOD_RES
 <222> (239)..(239)
 <223> His or Pro

<220>
 <221> MOD_RES
 <222> (240)..(240)
 <223> Leu, Asp, Asn, or Tyr

<220>
 <221> MOD_RES
 <222> (241)..(241)
 <223> Arg, Ala, Asp, Leu, Gln, or Tyr

<220>
 <221> MOD_RES
 <222> (242)..(242)
 <223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser,
 Val, Trp, or Tyr

<220>
 <221> MOD_RES
 <222> (244)..(244)
 <223> Val, Ile, or Lys

<220>
 <221> MOD_RES

<222> (249)..(249)

<223> Thr or Ala

<220>

<221> MOD_RES

<222> (251)..(251)

<223> Asp or Gly

<220>

<221> MOD_RES

<222> (257)..(257)

<223> Glu, Lys, or Pro

<220>

<221> MOD_RES

<222> (258)..(258)

<223> Ser or Cys

<220>

<221> MOD_RES

<222> (260)..(260)

<223> Leu, Asp, Phe, Gln, or Thr

<220>

<221> MOD_RES

<222> (265)..(265)

<223> Val or Phe

<220>

<221> MOD_RES

<222> (270)..(270)

<223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>

<221> MOD_RES

<222> (272)..(272)

<223> Cys or Val

<220>

<221> MOD_RES

<222> (292)..(292)

<223> Trp or Arg

<220>

<221> MOD_RES

<222> (301)..(301)

<223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Thr, Val, Trp, or Tyr

<220>

<221> MOD_RES

<222> (302)..(302)

<223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>
 <221> MOD_RES
 <222> (325)..(325)
 <223> Lys or Val

<220>
 <221> MOD_RES
 <222> (332)..(332)
 <223> Ala, Cys, Ser, or Val

<220>
 <221> MOD_RES
 <222> (352)..(352)
 <223> Cys, Leu, or Val

<220>
 <221> MOD_RES
 <222> (363)..(363)
 <223> Val or Arg

<220>
 <221> MOD_RES
 <222> (365)..(365)
 <223> Leu, Gln, His, Ile, Lys, or Ser

<220>
 <221> MOD_RES
 <222> (381)..(390)
 <223> This region may encompass one of the following sequences:
 "GGGGS" or "GGGSGGGGS" or "EPKSS"

<400> 201
 Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Xaa Ser Xaa Xaa Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
 50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Xaa
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly

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

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Xaa Xaa Xaa
 370 375 380

Xaa Xaa Xaa Xaa Xaa Xaa Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

515

520

525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 202

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<221> MOD_RES

<222> (1)..(1)

<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr, Val, or not present

<220>

<221> MOD_RES

<222> (6)..(6)

<223> Phe, Trp, Tyr or Val

<220>

<221> MOD_RES

<222> (9)..(9)

<223> Lys or Asp

<220>

<221> MOD_RES
 <222> (42)..(42)
 <223> Arg or Ala

<220>
 <221> MOD_RES
 <222> (62)..(62)
 <223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
 <221> MOD_RES
 <222> (93)..(93)
 <223> Ala, Glu, or Lys

<220>
 <221> MOD_RES
 <222> (126)..(126)
 <223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>
 <221> MOD_RES
 <222> (187)..(187)
 <223> Arg, Ile, or Lys

<220>
 <221> MOD_RES
 <222> (242)..(242)
 <223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser, Val, Trp, or Tyr

<220>
 <221> MOD_RES
 <222> (270)..(270)
 <223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>
 <221> MOD_RES
 <222> (301)..(301)
 <223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Thr, Val, Trp, or Tyr

<220>
 <221> MOD_RES
 <222> (302)..(302)
 <223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>
 <221> MOD_RES
 <222> (332)..(332)
 <223> Ala, Cys, Ser, or Val

<220>
 <221> MOD_RES

<222> (363)..(363)

<223> Val or Arg

<220>

<221> MOD_RES

<222> (365)..(365)

<223> Leu, Gln, His, Ile, Lys, or Ser

<220>

<221> MOD_RES

<222> (381)..(390)

<223> This region may encompass one of the following sequences:
"GGGGS" or "GGGGSGGGGS" or "EPKSS" ,

<400> 202

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

Ala	His	Ala	Tyr	Arg	Ile	Pro	Ala	Leu	Leu	Tyr	Leu	Pro	Gly	Gln	Gln
			20					25					30		

Ser	Leu	Leu	Ala	Phe	Ala	Glu	Gln	Arg	Xaa	Ser	Lys	Lys	Asp	Glu	His
		35					40					45			

Ala	Glu	Leu	Ile	Val	Leu	Arg	Arg	Gly	Asp	Tyr	Asp	Ala	Xaa	Thr	His
	50					55					60				

Gln	Val	Gln	Trp	Gln	Ala	Gln	Glu	Val	Val	Ala	Gln	Ala	Arg	Leu	Asp
65					70					75				80	

Gly	His	Arg	Ser	Met	Asn	Pro	Cys	Pro	Leu	Tyr	Asp	Xaa	Gln	Thr	Gly
				85					90					95	

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

Gln	Gln	Leu	Gln	Thr	Arg	Ala	Asn	Val	Thr	Arg	Leu	Cys	Xaa	Val	Thr
		115					120					125			

Ser	Thr	Asp	His	Gly	Arg	Thr	Trp	Ser	Ser	Pro	Arg	Asp	Leu	Thr	Asp
		130				135					140				

Ala	Ala	Ile	Gly	Pro	Ala	Tyr	Arg	Glu	Trp	Ser	Thr	Phe	Ala	Val	Gly
145					150					155					160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Xaa Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Xaa Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Xaa Xaa Xaa

370

375

380

Xaa Xaa Xaa Xaa Xaa Xaa Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

<210> 203

<211> 612

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 203

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 204

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 204

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys

340

345

350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly
 370 375 380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 205

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 205

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 206

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 206

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

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

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

Thr Lys Asn Gln Val Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 207

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 207

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 610 615

<210> 208

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 208

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Thr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 209

<211> 617

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 209

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys

260		265		270
Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser	275	280		285
Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg	290	295	300	
Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala	305	310	315	320
Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp	325	330		335
Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys	340	345		350
Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr	355	360		365
Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly	370	375	380	
Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro	385	390	395	400
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys	405	410		415
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val	420	425		430
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr	435	440		445
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu	450	455	460	
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His	465	470	475	480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys
610 615

 $\langle 210 \rangle$ 210

<211> 612

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 210

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln

			245					250						255	
Glu	Ser	Gln	Leu	Val	Lys	Lys	Leu	Val	Glu	Pro	Pro	Pro	Thr	Gly	Cys
			260					265					270		
Gln	Gly	Ser	Val	Ile	Ser	Phe	Pro	Ser	Pro	Arg	Ser	Gly	Pro	Gly	Ser
		275					280					285			
Pro	Ala	Gln	Trp	Leu	Leu	Tyr	Thr	His	Pro	Thr	His	Ser	Trp	Gln	Arg
	290					295					300				
Ala	Asp	Leu	Gly	Ala	Tyr	Leu	Asn	Pro	Arg	Pro	Pro	Ala	Pro	Glu	Ala
305					310					315					320
Trp	Ser	Glu	Pro	Val	Leu	Leu	Ala	Lys	Gly	Ser	Ala	Ala	Tyr	Ser	Asp
				325					330					335	
Leu	Gln	Ser	Met	Gly	Thr	Gly	Pro	Asp	Gly	Ser	Pro	Leu	Phe	Gly	Cys
			340					345					350		
Leu	Tyr	Glu	Ala	Asn	Asp	Tyr	Glu	Glu	Ile	Val	Phe	Leu	Met	Phe	Thr
		355					360					365			
Leu	Lys	Gln	Ala	Phe	Pro	Ala	Glu	Tyr	Leu	Pro	Gln	Glu	Pro	Lys	Ser
	370					375					380				
Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
385					390					395					400
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
				405					410					415	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
			420					425					430		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
		435					440					445			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
	450					455					460				

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 211

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 211

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

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80

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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

225 230 235 240
 Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330
 <210> 212
 <211> 330
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide
 <400> 212
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1 5 10 15
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

<210> 213

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 213

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

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80

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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285

Leu Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

<210> 214

<211> 330
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 214

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

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80

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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu

180

185

190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr
 245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

<210> 215

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 215

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

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

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

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285

Leu Thr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

<210> 216

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 216

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

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80

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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Tyr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

290

295

300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

<210> 217

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 217

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agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag      120
cggcggagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac      180
gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac      240
ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg      300
ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac      360
gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga      420
gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga      480
cctggacact gtctccagct gcacgacagg gctagatctc tgggtggtgcc tgcctacgcc      540
tatagaaagc tgcaccccaa acagcggcct attcctagcg ctttctgctt tctgagccac      600
gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag      660
gtggccgaag tggaaccggg cgagcagaga gtcgtgacct tgaacgccag atctcacctg      720
agattcagag tgcaggccca gagcacaac gacggcctgg atttccaaga gagccagctg      780
gtcaagaaac tgggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca      840
tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca cccacacac      900
agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct      960
tggagcgaac ctgttctgct ggccaagggc agcgtgcct acagcgatct gcagtctatg     1020

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```

ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa      1080
gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa      1140
gagcccaaatt cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg      1200
gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg      1260
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      1320
aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag      1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc      1500
atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg      1560
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc      1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      1680
cccgctgctgg actccgacgg ctctttcttc ctctatagca agctcaccgt ggacaagagc      1740
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      1800
tacacgcaga agagcctctc cctgtctccg ggtaaa                                1836

```

<210> 218

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 218

```

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

```

```

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
          20           25           30

```

```

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
          35           40           45

```

```

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
          50           55           60

```

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 219

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 219

gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60

agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cggcggagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac	360
gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga	420
gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga	480
cctggacact gtctccagct gcacgacagg gctagatctc tgggtggtgcc tgcctacgcc	540
tatagaaagc tgcaccccaa acagcggcct attcctagcg ctttctgctt tctgagccac	600
gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag	660
gtggccgaag tggaaaccgg cgagcagaga gtcgtgacct tgaacgccag atctcacctg	720
agattcagag tgcaggccca gagcacaac gacggcctgg atttccaaga gagccagctg	780
gtcaagaaac tgggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca	840
tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca cccacacac	900
agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct	960
tggagcgaac ctgttctgct ggccaagggc agcgtgcct acagcgatct gcagtctatg	1020
ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa	1080
gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa	1140
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg	1200
gggggaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctcccgg	1260
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	1320
aactggtacg tggacggcgt ggagggtgat aatgccaaga caaagccgcg ggaggagcag	1380
tacgccagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc	1500
atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg	1560
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1620
gacatgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1680
cccgtgctgg actccgacgg ctctttcttc ctctatagca agctcaccgt ggacaagagc	1740
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	1800
tacacgcaga agagcctaag cttgtctccg ggtaaa	1836

<211> 612
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 220

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro

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

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys

610

<210> 221

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 221

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agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag	120
cggcggagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac	180
gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac	240
ggccacagat ctatgaacct ctgtcctctg tacgatgaac agaccggcac actgtttctg	300
ttctttatcg ctatccccgg ccaagtgacc gaggaacagc agctgcagac aagagccaac	360
gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga	420
gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga	480
cctggacact gtctccagct gcacgacagg gctagatctc tgggtggtgcc tgcctacgcc	540
tatagaaagc tgcaccccaa acagcggcct attcctagcg ctttctgctt tctgagccac	600
gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag	660
gtggccgaag tggaaccgg cgagcagaga gtcgtgacct tgaacgccag atctcacctg	720
agattcagag tgcaggccca gagcacaac gacggcctgg atttccaaga gagccagctg	780
gtcaagaaac tgggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca	840
tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca cccacacac	900
agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct	960
tggagcgaac ctgttctgct ggccaagggc agcgtgcct acagcgatct gcagtctatg	1020
ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa	1080
gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa	1140
gagcccaaact cttctgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg	1200
gggggaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctcccg	1260

```

accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      1320
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc      1500
atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg      1560
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc      1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      1680
cccgtgctgg actccgacgg ctcttcttct ctctatagca agctcaccgt ggacaagagc      1740
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      1800
tacacgcaga agagcctctc cctgtctccg ggtaaa                                1836

```

<210> 222

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 222

```

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

```

```

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
          20          25          30

```

```

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
          35          40          45

```

```

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
          50          55          60

```

```

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65          70          75          80

```

```

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
          85          90          95

```

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Cys Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Cys Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 223

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 223

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agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag	120
cggcggagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac	180
gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac	240
ggccacagat ctatgaacct ctgtcctctg tacgatgaac agaccggcac actgtttctg	300
ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac	360
gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga	420
gatctgaccg acgccgcat cggacctgcc tatagagagt ggtccacctt cgccgttgga	480
cctggacact gtctccagct gcacgacagg gctagatctc tgggtggtgcc tgcctacgcc	540

tatagaaagc tgcaccccaa acagcggcct attcctagcg ctttctgctt tctgagccac	600
gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag	660
gtggccgaag tgtgtaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg	720
agattcagag tgcaggccca gagcacaac gacggcctgg atttccaaga gagccagctg	780
gtcaagaaac tgggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca	840
tctcctagaa gcggccctgg ctctccttgt cagtggctgc tgtatacaca cccacacac	900
agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct	960
tggagcgaac ctgttctgct ggccaagggc agcgtgcct acagcgatct gcagtctatg	1020
ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa	1080
gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa	1140
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg	1200
gggggaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctcccgg	1260
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	1320
aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag	1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc	1500
atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg	1560
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1680
cccgtgctgg actccgacgg ctctttcttc ctctatagca agctcaccgt ggacaagagc	1740
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	1800
tacacgcaga agagcctctc cctgtctccg ggtaaa	1836

<210> 224

<211> 611

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 224

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

His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln Ser
 20 25 30

Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His Ala
 35 40 45

Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His Gln
 50 55 60

Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp Gly
 65 70 75 80

His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly Thr
 85 90 95

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

Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr Ser
 115 120 125

Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp Ala
 130 135 140

Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly Pro
 145 150 155 160

Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val Pro
 165 170 175

Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro Ser
 180 185 190

Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg Gly
 195 200 205

His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val Glu

210		215		220
Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu Arg				
225		230	235	240
Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln Glu				
	245	250		255
Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys Gln				
	260	265		270
Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser Pro				
	275	280		285
Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg Ala				
	290	295	300	
Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala Trp				
305		310	315	320
Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp Leu				
	325	330		335
Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys Leu				
	340	345		350
Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr Leu				
	355	360		365
Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser Ser				
	370	375	380	
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly				
385		390	395	400
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met				
	405	410		415
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His				
	420	425	430	

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 435 440 445

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

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 465 470 475 480

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 485 490 495

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 500 505 510

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 515 520 525

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 530 535 540

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 545 550 555 560

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 565 570 575

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 580 585 590

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 595 600 605

Pro Gly Lys
 610

<210> 225

<211> 1833

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 225

gcatctctgc cttacctgca gaaagaaagc gtgttccagt ctggcgccca cgcctacaga	60
attcccgcgc tgctgtatct gccaggccag cagtctctgc tggctttcgc tgaacagcgg	120
cggagcaaga aggatgagca cgccgaactg atcgtgctgc ggagaggcga ttacgacgcc	180
ggcacacatc aggtgcagtg gcaggctcaa gaggtgggtg ctcaggctag actggacggc	240
cacagatcta tgaacccctg tcctctgtac gatgaacaga ccggcacact gtttctgttc	300
tttatcgcta tccccggcca agtgaccgag cagcagcagc tgagacaag agccaacgtg	360
accagactgt gttacgtgac ctccaccgac cacggcagaa cctgggtctag ccctagagat	420
ctgaccgacg ccgccatcgg acctgcctat agagagtggc ccaccttcgc cgttggacct	480
ggacactgtc tccagctgca cgacagggct agatctctgg tggcgcctgc ctacgcctat	540
agaaagctgc accccaaaca gcggcctatt cctagcgcct tctgctttct gagccacgat	600
cacggcagga catgggccag aggacatttc gtggcccagg acacactgga atgccaggtg	660
gccgaagtgg aaaccggcga gcagagagtc gtgaccctga acgccagatc tcacctgaga	720
ttcagagtgc aggcccagag cacaaacgac ggcctggatt tccaagagag ccagctggtc	780
aagaaactgg tggaacctcc tccaaccggc tgtcaggga gcgatgatcag ctttccatct	840
cctagaagcg gccctggctc tcctgctcag tggctgctgt atacacacc caccacacagc	900
tggcagagag ccgatctggg cgcctacctg aatcctagac ctctgctcc tgaggcttgg	960
agcgaacctg ttctgctggc caagggcagc gctgcctaca gcgatctgca gtctatgggc	1020
acaggccctg atggcagccc tctgtttggc tgtctgtacg aggccaacga ctacgaagag	1080
atcgtgttcc tgatgttcac cctgaagcag gcctttccag ccgagtacct gcctcaagag	1140
cccaaattct ctgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg	1200
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc	1260
cctgaggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac	1320
tggtagctgg acggcgtgga ggtgcataat gccaaagaaa agccgcggga ggagcagtac	1380
aacagcacgt accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc	1440
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc	1500

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tccaaagcca aagggcagcc ccgagaacca caggtctaca ccctgcccc atcccgggag      1560
gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac      1620
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc      1680
gtgctggact ccgacggctc cttcttcctc tatagcaagc tcaccgtgga caagagcagg      1740
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac      1800
acgcagaaga gcctctccct gtctccgggt aaa                                  1833

```

<210> 226

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 226

```

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

```

```

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
          20           25           30

```

```

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
          35           40           45

```

```

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
          50           55           60

```

```

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65           70           75           80

```

```

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
          85           90           95

```

```

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

```

```

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
          115          120          125

```

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 227

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 227

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agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag	120
cggcggagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac	180
gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac	240
ggccacagat ctatgaacct ctgtcctctg tacgatgaac agaccggcac actgtttctg	300
ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac	360
gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga	420
gatctgaccg acgccgcat cggacctgcc tatagagagt ggtccacctt cgccgttgga	480
cctggacact gtctccagct gcacgacagg gctagatctc tgggtggtgcc tgcctacgcc	540
tatagaaagc tgcaccccaa acagcggcct attcctagcg ctttctgctt tctgagccac	600
gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag	660
gtggccgaag tggaaccgg cgagcagaga gtcgtgacct tgaacgccag atctcacctg	720
agattcagag tgcaggccca gagcacaac gacggcctgg atttccaaga gagccagctg	780

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gtcaagaaac tgggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca      840
tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca cccacacac      900
agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct      960
tggagcgaac ctgttctgct ggccaagggc agcgtgcct acagcgatct gcagtctatg     1020
ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa     1080
gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa     1140
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg     1200
gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg      1260
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc     1320
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag     1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat     1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc     1500
atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccg      1560
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc     1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct     1680
cccgtgctgg actccgacgg ctctttcttc ctctatagca agctcaccgt ggacaagagc     1740
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac     1800
tacacgcaga agagcctctc cctgtctccg ggtaaa                                1836

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<210> 228

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 228

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

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Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
          20          25          30

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Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln

			245					250						255	
Glu	Ser	Gln	Leu	Val	Lys	Lys	Leu	Val	Glu	Pro	Pro	Pro	Thr	Gly	Cys
			260					265					270		
Gln	Gly	Ser	Val	Ile	Ser	Phe	Pro	Ser	Pro	Arg	Ser	Gly	Pro	Gly	Ser
		275					280					285			
Pro	Ala	Gln	Trp	Leu	Leu	Tyr	Thr	His	Pro	Thr	His	Ser	Trp	Gln	Arg
	290					295					300				
Ala	Asp	Leu	Gly	Ala	Tyr	Leu	Asn	Pro	Arg	Pro	Pro	Ala	Pro	Glu	Ala
305					310					315					320
Trp	Ser	Glu	Pro	Val	Leu	Leu	Ala	Lys	Gly	Ser	Ala	Ala	Tyr	Ser	Asp
				325					330					335	
Leu	Gln	Ser	Met	Gly	Thr	Gly	Pro	Asp	Gly	Ser	Pro	Leu	Phe	Gly	Cys
			340					345					350		
Leu	Tyr	Glu	Ala	Asn	Asp	Tyr	Glu	Glu	Ile	Val	Phe	Leu	Met	Phe	Thr
		355					360					365			
Leu	Lys	Gln	Ala	Phe	Pro	Ala	Glu	Tyr	Leu	Pro	Gln	Glu	Pro	Lys	Ser
	370					375					380				
Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
385					390					395					400
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
				405					410					415	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
			420					425					430		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
		435					440					445			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
	450					455					460				

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
595 600 605

Ser Pro Gly Lys
610

<210> 229

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 229

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cgggccagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac	180
gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac	240
ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg	300
ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac	360
gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga	420
gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga	480
cctggacact gtctccagct gcacgacagg gctagatctc tgggtggtgcc tgcctacgcc	540
tatagaaagc tgcaccccaa acagcggcct attcctagcg ctttctgctt tctgagccac	600
gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag	660
gtggccgaag tggaaaccgg cgagcagaga gtcgtgacct tgaacgccag atctcacctg	720
agattcagag tgcaggccca gagcacaac gacggcctgg atttccaaga gagccagctg	780
gtcaagaaac tgggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca	840
tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca cccacacac	900
agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct	960
tggagcgaac ctgttctgct ggccaagggc agcgtgcct acagcgatct gcagtctatg	1020
ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa	1080
gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa	1140
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg	1200
gggggaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctcccgg	1260
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	1320
aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag	1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc	1500
atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg	1560
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1680
cccgtgctgg actccgacgg ctctttcttc ctctatagca agctcaccgt ggacaagagc	1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800

tacacgcaga agagcctctc cctgtctccg ggtaaa 1836

<210> 230

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 230

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 231
 <211> 1836
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 231
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 cggcggagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180
 gcccctacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240
 ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300
 ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360
 gtgaccagac tgtgttacgt gacctcacc gaccacggca gaacctggtc tagccctaga 420
 gatctgaccg acgccgcat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480
 cctggacact gtctccagct gcacgacagg gctagatctc tgggtggtgcc tgcctacgcc 540
 tatagaaagc tgcaccccaa acagcggcct attcctagcg ctttctgctt tctgagccac 600
 gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660
 gtggccgaag tggaaaccgg cgagcagaga gtcgtgacct tgaacgccag atctcacctg 720
 agattcagag tgcaggccca gagcacaac gacggcctgg atttccaaga gagccagctg 780
 gtcaagaaac tgggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca 840
 tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca cccacacac 900
 agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960
 tggagcgaac ctgttctgct ggccaagggc agcgtgcct acagcgatct gcagtctatg 1020

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ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa      1080
gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa      1140
gagcccaaatt cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg      1200
ggggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg      1260
acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      1320
aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag      1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      1440
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atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg      1560
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc      1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      1680
cccggtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc      1740
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      1800
tacacgcaga agagcctctc cctgtctccg ggtaaa                                1836

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<210> 232

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 232

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Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
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Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
          20           25           30

```

```

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
          35           40           45

```

```

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
          50           55           60

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Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser

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

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 233

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 233

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cggcggagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac 180

gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240

ggccacagat ctatgaaccc ctgtcctctg tacgatgccc agaccggcac actgtttctg 300

ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360

gtgaccagac	tgtgttacgt	gacctccacc	gaccacggca	gaacctggtc	tagccctaga	420
gatctgaccg	acgccgccat	cggacctgcc	tatagagagt	ggtccacctt	cgccgttgga	480
cctggacact	gtctccagct	gcacgacagg	gctagatctc	tggtgggtgcc	tgccctacgcc	540
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gatcacggca	ggacatgggc	cagaggacat	ttcgtggccc	aggacacact	ggaatgccag	660
gtggccgaag	tggaaaccgg	cgagcagaga	gtcgtgaccc	tgaacgccag	atctcacctg	720
agattcagag	tgaggccca	gagcacaac	gacggcctgg	atttccaaga	gagccagctg	780
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tggagcgaac	ctgttctgct	ggccaagggc	agcgtgcct	acagcgatct	gcagtctatg	1020
ggcacaggcc	ctgatggcag	ccctctgttt	ggctgtctgt	acgaggccaa	cgactacgaa	1080
gagatcgtgt	tcctgatgtt	caccctgaag	caggcctttc	cagccgagta	cctgcctcaa	1140
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gggggaccgt	cagtcttctt	cttccccca	aaaccaagg	acaccctcat	gatctcccgg	1260
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aactgggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	1380
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgaccagga	ctggctgaat	1440
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atctccaaag	caaaggga	gccccgagaa	ccacaggtct	acaccctgcc	cccatcccgg	1560
gaggagatga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatcccagc	1620
gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	1680
cccgtgctgg	actccgacgg	ctccttcttc	ctctatagca	agctcaccgt	ggacaagagc	1740
aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	1800
tacacgcaga	agagcctctc	cctgtctccg	ggtaaa			1836

<210> 234

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 234

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 235
 <211> 1836
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 235
 gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac 60
 agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120
 cggcggagca agaaggatga gcacgccgaa ctgacgtgc tgccggagagg cgattacgac 180
 gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac 240
 ggccacagat ctatgaacc ctgtcctctg tacgatgaac agaccggcac actgtttctg 300
 ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac 360
 gtgaccagac tgtgtcaggt gacctccacc gaccacggca gaacctggtc tagccctaga 420
 gatctgaccg acgccgccat cggacctgcc tatagagagt ggtccacctt cgccgttgga 480
 cctggacact gtctccagct gcacgacagg gctagatctc tgggtggtgcc tgcctacgcc 540
 tatagaaagc tgcaccccaa acagcggcct attcctagcg ctttctgctt tctgagccac 600
 gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag 660
 gtggccgaag tggaaaccgg cgagcagaga gtcgtgacct tgaacgccag atctcacctg 720
 agattcagag tgcaggccca gagcacaac gacggcctgg atttccaaga gagccagctg 780
 gtcaagaaac tgggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca 840
 tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca cccacacac 900
 agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct 960
 tggagcgaac ctgttctgct ggccaagggc agcgtgcct acagcgatct gcagtctatg 1020
 ggacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa 1080
 gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa 1140
 gagcccaa at cttctgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 1200
 gggggaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctcccg 1260

```

acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      1320
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc      1500
atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg      1560
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc      1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      1680
cccgctgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc      1740
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      1800
tacacgcaga agagcctctc cctgtctccg ggtaaa                                1836

```

<210> 236

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 236

```

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

```

```

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
          20          25          30

```

```

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
          35          40          45

```

```

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
          50          55          60

```

```

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65          70          75          80

```

```

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
          85          90          95

```

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Ile Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

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

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 237

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 237

gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac	60
agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag	120
cggcggagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac	180
gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac	240
ggccacagat ctatgaacct ctgtcctctg tacgatgaac agaccggcac actgtttctg	300
ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac	360
gtgaccagac tgtgttacgt gacctcacc gaccacggca gaacctggtc tagccctaga	420
gatctgaccg acgccgcat cggacctgcc tatagagagt ggtccacctt cgccgttgga	480
cctggacact gtctccagct gcacgacagg gctagatctc tgggtggtgcc tgcctacgcc	540
tatagaaagc tgcaccccat ccagcggcct attcctagcg ctttctgctt tctgagccac	600

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gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag      660
gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg      720
agattcagag tgcaggccca gagcacaac gacggcctgg atttccaaga gagccagctg      780
gtcaagaaac tgggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca      840
tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca cccacacac      900
agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct      960
tggagcgaac ctgttctgct ggccaagggc agcgtgcct acagcgatct gcagtctatg     1020
ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa     1080
gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa     1140
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg     1200
gggggaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctcccgg     1260
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc     1320
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag     1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat     1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc     1500
atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg     1560
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc     1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct     1680
cccgtgctgg actccgacgg ctctttcttc ctctatagca agctcaccgt ggacaagagc     1740
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac     1800
tacacgcaga agagcctctc cctgtctccg ggtaaa                                1836

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<210> 238

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 238

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 239

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 239

gatgcatctc tgccttacct gcagaaagaa agcgtgttcc agtctggcgc ccacgcctac	60
agaattcccc ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag	120
cggcggagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac	180
gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac	240
ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg	300
ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac	360
gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga	420
gatctgaccg acgccgcat cggacctgcc tatagagagt ggtccacctt cgccgttgga	480
cctggacact gtctccagct gcacgacagg gctagatctc tgggtggtgcc tgcctacgcc	540
tatagaaagc tgcaccccaa acagcggcct attcctagcg ctttctgctt tctgagccac	600
gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag	660
gtggccgaag tggaaaccgg cgagcagaga gtcgtgacct tgaacgccag atctcacctg	720
agagccagag tgcaggccca gagcacaac gacggcctgg atttccaaga gagccagctg	780
gtcaagaaac tgggtgaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca	840
tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca cccacacac	900
agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct	960
tggagcgaac ctgttctgct ggccaagggc agcgtgcct acagcgatct gcagtctatg	1020
ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa	1080
gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa	1140
gagcccaa at cttctgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg	1200
gggggaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctcccgg	1260
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	1320
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag	1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc	1500

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atctccaaag ccaaaggga gccccgagaa ccacaggtct acaccctgcc cccatcccgg      1560
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc      1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      1680
cccgtgctgg actccgacgg ctctttcttc ctctatagca agctcaccgt ggacaagagc      1740
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      1800
tacacgcaga agagcctctc cctgtctccg ggtaaa                                1836

```

<210> 240

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 240

```

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

```

```

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20              25              30

```

```

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
35              40              45

```

```

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50              55              60

```

```

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65              70              75              80

```

```

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85              90              95

```

```

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

```

```

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115             120             125

```

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys

340

345

350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 241

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 241

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agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag	120
cggcggagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac	180
gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac	240
ggccacagat ctatgaacct ctgtcctctg tacgatgaac agaccggcac actgtttctg	300
ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac	360
gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga	420
gatctgaccg acgccgcat cggacctgcc tatagagagt ggtccacctt cgccgttgga	480
cctggacact gtctccagct gcacgacagg gctagatctc tgggtggtgcc tgcctacgcc	540
tatagaaagc tgcaccccaa acagcggcct attcctagcg ctttctgctt tctgagccac	600
gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag	660
gtggccgaag tggaaaccgg cgagcagaga gtcgtgacct tgaacgccag atctcacctg	720
agattcagag tgcaggccca gagcaciaaac gacggcctgg atttccaaga gagccagctg	780
gtcaagaaac tgggtggaacc tcctccacag ggctgtcagg gaagcgtgat cagctttcca	840


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tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca cccacacac      900
agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct      960
tggagcgaac ctgttctgct ggccaagggc agcgctgcct acagcgatct gcagtctatg     1020
ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa     1080
gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa     1140
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg     1200
gggggaccgt cagtcttctt cttccccca aaaccaagg acaccctcat gatctcccg      1260
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc     1320
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag     1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat     1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc     1500
atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccg      1560
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc     1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct     1680
cccgtgctgg actccgacgg ctcttcttct ctctatagca agctcaccgt ggacaagagc     1740
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac     1800
tacacgcaga agagcctctc cctgtctccg ggtaaa                                1836

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<210> 242

<211> 612

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 242

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

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Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
          20          25          30

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Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

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

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys
 610

<210> 243

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 243

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agaattcccg ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag 120

cggcggagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac	180
gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac	240
ggccacagat ctatgaaccc ctgtcctctg tacgatgaac agaccggcac actgtttctg	300
ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac	360
gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga	420
gatctgaccg acgccgcat cggacctgcc tatagagagt ggtccacctt cgccgttgga	480
cctggacact gtctccagct gcacgacagg gctagatctc tgggtggtgcc tgcctacgcc	540
tatagaaagc tgcaccccaa acagcggcct attcctagcg ctttctgctt tctgagccac	600
gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag	660
gtggccgaag tggaaaccgg cgagcagaga gtcgtgacct tgaacgccag atctcacctg	720
agattcagag tgcaggccca gagcacaac gacggcctgg atttccaaga gagccagctg	780
gtcaagaaac tgggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca	840
tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca cccacacac	900
agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct	960
tggagcgaac ctgttctgct ggccaagggc agctgtgcct acagcgatct gcagtctatg	1020
ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa	1080
gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa	1140
gagcccaaatt cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg	1200
gggggaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctcccgg	1260
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	1320
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag	1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc	1500
atctccaaag ccaaagggca gccccgagaa ccacaggtct acaccctgcc cccatcccgg	1560
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1680
cccgtgctgg actccgacgg ctctttcttc ctctatagca agctcaccgt ggacaagagc	1740

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1800
 tacacgcaga agagcctctc cctgtctccg ggtaaa 1836

<210> 244
 <211> 874
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 244
 Asp Ala Ser Leu Pro Tyr Leu Gln Lys Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
 50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
 85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
 180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Gly Gly Gly Gly

370

375

380

Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 625 630 635 640

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 645 650 655

Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala
 660 665 670

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly
 675 680 685

Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala
 690 695 700

Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
 705 710 715 720

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
 725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
 785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr

805

810

815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 820 825 830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
 850 855 860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 865 870

<210> 245

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 245

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tcttgtgccg ccagcggctt caacatcaag gacacctaca tccactgggt ccgacaggcc	120
cctggcaaag gacttgaatg ggtcgccaga atctacccca ccaacggcta caccagatac	180
gccgactctg tgaagggcag attcaccatc agcgccgaca ccagcaagaa caccgcctac	240
ctgcagatga acagcctgag agccgaggac accgccgtgt actactgttc tagatgggga	300
ggcgacggct tctacgcat ggattattgg ggccagggca ccctggtcac cgtttcttct	360
gctagcacca agggcccatc cgtcttcccc ctggcaccct cctccaagag cacctctggg	420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacggtgtcc	480
tggaactcag gcgctctgac cagcggcgtg cacaccttcc cggtgtcct acagtcctca	540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc	600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	660
aaatcttgtg acaaaaactca cacatgcca ccgtgcccag cacctgaact cctgggggga	720
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt	780

gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	840
tacgtggacg gcgtgggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac	900
agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag	960
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	1020
aaagccaaag ggcagccccg agaaccacag gtctacaccc tgcccccatc ccgggaggag	1080
atgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc	1140
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	1200
ctggactccg acggctcctt cttcctcacc agcaagctca ccgtggacaa gagcaggtgg	1260
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	1320
cagaagagcc tctccctgtc tccgggtaaa	1350

<210> 246

<211> 1836

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 246

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agaattcccc ctctgctgta tctgccaggc cagcagtctc tgctggcttt cgctgaacag	120
cggcggagca agaaggatga gcacgccgaa ctgatcgtgc tgcggagagg cgattacgac	180
gccggcacac atcaggtgca gtggcaggct caagaggtgg tggctcaggc tagactggac	240
ggccacagat ctatgaacct ctgtcctctg tacgatgaac agaccggcac actgtttctg	300
ttctttatcg ctatccccgg ccaagtgacc gagcagcagc agctgcagac aagagccaac	360
gtgaccagac tgtgttacgt gacctccacc gaccacggca gaacctggtc tagccctaga	420
gatctgaccg acgccgcat cggacctgcc tatagagagt ggtccacctt cgccgttgga	480
cctggacact gtctccagct gcacgacagg gctagatctc tgggtggcgcc tgcctacgcc	540
tatagaaagc tgcaccccaa acagcggcct attcctagcg ctttctgctt tctgagccac	600
gatcacggca ggacatgggc cagaggacat ttcgtggccc aggacacact ggaatgccag	660

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gtggccgaag tggaaaccgg cgagcagaga gtcgtgaccc tgaacgccag atctcacctg      720
agattcagag tgcaggccca gagcacaac gacggcctgg atttccaaga gagccagctg      780
gtcaagaaac tgggtggaacc tcctccaacc ggctgtcagg gaagcgtgat cagctttcca      840
tctcctagaa gcggccctgg ctctcctgct cagtggctgc tgtatacaca cccacacac      900
agctggcaga gagccgatct gggcgcctac ctgaatccta gacctcctgc tcctgaggct      960
tggagcgaac ctgttctgct ggccaagggc agcgtgcct acagcgatct gcagtctatg     1020
ggcacaggcc ctgatggcag ccctctgttt ggctgtctgt acgaggccaa cgactacgaa     1080
gagatcgtgt tcctgatgtt caccctgaag caggcctttc cagccgagta cctgcctcaa     1140
gagcccaaat cttctgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg     1200
gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg     1260
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc     1320
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag     1380
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat     1440
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc     1500
atctccaaag ccaaaggga gccccgagaa ccacaggtct acaccctgcc cccatcccgg     1560
gaggagatga ccaagaacca ggtcagcctg tactgcctgg tcaaaggctt ctatcccagc     1620
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct     1680
cccgtgctgg actccgacgg ctcttcttc ctctatagca agctcaccgt ggacaagagc     1740
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac     1800
tacacgcaga agagcctctc cctgtctccg ggtaaa                                1836

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<210> 247

<211> 874

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>

<221> MOD_RES

<222> (1)..(1)

<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr, Val, or not present

<220>

<221> MOD_RES

<222> (6)..(6)

<223> Phe, Trp, Tyr or Val

<220>

<221> MOD_RES

<222> (9)..(9)

<223> Lys or Asp

<220>

<221> MOD_RES

<222> (42)..(42)

<223> Arg or Ala

<220>

<221> MOD_RES

<222> (62)..(62)

<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>

<221> MOD_RES

<222> (93)..(93)

<223> Ala, Glu, or Lys

<220>

<221> MOD_RES

<222> (126)..(126)

<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>

<221> MOD_RES

<222> (187)..(187)

<223> Arg, Ile, or Lys

<220>

<221> MOD_RES

<222> (242)..(242)

<223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser, Val, Trp, or Tyr

<220>

<221> MOD_RES

<222> (270)..(270)

<223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>

<221> MOD_RES

<222> (301)..(301)

<223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Thr, Val, Trp, or Tyr

<220>

<221> MOD_RES

<222> (302)..(302)

<223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>

<221> MOD_RES

<222> (332)..(332)

<223> Ala, Cys, Ser, or Val

<220>

<221> MOD_RES

<222> (363)..(363)

<223> Val or Arg

<220>

<221> MOD_RES

<222> (365)..(365)

<223> Leu, Gln, His, Ile, Lys, or Ser

<220>

<221> MOD_RES

<222> (381)..(390)

<223> This region may encompass one of the following sequences:
"GGGGS" or "GGGSGGGGS" or "EPKSS"

<400> 247

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

Ala	His	Ala	Tyr	Arg	Ile	Pro	Ala	Leu	Leu	Tyr	Leu	Pro	Gly	Gln	Gln
			20					25					30		

Ser	Leu	Leu	Ala	Phe	Ala	Glu	Gln	Arg	Xaa	Ser	Lys	Lys	Asp	Glu	His
		35					40					45			

Ala	Glu	Leu	Ile	Val	Leu	Arg	Arg	Gly	Asp	Tyr	Asp	Ala	Xaa	Thr	His
	50					55					60				

Gln	Val	Gln	Trp	Gln	Ala	Gln	Glu	Val	Val	Ala	Gln	Ala	Arg	Leu	Asp
65					70					75				80	

Gly	His	Arg	Ser	Met	Asn	Pro	Cys	Pro	Leu	Tyr	Asp	Xaa	Gln	Thr	Gly
				85					90					95	

Thr	Leu	Phe	Leu	Phe	Phe	Ile	Ala	Ile	Pro	Gly	Gln	Val	Thr	Glu	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Xaa Xaa Xaa
 370 375 380

Xaa Xaa Xaa Xaa Xaa Xaa Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

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

530

535

540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 625 630 635 640

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 645 650 655

Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala
 660 665 670

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly
 675 680 685

Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala
 690 695 700

Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
 705 710 715 720

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
 725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
 785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 805 810 815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 820 825 830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
 850 855 860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 865 870

<210> 248

<211> 874

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<220>

<221> MOD_RES

<222> (1)..(1)

<223> Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Thr,
 Val, or not present

<220>

<221> MOD_RES

<222> (2)..(2)

<223> Ala or Lys

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Asn or Leu

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Pro or His

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Phe, Trp, Tyr or Val

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Lys or Asp

<220>
<221> MOD_RES
<222> (42)..(42)
<223> Ala or Arg

<220>
<221> MOD_RES
<222> (44)..(44)
<223> Lys, Arg, or Glu

<220>
<221> MOD_RES
<222> (45)..(45)
<223> Lys, Ala, Arg, or Glu

<220>
<221> MOD_RES
<222> (54)..(54)
<223> Leu or Met

<220>
<221> MOD_RES
<222> (62)..(62)
<223> Pro, Asn, Asp, His, Glu, Gly, Ser or Thr

<220>
<221> MOD_RES
<222> (69)..(69)
<223> Gln or His

<220>
<221> MOD_RES
<222> (78)..(78)
<223> Arg or Lys

<220>
<221> MOD_RES
<222> (80)..(80)
<223> Asp or Pro

<220>
<221> MOD_RES
<222> (93)..(93)
<223> Ala, Glu or Lys

<220>
<221> MOD_RES
<222> (107)..(107)
<223> Gly or Asp

<220>
<221> MOD_RES
<222> (108)..(108)
<223> Gln or His

<220>
<221> MOD_RES
<222> (112)..(112)
<223> Gln, Arg, or Lys

<220>
<221> MOD_RES
<222> (125)..(125)
<223> Ala, Cys, Ile, Ser, Val, or Leu

<220>
<221> MOD_RES
<222> (126)..(126)
<223> Gln, Leu, Glu, Phe, His, Ile, Leu, or Tyr

<220>
<221> MOD_RES
<222> (150)..(150)
<223> Ala or Val

<220>
<221> MOD_RES
<222> (164)..(164)
<223> Cys or Gly

<220>
<221> MOD_RES
<222> (170)..(170)
<223> Arg or Pro

<220>
<221> MOD_RES
<222> (171)..(171)

<223> Ala or Gly

<220>

<221> MOD_RES

<222> (187)..(187)

<223> Arg, Ile, or Lys

<220>

<221> MOD_RES

<222> (188)..(188)

<223> Gln or Pro

<220>

<221> MOD_RES

<222> (189)..(189)

<223> Arg or Pro

<220>

<221> MOD_RES

<222> (196)..(196)

<223> Ala, Cys, Leu, or Val

<220>

<221> MOD_RES

<222> (213)..(213)

<223> Ala, Cys, Asn, Ser, or Thr

<220>

<221> MOD_RES

<222> (217)..(217)

<223> Leu, Ala, or Val

<220>

<221> MOD_RES

<222> (225)..(225)

<223> Glu or Pro

<220>

<221> MOD_RES

<222> (239)..(239)

<223> His or Pro

<220>

<221> MOD_RES

<222> (240)..(240)

<223> Leu, Asp, Asn, or Tyr

<220>

<221> MOD_RES

<222> (241)..(241)

<223> Arg, Ala, Asp, Leu, Gln, or Tyr

<220>

<221> MOD_RES

<222> (242)..(242)
 <223> Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser,
 Val, Trp, or Tyr

<220>
 <221> MOD_RES
 <222> (244)..(244)
 <223> Val, Ile, or Lys

<220>
 <221> MOD_RES
 <222> (249)..(249)
 <223> Thr or Ala

<220>
 <221> MOD_RES
 <222> (251)..(251)
 <223> Asp or Gly

<220>
 <221> MOD_RES
 <222> (257)..(257)
 <223> Glu, Lys, or Pro

<220>
 <221> MOD_RES
 <222> (258)..(258)
 <223> Ser or Cys

<220>
 <221> MOD_RES
 <222> (260)..(260)
 <223> Leu, Asp, Phe, Gln, or Thr

<220>
 <221> MOD_RES
 <222> (265)..(265)
 <223> Val or Phe

<220>
 <221> MOD_RES
 <222> (270)..(270)
 <223> Gln, Ala, His, Phe, Pro, Ser, or Thr

<220>
 <221> MOD_RES
 <222> (272)..(272)
 <223> Cys or Val

<220>
 <221> MOD_RES
 <222> (292)..(292)
 <223> Trp or Arg

<220>
 <221> MOD_RES
 <222> (301)..(301)
 <223> Ser, Arg, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
 Pro, Gln, Thr, Val, Trp, or Tyr

<220>
 <221> MOD_RES
 <222> (302)..(302)
 <223> Trp, Lys, Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn,
 Pro, Gln, Arg, Ser, Thr, Val, or Tyr

<220>
 <221> MOD_RES
 <222> (325)..(325)
 <223> Lys or Val

<220>
 <221> MOD_RES
 <222> (332)..(332)
 <223> Ala, Cys, Ser, or Val

<220>
 <221> MOD_RES
 <222> (352)..(352)
 <223> Cys, Leu, or Val

<220>
 <221> MOD_RES
 <222> (363)..(363)
 <223> Val or Arg

<220>
 <221> MOD_RES
 <222> (365)..(365)
 <223> Leu, Gln, His, Ile, Lys, or Ser

<220>
 <221> MOD_RES
 <222> (381)..(390)
 <223> This region may encompass one of the following sequences:
 "GGGGS" or "GGGGSGGGGS" or "EPKSS"

<400> 248
 Xaa Xaa Ser Xaa Xaa Xaa Leu Gln Xaa Glu Ser Val Phe Gln Ser Gly
 1 5 10 15

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
 20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Xaa Ser Xaa Xaa Asp Glu His
 35 40 45

Ala Glu Leu Ile Val Xaa Arg Arg Gly Asp Tyr Asp Ala Xaa Thr His
 50 55 60

Gln Val Gln Trp Xaa Ala Gln Glu Val Val Ala Gln Ala Xaa Leu Xaa
 65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Xaa Gln Thr Gly
 85 90 95

Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Xaa Xaa Val Thr Glu Xaa
 100 105 110

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Xaa Xaa Val Thr
 115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
 130 135 140

Ala Ala Ile Gly Pro Xaa Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
 145 150 155 160

Pro Gly His Xaa Leu Gln Leu His Asp Xaa Xaa Arg Ser Leu Val Val
 165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Xaa Xaa Xaa Pro Ile Pro
 180 185 190

Ser Ala Phe Xaa Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
 195 200 205

Gly His Phe Val Xaa Gln Asp Thr Xaa Glu Cys Gln Val Ala Glu Val
 210 215 220

Xaa Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser Xaa Xaa
 225 230 235 240

Xaa Xaa Arg Xaa Gln Ala Gln Ser Xaa Asn Xaa Gly Leu Asp Phe Gln
 245 250 255

Xaa Xaa Gln Xaa Val Lys Lys Leu Xaa Glu Pro Pro Pro Xaa Gly Xaa
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Xaa Leu Leu Tyr Thr His Pro Thr His Xaa Xaa Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Xaa Leu Leu Ala Lys Gly Ser Xaa Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Xaa
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Xaa Phe Xaa Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Xaa Xaa Xaa Xaa
 370 375 380

Xaa Xaa Xaa Xaa Xaa Xaa Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 385 390 395 400

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 405 410 415

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 420 425 430

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 435 440 445

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 450 455 460

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 465 470 475 480

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 485 490 495

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 500 505 510

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 515 520 525

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 530 535 540

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 545 550 555 560

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 565 570 575

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 580 585 590

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 595 600 605

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
 625 630 635 640

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 645 650 655

Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala
 660 665 670

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly
 675 680 685

Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala
 690 695 700

Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala
 705 710 715 720

Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe
 725 730 735

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 755 760 765

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 770 775 780

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val
 785 790 795 800

Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 805 810 815

Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 820 825 830

Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 835 840 845

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
 850 855 860

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 865 870

<210> 249

<211> 869

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 249

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

Ala His Ala Tyr Arg Ile Pro Ala Leu Leu Tyr Leu Pro Gly Gln Gln
20 25 30

Ser Leu Leu Ala Phe Ala Glu Gln Arg Arg Ser Lys Lys Asp Glu His
35 40 45

Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Gly Thr His
50 55 60

Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp
65 70 75 80

Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Glu Gln Thr Gly
85 90 95

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

Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Tyr Val Thr
115 120 125

Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp
130 135 140

Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly
145 150 155 160

Pro Gly His Cys Leu Gln Leu His Asp Arg Ala Arg Ser Leu Val Val
165 170 175

Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Lys Gln Arg Pro Ile Pro
180 185 190

Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg
195 200 205

Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val
 210 215 220

Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu
 225 230 235 240

Arg Phe Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln
 245 250 255

Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Thr Gly Cys
 260 265 270

Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser
 275 280 285

Pro Ala Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg
 290 295 300

Ala Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala
 305 310 315 320

Trp Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Ala Ala Tyr Ser Asp
 325 330 335

Leu Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys
 340 345 350

Leu Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr
 355 360 365

Leu Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln Glu Pro Lys Ser
 370 375 380

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 385 390 395 400

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 420 425 430

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 435 440 445

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 450 455 460

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 465 470 475 480

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 485 490 495

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 500 505 510

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 515 520 525

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 530 535 540

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 545 550 555 560

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 565 570 575

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 580 585 590

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 595 600 605

Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 610 615 620

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 625 630 635 640

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile
645 650 655

Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
660 665 670

Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala
675 680 685

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

Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
705 710 715 720

Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr
725 730 735

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
740 745 750

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
755 760 765

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
770 775 780

Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
785 790 795 800

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu
805 810 815

Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp
820 825 830

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
835 840 845

Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr
 850 855 860

Lys Val Glu Ile Lys
 865

<210> 250
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 10xHis tag

<400> 250
 His His His His His His His His His His His
 1 5 10

<210> 251
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<220>
 <221> SITE
 <222> (1)..(15)
 <223> This sequence may encompass 1-5 "Gly Gly Pro"
 repeating units

<400> 251
 Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Gly Pro
 1 5 10 15

<210> 252
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<220>

<221> SITE
 <222> (1)..(25)
 <223> This sequence may encompass 1-5 "Gly Gly Gly Gly Ser"
 repeating units

<400> 252
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
 20 25

<210> 253
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 6xHis tag

<400> 253
 His His His His His His
 1 5

<210> 254
 <211> 5
 <212> PRT
 <213> Homo sapiens

<400> 254
 Leu His Pro Ile Gln
 1 5

<210> 255
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 255
 Thr Phe Ala Val Gly Pro Gly His Cys Leu
 1 5 10

<210> 256
 <211> 7
 <212> PRT
 <213> Petromyzon marinus

<400> 256

Cys His Cys Arg Ile Val Met
1 5

<210> 257
<211> 7
<212> PRT
<213> Carlito syrichta

<400> 257
Leu Arg Ala Arg Val Gln Ala
1 5

<210> 258
<211> 7
<212> PRT
<213> Saccoglossus kowalevskii

<400> 258
Cys Arg Cys Arg Ile Ile Ala
1 5

<210> 259
<211> 7
<212> PRT
<213> Lygus hesperus

<400> 259
His Pro Thr His Gln Gly Val
1 5

<210> 260
<211> 7
<212> PRT
<213> Rattus norvegicus

<400> 260
Ile Gly Ala Arg Val Gln Ala
1 5

<210> 261
<211> 7
<212> PRT
<213> Branchiostoma floridae

<400> 261
Cys His Cys Lys Ala Phe Leu
1 5

<210> 262
 <211> 7
 <212> PRT
 <213> Alces americanus

<400> 262
 Leu Gly Ala Arg Val Gln Ala
 1 5

<210> 263
 <211> 7
 <212> PRT
 <213> Pan troglodytes

<400> 263
 Leu Gln Ala Arg Val Gln Ala
 1 5

<210> 264
 <211> 7
 <212> PRT
 <213> Xenopus tropicalis

<400> 264
 Lys His Phe Arg Val Glu Ala
 1 5

<210> 265
 <211> 7
 <212> PRT
 <213> Gallus gallus

<400> 265
 Arg Gly Ala Arg Ile Gln Ala
 1 5

<210> 266
 <211> 7
 <212> PRT
 <213> Anolis carolinensis

<400> 266
 Asp Lys Ser Arg Ala Glu Ala
 1 5

<210> 267
 <211> 7
 <212> PRT
 <213> Ornithorhynchus anatinus

<400> 267

Arg Gly Ser Arg Val Gln Ala
1 5

<210> 268

<211> 7

<212> PRT

<213> Branchiostoma floridae

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Cys Ser Cys Lys Ala Phe Met
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<210> 269

<211> 7

<212> PRT

<213> Strongylocentrotus purpuratus

<400> 269

Cys His Cys Arg Leu Gln Ser
1 5

<210> 270

<211> 7

<212> PRT

<213> Strongylocentrotus purpuratus

<400> 270

Cys Asn Cys Arg Ile Gln Ala
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<210> 271

<211> 7

<212> PRT

<213> Otolemur garnettii

<400> 271

Leu Arg Ala Arg Val Gln Ala
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<210> 272

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<213> Alligator sinensis

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Arg Gly Ala Arg Val Gln Ala
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 <213> Chlorocebus sabaeus

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<210> 274
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 <213> Anas platyrhynchos platyrhynchos

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<210> 275
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 <213> Latimeria chalumnae

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 Leu Gly Ser Arg Val Gln Ala
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<400> 277
 Leu Gly Ser Arg Val Gln Ala
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<210> 278
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 <213> *Lonchura striata domestica*

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<210> 279
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<210> 280
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 <213> *Ovis aries*

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 His Gln Ala Arg Val Gln Ala
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<210> 282
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 <213> *Equus caballus*

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 Leu Arg Ala Arg Val Gln Ala
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<210> 283
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<400> 283

Leu Arg Ala Arg Val Gln Ala
1 5

<210> 284
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<213> *Xenopus tropicalis*

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Cys Gly Lys Arg Ile Glu Ala
1 5

<210> 285
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<213> *Branchiostoma floridae*

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His Ala Arg Arg Gln Gln Ser
1 5

<210> 286
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<213> *Karenia brevis*

<400> 286
Phe Phe Arg Thr Arg Thr
1 5

<210> 287
<211> 7
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<213> *Patagioenas fasciata monilis*

<400> 287
Arg Gly Ala Arg Ile Gln Ala
1 5

<210> 288
<211> 7
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<213> *Saccoglossus kowalevskii*

<400> 288
Cys Lys Cys Arg Ile Phe Ser
1 5

<210> 289
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 <212> PRT
 <213> *Petromyzon marinus*

<400> 289
 Cys Arg Cys Arg Ile Val Ile
 1 5

<210> 290
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 <213> *Anolis carolinensis*

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 Glu Gln Cys Arg Ala Glu Ala
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<210> 291
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<400> 291
 Cys Ser Cys Arg Ile Ile Thr
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<210> 292
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 His Glu Phe Arg Val Gln Ala
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<210> 293
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<400> 293
 Arg Gly Ala Arg Ile Gln Ala
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<210> 294
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 <213> *Branchiostoma floridae*

<400> 294
 Cys Asn Cys Lys Met Ile Met
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 <211> 7
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<400> 295
 Leu Arg Ala Arg Ile Gln Ala
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<210> 296
 <211> 7
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 Leu Gly Arg Arg Val Gln Ala
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<210> 297
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 His Lys Leu Arg Val Gln Ala
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<400> 298
 Leu Arg Ala Arg Ile Gln Ala
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<210> 299
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 <213> Ailuropoda melanoleuca

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<210> 300

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<213> *Anolis carolinensis*

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Asp Arg Tyr Arg Ala Glu Ala
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<210> 301

<211> 7

<212> PRT

<213> *Mesocricetus auratus*

<400> 301

Leu Gly Ala Arg Val Gln Ala
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<210> 302

<211> 7

<212> PRT

<213> *Alligator mississippiensis*

<400> 302

Arg Gly Ala Arg Val Gln Ala
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<210> 303

<211> 7

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<213> *Mustela putorius furo*

<400> 303

Leu Gly Ala Arg Val Gln Ala
1 5

<210> 304

<211> 7

<212> PRT

<213> *Castor fiber*

<400> 304

Leu Gly Ala Arg Val Gln Ala
1 5

<210> 305

<211> 7

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<400> 305
 Gln Ala Thr Arg Gln Glu Ser
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<210> 306
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 <213> *Paracentrotus lividus*

<400> 306
 Lys Lys Pro His Pro Arg Ser
 1 5

<210> 307
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 <213> *Ictidomys tridecemlineatus*

<400> 307
 Arg Gly Ala Arg Val Gln Ala
 1 5

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<400> 308
 Lys Gly Ala Arg Ile Gln Ala
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<210> 309
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 <213> *Cavia porcellus*

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 Gln Lys Ala Arg Val Gln Ala
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<210> 310
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 <213> *Sus scrofa*

<400> 310

Leu Gln Ala Arg Val Gln Ala
1 5

<210> 311
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<213> Canis lupus familiaris

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Arg Arg Ala Arg Val Gln Ala
1 5

<210> 312
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Cys Ser Cys Arg Ile Gln Ala
1 5

<210> 313
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Leu Arg Ala Arg Val Gln Ala
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Arg Gly Cys Arg Ala Val Ala
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Arg Gly Ala Arg Ile Gln Ala
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<210> 316
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 Trp Gly Ala Arg Ile Gln Ala
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 <213> *Mus musculus*

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 Leu Gly Ala Arg Val Gln Ala
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 Leu Gly Ala Arg Val Gln Ala
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 Leu Gly Ala Arg Val Gln Ala
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 Leu Gly Ala Arg Val Gln Ala
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 Gly Lys Lys Arg Ile Glu Ala
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 Leu Arg Ala Arg Val Gln Ala
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<210> 323
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 Gln Gln Thr Arg Ala Ala Ile
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<210> 324
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 <213> *Macaca mulatta*

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 Leu Arg Ala Arg Ile Gln Ala
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 Leu Gly Phe Arg Val Gln Ala
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<210> 327
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 His Lys Tyr Arg Ala Gly Ala
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 Ile Gly Ala Arg Val Gln Ala
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<210> 329
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 Arg Gly Ala Arg Val Gln Ala
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 Arg Gly Ala Arg Val Gln Ala
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 Leu Arg Ala Arg Val Gln Ala
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<210> 332
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<212> PRT
 <213> *Karenia brevis*

<400> 332
 Gly Arg Gly Val Ala
 1 5

<210> 333
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<400> 333
 Cys Ser Cys Arg Ile Val Ile
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<210> 334
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 <213> *Myotis lucifugus*

<400> 334
 Arg Gly Ala Arg Ile Gln Ala
 1 5

<210> 335
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 <213> *Gorilla gorilla gorilla*

<400> 335
 Leu Arg Ala Arg Val Gln Ala
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<210> 336
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<400> 336
 Arg Gly Ala Arg Ile Gln Ala
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<210> 337
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<400> 337

Arg Arg Ala Arg Val Gln Ala
1 5

<210> 338
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Leu Gly Ala Arg Val Gln Ala
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<210> 339
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Leu Arg Ala Arg Val Gln
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Leu Arg Ala Arg Ile Gln
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Leu Arg Tyr Arg Pro Gln
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Leu Arg Asn Arg Pro Gln
1 5