

SEQUENCE LISTING

<110> Massachusetts Institute of Technology

<120> LIGAND DISCOVERY AND GENE DELIVERY VIA RETROVIRAL SURFACE DISPLAY

<130> 12165MAS/VB

<140> NZ 782090

<141> 2021-11-06

<150> PCT/US2020/024175

<151> 2020-03-23

<150> US 62/851,889

<151> 2019-05-23

<160> 54

<170> PatentIn version 3.5

<210> 1

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 1

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Gly	Leu	Glu	Ala
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Pro Phe Lys

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Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Ala
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Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
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Lys

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Gly Ala Pro Gly Ala Ser
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<213> Artificial Sequence

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<211> 5

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<213> Artificial Sequence

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<400> 7

Gly Gly Gly Gly Ser
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<211> 33

<212> PRT

<213> Artificial Sequence

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<223> Synthetic Polypeptide

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Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu Pro Phe

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25

30

Lys

<210> 9

<211> 39

<212> PRT

<213> Artificial Sequence

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<223> Synthetic Polypeptide

<400> 9

Ala Ser Gly Gly Gly Gly Ser Gly Glu Leu Ala Ala Ile Lys Gln Glu
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Leu Ala Ala Ile Lys Lys Glu Leu Ala Ala Ile Lys Trp Glu Leu Ala
 20 25 30

Ala Ile Lys Gln Gly Ala Gly
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<210> 10

<211> 14

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<213> Artificial Sequence

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<223> Synthetic Polypeptide

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Ala Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
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<210> 11

<211> 1536

<212> DNA

<213> Artificial Sequence

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ccgtcaagct cagatttaaa ttggcataat gacttaatag gcacagccat acaagtcaaa	180
atgccaaga gtcacaaggc tattcaagca gacggttgga tgtgtcatgc ttccaaatgg	240
gtcactactt gtgatttccg ctggtatgga ccgaagtata taacacagtc catccgatcc	300
ttcactccat ctgtagaaca atgcaaggaa agcattgaac aaacgaaaca aggaacttgg	360
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gattcacagt tcatcaacgg aaaatgcagc aattacatat gccccactgt ccataactct	540
acaacctggc attctgacta taaggtcaaa gggctatgtg attctaact cattttccatg	600
gacatcacct tcttctcaga ggacggagag ctatcatccc tgggaaagga gggcacaggg	660
ttcagaagta actactttgc ttatgaaact ggaggcaagg cctgcaaaat gcaatactgc	720
aagcattggg gagtcaact cccatcaggt gtctggttcg agatggctga taaggatctc	780
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tggaagct ctattgcctc ttttttcttt atcatagggt taatcattgg actattcttg	1440
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tatacagaca tagagatgaa ccgacttgga aagtaa	1536

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<213> Artificial Sequence

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<223> Synthetic Polypeptide

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

His Asn Asp Leu Ile Gly Thr Ala Ile Gln Val Lys Met Pro Lys Ser
50 55 60

His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala Ser Lys Trp
65 70 75 80

Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr Gln
85 90 95

Ser Ile Arg Ser Phe Thr Pro Ser Val Glu Gln Cys Lys Glu Ser Ile
100 105 110

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

Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala Glu Ala Val Ile Val Gln
130 135 140

Val Thr Pro His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp Val
145 150 155 160

Asp Ser Gln Phe Ile Asn Gly Lys Cys Ser Asn Tyr Ile Cys Pro Thr
165 170 175

Val His Asn Ser Thr Thr Trp His Ser Asp Tyr Lys Val Lys Gly Leu
180 185 190

Cys Asp Ser Asn Leu Ile Ser Met Asp Ile Thr Phe Phe Ser Glu Asp
195 200 205

Gly Glu Leu Ser Ser Leu Gly Lys Glu Gly Thr Gly Phe Arg Ser Asn
210 215 220

Tyr Phe Ala Tyr Glu Thr Gly Gly Lys Ala Cys Lys Met Gln Tyr Cys
225 230 235 240

Lys His Trp Gly Val Arg Leu Pro Ser Gly Val Trp Phe Glu Met Ala
245 250 255

Asp Lys Asp Leu Phe Ala Ala Ala Arg Phe Pro Glu Cys Pro Glu Gly
260 265 270

Ser Ser Ile Ser Ala Pro Ser Gln Thr Ser Val Asp Val Ser Leu Ile
275 280 285

Gln Asp Val Glu Arg Ile Leu Asp Tyr Ser Leu Cys Gln Glu Thr Trp
290 295 300

Ser Lys Ile Arg Ala Gly Leu Pro Ile Ser Pro Val Asp Leu Ser Tyr
305 310 315 320

Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro Ala Phe Thr Ile Ile Asn
325 330 335

Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Val Asp Ile Ala
340 345 350

Ala Pro Ile Leu Ser Arg Met Val Gly Met Ile Ser Gly Thr Thr Thr
355 360 365

Glu Arg Glu Leu Trp Asp Asp Trp Ala Pro Tyr Glu Asp Val Glu Ile
370 375 380

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

Tyr Met Ile Gly His Gly Met Leu Asp Ser Asp Leu His Leu Ser Ser

405

410

415

Lys Ala Gln Val Phe Glu His Pro His Ile Gln Asp Ala Ala Ser Gln
 420 425 430

Leu Pro Asp Asp Glu Ser Leu Phe Phe Gly Asp Thr Gly Leu Ser Lys
 435 440 445

Asn Pro Ile Glu Leu Val Glu Gly Trp Phe Ser Ser Trp Lys Ser Ser
 450 455 460

Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu Ile Ile Gly Leu Phe Leu
 465 470 475 480

Val Leu Arg Val Gly Ile His Leu Cys Ile Lys Leu Lys His Thr Lys
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Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys
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<210> 13

<211> 495

<212> PRT

<213> Artificial Sequence

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<223> Synthetic Polypeptide

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Val Pro Ser Asn Tyr His Tyr Cys Pro Ser Ser Ser Asp Leu Asn Trp
 20 25 30

His Asn Asp Leu Ile Gly Thr Ala Ile Gln Val Lys Met Pro Lys Ser
 35 40 45

His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala Ser Lys Trp
 50 55 60

Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr Gln

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

Ser Lys Ile Arg Ala Gly Leu Pro Ile Ser Pro Val Asp Leu Ser Tyr
290 295 300

Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro Ala Phe Thr Ile Ile Asn
305 310 315 320

Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Val Asp Ile Ala
325 330 335

Ala Pro Ile Leu Ser Arg Met Val Gly Met Ile Ser Gly Thr Thr Thr
340 345 350

Glu Arg Glu Leu Trp Asp Asp Trp Ala Pro Tyr Glu Asp Val Glu Ile
355 360 365

Gly Pro Asn Gly Val Leu Arg Thr Ser Ser Gly Tyr Lys Phe Pro Leu
370 375 380

Tyr Met Ile Gly His Gly Met Leu Asp Ser Asp Leu His Leu Ser Ser
385 390 395 400

Lys Ala Gln Val Phe Glu His Pro His Ile Gln Asp Ala Ala Ser Gln
405 410 415

Leu Pro Asp Asp Glu Ser Leu Phe Phe Gly Asp Thr Gly Leu Ser Lys
420 425 430

Asn Pro Ile Glu Leu Val Glu Gly Trp Phe Ser Ser Trp Lys Ser Ser
435 440 445

Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu Ile Ile Gly Leu Phe Leu
450 455 460

Val Leu Arg Val Gly Ile His Leu Cys Ile Lys Leu Lys His Thr Lys
465 470 475 480

Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys
485 490 495

<210> 14

<211> 1536
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

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gacatcacct tcttctcaga ggacggagag ctatcatccc tgggaaagga gggcacaggg 660
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tatacagaca tagagatgaa ccgacttgga aagtaa	1536

<210> 15
 <211> 511
 <212> PRT
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<400> 15

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			20					25					30		

Val	Pro	Ser	Asn	Tyr	His	Tyr	Cys	Pro	Ser	Ser	Ser	Asp	Leu	Asn	Trp
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His	Asn	Asp	Leu	Ile	Gly	Thr	Ala	Leu	Gln	Val	Lys	Met	Pro	Gln	Ser
	50					55					60				

His	Lys	Ala	Ile	Gln	Ala	Asp	Gly	Trp	Met	Cys	His	Ala	Ser	Lys	Trp
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Val	Thr	Thr	Cys	Asp	Phe	Arg	Trp	Tyr	Gly	Pro	Lys	Tyr	Ile	Thr	Gln
			85						90					95	

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

Ser	Cys	Gly	Tyr	Ala	Thr	Val	Thr	Asp	Ala	Glu	Ala	Val	Ile	Val	Gln
	130					135					140				

Val	Thr	Pro	His	His	Val	Leu	Val	Asp	Glu	Tyr	Thr	Gly	Glu	Trp	Val
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Val	His	Asn	Ser	Thr	Thr	Trp	His	Ser	Asp	Tyr	Lys	Val	Lys	Gly	Leu
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Cys	Asp	Ser	Asn	Leu	Ile	Ser	Met	Asp	Ile	Thr	Phe	Phe	Ser	Glu	Asp
		195					200					205			
Gly	Glu	Leu	Ser	Ser	Leu	Gly	Lys	Glu	Gly	Thr	Gly	Phe	Arg	Ser	Asn
	210					215					220				
Tyr	Phe	Ala	Tyr	Glu	Thr	Gly	Gly	Lys	Ala	Cys	Lys	Met	Gln	Tyr	Cys
225					230					235					240
Lys	His	Trp	Gly	Val	Arg	Leu	Pro	Ser	Gly	Val	Trp	Phe	Glu	Met	Ala
				245					250					255	
Asp	Lys	Asp	Leu	Phe	Ala	Ala	Ala	Arg	Phe	Pro	Glu	Cys	Pro	Glu	Gly
			260					265					270		
Ser	Ser	Ile	Ser	Ala	Pro	Ser	Gln	Thr	Ser	Val	Asp	Val	Ser	Leu	Ile
		275					280					285			
Gln	Asp	Val	Glu	Arg	Ile	Leu	Asp	Tyr	Ser	Leu	Cys	Gln	Glu	Thr	Trp
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Ser	Lys	Ile	Arg	Ala	Gly	Leu	Pro	Ile	Ser	Pro	Val	Asp	Leu	Ser	Tyr
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Leu	Ala	Pro	Lys	Asn	Pro	Gly	Thr	Gly	Pro	Ala	Phe	Thr	Ile	Ile	Asn
				325					330					335	
Gly	Thr	Leu	Lys	Tyr	Phe	Glu	Thr	Arg	Tyr	Ile	Arg	Val	Asp	Ile	Ala
			340					345					350		
Ala	Pro	Ile	Leu	Ser	Arg	Met	Val	Gly	Met	Ile	Ser	Gly	Thr	Thr	Thr
		355					360					365			

Glu Ala Glu Leu Trp Asp Asp Trp Ala Pro Tyr Glu Asp Val Glu Ile
370 375 380

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

Tyr Met Ile Gly His Gly Met Leu Asp Ser Asp Leu His Leu Ser Ser
405 410 415

Lys Ala Gln Val Phe Glu His Pro His Ile Gln Asp Ala Ala Ser Gln
420 425 430

Leu Pro Asp Asp Glu Ser Leu Phe Phe Gly Asp Thr Gly Leu Ser Lys
435 440 445

Asn Pro Ile Glu Leu Val Glu Gly Trp Phe Ser Ser Trp Lys Ser Ser
450 455 460

Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu Ile Ile Gly Leu Phe Leu
465 470 475 480

Val Leu Arg Val Gly Ile His Leu Cys Ile Lys Leu Lys His Thr Lys
485 490 495

Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys
500 505 510

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

<220>
<223> Synthetic Polypeptide

<400> 16

Lys Phe Thr Ile Val Phe Pro His Asn Gln Lys Gly Asn Trp Lys Asn
1 5 10 15

Val Pro Ser Asn Tyr His Tyr Cys Pro Ser Ser Ser Asp Leu Asn Trp
20 25 30

His Asn Asp Leu Ile Gly Thr Ala Leu Gln Val Lys Met Pro Gln Ser
35 40 45

His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala Ser Lys Trp
50 55 60

Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr Gln
65 70 75 80

Ser Ile Arg Ser Phe Thr Pro Ser Val Glu Gln Cys Lys Glu Ser Ile
85 90 95

Glu Gln Thr Lys Gln Gly Thr Trp Leu Asn Pro Gly Phe Pro Pro Gln
100 105 110

Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala Glu Ala Val Ile Val Gln
115 120 125

Val Thr Pro His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp Val
130 135 140

Asp Ser Gln Phe Ile Asn Gly Lys Cys Ser Asn Tyr Ile Cys Pro Thr
145 150 155 160

Val His Asn Ser Thr Thr Trp His Ser Asp Tyr Lys Val Lys Gly Leu
165 170 175

Cys Asp Ser Asn Leu Ile Ser Met Asp Ile Thr Phe Phe Ser Glu Asp
180 185 190

Gly Glu Leu Ser Ser Leu Gly Lys Glu Gly Thr Gly Phe Arg Ser Asn
195 200 205

Tyr Phe Ala Tyr Glu Thr Gly Gly Lys Ala Cys Lys Met Gln Tyr Cys
210 215 220

Lys His Trp Gly Val Arg Leu Pro Ser Gly Val Trp Phe Glu Met Ala
225 230 235 240

Asp Lys Asp Leu Phe Ala Ala Ala Arg Phe Pro Glu Cys Pro Glu Gly

	245		250		255										
Ser	Ser	Ile	Ser	Ala	Pro	Ser	Gln	Thr	Ser	Val	Asp	Val	Ser	Leu	Ile
			260					265					270		
Gln	Asp	Val	Glu	Arg	Ile	Leu	Asp	Tyr	Ser	Leu	Cys	Gln	Glu	Thr	Trp
		275					280					285			
Ser	Lys	Ile	Arg	Ala	Gly	Leu	Pro	Ile	Ser	Pro	Val	Asp	Leu	Ser	Tyr
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Leu	Ala	Pro	Lys	Asn	Pro	Gly	Thr	Gly	Pro	Ala	Phe	Thr	Ile	Ile	Asn
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Gly	Thr	Leu	Lys	Tyr	Phe	Glu	Thr	Arg	Tyr	Ile	Arg	Val	Asp	Ile	Ala
				325					330					335	
Ala	Pro	Ile	Leu	Ser	Arg	Met	Val	Gly	Met	Ile	Ser	Gly	Thr	Thr	Thr
			340					345					350		
Glu	Ala	Glu	Leu	Trp	Asp	Asp	Trp	Ala	Pro	Tyr	Glu	Asp	Val	Glu	Ile
		355					360					365			
Gly	Pro	Asn	Gly	Val	Leu	Arg	Thr	Ser	Ser	Gly	Tyr	Lys	Phe	Pro	Leu
	370					375					380				
Tyr	Met	Ile	Gly	His	Gly	Met	Leu	Asp	Ser	Asp	Leu	His	Leu	Ser	Ser
385					390					395					400
Lys	Ala	Gln	Val	Phe	Glu	His	Pro	His	Ile	Gln	Asp	Ala	Ala	Ser	Gln
				405					410					415	
Leu	Pro	Asp	Asp	Glu	Ser	Leu	Phe	Phe	Gly	Asp	Thr	Gly	Leu	Ser	Lys
			420					425					430		
Asn	Pro	Ile	Glu	Leu	Val	Glu	Gly	Trp	Phe	Ser	Ser	Trp	Lys	Ser	Ser
		435					440					445			
Ile	Ala	Ser	Phe	Phe	Phe	Ile	Ile	Gly	Leu	Ile	Ile	Gly	Leu	Phe	Leu
	450					455					460				

Val Leu Arg Val Gly Ile His Leu Cys Ile Lys Leu Lys His Thr Lys
 465 470 475 480

Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys
 485 490 495

<210> 17
 <211> 495
 <212> PRT
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<220>
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<400> 17

Lys Phe Thr Ile Val Phe Pro His Asn Gln Lys Gly Asn Trp Lys Asn
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Val Pro Ser Asn Tyr His Tyr Cys Pro Ser Ser Ser Asp Leu Asn Trp
 20 25 30

His Asn Asp Leu Ile Gly Thr Ala Ile Gln Val Lys Met Pro Gln Ser
 35 40 45

His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala Ser Lys Trp
 50 55 60

Val Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr Gln
 65 70 75 80

Ser Ile Arg Ser Phe Thr Pro Ser Val Glu Gln Cys Lys Glu Ser Ile
 85 90 95

Glu Gln Thr Lys Gln Gly Thr Trp Leu Asn Pro Gly Phe Pro Pro Gln
 100 105 110

Ser Cys Gly Tyr Ala Thr Val Thr Asp Ala Glu Ala Val Ile Val Gln
 115 120 125

Val Thr Pro His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp Val
 130 135 140

Asp Ser Gln Phe Ile Asn Gly Lys Cys Ser Asn Tyr Ile Cys Pro Thr
 145 150 155 160

Val His Asn Ser Thr Thr Trp His Ser Asp Tyr Lys Val Lys Gly Leu
 165 170 175

Cys Asp Ser Asn Leu Ile Ser Met Asp Ile Thr Phe Phe Ser Glu Asp
 180 185 190

Gly Glu Leu Ser Ser Leu Gly Lys Glu Gly Thr Gly Phe Arg Ser Asn
 195 200 205

Tyr Phe Ala Tyr Glu Thr Gly Gly Lys Ala Cys Lys Met Gln Tyr Cys
 210 215 220

Lys His Trp Gly Val Arg Leu Pro Ser Gly Val Trp Phe Glu Met Ala
 225 230 235 240

Asp Lys Asp Leu Phe Ala Ala Ala Arg Phe Pro Glu Cys Pro Glu Gly
 245 250 255

Ser Ser Ile Ser Ala Pro Ser Gln Thr Ser Val Asp Val Ser Leu Ile
 260 265 270

Gln Asp Val Glu Arg Ile Leu Asp Tyr Ser Leu Cys Gln Glu Thr Trp
 275 280 285

Ser Lys Ile Arg Ala Gly Leu Pro Ile Ser Pro Val Asp Leu Ser Tyr
 290 295 300

Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro Ala Phe Thr Ile Ile Asn
 305 310 315 320

Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Val Asp Ile Ala
 325 330 335

Ala Pro Ile Leu Ser Arg Met Val Gly Met Ile Ser Gly Thr Thr Thr
 340 345 350

Glu Ala Glu Leu Trp Asp Asp Trp Ala Pro Tyr Glu Asp Val Glu Ile

355

360

365

Gly Pro Asn Gly Val Leu Arg Thr Ser Ser Gly Tyr Lys Phe Pro Leu
 370 375 380

Tyr Met Ile Gly His Gly Met Leu Asp Ser Asp Leu His Leu Ser Ser
 385 390 395 400

Lys Ala Gln Val Phe Glu His Pro His Ile Gln Asp Ala Ala Ser Gln
 405 410 415

Leu Pro Asp Asp Glu Ser Leu Phe Phe Gly Asp Thr Gly Leu Ser Lys
 420 425 430

Asn Pro Ile Glu Leu Val Glu Gly Trp Phe Ser Ser Trp Lys Ser Ser
 435 440 445

Ile Ala Ser Phe Phe Phe Ile Ile Gly Leu Ile Ile Gly Leu Phe Leu
 450 455 460

Val Leu Arg Val Gly Ile His Leu Cys Ile Lys Leu Lys His Thr Lys
 465 470 475 480

Lys Arg Gln Ile Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys
 485 490 495

<210> 18

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 18

atgggcagcc ggatcgtgat caaccgggag cacctgatga tcgaccggcc ctacgtgctg 60

ctggccgtgc tgttcgtgat gttcctgagc ctgatcggct tgctagccat tgctggaatc 120

cggctgcaca gagccgcat ctacaccgcc gagatccaca agagcctgag caccaacctg 180

gacgtgacca acagcatcga gcatcaggtc aaggacgtgc tgacccccct gtttaagatc 240

atcggcgacg aagtgggcct gcggaccccc cagagattca ccgacctggt caagttcatc 300

agcgacaaga tcaagttcct gaaccccgac cgggagtagc acttccggga cctgacctgg	360
tgcatacaacc ccccgagcg gatcaagctg gactacgacc agtactgcgc cgatgtggcc	420
gccgaggaac tgatgaatgc attggtgaac tcaactctac tggagaccag aacaaccaat	480
cagttcctag ctgtctcaaa gggaaactgc tcagggccca ctacaatcag aggtcaattc	540
tcaaacaatgt cgctgtccct gttagacttg tatttaggtc gaggttaca tgtgtcatct	600
atagtcacta tgacatccca gggaatgtat gggggaactt acctagtggg aaagcctaata	660
ctgagcagca aaaggtcaga gttgtcaca ctgagcatgt accgagtgtt tgaagtaggt	720
gttatcagaa atccgggttt gggggctccg gtgttccata tgacaaacta tcttgagcaa	780
ccagtcagta atgatctcag caactgtatg gtggctttgg gggagctcaa actcgcagcc	840
ctttgtcacg gggaagattc tatcacaatt ccctatcagg gatcaggga aggtgtcagc	900
ttccagctcg tcaagctagg tgtctggaaa tccccaccg acatgcaatc ctgggtcccc	960
ttatcaacgg atgatccagt gatagacagg ctttacctct catctcacag aggtgttatc	1020
gctgacaacc aagcaaatg ggctgtcccg acaacacgaa cagatgacaa gttgcgaatg	1080
gagacatgct tccaacaggc gtgtaagggt aaaatccaag cactctgcga gaatcccgag	1140
tgggcacat tgaaggataa caggattcct tcatacgggg tcttgtctgt tgatctgagt	1200
ctgacagttg agcttaaaat caaaattgct tcgggattcg ggccattgat cacacacggt	1260
tcagggatgg acctatacaa atccaaccac aacaatgtgt attggctgac tatcccgcca	1320
atgaagaacc tagccttagg tgtaatcaac acattggagt ggataccgag attcaaggtt	1380
agtccctatc tcttcacagt cccaattaag gaagcaggcg gagactgcca tgccccaaca	1440
tacctacctg cggaggtgga tggatgatgt aaactcagtt ccaatctggt gattctacct	1500
ggtcaagatc tccaatatgt tttggcaacc tacgatactt cccgggttga acatgctgtg	1560
gtttattacg ttacagccc aagccgctca ttttcttact tttatccttt taggttgcct	1620
ataaaggggg tccccatcga attacaagtg gaatgcttca catgggacca aaaactctgg	1680
tgccgtcact tctgtgtgct tgcggactca gaatctggtg gacatatcac tcaactctggg	1740
atggtgggca tgggagtcag ctgcacagtc acccggaag atggaaccaa tgactacaaa	1800
gacgatgacg acaagtga	1818

<211> 605
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 19

Met Gly Ser Arg Ile Val Ile Asn Arg Glu His Leu Met Ile Asp Arg
1 5 10 15

Pro Tyr Val Leu Leu Ala Val Leu Phe Val Met Phe Leu Ser Leu Ile
20 25 30

Gly Leu Leu Ala Ile Ala Gly Ile Arg Leu His Arg Ala Ala Ile Tyr
35 40 45

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

Ser Ile Glu His Gln Val Lys Asp Val Leu Thr Pro Leu Phe Lys Ile
65 70 75 80

Ile Gly Asp Glu Val Gly Leu Arg Thr Pro Gln Arg Phe Thr Asp Leu
85 90 95

Val Lys Phe Ile Ser Asp Lys Ile Lys Phe Leu Asn Pro Asp Arg Glu
100 105 110

Tyr Asp Phe Arg Asp Leu Thr Trp Cys Ile Asn Pro Pro Glu Arg Ile
115 120 125

Lys Leu Asp Tyr Asp Gln Tyr Cys Ala Asp Val Ala Ala Glu Glu Leu
130 135 140

Met Asn Ala Leu Val Asn Ser Thr Leu Leu Glu Thr Arg Thr Thr Asn
145 150 155 160

Gln Phe Leu Ala Val Ser Lys Gly Asn Cys Ser Gly Pro Thr Thr Ile
165 170 175

Arg Gly Gln Phe Ser Asn Met Ser Leu Ser Leu Leu Asp Leu Tyr Leu

190

Lys Asp Asn Arg Ile Pro Ser Tyr Gly Val Leu Ser Val Asp Leu Ser
385 390 395 400

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

Ile Thr His Gly Ser Gly Met Asp Leu Tyr Lys Ser Asn His Asn Asn
420 425 430

Val Tyr Trp Leu Thr Ile Pro Pro Met Lys Asn Leu Ala Leu Gly Val
435 440 445

Ile Asn Thr Leu Glu Trp Ile Pro Arg Phe Lys Val Ser Pro Tyr Leu
450 455 460

Phe Thr Val Pro Ile Lys Glu Ala Gly Gly Asp Cys His Ala Pro Thr
465 470 475 480

Tyr Leu Pro Ala Glu Val Asp Gly Asp Val Lys Leu Ser Ser Asn Leu
485 490 495

Val Ile Leu Pro Gly Gln Asp Leu Gln Tyr Val Leu Ala Thr Tyr Asp
500 505 510

Thr Ser Arg Val Glu His Ala Val Val Tyr Tyr Val Tyr Ser Pro Ser
515 520 525

Arg Ser Phe Ser Tyr Phe Tyr Pro Phe Arg Leu Pro Ile Lys Gly Val
530 535 540

Pro Ile Glu Leu Gln Val Glu Cys Phe Thr Trp Asp Gln Lys Leu Trp
545 550 555 560

Cys Arg His Phe Cys Val Leu Ala Asp Ser Glu Ser Gly Gly His Ile
565 570 575

Thr His Ser Gly Met Val Gly Met Gly Val Ser Cys Thr Val Thr Arg
580 585 590

Glu Asp Gly Thr Asn Asp Tyr Lys Asp Asp Asp Asp Lys
595 600 605

<210> 20

<211> 1818
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 20
 atgggcagcc ggatcgtgat caaccgggag cacctgatga tcgaccggcc ctacgtgctg 60
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 cggctgcaca gagccgcat ctacaccgcc gagatccaca agagcctgag caccaacctg 180
 gacgtgacca acagcatcga gcatcaggtc aaggacgtgc tgacccccct gtttaagatc 240
 atcggcgacg aagtgggcct gcggaccccc cagagattca ccgacctggt caagttcatc 300
 agcgacaaga tcaagttcct gaaccccgac cgggagtagc acttccggga cctgacctgg 360
 tgcatacaacc ccccgagcg gatcaagctg gactacgacc agtactgcgc cgatgtggcc 420
 gccgaggaac tgatgaatgc attggtgaac tcaactctac tggagaccag aacaaccaat 480
 cagttcctag ctgtctcaaa gggaaactgc tcagggccca ctacaatcag aggtcaattc 540
 tcaaacatgt cgctgtccct gttagacttg tatttaggtc gaggttaca tgtgtcatct 600
 atagtcacta tgacatccca gggaatgtat gggggaactt acctagtggg aaagcctaata 660
 ctgagcagca aaaggtcaga gttgtcaca ctgagcatgt accgagtgtt tgaagtaggt 720
 gttatcagaa atccgggttt gggggctccg gtgttccata tgacaaacta tcttgagcaa 780
 ccagtcagta atgatctcag caactgtatg gtggctttgg gggagctcaa actcgcagcc 840
 ctttgtcacg gggaagattc tatcacaatt ccctatcagg gatcagggaa aggtgtcagc 900
 ttccagctcg tcaagctagg tgtctggaaa tccccaaccg acatgcaatc ctgggtcccc 960
 ttatcaacgg atgatccagt gatagacagg ctttacctct catctcacag aggtgttatc 1020
 gctgacaacc aagcaaaatg ggctgtcccg acaacacgaa cagatgacaa gttgcgaatg 1080
 gagacatgct tccaacaggc gtgtaagggt aaaatccaag cactctgcga gaatcccag 1140
 tgggcacat tgaaggataa caggattcct tcatacgggg tcttgtctgt tgatctgagt 1200
 ctgacagttg agcttaaaat caaaattgct tcgggattcg ggccattgat cacacacggt 1260
 tcagggatgg acctatacaa atccaaccac aacaatgtgt attggctgac tatcccgcca 1320
 atgaagaacc tagccttagg tgtaatcaac acattggagt ggataccgag attcaaggtt 1380

agtcccgcgc tcttcaatgt cccaattaag gaagcaggcg gagactgcca tgccccaaca 1440
 tacctacctg cggagggtgga tggatgatgtc aaactcagtt ccaatctggt gattctacct 1500
 ggtcaagatc tccaatatgt tttggcaacc tacgatactt ccgcggttga acatgctgtg 1560
 gtttattacg ttacagccc aagccgctca ttttcttact ttatccttt taggttgctt 1620
 ataaaggggg tccccatcga attacaagtg gaatgcttca catgggacca aaaactctgg 1680
 tgccgtcact tctgtgtgct tgcggactca gaatctggtg gacatatcac tcactctggg 1740
 atggtgggca tgggagtcag ctgcacagtc acccggaag atggaaccaa tgactacaaa 1800
 gacgatgacg acaagtga 1818

<210> 21
 <211> 605
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 21

Met Gly Ser Arg Ile Val Ile Asn Arg Glu His Leu Met Ile Asp Arg
 1 5 10 15

Pro Tyr Val Leu Leu Ala Val Leu Phe Val Met Phe Leu Ser Leu Ile
 20 25 30

Gly Leu Leu Ala Ile Ala Gly Ile Arg Leu His Arg Ala Ala Ile Tyr
 35 40 45

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

Ser Ile Glu His Gln Val Lys Asp Val Leu Thr Pro Leu Phe Lys Ile
 65 70 75 80

Ile Gly Asp Glu Val Gly Leu Arg Thr Pro Gln Arg Phe Thr Asp Leu
 85 90 95

Val Lys Phe Ile Ser Asp Lys Ile Lys Phe Leu Asn Pro Asp Arg Glu
 100 105 110

Tyr Asp Phe Arg Asp Leu Thr Trp Cys Ile Asn Pro Pro Glu Arg Ile
115 120 125

Lys Leu Asp Tyr Asp Gln Tyr Cys Ala Asp Val Ala Ala Glu Glu Leu
130 135 140

Met Asn Ala Leu Val Asn Ser Thr Leu Leu Glu Thr Arg Thr Thr Asn
145 150 155 160

Gln Phe Leu Ala Val Ser Lys Gly Asn Cys Ser Gly Pro Thr Thr Ile
165 170 175

Arg Gly Gln Phe Ser Asn Met Ser Leu Ser Leu Leu Asp Leu Tyr Leu
180 185 190

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

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

Arg Ser Glu Leu Ser Gln Leu Ser Met Tyr Arg Val Phe Glu Val Gly
225 230 235 240

Val Ile Arg Asn Pro Gly Leu Gly Ala Pro Val Phe His Met Thr Asn
245 250 255

Tyr Leu Glu Gln Pro Val Ser Asn Asp Leu Ser Asn Cys Met Val Ala
260 265 270

Leu Gly Glu Leu Lys Leu Ala Ala Leu Cys His Gly Glu Asp Ser Ile
275 280 285

Thr Ile Pro Tyr Gln Gly Ser Gly Lys Gly Val Ser Phe Gln Leu Val
290 295 300

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

Leu Ser Thr Asp Asp Pro Val Ile Asp Arg Leu Tyr Leu Ser Ser His

325	330	335
Arg Gly Val Ile Ala Asp Asn Gln Ala Lys Trp Ala Val Pro Thr Thr		
340	345	350
Arg Thr Asp Asp Lys Leu Arg Met Glu Thr Cys Phe Gln Gln Ala Cys		
355	360	365
Lys Gly Lys Ile Gln Ala Leu Cys Glu Asn Pro Glu Trp Ala Pro Leu		
370	375	380
Lys Asp Asn Arg Ile Pro Ser Tyr Gly Val Leu Ser Val Asp Leu Ser		
385	390	395
Leu Thr Val Glu Leu Lys Ile Lys Ile Ala Ser Gly Phe Gly Pro Leu		
405	410	415
Ile Thr His Gly Ser Gly Met Asp Leu Tyr Lys Ser Asn His Asn Asn		
420	425	430
Val Tyr Trp Leu Thr Ile Pro Pro Met Lys Asn Leu Ala Leu Gly Val		
435	440	445
Ile Asn Thr Leu Glu Trp Ile Pro Arg Phe Lys Val Ser Pro Ala Leu		
450	455	460
Phe Asn Val Pro Ile Lys Glu Ala Gly Gly Asp Cys His Ala Pro Thr		
465	470	475
Tyr Leu Pro Ala Glu Val Asp Gly Asp Val Lys Leu Ser Ser Asn Leu		
485	490	495
Val Ile Leu Pro Gly Gln Asp Leu Gln Tyr Val Leu Ala Thr Tyr Asp		
500	505	510
Thr Ser Ala Val Glu His Ala Val Val Tyr Tyr Val Tyr Ser Pro Ser		
515	520	525
Arg Ser Phe Ser Tyr Phe Tyr Pro Phe Arg Leu Pro Ile Lys Gly Val		
530	535	540

Pro Ile Glu Leu Gln Val Glu Cys Phe Thr Trp Asp Gln Lys Leu Trp
 545 550 555 560

Cys Arg His Phe Cys Val Leu Ala Asp Ser Glu Ser Gly Gly His Ile
 565 570 575

Thr His Ser Gly Met Val Gly Met Gly Val Ser Cys Thr Val Thr Arg
 580 585 590

Glu Asp Gly Thr Asn Asp Tyr Lys Asp Asp Asp Asp Lys
 595 600 605

<210> 22
 <211> 1785
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 22
 atgaagaaga tcaacgaggg cctgctggac agcaagatcc tgagcgcctt caacaccgtg 60
 attgccctgc tgggctctat cgtgatcatc gtgatgaaca tcatgatcat ccagaactac 120
 acccggtcca ccgacaacca ggccgtgatt aaggatgctc tgcagggaat ccagcagcag 180
 atcaaaggcc tggccgacaa gatcggcaca gagatcggcc ctaaggtgtc cctgatcgac 240
 accagcagca ccatcacaat ccccgccaat atcggactgc tgggaagcaa gatcagccag 300
 agcaccgcca gcatcaacga gaacgtgaac gagaagtga agttcacct gcctccactg 360
 aagatccacg agtgcaacat cagctgcccc aatcctctgc cattcagaga gtacagaccc 420
 cagacagagg gcgtgtccaa tctcgtgggc ctgcctaaca acatctgcct gcagaaaacc 480
 agcaaccaga tcctgaagcc taagctgata tcctacacac tgcccgtcgt gggccagagc 540
 ggacactgta ttacagatcc tctgctggcc atggacgagg gctactttgc ctacagccac 600
 ctggaaagaa tcggcagctg tagccgggga gtgtccaagc agagaatcat cggcgtgggc 660
 gaagtgtggt atagaggcga cgaagtggcc agcctgttca tgaccaatgt gtggaccctt 720
 cctaataccta acaccgtgta ccactgcagc gccgtgtaca acaacgagtt ctactacgtg 780
 ctgtgcgccg tgtccacagt gggcgaccct atcctgaaca gcacctattg gagcggcagc 840

ctgatgatga ccagactggc cgtgaagccc aagagcaatg gcggcggata caaccagcat 900
 cagctggccc tgcggtccat cgagaagggc agatacgaca aagtgatgcc ttacggcccc 960
 agcggcatca agcaaggcga taccctgtac tttcccgccg tgggatttct cgtgcgggacc 1020
 gagttcaagt acaacgacag caactgcccc atcaccaagt gccagtacag caagcccagag 1080
 aactgcagac tgagcatggg catcagaccc aacagccact acatcctgag aagcggcctg 1140
 ctgaagtaca acctgagcga cggcgagaac cccaaggtgg tgttcacga gatcagcgac 1200
 cagcggctgt ctatcggcag cccctccaag atctacgact ctctgggcca gccagtgttc 1260
 taccaggcca gctttagctg ggacaccatg atcaagttcg gcgacgtgct gaccgtgaat 1320
 cccctggtgg tcaactggcg gaacaatacc gtgatcagcc ggcctggcca gtctcagtgc 1380
 cccagattca atacctgtcc tgccatttgc gccgaaggcg tgtacaatga cgccttcctg 1440
 atcgatcgga tcaactggat ctctgccggc gtgttcctgg actctaagtc cacagccgcc 1500
 aatcctgtgt tcaccgtgtt caaggacaat gagatcctgt atcgggcccga gctggcctcc 1560
 gaggacacaa atgcccagaa aacaatcacc aactgctttc tgctcaagaa caagatctgg 1620
 tgcacagcc tgggtggaaat ctacgacacc ggcgacaacg tgatcaggcc caagctgttc 1680
 gccgtgaaga tccctgagca gtgtacaggc ggcggaggat ctggcggagg tggaagcgga 1740
 ggcggtggat ctgctagcga ttacaaggat gacgacgata agtga 1785

<210> 23
 <211> 594
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 23

Met Lys Lys Ile Asn Glu Gly Leu Leu Asp Ser Lys Ile Leu Ser Ala
 1 5 10 15

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

Asn Ile Met Ile Ile Gln Asn Tyr Thr Arg Ser Thr Asp Asn Gln Ala
 35 40 45

Val Ile Lys Asp Ala Leu Gln Gly Ile Gln Gln Gln Ile Lys Gly Leu
50 55 60

Ala Asp Lys Ile Gly Thr Glu Ile Gly Pro Lys Val Ser Leu Ile Asp
65 70 75 80

Thr Ser Ser Thr Ile Thr Ile Pro Ala Asn Ile Gly Leu Leu Gly Ser
85 90 95

Lys Ile Ser Gln Ser Thr Ala Ser Ile Asn Glu Asn Val Asn Glu Lys
100 105 110

Cys Lys Phe Thr Leu Pro Pro Leu Lys Ile His Glu Cys Asn Ile Ser
115 120 125

Cys Pro Asn Pro Leu Pro Phe Arg Glu Tyr Arg Pro Gln Thr Glu Gly
130 135 140

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

Ser Asn Gln Ile Leu Lys Pro Lys Leu Ile Ser Tyr Thr Leu Pro Val
165 170 175

Val Gly Gln Ser Gly Thr Cys Ile Thr Asp Pro Leu Leu Ala Met Asp
180 185 190

Glu Gly Tyr Phe Ala Tyr Ser His Leu Glu Arg Ile Gly Ser Cys Ser
195 200 205

Arg Gly Val Ser Lys Gln Arg Ile Ile Gly Val Gly Glu Val Leu Asp
210 215 220

Arg Gly Asp Glu Val Pro Ser Leu Phe Met Thr Asn Val Trp Thr Pro
225 230 235 240

Pro Asn Pro Asn Thr Val Tyr His Cys Ser Ala Val Tyr Asn Asn Glu
245 250 255

Phe Tyr Tyr Val Leu Cys Ala Val Ser Thr Val Gly Asp Pro Ile Leu

260

265

270

Asn Ser Thr Tyr Trp Ser Gly Ser Leu Met Met Thr Arg Leu Ala Val
 275 280 285

Lys Pro Lys Ser Asn Gly Gly Tyr Asn Gln His Gln Leu Ala Leu
 290 295 300

Arg Ser Ile Glu Lys Gly Arg Tyr Asp Lys Val Met Pro Tyr Gly Pro
 305 310 315 320

Ser Gly Ile Lys Gln Gly Asp Thr Leu Tyr Phe Pro Ala Val Gly Phe
 325 330 335

Leu Val Arg Thr Glu Phe Lys Tyr Asn Asp Ser Asn Cys Pro Ile Thr
 340 345 350

Lys Cys Gln Tyr Ser Lys Pro Glu Asn Cys Arg Leu Ser Met Gly Ile
 355 360 365

Arg Pro Asn Ser His Tyr Ile Leu Arg Ser Gly Leu Leu Lys Tyr Asn
 370 375 380

Leu Ser Asp Gly Glu Asn Pro Lys Val Val Phe Ile Glu Ile Ser Asp
 385 390 395 400

Gln Arg Leu Ser Ile Gly Ser Pro Ser Lys Ile Tyr Asp Ser Leu Gly
 405 410 415

Gln Pro Val Phe Tyr Gln Ala Ser Phe Ser Trp Asp Thr Met Ile Lys
 420 425 430

Phe Gly Asp Val Leu Thr Val Asn Pro Leu Val Val Asn Trp Arg Asn
 435 440 445

Asn Thr Val Ile Ser Arg Pro Gly Gln Ser Gln Cys Pro Arg Phe Asn
 450 455 460

Thr Cys Pro Ala Ile Cys Ala Glu Gly Val Tyr Asn Asp Ala Phe Leu
 465 470 475 480

Ile Asp Arg Ile Asn Trp Ile Ser Ala Gly Val Phe Leu Asp Ser Asn
485 490 495

Ala Thr Ala Ala Asn Pro Val Phe Thr Val Phe Lys Asp Asn Glu Ile
500 505 510

Leu Tyr Arg Ala Gln Leu Ala Ser Glu Asp Thr Asn Ala Gln Lys Thr
515 520 525

Ile Thr Asn Cys Phe Leu Leu Lys Asn Lys Ile Trp Cys Ile Ser Leu
530 535 540

Val Glu Ile Tyr Asp Thr Gly Asp Asn Val Ile Arg Pro Lys Leu Phe
545 550 555 560

Ala Val Lys Ile Pro Glu Gln Cys Thr Gly Gly Gly Gly Ser Gly Gly
565 570 575

Gly Gly Ser Gly Gly Gly Gly Ser Ala Ser Asp Tyr Lys Asp Asp Asp
580 585 590

Asp Lys

<210> 24

<211> 609

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 24

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
1 5 10 15

Gly Pro Val Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu
20 25 30

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
65 70 75 80

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

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

Ser Tyr Val Gly Asn Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg
115 120 125

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

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

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
245 250 255

Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln

260	265	270
Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala		
275	280	285
Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val		
290	295	300
Lys Arg Lys Asp Ser Arg Gly Gly Ser Ala Thr Asn Phe Ser Leu Leu		
305	310	315
Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Thr Leu		
325	330	335
Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp Val Ser Ser Lys		
340	345	350
Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val Pro Glu Gly Glu		
355	360	365
Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn Leu		
370	375	380
Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu Leu		
385	390	395
Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala Ser		
405	410	415
Leu Asp Lys Ser Ser Gly Ser Ser Thr Leu Tyr Ile Ala Ala Ser Gln		
420	425	430
Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Arg Pro Thr Ser Gly		
435	440	445
Gly Ser Tyr Ile Pro Thr Phe Gly Arg Gly Thr Ser Leu Ile Val His		
450	455	460
Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser		
465	470	475
		480

Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
485 490 495

Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
500 505 510

Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val
515 520 525

Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
530 535 540

Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys
545 550 555 560

Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn
565 570 575

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

Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser Ala Ala
595 600 605

Ala

<210> 25
<211> 609
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 25

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
1 5 10 15

Gly Pro Val Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu
20 25 30

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
50 55 60

Ile His Tyr Ser Val Gly Ala Gln Thr Thr Asp Gln Gly Glu Val Pro
65 70 75 80

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

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

Ser Tyr Leu Gly Asn Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg
115 120 125

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

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

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu

245

250

255

Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln
 260 265 270

Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
 275 280 285

Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
 290 295 300

Lys Arg Lys Asp Ser Arg Gly Gly Ser Ala Thr Asn Phe Ser Leu Leu
 305 310 315 320

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Thr Leu
 325 330 335

Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp Val Ser Ser Lys
 340 345 350

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

Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn Leu
 370 375 380

Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu Leu
 385 390 395 400

Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala Ser
 405 410 415

Leu Asp Lys Ser Ser Gly Ser Ser Thr Leu Tyr Ile Ala Ala Ser Gln
 420 425 430

Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Arg Pro Met Ile Gly
 435 440 445

Gly Thr Tyr Ile Pro Thr Phe Gly Arg Gly Thr Ser Leu Ile Val His
 450 455 460

Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
 465 470 475 480

Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
 485 490 495

Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
 500 505 510

Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val
 515 520 525

Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
 530 535 540

Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys
 545 550 555 560

Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn
 565 570 575

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

Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser Ala Ala
 595 600 605

Ala

<210> 26
 <211> 609
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 26

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
 1 5 10 15

Gly Pro Val Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu
20 25 30

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
50 55 60

Ile His Tyr Ser Val Gly Ala Gly Thr Thr Asp Arg Gly Glu Val Pro
65 70 75 80

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

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

Ser Tyr Val Gly Asp Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg
115 120 125

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

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

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu

225		230		235		240
Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu						
		245		250		255
Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln						
		260		265		270
Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala						
		275		280		285
Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val						
		290		295		300
Lys Arg Lys Asp Ser Arg Gly Gly Ser Ala Thr Asn Phe Ser Leu Leu						
305		310		315		320
Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Thr Leu						
		325		330		335
Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp Val Ser Ser Lys						
		340		345		350
Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val Pro Glu Gly Glu						
		355		360		365
Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr Asn Leu						
		370		375		380
Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu Leu Leu						
385		390		395		400
Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn Ala Ser						
		405		410		415
Leu Asp Lys Ser Ser Gly Ser Ser Thr Leu Tyr Ile Ala Ala Ser Gln						
		420		425		430
Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Arg Pro Leu Leu Asp						
		435		440		445

Gly Thr Tyr Ile Pro Thr Phe Gly Arg Gly Thr Ser Leu Ile Val His
450 455 460

Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
465 470 475 480

Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
485 490 495

Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
500 505 510

Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val
515 520 525

Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
530 535 540

Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys
545 550 555 560

Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn
565 570 575

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

Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser Ala Ala
595 600 605

Ala

<210> 27
<211> 609
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 27

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
 1 5 10 15

Gly Pro Val Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu
 20 25 30

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
 35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
 50 55 60

Ile His Tyr Ser Val Ala Ile Gln Thr Thr Asp Gln Gly Glu Val Pro
 65 70 75 80

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

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

Ser Tyr Leu Gly Asn Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg
 115 120 125

Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
 130 135 140

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
 145 150 155 160

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

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
 180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
 195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn

210		215		220
His 225	Phe	Arg	Cys	Gln 230
	Val	Gln	Phe	Tyr
		Gly	Leu 235	Ser
			Glu	Asn
			Asp	Glu 240
Trp	Thr	Gln	Asp	Arg 245
		Ala	Lys	Pro
		Val	Thr 250	Gln
			Ile	Val
			Ser	Ala 255
Ala	Trp	Gly	Arg	Ala 260
		Asp	Cys	Gly
			Phe	Thr 265
			Ser	Glu
			Ser	Tyr 270
			Gln	Gln
Gly	Val	Leu	Ser	Ala
			Thr	Ile
			Leu 280	Tyr
			Glu	Ile
			Leu 285	Leu
			Gly	Lys
			Ala	
Thr	Leu	Tyr	Ala	Val
			Leu 295	Val
			Ser	Ala
			Leu	Val
			Leu 300	Met
			Ala	Met
			Val	
Lys 305	Arg	Lys	Asp	Ser
			Arg 310	Gly
			Gly	Ser
			Ala	Thr
			Asn 315	Phe
			Ser	Leu
			Leu 320	
Lys	Gln	Ala	Gly	Asp
			Val	Glu
			Glu	Asn
			Pro 330	Gly
			Pro	Met
			Glu	Thr
			Leu 335	
Leu	Gly	Leu	Leu	Ile
			Leu 340	Trp
			Leu	Gln
			Leu 345	Gln
			Trp	Val
			Ser 350	Ser
			Lys	
Gln	Glu	Val	Thr	Gln
			Ile	Pro
			Ala 360	Ala
			Leu	Ser
			Val 365	Pro
			Glu	Gly
			Glu	
Asn	Leu	Val	Leu	Asn
			Cys 375	Ser
			Phe	Thr
			Asp	Ser
			Ala 380	Ile
			Tyr	Asn
			Leu	
Gln	Trp	Phe	Arg	Gln
			Asp 390	Pro
			Gly	Lys
			Gly	Leu
			Thr 395	Ser
			Leu	Leu
			Leu 400	
Ile	Thr	Pro	Trp	Gln
			Arg	Glu
			Gln	Thr
			Ser 410	Gly
			Arg	Leu
			Asn	Ala
			Ser 415	
Leu	Asp	Lys	Ser	Ser
			Gly 420	Ser
			Ser	Thr
			Leu 425	Tyr
			Ile	Ala
			Ala 430	Ser
			Gln	

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

Gly Thr Tyr Ile Pro Thr Phe Gly Arg Gly Thr Ser Leu Ile Val His
450 455 460

Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
465 470 475 480

Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
485 490 495

Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
500 505 510

Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val
515 520 525

Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
530 535 540

Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys
545 550 555 560

Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn
565 570 575

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

Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser Ala Ala
595 600 605

Ala

<210> 28
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 28

Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr Ile Ile
1 5 10 15

Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg
20 25 30

<210> 29
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<220>
<221> MISC_FEATURE
<222> (7)..(60)
<223> may be absent

<400> 29

Gly Ala Pro Gly Ala Ser Gly Ala Pro Gly Ala Ser Gly Ala Pro Gly
1 5 10 15

Ala Ser Gly Ala Pro Gly Ala Ser Gly Ala Pro Gly Ala Ser Gly Ala
20 25 30

Pro Gly Ala Ser Gly Ala Pro Gly Ala Ser Gly Ala Pro Gly Ala Ser
35 40 45

Gly Ala Pro Gly Ala Ser Gly Ala Pro Gly Ala Ser
50 55 60

<210> 30
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<220>
<221> MISC_FEATURE
<222> (6)..(50)
<223> may be absent

<400> 30

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 Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser
50

<210> 31
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 31

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
1 5 10 15

Gly Pro Val Asn Ala Asp Ala Gly Val Thr Gln Ser Pro Thr His Leu
20 25 30

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

Gly His Asp Thr Val Ser Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro
50 55 60

Gln Phe Ile Phe Gln Tyr Tyr Glu Glu Glu Glu Arg Gln Arg Gly Asn
65 70 75 80

Phe Pro Asp Arg Phe Ser Gly His Gln Phe Pro Asn Tyr Ser Ser Glu

85

90

95

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

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

Arg Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val
 130 135 140

Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala
 145 150 155 160

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

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
 180 185 190

Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys
 195 200 205

Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg
 210 215 220

Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp
 225 230 235 240

Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala
 245 250 255

Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln
 260 265 270

Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys
 275 280 285

Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met
 290 295 300

Val Lys Arg Lys Asp Ser Arg Gly Gly Ser Ala Thr Asn Phe Ser Leu
305 310 315 320

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Thr
325 330 335

Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp Val Ser Ser
340 345 350

Lys Glu Val Glu Gln Asn Ser Gly Pro Leu Ser Val Pro Glu Gly Ala
355 360 365

Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg Gly Ser Gln Ser Phe
370 375 380

Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro Glu Leu Ile Met Phe
385 390 395 400

Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg Phe Thr Ala Gln Leu
405 410 415

Asn Lys Ala Ser Gln Tyr Ile Ser Leu Leu Ile Arg Asp Ser Lys Leu
420 425 430

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

Ala Leu Asn Phe Gly Lys Gly Thr Ser Leu Leu Val Thr Pro His Ile
450 455 460

Gln Lys Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser
465 470 475 480

Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val
485 490 495

Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu
500 505 510

Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser

515

520

525

Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile
 530 535 540

Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys
 545 550 555 560

Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn
 565 570 575

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

Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
 595 600

<210> 32
 <211> 1812
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

<400> 32
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 gctgatgctg gcgtaacgca gagcccgaca catctgataa aaacaagagg ccaacaagtt 120
 actctgaggt gcagtccaaa gcaagggcac gatactgtgt cttggtacca acaggctctt 180
 gggcaagggc cacaattcat ctttcaatac tacgaggaag aagagcgcca acgaggaaac 240
 tttcctgata gcttcagcgg tcaccaatct cctaattaca gttccgaatt gaatgtaaat 300
 gctctcctgc tcggcgatag cgctctgtac ctttgtgcct cctccgacac cgtaagctat 360
 gaacaatact ttggctctgg cactcgcctc accgtaaccg aagatctgaa gaacgttttt 420
 ccgccagagg tcgccgtttt tgaaccaagc gaagcggaaa tcagtcacac acagaaggca 480
 acactcgttt gtctggccac tggcttctac cccgatcacg tcgaactttc atgggtgggtc 540
 aatggaaagg aagttcacag cgggtgtaagt actgatccac agcctctcaa agagcagccc 600
 gccttgaatg acagcagata ttgtttgagt tcacggttga gagtaagcgc taccttctgg 660

caagatcctc gcaatcactt ccgatgtcag gtgcagtttt atggactgtc agaaaatgat	720
gaatggacac aagatagggc taaacccgtg acccaaatcg tgagcgctga ggcatgggggt	780
cgagcagact gcggcttcac aagtgaatca taccagcagg ggggtgctgag cgccactatc	840
ctgtacgaga ttctgctggg aaaggctacc ctgtatgcag tgctgggtctc cgccctgggtg	900
ctgatggcta tgggtcaagcg aaaagacagc cggggcggggt ccgcaacaaa cttttccctg	960
ctgaaacagg ccggcgatgt ggaggaaaat cctgggccaa tggagactct gctgggactg	1020
ctgatcctgt ggctgcagct gcagtgggtg tcaagcaaag aagtagaaca aaactcaggc	1080
cccctgtccg taccagaggg agctatagcg tctctcaatt gtacgtacag cgaccggggc	1140
tccaatcat tcttctggta tcggcagtac agcgggaaaa gtccggaatt gattatgttc	1200
atatattcta acggcgacaa agaggacggg cgattttacgg cacaactgaa caaagcgagc	1260
caatacatca gtcttcttat tcgagatagc aaattgtctg actccgctac atacctctgt	1320
gcagtccgga ctaactccgg ttacgccttg aactttggga aagggacgtc attgttggtc	1380
acgccgcaca tacagaagcc cgatcctgca gtttaccaac tccgggactc aaagtcttcc	1440
gataagagtg tctgtctttt caccgacttc gatagtcaaa cgaatgttag ccagtctaag	1500
gacagcgatg tttatatcac cgacaaaacc gtcctcgaca tgaggtctat ggacttcaag	1560
agcaacagcg cggtagcgtg gtcaaataag agcgactttg cttgcgcgaa cgctttcaat	1620
aattcaatca tacccgagga tactttcttc ccaagtccgg aatctagttg tgacgtgaag	1680
ctggctcgaga aaagtttcga aacagatact aacctgaatt ttcagaacct gtcagtgatc	1740
ggcttccgga ttctgctgct gaaggtcgcc gggttcaatc tgctgatgac cctgagactg	1800
tgggtcaagct ga	1812

<210> 33
 <211> 609
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 33

Met	Gly	Thr	Arg	Leu	Leu	Phe	Trp	Val	Ala	Phe	Cys	Leu	Leu	Gly	Ala
1				5					10					15	

Asp His Thr Gly Ala Gly Val Ser Gln Ser Pro Ser Asn Lys Val Thr
20 25 30

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

Thr Ala Leu Tyr Trp Tyr Arg Gln Arg Leu Gly Gln Gly Leu Glu Phe
50 55 60

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

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

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

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

Arg Leu Leu Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val
130 135 140

Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala
145 150 155 160

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

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys
195 200 205

Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg
210 215 220

Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp

225		230		235		240
Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala						
		245		250		255
Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln						
		260		265		270
Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys						
		275		280		285
Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met						
		290		295		300
Val Lys Arg Lys Asp Ser Arg Gly Gly Ser Ala Thr Asn Phe Ser Leu						
305		310		315		320
Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Glu Lys						
		325		330		335
Asn Pro Leu Ala Ala Pro Leu Leu Ile Leu Trp Phe His Leu Asp Cys						
		340		345		350
Val Ser Ser Ile Leu Asn Val Glu Gln Ser Pro Gln Ser Leu His Val						
		355		360		365
Gln Glu Gly Asp Ser Thr Asn Phe Thr Cys Ser Phe Pro Ser Ser Asn						
		370		375		380
Phe Tyr Ala Leu His Trp Tyr Arg Trp Glu Thr Ala Lys Ser Pro Glu						
385		390		395		400
Ala Leu Phe Val Met Thr Leu Asn Gly Asp Glu Lys Lys Lys Gly Arg						
		405		410		415
Ile Ser Ala Thr Leu Asn Thr Lys Glu Gly Tyr Ser Tyr Leu Tyr Ile						
		420		425		430
Lys Gly Ser Gln Pro Glu Asp Ser Ala Thr Tyr Leu Cys Ala Phe Ile						
		435		440		445

Thr Gly Asn Gln Phe Tyr Phe Gly Thr Gly Thr Ser Leu Thr Val Ile
450 455 460

Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
465 470 475 480

Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln
485 490 495

Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys
500 505 510

Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val
515 520 525

Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn
530 535 540

Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys
545 550 555 560

Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn
565 570 575

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

Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser Ala Ala
595 600 605

Ala

<210> 34
<211> 1830
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<400> 34

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gcgggggtta gtcagtcccc tagcaataaa gtgacggaaa aagggaaga tgtcgagctg	120
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<210> 35
<211> 474
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic Polypeptide
<400> 35

Met Ser Arg Ser Val Ala Leu Ala Val Leu Ala Leu Leu Ser Leu Ser
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Gly Leu Glu Ala Ser Leu Tyr Asn Thr Val Ala Thr Leu Gly Gly Gly
20 25 30

Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Gln Arg Thr
35 40 45

Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala Glu Asn Gly Lys Ser
50 55 60

Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro Ser Asp Ile Glu
65 70 75 80

Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys Val Glu His Ser
85 90 95

Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr
100 105 110

Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys Arg Val Asn His
115 120 125

Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp Arg Asp Met Gly
130 135 140

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

Gly Gly Ser His Ser Met Arg Tyr Phe Phe Thr Ser Val Ser Arg Pro
165 170 175

Gly Arg Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr
180 185 190

Gln Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met Glu Pro
195 200 205

Arg Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp Asp Gly Glu
210 215 220

Thr Arg Lys Val Lys Ala His Ser Gln Thr His Arg Val Asp Leu Gly
225 230 235 240

Thr Leu Arg Gly Ala Tyr Asn Gln Ser Glu Ala Gly Ser His Thr Val
245 250 255

Gln Arg Met Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg Phe Leu Arg
260 265 270

Gly Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Ile Ala Leu Lys
275 280 285

Glu Asp Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala Gln Thr Thr
290 295 300

Lys His Lys Trp Glu Ala Ala His Val Ala Glu Gln Leu Arg Ala Tyr
305 310 315 320

Leu Glu Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly
325 330 335

Lys Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys Thr His Met Thr His
340 345 350

His Ala Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser

355

360

365

Phe Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp
 370 375 380

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

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

Arg Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr
 420 425 430

Leu Arg Trp Glu Pro Ser Ser Gln Pro Thr Ile Pro Ile Val Gly Ile
 435 440 445

Ile Ala Gly Leu Val Leu Phe Gly Ala Val Ile Thr Gly Ala Val Val
 450 455 460

Ala Ala Val Met Trp Arg Arg Lys Ser Ser
 465 470

<210> 36

<211> 1425

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 36

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aacggtaaat ctaatttctt gaactgttac gtctccggtt tccaccaag tgatatagaa 240

gttgacttgt tgaaaaatgg tgaaagaatc gaaaagggtg aacattcaga tttgtctttt 300

tctaaggact ggtccttcta tttgttgtac tacacagagt tcactccaac tgaaaaggat 360

gaatacgctt gcagagttaa tcatgtaacc ttgtctcaac ctaaaatcgt taagtgggat 420

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cctagattca tcgcagtcgg ttacgttgat gacacacaat ttgtaagatt cgattccgac	600
gctgcaagtc aaagaatgga accaagagca ccttggttg aacaagaagg tccagaatat	660
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catgtccaac acgaaggttt accaaagcca ttgacattga gatgggaacc atcctctcag	1320
cctacaatac caatagtcgg cataatcgct ggactgggtc tgttcggggc ggtaatcacg	1380
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<210> 37
 <211> 474
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 37

Met	Ser	Arg	Ser	Val	Ala	Leu	Ala	Val	Leu	Ala	Leu	Leu	Ser	Leu	Ser
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Gly	Leu	Glu	Ala	Asn	Leu	Val	Pro	Met	Val	Ala	Thr	Val	Gly	Ala	Ser
			20					25					30		

Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ile	Gln	Arg	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35

40

45

Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala Glu Asn Gly Lys Ser
 50 55 60

Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro Ser Asp Ile Glu
 65 70 75 80

Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys Val Glu His Ser
 85 90 95

Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr
 100 105 110

Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys Arg Val Asn His
 115 120 125

Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp Arg Asp Met Gly
 130 135 140

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

Gly Gly Ser His Ser Met Arg Tyr Phe Phe Thr Ser Val Ser Arg Pro
 165 170 175

Gly Arg Gly Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr
 180 185 190

Gln Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met Glu Pro
 195 200 205

Arg Ala Pro Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp Asp Gly Glu
 210 215 220

Thr Arg Lys Val Lys Ala His Ser Gln Thr His Arg Val Asp Leu Gly
 225 230 235 240

Thr Leu Arg Gly Ala Tyr Asn Gln Ser Glu Ala Gly Ser His Thr Val
 245 250 255

Gln Arg Met Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg Phe Leu Arg
260 265 270

Gly Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Ile Ala Leu Lys
275 280 285

Glu Asp Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala Gln Thr Thr
290 295 300

Lys His Lys Trp Glu Ala Ala His Val Ala Glu Gln Leu Arg Ala Tyr
305 310 315 320

Leu Glu Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly
325 330 335

Lys Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys Thr His Met Thr His
340 345 350

His Ala Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser
355 360 365

Phe Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp
370 375 380

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

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

Arg Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr
420 425 430

Leu Arg Trp Glu Pro Ser Ser Gln Pro Thr Ile Pro Ile Val Gly Ile
435 440 445

Ile Ala Gly Leu Val Leu Phe Gly Ala Val Ile Thr Gly Ala Val Val
450 455 460

Ala Ala Val Met Trp Arg Arg Lys Ser Ser

465

470

<210> 38

<211> 1425

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 38

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gatggtgaag accaaacca agatactgaa ttagttgaaa ccagaccagc aggtgacggt     1200
actttccaaa aatgggccgc tgtttagtc cttcaggtc aagaacaaag atacacatgc     1260

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catgtccaac acgaaggttt accaaagcca ttgacattga gatgggaacc atcctctcag 1320
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<210> 39
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

<400> 39

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Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Gly Ile Leu Gly Phe Val
20 25 30

Phe Thr Leu Gly Cys Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro
50 55 60

Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe
65 70 75 80

His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile
85 90 95

Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe
100 105 110

Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr
115 120 125

Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys
130 135 140

Trp Asp Arg Asp Met Gly Gly Gly Gly Ser Gly Gly Ser Gly Ser Gly

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

Thr Leu Arg Cys Trp Ala Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu
 370 375 380

Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val
 385 390 395 400

Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val
 405 410 415

Val Val Pro Ser Gly Gln Glu Gln Arg Tyr Thr Cys His Val Gln His
 420 425 430

Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu Pro Ser Ser Gln
 435 440 445

Pro Thr Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Phe Gly
 450 455 460

Ala Val Ile Thr Gly Ala Val Val Ala Ala Val Met Trp Arg Arg Lys
 465 470 475 480

Ser Ser

<210> 40
 <211> 1449
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Polynucleotide

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 cacccaagtg atatagaagt tgacttggtg aaaaatggtg aaagaatcga aaaggttgaa 300
 cattcagatt tgtctttttc taaggactgg tccttctatt tgttgacta cacagagttc 360

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aaaatcgtta agtgggtag agacatggga ggcggcggct ctggtggcag cggctctgga	480
ggttctggaa gtggaggcgg ctctggaggc tcccatagta tgagatattt ctttacttct	540
gtttcaagac caggtagagg tgaacctaga ttcacgcag tcggttacgt tgatgacaca	600
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<210> 41
 <211> 474
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 41

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

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

Thr Leu Arg Gly Ala Tyr Asn Gln Ser Glu Ala Gly Ser His Thr Val
245 250 255

Gln Arg Met Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg Phe Leu Arg
260 265 270

Gly Tyr His Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Ile Ala Leu Lys
275 280 285

Glu Asp Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala Gln Thr Thr
290 295 300

Lys His Lys Trp Glu Ala Ala His Val Ala Glu Gln Leu Arg Ala Tyr
305 310 315 320

Leu Glu Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly
325 330 335

Lys Glu Thr Leu Gln Arg Thr Asp Ala Pro Lys Thr His Met Thr His
340 345 350

His Ala Val Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser
355 360 365

Phe Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp
370 375 380

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

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

Arg Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr
420 425 430

Leu Arg Trp Glu Pro Ser Ser Gln Pro Thr Ile Pro Ile Val Gly Ile
435 440 445

Ile Ala Gly Leu Val Leu Phe Gly Ala Val Ile Thr Gly Ala Val Val

450

455

460

Ala Ala Val Met Trp Arg Arg Lys Ser Ser
465 470

<210> 42

<211> 1425

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 42

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cctagattca tcgcagtcgg ttacgttgat gacacacaat ttgtaagatt cgattccgac      600
gctgcaagtc aaagaatgga accaagagca ccttggttg aacaagaagg tccagaatat      660
tgggatggtg aaactagaaa agttaaggcc cattctcaaa ctcacagagt agatttgggt      720
acattaagag gtgcttataa tcaatctgaa gcaggttcac atacagtaca aagaatgtac      780
ggttgtgatg tcggttcaga ctggagattt ttgagagggt atcaccaata tgcttacgat      840
ggtaaagact acattgcatt gaaggaagat ttgagatcct ggaccgccgc tgacatggca      900
gcccuaacta caaaacataa gtgggaagct gcacacgtag cagaacaatt gagagcctat      960
ttggaaggta catgtgtcga atgggtgaga agatacttag aaaacggtaa agaaacattg     1020
caaagaaccg atgctccaaa gactcatatg acacatcacg ccgttagtga tcacgaagct     1080
actttgagat gctgggcatt atctttttac cctgccgaaa tcacattgac ctggcaaaga     1140

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gatggtgaag accaaaccca agatactgaa ttagttgaaa ccagaccagc aggtgacggt 1200
 actttccaaa aatgggccgc tgttgtagtc ctttcaggctc aagaacaaag atacacatgc 1260
 catgtccaac acgaagggtt accaaagcca ttgacattga gatgggaacc atcctctcag 1320
 cctacaatac caatagtcgg cataatcgct ggactgggtcc tgttcggggc ggtaatcacg 1380
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<210> 43
 <211> 273
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 43

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 1 5 10 15

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

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
 35 40 45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
 50 55 60

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
 65 70 75 80

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
 85 90 95

Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
 100 105 110

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
 115 120 125

Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr

130

135

140

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
 145 150 155 160

Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
 165 170 175

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

Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
 195 200 205

Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
 210 215 220

Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
 225 230 235 240

Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
 245 250 255

Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
 260 265 270

Glu

<210> 44

<211> 822

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 44

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gaggtcaagg aggtcgcaac attgagttgt ggccataacg tatcagttga agaactcgcg 180

cagacacgga tttactggca aaaggaaaag aagatggtgt tgacaatgat gagcggtagac 240
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 atagtaatac ttgccttgcg accttctgac gagggaaacgt atgaatgtgt agtgcttaag 360
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 gaacttaacg caatcaatac cacggtgtcc caagaccgg agacagagct gtacgccgtg 600
 tcatccaaac tggattttaa catgacgaca aatcatagtt tcatgtgtct gatcaaatat 660
 gggcatctca gggatgaatca gacttttaat tggaacacta ccaaacaaga gcacttccca 720
 gataatctgt tgccaagctg ggcgataact cttatctccg tcaacggtat cttcgtaatt 780
 tgctgcctca cctattgttt cgcgctcga tgccgagaat ga 822

<210> 45
 <211> 275
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic Polypeptide

 <400> 45

Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met
 1 5 10 15

Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe
 20 25 30

Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
 35 40 45

Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
 50 55 60

Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
 65 70 75 80

Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg

85

90

95

Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
 100 105 110

His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
 115 120 125

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

Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile
 145 150 155 160

His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys
 165 170 175

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

Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro
 195 200 205

Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys
 210 215 220

Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln
 225 230 235 240

Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
 245 250 255

Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys
 260 265 270

Lys Lys Arg
 275

<210> 46

<211> 828

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Polynucleotide

<400> 46

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cagttcgcaa atagtcagaa tcaaagtctc agtgagttgg tcgtattttg gcaggatcaa      180
gagaatctcg tcctgaacga ggtttacctg ggcaaagaga agtttgattc cgtgcatagt      240
aagtacatgg gtcgcacgtc ctttgactcc gacagctgga cacttaggct gcacaacctc      300
cagatcaaag ataagggtct ttaccagtgc attatacacc ataaaaaacc tactgggatg      360
atcaggattc accagatgaa cagcgagttg tcagtgttgg caaatcttc acaaccagaa      420
atagtaccta tctcaaacat caccgaaaac gtatatatta acctcacctg ttctagtatc      480
catggttatc cagagccaaa gaaaatgtcc gtgttgctga gaacaaagaa ctctacaata      540
gagtacgacg gagtgatgca aaaatcccag gacaacgtaa cagaactgta cgatgttagc      600
atctctcttt ctgtgagctt tcctgatgtg acatccaaca tgaccatttt ttgcatactc      660
gaaacagaca aaacgcgact tttgtcctcc cccttttcaa tcgagttgga ggatccccaa      720
cctccccccg accatatccc gtggatcacc gctgttcttc ctaccgtaat catctgtgtc      780
atggtattct gccttattct ctggaaatgg aagaaaaaga agcgatga      828
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<210> 47

<211> 551

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Polypeptide

<400> 47

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Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1           5           10          15
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Gly Ser Thr Gly Ala Asp Tyr Lys Asp Asp Asp Asp Lys Asp Ile Gln
          20          25          30
```

```
Met Thr Gln Ser Pro Ser Ser Leu Pro Ala Ser Leu Gly Asp Arg Val
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35

40

45

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

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

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

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

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

Pro Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Lys Pro Thr Val
 130 135 140

Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Gly Thr Gly Ser Ala Thr
 145 150 155 160

Leu Val Cys Phe Val Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys
 165 170 175

Trp Lys Val Asp Gly Ser Glu Lys Arg Asp Gly Val Leu Gln Ser Val
 180 185 190

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

Ser Leu Thr Lys Ala Asp Tyr Glu Arg His Asn Leu Tyr Thr Cys Glu
 210 215 220

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

Asn Glu Cys Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala
 245 250 255

Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Pro Cys Thr Leu Leu
260 265 270

Leu Leu Leu Ala Ala Ala Leu Ala Pro Thr Gln Thr Arg Ala Glu Val
275 280 285

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys Ser Leu
290 295 300

Lys Leu Ser Cys Glu Ala Ser Gly Phe Thr Phe Ser Gly Tyr Gly Met
305 310 315 320

His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Ser Val Ala Tyr
325 330 335

Ile Thr Ser Ser Ser Ile Asn Ile Lys Tyr Ala Asp Ala Val Lys Gly
340 345 350

Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Leu Leu Phe Leu Gln
355 360 365

Met Asn Ile Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg
370 375 380

Phe Asp Trp Asp Lys Asn Tyr Trp Gly Gln Gly Thr Met Val Thr Val
385 390 395 400

Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Ala
405 410 415

Cys Asp Ser Thr Thr Ser Thr Thr Asn Thr Val Thr Leu Gly Cys Leu
420 425 430

Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Ile Trp Asn Ser Gly
435 440 445

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu His Ser Gly
450 455 460

Leu Tyr Ser Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro

tatacgtgtg aggtcactca taaaaccagt actgcggcga ttgtaaaaac gctgaacagg	720
aacgaatgtg gaagtgggtg tacgaacttc tctactgctta agcaagctgg agatgttgag	780
gaaaaccctg gaccaatggt gccgtgcacc ctccttttgc ttttggccgc tgcgttggct	840
ccaaccaga ctagggcaga agtacagctt gtggaaagcg gcggagggtt tgtgcagcct	900
ggcaaatccc tcaaactcag ttgtgaggct agtggcttca catttagcgg gtacggtatg	960
cactgggtcc gacaggcacc tgggcgcgga ttggaaagcg tcgcatacat tacaagctca	1020
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gcgaagaacc ttttgttcct gcaaatgaac attctcaaga gcgaggacac ggctatgtac	1140
tattgtgcta ggttcgactg ggacaagaat tattggggac aaggtactat ggttacagta	1200
agtagtgcta aaactactgc tccgtcagta tatcccctcg caccagcctg cgattctact	1260
accagcacta ctaatacagt aacactcggg tgcctcgtga aggggtatth ccctgaacca	1320
gttacgggtc tctggaatag tggggccttg actagtgggtg tacatacgtt cccatccgtc	1380
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tctcagacag ttacgtgcaa cgtcgtcat cctgcaagtt ccacgactgt ggaccttaaa	1500
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aaggtgggtc tgatctctgc gatcctcgcg ctcgtcgttt tgacgatcat tagcctcatc	1620
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<210> 49
 <211> 555
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 49

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1				5				10					15		

Gly	Ser	Thr	Gly	Ala	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Tyr	Glu	Leu
			20					25					30		

Ile Gln Pro Ser Ser Ala Ser Val Thr Val Gly Glu Thr Val Lys Ile

35

40

45

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

Gln Lys Ser Asp Lys Asn Ile Leu Leu Leu Ile Tyr Met Asp Asn Lys
 65 70 75 80

Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Thr Ser Gly Thr
 85 90 95

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

Tyr Tyr Cys Leu Ser Ser Tyr Gly Asp Asn Asn Asp Leu Val Phe Gly
 115 120 125

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

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

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

Thr Trp Lys Ala Asn Gly Ala Thr Ile Asn Asp Gly Val Lys Thr Thr
 180 185 190

Lys Pro Ser Lys Gln Gly Gln Asn Tyr Met Thr Ser Ser Tyr Leu Ser
 195 200 205

Leu Thr Ala Asp Gln Trp Lys Ser His Asn Arg Val Ser Cys Gln Val
 210 215 220

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

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

Val Glu Glu Asn Pro Gly Pro Met Val Pro Cys Thr Leu Leu Leu Leu
260 265 270

Leu Ala Ala Ala Leu Ala Pro Thr Gln Thr Arg Ala Glu Val Tyr Leu
275 280 285

Val Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Ser Ser Leu Lys Val
290 295 300

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Phe Trp Met Tyr Trp
305 310 315 320

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Arg Ile Lys
325 330 335

Asn Ile Pro Asn Asn Tyr Ala Thr Glu Tyr Ala Asp Ser Val Arg Gly
340 345 350

Arg Phe Thr Ile Ser Arg Asp Asp Ser Arg Asn Ser Ile Tyr Leu Gln
355 360 365

Met Asn Arg Leu Arg Val Asp Asp Thr Ala Ile Tyr Tyr Cys Thr Arg
370 375 380

Ala Gly Arg Phe Asp His Phe Asp Tyr Trp Gly Gln Gly Thr Met Val
385 390 395 400

Thr Val Ser Ser Ala Thr Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala
405 410 415

Pro Ala Cys Asp Ser Thr Thr Ser Thr Thr Asp Thr Val Thr Leu Gly
420 425 430

Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
435 440 445

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu His
450 455 460

Ser Gly Leu Tyr Ser Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr


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tcacttccat tcaaggtggt cgtgatctct gcgatcctcg cgctcgtcgt tttgacgac      1620
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<210> 51
<211> 512
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Polypeptide

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<400> 51

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Met Asn Phe Leu Leu Leu Thr Phe Ile Val Leu Pro Leu Cys Ser His
1           5           10          15

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Ala Lys Phe Ser Ile Val Phe Pro Gln Ser Gln Lys Gly Asn Trp Lys
          20          25          30

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Asn Val Pro Ser Ser Tyr His Tyr Cys Pro Ser Ser Ser Asp Gln Asn

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35

40

45

Trp His Asn Asp Leu Leu Gly Ile Thr Met Lys Val Lys Met Pro Lys
 50 55 60

Thr His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala Ala Lys
 65 70 75 80

Trp Ile Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr
 85 90 95

His Ser Ile His Ser Ile Gln Pro Thr Ser Glu Gln Cys Lys Glu Ser
 100 105 110

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

Gln Asn Cys Gly Tyr Ala Thr Val Thr Asp Ser Val Ala Val Val Val
 130 135 140

Gln Ala Thr Pro His His Val Leu Val Asp Glu Tyr Thr Gly Glu Trp
 145 150 155 160

Ile Asp Ser Gln Phe Pro Asn Gly Lys Cys Glu Thr Glu Glu Cys Glu
 165 170 175

Thr Val His Asn Ser Thr Val Trp Tyr Ser Asp Tyr Lys Val Thr Gly
 180 185 190

Leu Cys Asp Ala Thr Leu Val Asp Thr Glu Ile Thr Phe Phe Ser Glu
 195 200 205

Asp Gly Lys Lys Glu Ser Ile Gly Lys Pro Asn Thr Gly Tyr Arg Ser
 210 215 220

Asn Tyr Phe Ala Tyr Glu Lys Gly Asp Lys Val Cys Lys Met Asn Tyr
 225 230 235 240

Cys Lys His Ala Gly Val Arg Leu Pro Ser Gly Val Trp Phe Glu Phe
 245 250 255

Val Asp Gln Asp Val Tyr Ala Ala Ala Lys Leu Pro Glu Cys Pro Val
260 265 270

Gly Ala Thr Ile Ser Ala Pro Thr Gln Thr Ser Val Asp Val Ser Leu
275 280 285

Ile Leu Asp Val Glu Arg Ile Leu Asp Tyr Ser Leu Cys Gln Glu Thr
290 295 300

Trp Ser Lys Ile Arg Ser Lys Gln Pro Val Ser Pro Val Asp Leu Ser
305 310 315 320

Tyr Leu Ala Pro Lys Asn Pro Gly Thr Gly Pro Ala Phe Thr Ile Ile
325 330 335

Asn Gly Thr Leu Lys Tyr Phe Glu Thr Arg Tyr Ile Arg Ile Asp Ile
340 345 350

Asp Asn Pro Ile Ile Ser Lys Met Val Gly Lys Ile Ser Gly Ser Gln
355 360 365

Thr Glu Arg Glu Leu Trp Thr Glu Trp Phe Pro Tyr Glu Gly Val Glu
370 375 380

Ile Gly Pro Asn Gly Ile Leu Lys Thr Pro Thr Gly Tyr Lys Phe Pro
385 390 395 400

Leu Phe Met Ile Gly His Gly Met Leu Asp Ser Asp Leu His Lys Thr
405 410 415

Ser Gln Ala Glu Val Phe Glu His Pro His Leu Ala Glu Ala Pro Lys
420 425 430

Gln Leu Pro Glu Glu Glu Thr Leu Phe Phe Gly Asp Thr Gly Ile Ser
435 440 445

Lys Asn Pro Val Glu Leu Ile Glu Gly Trp Phe Ser Ser Trp Lys Ser
450 455 460

Thr Val Val Thr Phe Phe Phe Ala Ile Gly Val Phe Ile Leu Leu Tyr

465 470 475 480

Val Val Ala Arg Ile Val Ile Ala Val Arg Tyr Arg Tyr Gln Gly Ser
485 490 495

<210>	52
<211>	1539
<212>	DNA
<213>	Artificial Sequence

<400>	52						
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tggatcacta	catgcgattt	ccggtgggtat	ggccctaagt	acattacaca	ctctatccat		300
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caaacgtccg	ttgacgtctc	cttgatactg	gatgtagagc	gaatcctgga	ctacagtctc		900
tgccaggaaa	cgtgggtcaaa	aataagaagt	aagcagccag	tttcacccgt	ggatctgtct		960
tatctggcgc	caaaaaaccc	gggcacgggc	cctgctttta	ccataattaa	cgggaacgctt		1020

aaatacttcg aaacccgcta cattagaatc gatatagaca atcctattat cagcaagatg 1080
 gtagggaaga tatctgggtc tcaaacggag cgagaattgt ggacggagtg gttcccttat 1140
 gagggagtgg aaattgggcc caacgggatc ctcaagaccc caacgggtta caagttccct 1200
 ctgtttatga tcggccatgg catgttggac agtgacttgc acaaaacatc tcaggcagag 1260
 gttttcgaac atccacattt ggcggaggcg cccaagcaac ttccagaaga agaaactctc 1320
 ttctttggag atacaggcat ttcaaaaaat cctgtagaac tgatagaagg gtggttctct 1380
 tcctggaaat caacggttgt cacgtttttc tttgcaatag gcgtatttat actcctgtac 1440
 gtcgtagccc gcattgtgat cgcagtacga tacagatacc agggcagtaa caataaacgc 1500
 atatataatg acatcgaaat gtcaaggttc cgaaagtga 1539

<210> 53
 <211> 512
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Polypeptide

<400> 53

Met Asn Phe Leu Leu Leu Thr Phe Ile Val Leu Pro Leu Cys Ser His
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Ala Lys Phe Ser Ile Val Phe Pro Gln Ser Gln Lys Gly Asn Trp Lys
 20 25 30

Asn Val Pro Ser Ser Tyr His Tyr Cys Pro Ser Ser Ser Asp Gln Asn
 35 40 45

Trp His Asn Asp Leu Leu Gly Ile Thr Met Lys Val Lys Met Pro Gln
 50 55 60

Thr His Lys Ala Ile Gln Ala Asp Gly Trp Met Cys His Ala Ala Lys
 65 70 75 80

Trp Ile Thr Thr Cys Asp Phe Arg Trp Tyr Gly Pro Lys Tyr Ile Thr
 85 90 95

His Ser Ile His Ser Ile Gln Pro Thr Ser Glu Gln Cys Lys Glu Ser

100					105					110					
Ile	Lys	Gln	Thr	Lys	Gln	Gly	Thr	Trp	Met	Ser	Pro	Gly	Phe	Pro	Pro
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Gln	Asn	Cys	Gly	Tyr	Ala	Thr	Val	Thr	Asp	Ser	Val	Ala	Val	Val	Val
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Ile Gly Pro Asn Gly Ile Leu Lys Thr Pro Thr Gly Tyr Lys Phe Pro
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Leu Phe Met Ile Gly His Gly Met Leu Asp Ser Asp Leu His Lys Thr
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Ser Gln Ala Glu Val Phe Glu His Pro His Leu Ala Glu Ala Pro Lys
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Gln Leu Pro Glu Glu Glu Thr Leu Phe Phe Gly Asp Thr Gly Ile Ser
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Lys Asn Pro Val Glu Leu Ile Glu Gly Trp Phe Ser Ser Trp Lys Ser
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Thr Val Val Thr Phe Phe Phe Ala Ile Gly Val Phe Ile Leu Leu Tyr
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