

PAT056489WOPCTB_ST25
SEQUENCE LISTING

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<120> COMPOSITIONS AND METHODS OF USE FOR AUGMENTED IMMUNE RESPONSE
AND CANCER THERAPY

<130> PAT056489-WO-PCT

<150> 62/061,644
<151> 2014-10-08

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<151> 2015-09-18

<150> 62/198,673
<151> 2015-07-29

<160> 113

<170> PatentIn version 3.5

<210> 1
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<212> PRT
<213> Homo sapiens

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Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
1 5 10 15

Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
20 25 30

Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
35 40 45

Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
50 55 60

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Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
65 70 75 80

Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
85 90 95

Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
100 105 110

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

Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
130 135 140

Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
145 150 155 160

Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
165 170 175

Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
180 185 190

Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
195 200 205

Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
210 215 220

Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
225 230 235 240

Val

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Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
 1 5 10 15

Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
 20 25 30

Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
 35 40 45

Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
 50 55 60

Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
 65 70 75 80

Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
 85 90 95

Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
 100 105 110

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

Lys Pro Trp Thr Asp Cys Cys Trp Arg Cys Arg Arg Arg Pro Lys Thr
 130 135 140

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

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Arg Arg Arg Gly Gly Trp Glu Thr Cys Gly Cys Glu Pro Gly Arg Pro
165 170 175

Pro Gly Pro Pro Thr Ala Ala Ser Pro Ser Pro Gly Ala Pro Gln Ala
180 185 190

Ala Gly Ala Leu Arg Ser Ala Leu Gly Arg Ala Leu Leu Pro Trp Gln
195 200 205

Gln Lys Trp Val Gln Glu Gly Gly Ser Asp Gln Arg Pro Gly Pro Cys
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Ser Ser Ala Ala Ala Ala Gly Pro Cys Arg Arg Glu Arg Glu Thr Gln
225 230 235 240

Ser Trp Pro Pro Ser Ser Leu Ala Gly Pro Asp Gly Val Gly Ser
245 250 255

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Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
1 5 10 15

Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
20 25 30

Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
35 40 45

Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
50 55 60

Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His

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65		70		75		80									
Cys	Gly	Asp	Pro	Cys	Cys	Thr	Thr	Cys	Arg	His	His	Pro	Cys	Pro	Pro
				85				90					95		
Gly	Gln	Gly	Val	Gln	Ser	Gln	Gly	Lys	Phe	Ser	Phe	Gly	Phe	Gln	Cys
			100					105					110		
Ile	Asp	Cys	Ala	Ser	Gly	Thr	Phe	Ser	Gly	Gly	His	Glu	Gly	His	Cys
		115					120					125			
Lys	Pro	Trp	Thr	Asp	Cys	Thr	Gln	Phe	Gly	Phe	Leu	Thr	Val	Phe	Pro
	130					135					140				
Gly	Asn	Lys	Thr	His	Asn	Ala	Val	Cys	Val	Pro	Gly	Ser	Pro	Pro	Ala
145					150					155					160
Glu	Pro	Leu	Gly	Trp	Leu	Thr	Val	Val	Leu	Leu	Ala	Val	Ala	Ala	Cys
				165					170					175	
Val	Leu	Leu	Leu	Thr	Ser	Ala	Gln	Leu	Gly	Leu	His	Ile	Trp	Gln	Leu
			180					185					190		
Arg	Lys	Thr	Gln	Leu	Leu	Leu	Glu	Val	Pro	Pro	Ser	Thr	Glu	Asp	Ala
		195					200					205			
Arg	Ser	Cys	Gln	Phe	Pro	Glu	Glu	Glu	Arg	Gly	Glu	Arg	Ser	Ala	Glu
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Glu	Lys	Gly	Arg	Leu	Gly	Asp	Leu	Trp	Val						
225					230										

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

Cys	Cys	Ser	Glu	Trp	Asp	Cys
			35			

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Met	Cys	Val	Gln	Pro	Glu	Phe	His	Cys	Gly	Asp	Pro	Cys	Cys	Thr	Thr
1				5				10						15	

Cys	Arg	His	His	Pro	Cys	Pro	Pro	Gly	Gln	Gly	Val	Gln	Ser	Gln	Gly
			20					25					30		

Lys	Phe	Ser	Phe	Gly	Phe	Gln	Cys
			35			40	

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Gln 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 Ser Leu Ser Ser Tyr
20 25 30

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

Gly Val Ile Trp Gly Gly Gly Gly Thr Tyr Tyr Ala Ser Ser Val Met
50 55 60

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

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

Lys His Ala Tyr Gly His Asp Gly Gly Phe Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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<400> 7

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Glu Ser Val Ser Ser Asn

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20

25

30

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

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Gln 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 Ser Leu Ser Ser Tyr
20 25 30

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

Gly Val Ile Trp Gly Gly Gly Gly Thr Tyr Tyr Thr Ala Ser Leu Met
50 55 60

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

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

Lys His Ala Tyr Gly His Asp Gly Gly Phe Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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

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

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

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

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

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

85

90

95

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

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

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

Gly Val Ile Trp Gly Gly Gly Gly Thr Tyr Tyr Ala Ser Ser Leu Met
 50 55 60

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

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

Lys His Ala Tyr Gly His Asp Gly Gly Phe Ala Met Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

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

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

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

Gly Val Ile Trp Gly Gly Gly Gly Thr Tyr Tyr Thr Ser Ser Leu Met
 50 55 60

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

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

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Lys His Ala Tyr Gly His Asp Gly Gly Phe Ala Met Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

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Ala Ala Gly Ala Ser His His His His His His
 1 5 10

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

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

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

Gly Val Ile Trp Gly Gly Gly Gly Thr Tyr Tyr Thr Ser Ser Leu Met
 50 55 60

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

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

Lys His Ala Tyr Gly His Asp Gly Gly Phe Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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Gly Gly Gly Gly Ser
1 5

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<223> (K/R)

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<223> (H/N)

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

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

Gly	Val	Asp	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Xaa
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35

40

45

Gly Val Ile Trp Gly Gly Gly Gly Thr Tyr Tyr Xaa Xaa Ser Xaa Met
 50 55 60

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

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

Xaa Xaa Ala Tyr Gly His Asp Gly Gly Phe Ala Met Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Xaa Ser Val Ser Ser Asn
 20 25 30

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

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 gcgtctagaa ctggatggtg ggaagatgg

29

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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

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110

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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

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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

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

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

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Ser Tyr Gly Val Asp
1 5

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Val Ile Trp Gly Gly Gly Gly Thr Tyr Tyr Ala Ser Ser Val Met Ala
1 5 10 15

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Val Ile Trp Gly Gly Gly Gly Thr Tyr Tyr Thr Ala Ser Leu Met Gly
1 5 10 15

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Val	Ile	Trp	Gly	Gly	Gly	Gly	Thr	Tyr	Tyr	Ala	Ser	Ser	Leu	Met	Gly
1				5					10					15	

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Val	Ile	Trp	Gly	Gly	Gly	Gly	Thr	Tyr	Tyr	Thr	Ser	Ser	Leu	Met	Gly
1				5					10					15	

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Val	Ile	Trp	Gly	Gly	Gly	Gly	Thr	Tyr	Tyr	Thr	Ser	Ser	Leu	Met	Ala
1				5					10					15	

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<222> (14)..(14)

<223> (L/V)

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<222> (16)..(16)

<223> (A/G)

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Val	Ile	Trp	Gly	Gly	Gly	Gly	Thr	Tyr	Tyr	Xaa	Xaa	Ser	Xaa	Met	Xaa
1				5					10					15	

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His	Ala	Tyr	Gly	His	Asp	Gly	Gly	Phe	Ala	Met	Asp	Tyr
1				5				10				

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Arg Ala Ser Glu Ser Val Ser Ser Asn Val Ala

1 5 10

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Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
1 5 10

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Arg Ala Ser Xaa Ser Val Ser Ser Asn Xaa Ala
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Gly Ala Ser Asn Arg Ala Thr
1 5

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<400> 34

Gly Gln Ser Tyr Ser Tyr Pro Phe Thr
1 5

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<213> Artificial Sequence

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<223> synthetic sequence

<400> 35

Gln 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 Ser Leu Ser
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<211> 30

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

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

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<223> (P/S)

<400> 37

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

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

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<400> 38

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Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly
1 5 10

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Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu Gly
1 5 10

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Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Xaa Gly
1 5 10

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<223> (K/R)

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Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln
1				5					10					15	

Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Xaa
			20					25					30		

<210> 42

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 42

Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 43

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 43

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

Glu	Arg	Ala	Thr	Leu	Ser	Cys
				20		

<210> 44

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

<220>
 <223> synthetic sequence

<400> 44

Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr
1				5					10					15

<210> 45
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 45

Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr
1				5					10					15

<210> 46
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<220>
 <221> VARIANT
 <222> (5)..(5)
 <223> (K/R)

<400> 46

Trp	Tyr	Gln	Gln	Xaa	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr
1				5					10					15

<210> 47

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

<220>
 <223> synthetic sequence

<400> 47

Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr
1				5				10					15		

Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys
			20					25					30		

<210> 48
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 48

Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr
1				5				10					15		

Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys
			20					25					30		

<210> 49
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<220>
 <221> VARIANT
 <222> (4)..(4)
 <223> (A/D)

<400> 49

Gly	Ile	Pro	Xaa	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys
			20				25						30		

<210> 50

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 50

Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
1				5					10

<210> 51

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 51

caggtgcagc	tggtggagtc	tgggggaggc	ttggtacagc	ctgggggggtc	cctgagactc	60
tcctgtgcag	cctctggatt	ctccctcagc	agctatgggtg	tggactgggt	tcgccaggct	120
ccaggaaaagg	gtctggagtg	ggtgggagtt	atatgggggtg	gtggaggcac	atattatgct	180
tcttctgtca	tggccagatt	caccatctcc	agagacaatt	ccaagaacac	gctgtatctg	240
caaatgaaca	gcctgagagc	tgaggacacg	gccgtgtatt	actgcgccaa	acatgcctat	300
ggccatgatg	gcggttttgc	tatggattat	tggggccagg	gtacccttgt	gaccgtgagc	360
tca						363

<210> 52
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 52
 gaaatagtga tgacgcagtc tccagccacc ctgtctgttt ctccaggaga aagagccacc 60
 ctctcctgca gggccagtga gagtgtagc agtaatgtag cctggtacca gcagagacct 120
 ggccaggcac ccaggctcct catctacggg gcatccaacc gggccactgg catcccagcc 180
 aggttcagtg gcagtgggtc tgggacagac ttactctca ccatcagcag actggagcct 240
 gaagattttg cagtgtacta ctgcggccag agctatagct atccatttac ctttggccag 300
 ggcaccaagc ttgaaattaa g 321

<210> 53
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 53
 caggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt ctccctcagc agctatgggtg tggactgggt tcgccaggct 120
 ccaggaaagg gtctggagtg gctgggagtt atatgggggtg gtggaggcac atattatact 180
 gcttctctca tgggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctg 240
 caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgcgcaa acatgcctat 300
 ggccatgatg gcggctttgc tatggattat tggggccagg gtacccttgt gaccgtgagc 360
 tca 363

<210> 54

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<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 54
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgtttagc agcaacttag cctggtagca gcagaaacct 120
ggccaggctc ccaggctcct catctacggg gcatccaacc gggccactgg catcccagac 180
aggttcagtg gcagtgggtc tgggacagac ttactctca ccatcagcag actggagcct 240
gaagattttg cagtttacta ctgcggccag agctatagct atccatttac ctttggccag 300
ggcaccaagc ttgaaattaa a 321

<210> 55
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 55
gaggtgcagc tgggtggagtc cgggggaggc ttagttcagt ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt ctccctcagc agctatggtg tggactgggt tcgccaggct 120
ccaggaaagg gtctggagtg ggtgggagtt atatgggggtg gtggaggcac atattatgct 180
tcttctctca tgggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctg 240
caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgcgcaa acatgcctat 300
ggccatgatg gcggctttgc tatggattat tggggccagg gtacccttgt gaccgtgagc 360
tca 363

<210> 56
<211> 363
<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 56

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gaggtgcagc tgggtggagtc cgggggaggc ttagttcagt ctgggggggtc cctgagactc      60
tcctgtgcag cctctggatt ctccctcagc agctatgggtg tggactgggt tcgccaggct      120
ccaggaaagg gtctggagtg gctgggagtt atatgggggtg gtggaggcac atattatact      180
tcttctctca tgggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctg      240
caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgcgcaa acatgcctat      300
ggccatgatg gcggctttgc tatggattat tggggccagg gtacccttgt gaccgtgagc      360
tca                                          363

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<210> 57

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 57

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gaggtgcagc tgggtggagtc cgggggaggc ttagttcagt ctgggggggtc cctgagactc      60
tcctgtgcag cctctggatt ctccctcagc agctatgggtg tggactgggt tcgccaggct      120
ccaggaaagg gtctggagtg gctgggagtt atatgggggtg gtggaggcac atattatact      180
tcttctctca tggccagatt caccatctcc agagacaatt ccaagaacac gctgtatctg      240
caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgcgcaa acatgcctat      300
ggccatgatg gcggctttgc tatggattat tggggccagg gtacccttgt gaccgtgagc      360
tca                                          363

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<210> 58

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 58

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aacattgtaa tgaccaatc tcccaaatcc atgtccatgt cagtaggaga gagggtcacc      60
ttgagctgca aggccagtga gaatgtggat acttttgtat cctggatatca acagaaacca    120
gaccactctc ctaaactact gatatacggg gcatccaacc ggtacactgg ggtccccgat     180
cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct     240
gaagaccttg cagattatca ctgtggacag agttacagct atccattcac gttcggctcg     300
gggacaaaagt tggaaataaa a                                              321

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<210> 59

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 59

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Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly
1           5           10          15

Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Thr Phe
          20          25          30

Val Ser Trp Tyr Gln Gln Lys Pro Asp His Ser Pro Lys Leu Leu Ile
          35          40          45

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

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

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

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 60
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 60
cagggtgcagc tgaaggagtc aggacctggc ctggtggcgc cctcacagag cctgtccatc 60
acttgactg tctctgggtt ttcattaagg agctatggtg tagactgggt tcgccagcct 120
ccaggaaaagg gtctggagtg gctgggagtt atatggggtg gtggaggcac aaattataat 180
tcagctctca tggccaaact gagtatcagc aaagacaagt ccaagagcca agttttctta 240
aaaatgaaca gtctgcaaac tgatgacaca gccatgtact actgtgccaac acatgcctat 300
ggtcacgacg gcggttttgc tatggactac tgggggtcaag gaacctcagt caccgtctcc 360
tca 363

<210> 61
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 61

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

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

20

25

30

Gly Val Asp Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45

Gly Val Ile Trp Gly Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
 50 55 60

Ala Lys Leu Ser Ile Ser Lys Asp Lys Ser Lys Ser Gln Val Phe Leu
 65 70 75 80

Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
 85 90 95

Lys His Ala Tyr Gly His Asp Gly Gly Phe Ala Met Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser
 115 120

<210> 62

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 62

Val Ile Trp Gly Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met Ala
 1 5 10 15

<210> 63

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 63

Lys Ala Ser Glu Asn Val Asp Thr Phe Val Ser
1 5 10

<210> 64

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 64

Gly Ala Ser Asn Arg Tyr Thr
1 5

<210> 65

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 65

Gln 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 Ser Leu Ser Ser Tyr
20 25 30

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

Gly Val Ile Trp Gly Gly Gly Gly Thr Tyr Tyr Ala Ser Ser Val Met
50 55 60

Ala Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu

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

260

265

270

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys

450

<210> 66
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 66

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu 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

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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> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 67
caggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt ctccctcagc agctatggtg tggactgggt tcgccaggct 120
ccaggaaagg gtctggagtg ggtgggagtt atatgggggtg gtggaggcac atattatgct 180
tcttctgtca tggccagatt caccatctcc agagacaatt ccaagaacac gctgtatctg 240
caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgcgcaa acatgcctat 300
ggccatgatg gcggccttgc tatggattat tggggccagg gtacccttgt gaccgtgagc 360
tcagctagca ccaaggggcc cagcgtgttc cccctggccc ccagcagcaa gagcaccagc 420
ggcggcacag ccgcccctggg ctgcctgggtg aaggactact tccccgagcc cgtgaccgtg 480
tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagc 540

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agcggcctgt acagcctgtc cagcgtggtg acagtgccca gcagcagcct gggcaccacag	600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gagagtggag	660
cccaagagct gcgacaagac ccacacctgc cccccctgcc cagccccaga gctgctgggc	720
ggaccctccg tgttcctgtt ccccccaag cccaaggaca ccctgatgat cagcaggacc	780
cccgaggatga cctgcgtggt ggtggacgtg agccacgagg acccagaggt gaagttcaac	840
tggtacgtgg acggcgtgga ggtgcacaac gccaaagacca agcccagaga ggagcagtac	900
aacagcacct acagggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc	960
aaggaataca agtgcaaggt ctccaacaag gccctgccag ccccatcga aaagaccatc	1020
agcaaggcca agggccagcc acgggagccc caggtgtaca ccctgcccc ctcccgggag	1080
gagatgacca agaaccaggt gtccctgacc tgtctggtga agggcttcta ccccagcgac	1140
atgcccgtag agtgggagag caacggccag cccgagaaca actacaagac cccccccca	1200
gtgctggaca gcgacggcag cttcttcctg tacagcaagc tgaccgtgga caagtccagg	1260
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac	1320
accagaaga gcctgagcct gtcccccggc aag	1353

<210> 68
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 68	
gaaatagtga tgacgcagtc tccagccacc ctgtctgttt ctccaggaga aagagccacc	60
ctctcctgca gggccagtga gagtgttagc agtaatgtag cctggtacca gcagagacct	120
ggccaggcac ccaggctcct catctacggg gcatccaacc gggccactgg catcccagcc	180
aggttcagtg gcagtgggtc tgggacagac ttactctca ccatcagcag actggagcct	240
gaagattttg cagtgtacta ctgcggccag agctatagct atccatttac ctttggccag	300

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ggcaccaagc ttgaaattaa gcgtacgggtg gccgctccca gcgtgttcat cttccccccc 360
 agcgacgagc agctgaagag cggcaccgcc agcgtgggtgt gcctgctgaa caacttctac 420
 ccccgaggagg ccaaggtgca gtggaagggtg gacaacgccc tgcagagcgg caacagccag 480
 gagagcgtca ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540
 ctgagcaagg ccgactacga gaagcataag gtgtacgcct gcgaggtgac ccaccagggc 600
 ctgtccagcc ccgtgaccaa gagcttcaac aggggcgagt gc 642

<210> 69
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 69

Gln 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 Ser Leu Ser Ser Tyr
 20 25 30

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

Gly Val Ile Trp Gly Gly Gly Gly Thr Tyr Tyr Thr Ala Ser Leu Met
 50 55 60

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

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

Lys His Ala Tyr Gly His Asp Gly Gly Phe Ala Met Asp Tyr Trp Gly

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100

105

110

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

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

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

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

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

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

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

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

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

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

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

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

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290

295

300

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

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

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

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

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

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

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

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

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

Pro Gly Lys
 450

<210> 70

<211> 214

<212> PRT

<213> Artificial Sequence

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<220>

<223> synthetic sequence

<400> 70

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu 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

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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> 71
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 71
 caggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt ctccctcagc agctatgggtg tggactgggt tcgccaggct 120
 ccaggaaagg gtctggagtg gctgggagtt atatgggggtg gtggaggcac atattatact 180
 gcttctctca tgggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctg 240
 caaatgaaca gcctgagagc tggaggacacg gccgtgtatt actgcgccaa acatgcctat 300
 ggccatgatg gcggctttgc tatggattat tggggccagg gtacccttgt gaccgtgagc 360
 tcagctagca ccaagggccc cagcgtgttc cccctggccc ccagcagcaa gagcaccagc 420
 ggccggcacag ccgccctggg ctgcctgggtg aaggactact tccccgagcc cgtgaccgtg 480
 tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagc 540
 agcggcctgt acagcctgtc cagcgtgggtg acagtgccca gcagcagcct gggcacccag 600
 acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gagagtggag 660
 cccaagagct gcgacaagac ccacacctgc cccccctgcc cagccccaga gctgctgggc 720
 ggaccctccg tgttcctgtt cccccccaag cccaaggaca ccctgatgat cagcaggacc 780

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cccgaggtga cctgcgtggt ggtggacgtg agccacgagg acccagaggt gaagttcaac	840
tggtagctgg acggcgtgga ggtgcacaac gccaagacca agcccagaga ggagcagtag	900
aacagcacct acaggggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc	960
aaggaataca agtgcaaggt ctccaacaag gccctgccag ccccatcga aaagaccatc	1020
agcaaggcca agggccagcc acgggagccc caggtgtaca ccctgcccc ctcccgggag	1080
gagatgacca agaaccaggt gtccctgacc tgtctggtga agggcttcta cccagcgac	1140
atgccgtgg agtgggagag caacggccag cccgagaaca actacaagac cccccccca	1200
gtgctggaca gcgacggcag cttcttcctg tacagcaagc tgaccgtgga caagtccagg	1260
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac	1320
accagaaga gcctgagcct gtcccccggc aag	1353

<210> 72
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 72	
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc	60
ctctcctgca gggccagtca gtagttagc agcaacttag cctggtacca gcagaaacct	120
ggccaggctc ccaggctcct catctacggg gcatccaacc gggccactgg catcccagac	180
aggttcagtg gcagtgggtc tgggacagac ttactctca ccatcagcag actggagcct	240
gaagattttg cagtttacta ctgcggccag agctatagct atccatttac ctttggccag	300
ggcaccaagc ttgaaattaa acgtacggtg gccgctcca gcgtgttcat cttccccccc	360
agcgacgagc agctgaagag cggcaccgcc agcgtggtgt gcctgctgaa caacttctac	420
ccccgggagg ccaaggtgca gtggaagggt gacaacgccc tgacagcgg caacagccag	480
gagagcgtca ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc	540

ctgagcaagg ccgactacga gaagcataag gtgtacgcct gcgaggtgac ccaccagggc 600

ctgtccagcc ccgtgaccaa gagcttcaac aggggcgagt gc 642

<210> 73

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 73

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

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

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

Gly Val Ile Trp Gly Gly Gly Gly Thr Tyr Tyr Ala Ser Ser Leu Met
50 55 60

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

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

Lys His Ala Tyr Gly His Asp Gly Gly Phe Ala Met Asp Tyr Trp Gly
100 105 110

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala

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130

135

140

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

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

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

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

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

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

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

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

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

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

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

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile

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325

330

335

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

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

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

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

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

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

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

Pro Gly Lys
450

<210> 74
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 74
gaggtgcagc tgggtggagtc cggggggaggc ttagttcagt ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt ctccctcagc agctatggtg tggactgggt tcgccaggct 120

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ccaggaaagg gtctggagtg ggtgggagtt atatgggggtg gtggaggcac atattatgct	180
tcttctctca tgggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctg	240
caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgcgcaa acatgcctat	300
ggccatgatg gcggctttgc tatggattat tggggccagg gtacccttgt gaccgtgagc	360
tcagctagca ccaagggccc cagcgtgttc cccctggccc ccagcagcaa gagcaccagc	420
ggcggcacag ccgccctggg ctgcctgggtg aaggactact tccccgagcc cgtgaccgtg	480
tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagc	540
agcggcctgt acagcctgtc cagcgtgggtg acagtgccca gcagcagcct gggcacccag	600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gagagtggag	660
cccaagagct gcgacaagac ccacacctgc cccccctgcc cagccccaga gctgctgggc	720
ggaccctccg tgttcctgtt ccccccaag cccaaggaca ccctgatgat cagcaggacc	780
cccgagggtga cctgcgtggg ggtggacgtg agccacgagg acccagaggt gaagttcaac	840
tggtacgtgg acggcgtgga ggtgcacaac gccaagacca agcccagaga ggagcagtac	900
aacagcacct acaggggtggg gtccgtgctg accgtgctgc accaggactg gctgaacggc	960
aaggaataca agtgcaaggt ctccaacaag gccctgccag ccccatcga aaagaccatc	1020
agcaaggcca agggccagcc acgggagccc caggtgtaca ccctgcccc ctcccgggag	1080
gagatgacca agaaccaggt gtccctgacc tgtctgggtga agggcttcta ccccagcgac	1140
atcgccgtgg agtgggagag caacggccag cccgagaaca actacaagac cccccccca	1200
gtgctggaca gcgacggcag cttcttcctg tacagcaagc tgaccgtgga caagtccagg	1260
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac	1320
accagaaga gcctgagcct gtcccccggc aag	1353

<210> 75

<211> 451

<212> PRT

<213> Artificial Sequence

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<220>

<223> synthetic sequence

<400> 75

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

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

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

Gly Val Ile Trp Gly Gly Gly Gly Thr Tyr Tyr Thr Ser Ser Leu Met
50 55 60

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

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

Lys His Ala Tyr Gly His Asp Gly Gly Phe Ala Met Asp Tyr Trp Gly
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
450

<210> 76
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 76
gaggtgcagc tgggtggagtc cggggggaggc ttagttcagt ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt ctccctcagc agctatgggtg tggactgggt tcgccaggct 120
ccaggaaaagg gtctggagtg gctggggagtt atatgggggtg gtggaggcac atattatact 180
tcttctctca tgggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctg 240
caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgcgcaa acatgcctat 300
ggccatgatg gcggtcttgc tatggattat tggggccagg gtacccttgt gaccgtgagc 360
tcagctagca ccaagggccc cagcgtgttc cccctggccc ccagcagcaa gagcaccagc 420

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ggcggcacag ccgccctggg ctgcctggtg aaggactact tccccgagcc cgtgaccgtg	480
tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagc	540
agcggcctgt acagcctgtc cagcgtggtg acagtgccca gcagcagcct gggcacccag	600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gagagtggag	660
cccaagagct gcgacaagac ccacacctgc cccccctgcc cagccccaga gctgctgggc	720
ggaccctccg tgttcctgtt ccccccaag cccaaggaca ccctgatgat cagcaggacc	780
cccgagggtga cctgcgtggt ggtggacgtg agccacgagg acccagaggt gaagttcaac	840
tggtacgtgg acggcgtgga ggtgcacaac gccaagacca agcccagaga ggagcagtac	900
aacagcacct acagggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc	960
aaggaatata agtgcaaggt ctccaacaag gccctgccag ccccatcga aaagaccatc	1020
agcaaggcca agggccagcc acgggagccc caggtgtaca ccctgcccc ctcccgggag	1080
gagatgacca agaaccaggt gtccctgacc tgtctggtga agggcttcta ccccagcgac	1140
atcgccgtgg agtgggagag caacggccag cccgagaaca actacaagac cccccccca	1200
gtgctggaca gcgacggcag cttcttcctg tacagcaagc tgaccgtgga caagtccagg	1260
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac	1320
accagaaga gcctgagcct gtcccccggc aag	1353

<210> 77
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 77

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Ser Ser Tyr

20

25

30

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

Gly Val Ile Trp Gly Gly Gly Gly Thr Tyr Tyr Thr Ser Ser Leu Met
 50 55 60

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

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

Lys His Ala Tyr Gly His Asp Gly Gly Phe Ala Met Asp Tyr Trp Gly
 100 105 110

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

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

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

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

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

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

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys

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210

215

220

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

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

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

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

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

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

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

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

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

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

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

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

405

410

415

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

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

Pro Gly Lys
 450

<210> 78
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 78
 gaggtgcagc tgggtggagtc cggggggaggc ttagttcagt ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt ctccctcagc agctatgggtg tggactgggt tcgccaggct 120
 ccaggaaagg gtctggagtg gctgggagtt atatgggggtg gtggaggcac atattatact 180
 tcttctctca tggccagatt caccatctcc agagacaatt ccaagaacac gctgtatctg 240
 caaatgaaca gcctgagagc tgaggacacg gccgtgtatt actgcgcaa acatgcctat 300
 ggccatgatg gcggctttgc tatggattat tggggccagg gtacccttgt gaccgtgagc 360
 tcagctagca ccaagggtccc cagcgtgttc cccctggccc ccagcagcaa gagcaccagc 420
 ggcggcacag ccgccctggg ctgcctgggtg aaggactact tccccgagcc cgtgaccgtg 480
 tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagc 540
 agcggcctgt acagcctgtc cagcgtgggtg acagtgccca gcagcagcct gggcaccacg 600
 acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gagagtggag 660
 cccaagagct gcgacaagac ccacacctgc cccccctgcc cagccccaga gctgctgggc 720

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ggaccctccg tgttcctgtt cccccccaag cccaaggaca ccctgatgat cagcaggacc	780
cccagggtga cctgcgtggt ggtggacgtg agccacgagg acccagaggt gaagttcaac	840
tggtagctgg acggcgtgga ggtgcacaac gccaaagacca agcccagaga ggagcagtac	900
aacagcacct acagggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc	960
aaggaataca agtgcaaggt ctccaacaag gccctgccag ccccatcga aaagaccatc	1020
agcaaggcca agggccagcc acgggagccc caggtgtaca ccctgcccc ctcccgggag	1080
gagatgacca agaaccaggt gtccctgacc tgtctggtga agggcttcta cccagcgac	1140
atcgccgtgg agtgggagag caacggccag cccgagaaca actacaagac cccccccca	1200
gtgctggaca gcgacggcag cttcttcctg tacagcaagc tgaccgtgga caagtccagg	1260
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac	1320
accagaaga gcctgagcct gtcccccggc aag	1353

<210> 79
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 79

Gly	Phe	Ser	Leu	Arg	Ser	Tyr
1				5		

<210> 80
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 80

Trp Gly Gly Gly Gly

1 5

<210> 81
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 81

Ser Glu Asn Val Asp Thr Phe
1 5

<210> 82
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 82

Gly Ala Ser
1

<210> 83
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 83

Ser Tyr Ser Tyr Pro Phe
1 5

<210> 84
<211> 7
<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 84

Gly Phe Ser Leu Ser Ser Tyr
1 5

<210> 85

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 85

Ser Glu Ser Val Ser Ser Asn
1 5

<210> 86

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 86

Ser Gln Ser Val Ser Ser Asn
1 5

<210> 87

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<220>

<221> VARIANT

<222> (2)..(2)

<223> (E/Q)

<400> 87

Ser Xaa Ser Val Ser Ser Asn

1 5

<210> 88

<211> 56

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 88

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

1 5 10 15

Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg

20 25 30

Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val

35 40 45

Gln Pro Glu Phe His Cys Gly Asp

50 55

<210> 89

<211> 98

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 89

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

1 5 10 — 15

<400> 91

Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10 15

<210> 92

<211> 95

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 92

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

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

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

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

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

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

<210> 93

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 93

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 94

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 94

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 95

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 95

gggtctagac accatggctg tcttggggct gctcttc

37

<210> 96

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 96

gcgtctagaa yctccacaca caggrccag tggatagac

39

<210> 97

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 97

gggtctagac accatggagw cacakwctca ggtctttrta

40

<210> 98

<211> 88

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 98

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

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

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

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

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

Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys
				85			

<210> 99

<211> 121

<212> PRT

<213> Artificial Sequence

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<220>

<223> synthetic sequence

<400> 99

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

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

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

Gly Val Ile Trp Gly Gly Gly Gly Thr Tyr Tyr Ala Ser Ser Leu Met
50 55 60

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

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

Arg His Ala Tyr Gly His Asp Gly Gly Phe Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 100

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 100

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

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

195

200

205

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

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

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

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

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

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

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

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

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

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

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

$\langle 210 \rangle$	102
$\langle 211 \rangle$	321
$\langle 212 \rangle$	DNA
$\langle 213 \rangle$	Artificial Sequence

<220>

<223> synthetic sequence

<400> 102

gagatcgtga tgacccagtc ccccgccacc ctgtctgtgt ctcccggcga gagagccacc 60
 ctgagctgca gaggcctccga gtccgtgtcc tccaacgtgg cctggatatca gcagagacct 120
 ggtcaggccc ctcggtgtgt gatctacggc gcctctaacc gggccaccgg catccctgcc 180
 agattctccg gctccggcag cggcaccgac ttcaccctga ccatctcccg gctggaaccc 240
 gaggacttcg cctgttacta ctgcggccag tcctactcat accccttcac cttcggccag 300
 ggcaccaagc tggaaatcaa g 321

<210> 103

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 103

gaggtgcagc tgggtggaatc tggcggcgga ctggtgcagt ccggcggctc tctgagactg 60
 tcttgcgctg cctccggctt ctccctgtcc tcttacggcg tggactgggt gcgacaggcc 120
 cctggcaagg gcctggaatg ggtgggagtg atctggggcg gaggcggcac ctactacgcc 180
 tcttccctga tgggccgggt caccatctcc cgggacaact ccaagaacac cctgtacctg 240
 cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgcgccag acacgcctac 300
 ggccacgacg gcggcttcgc catggattat tggggccagg gcaccctggg gacagtgtcc 360
 tccgctagca ccaaggggccc aagtgtgttt cccctggccc ccagcagcaa gtctacttcc 420
 ggcggaactg ctgccctggg ttgcctgggt aaggactact tccccgagcc cgtgacagtg 480
 tcctggaact ctggggctct gacttccggc gtgcacacct tccccgccgt gctgcagagc 540
 agcggcctgt acagcctgag cagcgtgggt acagtgccct ccagctctct gggaacccag 600
 acctatatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gagagtggag 660

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cccaagagct gcgacaagac ccacacctgc cccccctgcc cagctccaga actgctggga	720
gggccttccg tgttcctggt ccccccaag cccaaggaca ccctgatgat cagcaggacc	780
cccgaggtga cctgcgtggt ggtggacgtg tcccacgagg acccagaggt gaagttcaac	840
tggtagctgg acggcgtgga ggtgcacaac gccaaagacca agcccagaga ggagcagtac	900
aacagcacct acagggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc	960
aaagaataca agtgcaaagt ctccaacaag gccctgccag cccaatcga aaagacaatc	1020
agcaaggcca agggccagcc acgggagccc cagggtgtaca ccctgcccc cagccgggag	1080
gagatgacca agaaccaggt gtccctgacc tgtctggtga agggcttcta cccagcgat	1140
atcgccgtgg agtgggagag caacggccag cccgagaaca actacaagac cccccccca	1200
gtgctggaca gcgacggcag cttcttcctg tacagcaagc tgaccgtgga caagtccagg	1260
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac	1320
accagaagt ccctgagcct gagccccggc aag	1353

<210> 104
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 104 gagatcgtga tgaccagtc ccccgccacc ctgtctgtgt ctcccggcga gagagccacc	60
ctgagctgca gagcctccga gtccgtgtcc tccaacgtgg cctggatatca gcagagacct	120
ggtcaggccc ctcggctgct gatctacggc gcctctaacc gggccaccgg catccctgcc	180
agattctccg gctccggcag cggcaccgac ttcaccctga ccatctcccg gctggaaccc	240
gaggacttcg ccgtgtacta ctgcggccag tcctactcat accccttcac cttcggccag	300
ggcaccaagc tggaatatcaa gcgtacgggtg gccgctccca gcgtgttcat cttccccccc	360
agcgacgagc agctgaagag cggcaccgcc agcgtgggtgt gcctgctgaa caacttctac	420

PAT056489WOPCTB_ST25

ccccgggagg ccaaggtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag 480
gagagcgtca ccgagcagga cagcaaggac tccacctaca gcctgagcag caccctgacc 540
ctgagcaagg ccgactacga gaagcataag gtgtacgcct gcgaggtgac ccaccagggc 600
ctgtccagcc ccgtgaccaa gagcttcaac aggggcgagt gc 642

<210> 105
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 105

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

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

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

Gly Val Ile Trp Gly Gly Gly Gly Thr Tyr Tyr Ala Ser Ser Leu Met
50 55 60

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

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

Arg Asn Ala Tyr Gly His Asp Gly Gly Phe Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 106
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 106

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

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

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

Gly Val Ile Trp Gly Gly Gly Gly Thr Tyr Tyr Ala Ser Ser Leu Met
 50 55 60

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

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

Arg Asn Ala Tyr Gly His Asp Gly Gly Phe Ala Met Asp Tyr Trp Gly
 100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
450

<210> 107
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic sequence

<400> 107
gaggtgcagc tgggtggaatc aggcggcgga ctggtgcagt caggcggtag cctgagactg 60
agctgcgccg cctccggctt tagcctgtct agctacggcg tggactgggt cgcacaggcc 120
cctggcaaag gcctggagtg ggtcggagtg atctggggcg gaggcggaac ctactacgcc 180

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tctagcctga tgggccggtt cactatctct agggacaact ctaagaacac cctgtacctg	240
cagatgaact cactgagagc cgaggacacc gccgtctact actgcgctag aaacgcctac	300
ggtcacgacg gcggcttcgc tatggactac tggggtcagg gcaccctggg caccgtgagt	360
tca	363

<210> 108
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 108	
gaggtgcagc tgggtggaatc aggcggcgga ctgggtgcagt caggcggtag cctgagactg	60
agctgcgccg cctccggctt tagcctgtct agctacggcg tggactgggt ccgacaggcc	120
cctggcaaag gcctggagtg ggtcggagtg atctggggcg gaggcggaac ctactacgcc	180
tctagcctga tgggccggtt cactatctct agggacaact ctaagaacac cctgtacctg	240
cagatgaact cactgagagc cgaggacacc gccgtctact actgcgctag aaacgcctac	300
ggtcacgacg gcggcttcgc tatggactac tggggtcagg gcaccctggg caccgtgagt	360
tcagctagca ctaaggggcc aagtgtgttt cccctggccc ccagcagcaa gtctacttcc	420
ggcgggaactg ctgccctggg ttgcctgggtg aaggactact tccccgagcc cgtgacagtg	480
tcctggaact ctggggctct gacttccggc gtgcacacct tccccgccgt gctgcagagc	540
agcggcctgt acagcctgag cagcgtgggt acagtgccct ccagctctct gggaaccag	600
acctatatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gagagtggag	660
ccaagagct gcgacaagac ccacacctgc cccccctgcc cagctccaga actgctggga	720
gggccttccg tgttcctgtt ccccccaag cccaaggaca ccctgatgat cagcaggacc	780
cccaggtga cctgcgtggg ggtggacgtg tcccacgagg acccagaggt gaagttcaac	840
tgggtacgtgg acggcgtgga ggtgcacaac gccaaagacca agcccagaga ggagcagtac	900

PAT056489WOPCTB_ST25

aacagcacct acaggggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc	960
aaagaatata agtgcaaagt ctccaacaag gccctgccag cccaatcga aaagacaatc	1020
agcaaggcca agggccagcc acgggagccc caggtgtaca ccctgcccc cagccgggag	1080
gagatgacca agaaccaggt gtccctgacc tgtctggtga agggcttcta cccagcgat	1140
atcgccgtgg agtgggagag caacggccag cccgagaaca actacaagac cccccccca	1200
gtgctggaca gcgacggcag cttcttcctg tacagcaagc tgaccgtgga caagtccagg	1260
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac	1320
accagaagt ccctgagcct gagccccggc aag	1353

<210> 109
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 109

Asn	Ala	Tyr	Gly	His	Asp	Gly	Gly	Phe	Ala	Met	Asp	Tyr
1				5					10			

<210> 110
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic sequence

<400> 110	
tctggcgcag taatacacgg cc	22

<210> 111
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetic sequence

<220>

<221> misc_feature

<222> (1)..(3)

<223> degenerate trinucleotide codon sequence nnk

<400> 111

nnkgcctatg gccatgatgg cg

22

<210> 112

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 112

gcctttctct ccacagg

17

<210> 113

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic sequence

<400> 113

ggcaaacaac agatggctgg

20