

SEQUENCE LISTING

<110> Merck Sharp & Dohme Corp.
 Chen, Zhu
 Ellsworth, Kenneth P
 Milligan, James
 Oldham, Elizabeth
 Seiffert, Dietmar

<120> ANTI-COAGULATION FACTOR XI ANTIBODIES

<130> 24339

<150> 62/349,888

<151> 2016-06-14

<160> 85

<170> PatentIn version 3.5

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Tyr	Ser	Ile	Ser	Ser	Gly	Tyr	Phe	Trp	Gly
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Ser	Ile	Leu	His	Ser	Gly	Val	Thr	Tyr	Tyr	Asn	Pro	Ser	Leu	Lys	Ser
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Ala	Arg	Asp	Arg	Thr	Thr	Val	Ser	Met	Ile	Glu	Tyr	Phe	Gln	His
1				5					10					15

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Ala	Arg	Asp	Arg	Thr	Thr	Val	Ser	Leu	Ile	Glu	Tyr	Phe	Gln	His
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Gln	Ala	Ser	Gln	Asp	Ile	Ser	Asn	Tyr	Leu	Asn
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Asp Ala Ser Asn Leu Glu Thr
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Gln Gln Phe His Leu Leu Pro Ile Thr
1 5

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Gly Ser Ile Tyr Ser Gly Ala Tyr Tyr Trp Ser
1 5 10

<210> 9

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Ser Ile His Tyr Ser Gly Leu Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 10

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<400> 10

Ala Arg Asp Val Asp Asp Ser Ser Gly Asp Glu His Tyr Gly Met Asp
 1 5 10 15

Val

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Arg Ala Ser Gln Gly Ile Asp Ser Trp Leu Ala
 1 5 10

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<400> 12

Ala Ala Ser Ser Leu Gln Ser
 1 5

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Gln Gln Tyr His Ile Val Pro Ile Thr
 1 5

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<400> 14

Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
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Asp Ala Arg Cys
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Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly
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Val His Ser

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<400> 16

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Glu Ser 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 Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
 325

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15

Ser Thr Ser Glu Ser 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 Lys Thr
 65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
 100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 305 310 315 320

Leu Ser Leu Ser Leu Gly
 325

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<400> 18

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

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

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
 225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

<210> 19
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<400> 19

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

20																25				12		30			
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser										
		35						40				45													
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser										
50							55				60														
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr										
65					70						75					80									
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys										
			85						90							95									
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys										
			100						105							110									
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro										
		115						120								125									
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys										
130							135								140										
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp										
145					150						155					160									
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu										
			165						170							175									
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu										
			180						185							190									
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn										
		195						200								205									
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly										
210							215								220										

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly
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<212> PRT

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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 14 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

<210> 21
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<400> 21

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

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95 15

Ala Arg Asp Arg Thr Thr Val Ser Met Ile Glu Tyr Phe Gln His Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 22
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<212> PRT
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<400> 22

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Met Ile Glu Tyr Phe Gln His Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

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<400> 23

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
 20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
 50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Leu Ile Glu Tyr Phe Gln His Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

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<400> 24

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
 20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
 50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Leu Ile Glu Tyr Phe Gln His Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 25
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 <212> PRT
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<400> 25

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

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 26

<211> 214

<212> PRT

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<400> 26

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
 20 25 30

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

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

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
 210

<210> 27

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<400> 27

Gly Ala Cys Ala Thr Cys Cys Ala Gly Ala Thr Gly Ala Cys Cys Cys
1 5 10 15

Ala Gly Ala Gly Cys Cys Cys Thr Ala Gly Cys Ala Gly Cys Cys Thr
20 25 30

Gly Ala Gly Cys Gly Cys Cys Ala Gly Cys Gly Thr Gly Gly Gly Cys
35 40 45

Gly Ala Cys Ala Gly Ala Gly Thr Gly Ala Cys Cys Ala Thr Cys Ala
50 55 60

Cys Cys Thr Gly Thr Cys Ala Ala Gly Cys Cys Thr Cys Cys Cys Ala
65 70 75 80

Gly Gly Ala Cys Ala Thr Cys Thr Cys Cys Ala Ala Cys Thr Ala Cys
85 90 95

Cys Thr Gly Ala Ala Cys Thr Gly Gly Thr Ala Cys Cys Ala Gly Cys
100 105 110

Ala Gly Ala Ala Gly Cys Cys Cys Gly Gly Cys Ala Ala Gly Gly Cys
115 120 125

Thr Cys Cys Cys Ala Ala Gly Cys Thr Gly Cys Thr Gly Ala Thr Cys
130 135 140

Thr Ala Cys Gly Ala Cys Gly Cys Cys Thr Cys Cys Ala Ala Cys Cys
145 150 155 160

Thr Gly Gly Ala Gly Ala Cys Cys Gly Gly Cys Gly Thr Gly Cys Cys
165 170 175

Thr Ala Gly Cys Ala Gly Ala Thr Thr Thr Ala Gly Cys Gly Gly Cys
 180 185 190

Ala Gly Cys Gly Gly Cys Thr Cys Cys Gly Gly Cys Ala Cys Ala Gly
 195 200 205

Ala Cys Thr Thr Cys Ala Cys Cys Thr Thr Cys Ala Cys Cys Ala Thr
 210 215 220

Cys Ala Gly Cys Thr Cys Cys Cys Thr Gly Cys Ala Gly Cys Cys Cys
 225 230 235 240

Gly Ala Gly Gly Ala Cys Ala Thr Thr Gly Cys Cys Ala Cys Cys Thr
 245 250 255

Ala Cys Thr Ala Cys Thr Gly Cys Cys Ala Gly Cys Ala Gly Thr Thr
 260 265 270

Thr Cys Ala Cys Cys Thr Gly Cys Thr Gly Cys Cys Thr Ala Thr Cys
 275 280 285

Ala Cys Cys Thr Thr Cys Gly Gly Cys Gly Gly Cys Gly Gly Cys Ala
 290 295 300

Cys Cys Ala Ala Gly Gly Thr Gly Gly Ala Gly Ala Thr Cys Ala Ala
 305 310 315 320

Ala Ala Gly Gly Ala Cys Cys Gly Thr Cys Gly Cys Cys Gly Cys Cys
 325 330 335

Cys Cys Thr Ala Gly Cys Gly Thr Gly Thr Thr Cys Ala Thr Cys Thr
 340 345 350

Thr Cys Cys Cys Cys Cys Cys Thr Ala Gly Cys Gly Ala Cys Gly Ala
 355 360 365

Gly Cys Ala Gly Cys Thr Cys Ala Ala Gly Thr Cys Cys Gly Gly Cys
 370 375 380

Ala Cys Cys Gly Cys Cys Ala Gly Cys Gly Thr Gly Gly Thr Gly Thr
 385 390 395 400

Gly Thr Cys Thr Gly Cys Thr Cys Ala Ala Cys Ala Ala Cys Thr Thr
 405 410 415

Cys Thr Ala Cys Cys Cys Cys Ala Gly Gly Gly Ala Gly Gly Cys Cys
 420 425 430

Ala Ala Gly Gly Thr Gly Cys Ala Gly Thr Gly Gly Ala Ala Gly Gly
 435 440 445

Thr Gly Gly Ala Cys Ala Ala Cys Gly Cys Cys Cys Thr Gly Cys Ala
 450 455 460

Gly Ala Gly Cys Gly Gly Cys Ala Ala Cys Ala Gly Cys Cys Ala Gly
 465 470 475 480

Gly Ala Gly Ala Gly Cys Gly Thr Gly Ala Cys Ala Gly Ala Ala Cys
 485 490 495

Ala Gly Gly Ala Cys Ala Gly Cys Ala Ala Gly Gly Ala Thr Thr Cys
 500 505 510

Cys Ala Cys Ala Thr Ala Cys Ala Gly Cys Cys Thr Gly Ala Gly Cys
 515 520 525

Thr Cys Cys Ala Cys Cys Cys Thr Gly Ala Cys Cys Cys Thr Gly Ala
 530 535 540

Gly Cys Ala Ala Gly Gly Cys Cys Gly Ala Cys Thr Ala Cys Gly Ala
 545 550 555 560

Gly Ala Ala Gly Cys Ala Cys Ala Ala Gly Gly Thr Gly Thr Ala Cys
 565 570 23 575

Gly Cys Cys Thr Gly Thr Gly Ala Gly Gly Thr Gly Ala Cys Ala Cys
 580 585 590

Ala Cys Cys Ala Gly Gly Gly Cys Cys Thr Cys Ala Gly Cys Thr Cys
 595 600 605

Cys Cys Cys Cys Gly Thr Gly Ala Cys Cys Ala Ala Gly Ala Gly Cys
 610 615 620

Thr Thr Cys Ala Ala Cys Ala Gly Ala Gly Gly Cys Gly Ala Ala Thr
 625 630 635 640

Gly Cys Thr Gly Ala
 645

<210> 28
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<400> 28

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

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

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

Trp Ile Gly Ser Ile His Tyr Ser Gly Leu Thr Tyr Tyr Asn Pro Ser
 50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Val Asp Asp Ser Ser Gly Asp Glu His Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 29

<211> 125

<212> PRT

<213> Artificial Sequence

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<400> 29

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

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

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

Trp Ile Gly Ser Ile His Tyr Ser Gly Leu Thr Tyr Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Val Asp Asp Ser Ser Gly Asp Glu His Tyr Gly Met
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 30
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<400> 30

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

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 31

<211> 214
 <212> PRT
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<220>
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<400> 31

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

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

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

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

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

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

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

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

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

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

27

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> 32
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Protein

<400> 32
gacatccaga tgacccagag ccctagcagc gtgagcgcca gcgtgggcga tagggtgacc 60
atcacctgca gagcctccca gggcatcgac agctggctgg cctggtacca gcagaagccc 120
ggcaaggccc ctaagctgct gatctacgcc gctagcagcc tgcagagcgg cgtgcctagc 180
aggttcagcg gaagcggcag cggcaccgac ttcacactga ccatcagcag cctgcaacct 240
gaggacttcg ccacctacta ctgccagcag tatcacatcg tgcccatcac cttcggcggc 300
ggaaccaagg tggagattaa gaggaccgtg gccgccccca gcgtgtttat ctttcccccc 360
agcgatgagc agctgaagag cggaaccgcc agcgtggtgt gcctgctgaa caacttctac 420
cccagagagg ccaagggtgca gtggaagggtg gacaacgccc tgcagtccgg aaacagccag 480
gagagcgtga ccgagcagga ttccaaggat agcacctaca gcctgagcag caccctgaca 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gtgaggtgac ccatcagggc 600
ctgagcagcc ctgtgaccaa gagcttcaac aggggcgagt gctga 645

<210> 33

<211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein

<400> 33

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
 20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
 50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Met Ile Glu Tyr Phe Gln His Trp
 100 105 110

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

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

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

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

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

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

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

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
260 265 270

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

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

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

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

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

Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr

1

gtccctgacc tgcgccgtga gcggctacag catctccagc ggctatttct ggggatggat 113
 cagacagccc cctggcaagg gcctggaatg gatcggttct atcctgcact ccggcgtgac 173
 atactataac cctagcctga agagcagggt gaccatctcc gtggatacca gcaagaatca 233
 gttcagcctg aagctcagca gcgtgaccgc cgccgatacc gctgtgtact actgcgccag 293
 agacaggacc accgtctcca tgatcgagta cttccagcac tggggccaag gcaccctggt 353
 caccgtgtcc tccgcctcca ccaagggccc tagcgtgttt cctctggccc cctgctccag 413
 atccacaagc gagagcaccg ctgccctggg ctgtctggtc aaggactact tccccgagcc 473
 cgtgacagtg tcctggaaca gcggcgccct gacaagcggc gtccatacat tccccgccgt 533
 gctgcagtcc agcggactgt atagcctgag ctccgtgggtg accgtgcctt ccagcagcct 593
 gggaaccaag acatatacct gcaacgtgga ccataagccc agcaacacaa aagtcgacaa 653
 gaggggtggag agcaagtacg gacccccctg tcccccttgt cctgctcccg agttcctcgg 713
 cggacctagc gtgttcctgt ttcctcccaa gcccaaggat accctgatga tcagcaggac 773
 ccctgagggtc acctgcgtgg tggtcgacgt gtcccaggag gaccctgagg tccagtttaa 833
 ctggtacgtg gacggagtgg aggtgcacaa cgccaagacc aagcccagag aggagcagtt 893
 caattccacc tacagggtgg tgagcgtcct gaccgtgctg caccaggact ggctgaatgg 953
 aaaggagtac aaatgcaagg tctccaacaa gggcctccct agcagcatcg agaagaccat 1013
 ctccaaggcc aagggccagc ctagggagcc ccagggtgtac accctgcctc ctagccagga 1073
 ggaaatgacc aagaaccagg tgtccctgac atgcctgggtg aagggttct atcctagcga 1133
 catcgccgtg gagtgggaga gcaatggcca gcccgagaat aactacaaga ccaccccccc 1193
 tgtgctcgat agcgacggca gcttctttct gtacagcagg ctgaccgtgg acaagagcag 1253
 gtggcaagag ggcaacgtgt ttagctgctc cgtcatgcac gaggccctgc ataaccacta 1313
 caccacaaaaa tccctgtccc tgtccctggg caagtga 1350

<210> 35

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein

<400> 35

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
 20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
 50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Met Ile Glu Tyr Phe Gln His Trp
 100 105 110

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

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

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

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro

33																
165						170						175				
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	
			180				185						190			
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	
		195					200				205					
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	
		210			215						220					
Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	
225				230						235						240
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	
			245						250				255			
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	
			260				265						270			
Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	
		275				280						285				
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	
		290				295				300						
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	
305				310						315				320		
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	
			325						330				335			
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	
			340				345						350			
Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	
		355				360						365				

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

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

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

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

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

Lys

<210> 36
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA

<220>
 <221> CDS
 <222> (1)..(3)
 <223> nnn=GAA or GAG

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> n is a, c, g, or t

<400> 36
 nnn gtccagctgc aggagagcgg ccctggcctg gtgaagccta gcgagacact
 Xaa
 1

gtccctgacc tgcgccgtga gcggctacag catctccagc ggctatattct ggggatggat 113
 cagacagccc cctggcaagg gcctggaatg gatcggttct atcctgcact ccggcgtgac 173
 atactataac cctagcctga agagcagggt gaccatctcc gtggatacca gcaagaatca 233
 gttcagcctg aagctcagca gcgtgaccgc cgccgatacc gctgtgtact actgcgccag 293
 agacaggacc accgtctcca tgatcgagta cttccagcac tggggccaag gcaccctggt 353
 caccgtgtcc tccgcctcca ccaagggccc tagcgtgttt cctctggccc cctgctccag 413
 atccacaagc gagagcaccg ctgccctggg ctgtctggtc aaggactact tccccgagcc 473
 cgtgacagtg tcctggaaca gcggcgccct gacaagcggc gtccatacat tccccgccgt 533
 gctgcagtcc agcggactgt atagcctgag ctccgtgggtg accgtgcctt ccagcagcct 593
 gggaaccaag acatatacct gcaacgtgga ccataagccc agcaacacaa aagtcgacaa 653
 gaggggtggag agcaagtacg gacccccctg tcccccttgt cctgctcccg agttcctcgg 713
 cggacctagc gtgttcctgt ttcctcccaa gcccaggat accctgatga tcagcaggac 773
 ccctgagggtc acctgcgtgg tggtcgacgt gtcccaggag gaccctgagg tccagtttaa 833
 ctggtacgtg gacggagtgg aggtgcacaa cgccaagacc aagcccagag aggagcagtt 893
 caattccacc tacagggtgg tgagcgtcct gaccgtgctg caccaggact ggctgaatgg 953
 aaaggagtac aaatgcaagg tctccaacaa gggcctccct agcagcatcg agaagaccat 1013
 ctccaaggcc aagggccagc ctagggagcc ccagggtgtac accctgcctc ctagccagga 1073
 ggaaatgacc aagaaccagg tgtccctgac atgcctgggtg aagggtttct atcctagcga 1133
 catcgccgtg gagtgggaga gcaatggcca gcccgagaat aactacaaga ccaccccccc 1193
 tgtgctcgat agcgacggca gcttctttct gtacagcagg ctgaccgtgg acaagagcag 1253
 gtggcaagag ggcaacgtgt ttagctgctc cgtcatgcac gaggccctgc ataaccacta 1313
 caccacaaaaa tccctgtccc tgtccctggg caagtga 1350

<210> 37
 <211> 449
 <212> PRT

<213> Artificial Sequence

<220>

<223> Protein

<400> 37

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Leu Ile Glu Tyr Phe Gln His Trp
100 105 110

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

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

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

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

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

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

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

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
 225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
 260 265 270

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

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

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

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

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

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

38

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

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

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

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

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

Lys

<210> 38
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA

<220>
<221> CDS
<222> (1)..(3)
<223> nnn= CAG or CAA

<220>
<221> misc_feature
<222> (1)..(3)
<223> n is a, c, g, or t

<400> 38
nnn gtccagctgc aggagagcgg ccctggactc gtgaagccct ccgaaaccct
Xaa
1

53

gagcctcaca tgcgccgtct ccggatacag catcagcagc ggatacttct ggggctggat 113
 cagacagccc cccggcaaag gcctggagtg gatcggttct attctccaca gcggcgtgac 173
 atactacaac ccctccctga agagcagggt gaccatcagc gtggacacct ccaagaacca 233
 gttttccctc aagctgagca gcgtgaccgc cgctgacaca gccgtgtatt actgcgccag 293
 ggacaggacc accgtgtccc tgattgagta cttccagcat tggggccagg gcacactggt 353
 gaccgtcagc agcgccagca ccaagggccc ttccgtcttc cctctggccc cttgcagcag 413
 aagcacctcc gagtccacag ccgccctggg atgcctcgtg aaggattact tccccgagcc 473
 cgtcacagtc tcctggaact ccggcgctct gaccagcgga gtgcacacct tccccgccgt 533
 gctgcaaagc agcggcctgt acagcctgtc cagcgtggtc accgtgcctt cctccagcct 593
 gggcaccaag acctacacat gcaacgtgga ccacaagcct tccaacacca aggtggacaa 653
 gagagtggaa agcaagtacg gccccccctg ccccccttgt cctgcccccg agtttctggg 713
 aggaccctcc gtgttcctct ttcctcccaa gcctaaggac accctgatga tctccaggac 773
 ccccgaagtg acctgcgtgg tcgtggacgt gtcccaggag gaccctgagg tgcagtttaa 833
 ctggtacgtg gacggcgtgg aggtgcacaa cgccaagacc aagcccaggg aggagcagtt 893
 caatagcacc tacagggtgg tgtccgtgct gaccgtgctg caccaggact ggctgaacgg 953
 caaagagtac aagtgcaaag tcagcaacaa gggcctgccc tcctccatcg agaagaccat 1013
 tagcaaggcc aagggccagc ctagggagcc tcaggtgtac accctgcccc ccagccagga 1073
 ggagatgacc aagaaccagg tgtccctgac ctgcctggtc aagggatttt accccagcga 1133
 catcgctgtg gaatgggaga gcaatggcca gcccgagaac aactacaaga ccaccctcc 1193
 cgtgctcgat tccgacggca gctttttcct gtacagcagg ctgaccgtgg ataagagcag 1253
 gtggcaggaa ggcaacgtgt tctcctgttc cgtgatgcat gaggccctgc acaaccacta 1313
 cacacagaag agcctgtccc tgtccctggg caagtga 1350

<210> 39

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein

<400> 39

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
 20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
 50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Leu Ile Glu Tyr Phe Gln His Trp
 100 105 110

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

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

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

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

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

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

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

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
 225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
 260 265 270

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

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

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

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

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

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

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 42 380

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

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

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

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

Lys

<210> 40
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA

<220>
 <221> CDS
 <222> (1)..(3)
 <223> nnn=GAA or GAG

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> n is a, c, g, or t

<400> 40
 nnn gtccagctgc aggagagcgg ccctggactc gtgaagccct ccgaaaccct 53
 Xaa
 1

gagcctcaca tgcgccgtct ccggatacag catcagcagc ggatacttct ggggctggat 113

cagacagccc cccggcaaag gcctggagtg gatcggttct attctccaca gcggcgtgac 173
 atactacaac ccctccctga agagcaggggt gaccatcagc gtggacacct ccaagaacca 233
 gttttccctc aagctgagca gcgtgaccgc cgctgacaca gccgtgtatt actgcgccag 293
 ggacaggacc accgtgtccc tgattgagta cttccagcat tggggccagg gcacactggt 353
 gaccgtcagc agcgccagca ccaagggccc ttccgtcttc cctctggccc cttgcagcag 413
 aagcacctcc gagtccacag ccgccctggg atgcctcgtg aaggattact tccccgagcc 473
 cgtcacagtc tcctggaact ccggcgctct gaccagcggg gtgcacacct tccccgccgt 533
 gctgcaaagc agcggcctgt acagcctgtc cagcgtggtc accgtgcctt cctccagcct 593
 gggcaccaag acctacacat gcaacgtgga ccacaagcct tccaacacca aggtggacaa 653
 gagagtggaa agcaagtacg gccccccctg ccccccttgt cctgcccccg agtttctggg 713
 aggaccctcc gtgttcctct ttcctcccaa gcctaaggac accctgatga tctccaggac 773
 ccccgaaagt acctgcgtgg tcgtggacgt gtcccaggag gaccctgagg tgcagtttaa 833
 ctggtacgtg gacggcgtgg aggtgcacaa cgccaagacc aagcccaggg aggagcagtt 893
 caatagcacc tacagggtgg tgtccgtgct gaccgtgctg caccaggact ggctgaacgg 953
 caaagagtac aagtgcaaag tcagcaacaa gggcctgccc tcctccatcg agaagaccat 1013
 tagcaaggcc aagggccagc ctagggagcc tcagggtgtac accctgcccc ccagccagga 1073
 ggagatgacc aagaaccagg tgtccctgac ctgcctggtc aagggatttt accccagcga 1133
 catcgctgtg gaatgggaga gcaatggcca gcccgagaac aactacaaga ccaccctcc 1193
 cgtgctcgat tccgacggca gctttttcct gtacagcagg ctgaccgtgg ataagagcag 1253
 gtggcaggaa ggcaacgtgt tctcctgttc cgtgatgcat gaggccctgc acaaccacta 1313
 cacacagaag agcctgtccc tgtccctggg caagtga 1350

<210> 41
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Protein

<400> 41

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

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

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

Trp Ile Gly Ser Ile His Tyr Ser Gly Leu Thr Tyr Tyr Asn Pro Ser
 50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
 85 90 95

Cys Ala Arg Asp Val Asp Asp Ser Ser Gly Asp Glu His Tyr Gly Met
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
 115 120 125

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

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

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

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
180 185 190 45

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

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

Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu
225 230 235 240

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

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

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

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

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

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

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

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

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

370

375

46

380

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

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

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

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

Ser Leu Gly Lys
450

<210> 42
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA

<220>
<221> CDS
<222> (1)..(3)
<223> nnn= CAG or CAA

<220>
<221> misc_feature
<222> (1)..(3)
<223> n is a, c, g, or t

<400> 42
nnn gtccagctgc aggaatccgg acccggcctg gtgaagccta gccagaccct 53
Xaa
1

gagcctgacc tgtaccgtgt ccggcggaag catctattcc ggcgccctact actggtcctg 113

gattaggcag caccccggca agggcctgga atggatcggc tccatccact acagcggcct 173
 gacctattac aacccctccc tgaagtccag ggtgaccatc agcgtcgaca caagcaagaa 233
 ccagttctcc ctcaagctga gcagcgtgac cgccgccgac accgccgtgt attattgcgc 293
 cagagacgtg gacgactcct ccggagacga gcactacggc atggacgtct ggggccaggg 353
 cacaacagtg acagtgagca gcgccagcac caaaggaccc tccgtcttcc ctctggcccc 413
 ttgctccagg agcacaagcg aaagcacagc cgccctgggc tgcctgggtga aggactactt 473
 tcccagagccc gtgaccgtga gctggaatag cggagccctc acctccggag tccacacatt 533
 tcccgccgtc ctgcagagca gcggcctgta ctccctgagc tccgtgggtga ccgtgccttc 593
 ctccagcctg ggcaccaaga cctacacctg caacgtggac cacaagccta gcaataccaa 653
 ggtggacaag aggggtggaat ccaagtacgg ccccccctgc cctccttgct ctgccccga 713
 atttctgggc ggcccttccg tgttcctgtt ccctccaag cccaaggata ccctgatgat 773
 cagcaggacc cctgagggtga cctgtgtggt ggtggacgtg agccaggagg accccgaggt 833
 gcagttcaac tggtagctgg atggcgtgga agtgcacaat gccaagacaa agcccaggga 893
 ggagcagttc aatagcacct acagggtggt cagcgtgctc acagtgtgc accaggactg 953
 gctgaacgga aaggagtaca agtgcaaagt gtccaacaag ggccctgccct cctccatcga 1013
 aaagaccatc tccaaggcca aaggccagcc caggaggccc caagtgtata ccctcccccc 1073
 tagccaggag gaaatgacca aaaaccaggt ctccctgacc tgtctgggtga agggcttcta 1133
 tcccagcgac atcgctgtgg agtgggagag caacggccaa cccgagaaca actataagac 1193
 cacaccccc gtcctggact ccgatggctc cttcttcctg tacagcaggc tgaccgtcga 1253
 caagtccagg tggcaggaag gaaacgtgtt ctctgtagc gtcatgcacg aggccctgca 1313
 caaccactat acccagaagt ccctgtccct gagcctgggc aagtga 1359

<210> 43

<211> 452

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein

<400> 43

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

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

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

Trp Ile Gly Ser Ile His Tyr Ser Gly Leu Thr Tyr Tyr Asn Pro Ser
 50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
 85 90 95

Cys Ala Arg Asp Val Asp Asp Ser Ser Gly Asp Glu His Tyr Gly Met
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
 115 120 125

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

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

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

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser

180

185

190

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

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

Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu
 225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Gly Lys
 450

<210> 44
 <211> 1359
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA

<220>
 <221> CDS
 <222> (1)..(3)
 <223> nnn=GAA or GAG

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> n is a, c, g, or t

<400> 44
 nnn gtccagctgc aggaatccgg acccggcctg gtgaagccta gccagaccct 53
 Xaa
 1

gagcctgacc tgtaccgtgt ccggcggaag catctattcc ggcgccctact actggtcctg 113

gattaggcag caccgccgca agggcctgga atggatcggc tccatccact acagcggcct 173

gacctattac aacccctccc tgaagtccag ggtgaccatc agcgtcgaca caagcaagaa 233
 ccagttctcc ctcaagctga gcagcgtgac cgccgccgac accgccgtgt attattgcgc 293
 cagagacgtg gacgactcct ccggagacga gcactacggc atggacgtct ggggccaggg 353
 cacaacagtg acagtgagca gcgccagcac caaaggaccc tccgtcttcc ctctggcccc 413
 ttgctccagg agcacaagcg aaagcacagc cgccctgggc tgcctgggtga aggactactt 473
 tcccagagccc gtgaccgtga gctggaatag cggagccctc acctccggag tccacacatt 533
 tcccgccgtc ctgcagagca gcggcctgta ctccctgagc tccgtgggtga ccgtgccttc 593
 ctccagcctg ggcaccaaga cctacacctg caacgtggac cacaagccta gcaataccaa 653
 ggtggacaag aggggtggaat ccaagtacgg ccccccctgc cctccttgtc ctgccccga 713
 atttctgggc ggcccttccg tgttcctgtt ccctcccaag cccaaggata ccctgatgat 773
 cagcaggacc cctgaggtga cctgtgtggt ggtggacgtg agccaggagg accccgaggt 833
 gcagttcaac tggtagctgg atggcgtgga agtgcacaat gccaagacaa agcccaggga 893
 ggagcagttc aatagcacct acagggtggt cagcgtgctc acagtgtgc accaggactg 953
 gctgaacgga aaggagtaca agtgcaaagt gtccaacaag ggcttgcctt cctccatcga 1013
 aaagaccatc tccaaggcca aaggccagcc cagggagccc caagtgtata ccctcccccc 1073
 tagccaggag gaaatgacca aaaaccaggt ctccctgacc tgtctgggtga agggcttcta 1133
 tcccagcgac atcgctgtgg agtgggagag caacggccaa ccgagaaca actataagac 1193
 cacaccccc gtcctggact ccgatggctc cttcttcctg tacagcaggc tgaccgtcga 1253
 caagtccagg tggcaggaag gaaacgtgtt ctctgtagc gtcatgcacg aggccctgca 1313
 caaccactat acccagaagt ccctgtccct gagcctgggc aagtga 1359

<210> 45

<211> 452

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein

<400> 45

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
 20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
 50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Met Ile Glu Tyr Phe Gln His Trp
 100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys
 450

<210> 46
 <211> 1359
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA

<220>
 <221> CDS
 <222> (1)..(3)
 <223> nnn= CAG or CAA

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> n is a, c, g, or t

<400> 46
 nnn gtccagctgc aggagagcgg ccctggcctg gtgaagccta gcgagacact 53
 Xaa
 1

gtccctgacc tgcgccgtga gcggctacag catctccagc ggctatttct ggggatggat 113

cagacagccc cctggcaagg gcctggaatg gatcggttct atcctgcact ccggcgtgac 173

atactataac cctagcctga agagcagggt gaccatctcc gtggatacca gcaagaatca 233
 gttcagcctg aagctcagca gcgtgaccgc cgccgatacc gctgtgtact actgcgccag 293
 agacaggacc accgtctcca tgatcgagta cttccagcac tggggccaag gcaccctggt 353
 caccgtgtcc tccgctagca caaaaggacc aagcgtgttt cactggcac ctagcagcaa 413
 atccaccagc ggcggaacag cagccctcgg gtgcctgggtg aaggattact tccctgagcc 473
 agtcacagtg tcctggaact ccggagccct gacatccggc gtgcacacct tccccgctgt 533
 gctgcaatcc agcggactgt atagcctcag ctccgtcgtg acagtccctt ccagcagcct 593
 gggcacacag acttacattht gcaacgtgaa ccacaaacct tccaacacta aggtggacaa 653
 aaaggtggaa cccaaatcct gtgataagac ccatacatgc ccaccttgct ccgctcctga 713
 gctgctgggg ggaccttccg tctttctgtt tcctccaaaa ccaaaagaca cactcatgat 773
 cagccggacc cccgaagtca cctgtgtggt ggtggacgtc agccacgaag atccagaggt 833
 caagttcaat tggtagctgg atggagtgga agtccacaac gcaaaaaacca aacctagaga 893
 agaacagtac aatagcacat acagggtggt gtccgtcctg acagtgtctc accaggactg 953
 gctcaatggc aaagagtata agtgcaagggt gagcaacaag gccctgcctg caccaattga 1013
 gaaaacaatt agcaaggcaa aggggcagcc acgggaaccc caggtgtata ccctgcccc 1073
 aagccgggat gaactgacca aaaaccagggt cagcctgaca tgcctgggtga aagggtttta 1133
 cccaagcgat attgccgtcg agtgggagag caacggacag ccagaaaaca attacaaaac 1193
 caccacact gtgctggact ccgatgggag ctttttctctg tacagcaagc tcacagtgga 1253
 caagtccaga tggcaacagg gcaacgtgtt ttctgtctcc gtgatgcacg aggccctcca 1313
 caaccactat acacaaaagt ccctctccct cagcccagga aagtga 1359

<210> 47
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein

<400> 47

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
 20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
 50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Met Ile Glu Tyr Phe Gln His Trp
 100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys
 450

<210> 48
 <211> 1359
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA

<220>
 <221> CDS
 <222> (1)..(3)
 <223> nnn=GAA or GAG

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> n is a, c, g, or t

<400> 48
 nnn gtccagctgc aggagagcgg ccctggcctg gtgaagccta gcgagacact 53
 Xaa
 1

gtccctgacc tgcgccgtga gcggctacag catctccagc ggctatttct ggggatggat 113

cagacagccc cctggcaagg gcctggaatg gatcggttct atcctgcact ccggcgtgac 173

atactataac cctagcctga agagcagggt gaccatctcc gtggatacca gcaagaatca 233

gttcagcctg aagctcagca gcgtgaccgc cgccgatacc gctgtgtact actgcgccag 293
 agacaggacc accgtctcca tgatcgagta cttccagcac tggggccaag gcaccctggt 353
 caccgtgtcc tccgctagca caaaaggacc aagcgtgttt ccactggcac ctagcagcaa 413
 atccaccagc ggcggaacag cagccctcgg gtgcctgggtg aaggattact tccctgagcc 473
 agtcacagtg tcctggaact ccggagccct gacatccggc gtgcacacct tccccgctgt 533
 gctgcaatcc agcggactgt atagcctcag ctccgtcgtg acagtccctt ccagcagcct 593
 gggcacacag acttacattht gcaacgtgaa ccacaaacct tccaacacta aggtggacaa 653
 aaaggtggaa cccaaatcct gtgataagac ccatacatgc ccaccttgct ccgctcctga 713
 gctgctgggg ggaccttccg tctttctgtt tcctccaaaa ccaaaagaca cactcatgat 773
 cagccggacc cccgaagtca cctgtgtggt ggtggacgtc agccacgaag atccagaggt 833
 caagttcaat tggtagctgg atggagtgga agtccacaac gcaaaaacca aacctagaga 893
 agaacagtac aatagcacat acagggtggt gtccgtcctg acagtgtctc accaggactg 953
 gctcaatggc aaagagtata agtgcaaggt gagcaacaag gccctgcctg caccaattga 1013
 gaaaacaatt agcaaggcaa aggggcagcc acgggaaccc caggtgtata ccctgcccc 1073
 aagccgggat gaactgacca aaaaccaggt cagcctgaca tgcctggtga aagggtttta 1133
 cccaagcgat attgccgtcg agtgggagag caacggacag ccagaaaaca attacaaaac 1193
 caccacact gtgctggact ccgatgggag ctttttcctg tacagcaagc tcacagtgga 1253
 caagtccaga tggcaacagg gcaacgtgtt ttcctgctcc gtgatgcacg aggccctcca 1313
 caaccactat acacaaaagt ccctctccct cagcccagga aagtga 1359

<210> 49
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein

<400> 49

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
 20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
 50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Leu Ile Glu Tyr Phe Gln His Trp
 100 105 110

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

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

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

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

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

61

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

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

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

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

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

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

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

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

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

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

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

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

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

385	390	62 395	400
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Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
405 410 415

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

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

Ser Pro Gly Lys
450

<210>	50
<211>	1359
<212>	DNA
<213>	Artificial Sequence

<220>
<223> DNA

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<220>
<221> CDS
<222> (1)..(3)
<223> nnn= CAG or CAA
```

```
<220>
<221> misc_feature
<222> (1)..(3)
<223> n is a, c, g, or t
```

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<400> 50
nnn gtccagctgc aggagagcgg ccctggactc gtgaagccct ccgaaaccct
Xaa
1
```

gagcctcaca tgcgccgtct ccggatacag catcagcagc ggatacttct ggggctggat 113

cagacagccc cccggcaaag gcctggagtg gatcggttct attctccaca gcggcgtgac 173

atactacaac ccctccctga agagcaggggt gaccatcagc gtggacacct ccaagaacca 233

gttttccctc aagctgagca gcgtgaccgc cgctgacaca gccgtgtatt actgcgccag 293
 ggacaggacc accgtgtccc tgattgagta cttccagcat tggggccagg gcacactggt 353
 gaccgtcagc agcgctagca caaaaggacc aagcgtgttt cactggcac ctagcagcaa 413
 atccaccagc ggcggaacag cagccctcgg gtgcctgggtg aaggattact tccctgagcc 473
 agtcacagtg tcctggaact ccggagccct gacatccggc gtgcacacct tccccgctgt 533
 gctgcaatcc agcggactgt atagcctcag ctccgtcgtg acagtccctt ccagcagcct 593
 gggcacacag acttacatit gcaacgtgaa ccacaaacct tccaacacta aggtggacaa 653
 aaaggtggaa cccaaatcct gtgataagac ccatacatgc ccaccttgtc ccgctcctga 713
 gctgctgggg ggaccttccg tctttctgtt tcctccaaaa ccaaaagaca cactcatgat 773
 cagccggacc cccgaagtca cctgtgtggt ggtggacgtc agccacgaag atccagaggt 833
 caagttcaat tggtagctgg atggagtgga agtccacaac gcaaaaacca aacctagaga 893
 agaacagtac aatagcacat acagggtggt gtccgtcctg acagtgtctc accaggactg 953
 gctcaatggc aaagagtata agtgcaaggt gagcaacaag gccctgcctg caccaattga 1013
 gaaaacaatt agcaaggcaa aggggcagcc acgggaaccc caggtgtata ccctgcccc 1073
 aagccgggat gaactgacca aaaaccaggt cagcctgaca tgcctggtga aagggtttta 1133
 cccaagcgat attgccgtcg agtgggagag caacggacag ccagaaaaa attacaaaac 1193
 caccacact gtgctggact ccgatgggag ctttttcttg tacagcaagc tcacagtgga 1253
 caagtccaga tggcaacagg gcaacgtgtt ttctgtctcc gtgatgcacg aggccctcca 1313
 caaccactat acacaaaagt ccctctccct cagcccagga aagtga 1359

<210> 51
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein

<400> 51

Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15 64

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
 20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
 50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Leu Ile Glu Tyr Phe Gln His Trp
 100 105 110

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

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

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

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

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

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn

195						200				65		205				
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	
210						215				220						
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	
225				230						235				240		
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	
				245				250						255		
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	
		260						265				270				
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	
		275				280						285				
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	
290						295				300						
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	
305				310						315				320		
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	
				325				330						335		
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	
		340						345				350				
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	
		355				360						365				
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	
370						375				380						
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	
385				390						395				400		

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

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

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

Ser Pro Gly Lys
 450

<210> 52
 <211> 1359
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA

<220>
 <221> CDS
 <222> (1)..(3)
 <223> nnn=GAA or GAG

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> n is a, c, g, or t

<400> 52
 nnn gtccagctgc aggagagcgg ccctggactc gtgaagccct ccgaaaccct 53
 Xaa
 1

gagcctcaca tgcgccgtct ccggatacag catcagcagc ggatacttct ggggctggat 113

cagacagccc cccggcaaaag gcctggagtg gatcggttct attctccaca gcggcgtgac 173

atactacaac ccctccctga agagcagggt gaccatcagc gtggacacct ccaagaacca 233

gttttccctc aagctgagca gcgtgaccgc cgctgacaca gccgtgtatt actgcgccag 293

ggacaggacc accgtgtccc tgattgagta cttccagcat tggggccagg gcacactggt 353
 gaccgtcagc agcgctagca caaaaggacc aagcgtgttt cactggcac ctagcagcaa 413
 atccaccagc ggcggaacag cagccctcgg gtgcctgggtg aaggattact tccctgagcc 473
 agtcacagtg tcctggaact ccggagccct gacatccggc gtgcacacct tccccgctgt 533
 gctgcaatcc agcggactgt atagcctcag ctccgtcgtg acagtccctt ccagcagcct 593
 gggcacacag acttacattht gcaacgtgaa ccacaaacct tccaacacta aggtggacaa 653
 aaaggtggaa cccaaatcct gtgataagac ccatacatgc ccaccttgtc ccgctcctga 713
 gctgctgggg ggaccttccg tctttctgtt tcctccaaaa ccaaaagaca cactcatgat 773
 cagccggacc cccgaagtca cctgtgtggt ggtggacgtc agccacgaag atccagaggt 833
 caagttcaat tgggtacgtgg atggagtggga agtccacaac gcaaaaacca aacctagaga 893
 agaacagtac aatagcacat acagggtggt gtccgtcctg acagtgtctc accaggactg 953
 gctcaatggc aaagagtata agtgcaaggt gagcaacaag gccctgcctg caccaattga 1013
 gaaaacaatt agcaaggcaa aggggcagcc acgggaaccc caggtgtata ccctgcccc 1073
 aagccgggat gaactgacca aaaaccagggt cagcctgaca tgcctggtga aagggtttta 1133
 cccaagcgat attgccgtcg agtgggagag caacggacag ccagaaaaaca attacaaaac 1193
 caccacacct gtgctggact ccgatgggag ctttttctctg tacagcaagc tcacagtgga 1253
 caagtccaga tggcaacagg gcaacgtgtt ttcctgctcc gtgatgcacg aggccctcca 1313
 caaccactat acacaaaagt ccctctccct cagcccagga aagtga 1359

<210> 53
 <211> 455
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein

<400> 53

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

1 5 10 15 68

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

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

Trp Ile Gly Ser Ile His Tyr Ser Gly Leu Thr Tyr Tyr Asn Pro Ser
 50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
 85 90 95

Cys Ala Arg Asp Val Asp Asp Ser Ser Gly Asp Glu His Tyr Gly Met
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
 115 120 125

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

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

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

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

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

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 245 250 255

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

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

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

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

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

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 370 375 380

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 54
 <211> 1368
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA

<220>
 <221> CDS
 <222> (1)..(3)
 <223> nnn= CAG or CAA

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> n is a, c, g, or t

<400> 54
 nnn gtccagctgc aggaatccgg acccggcctg gtgaagccta gccagaccct 53
 Xaa
 1

gagcctgacc tgtaccgtgt ccggcggaag catctattcc ggcgcctact actggtcctg 113

gattaggcag caccgccgca agggcctgga atggatcggc tccatccact acagcggcct 173

gacctattac aaccctccc tgaagtccag ggtgaccatc agcgtcgaca caagcaagaa 233

ccagttctcc ctcaagctga gcagcgtgac cgccgccgac accgccgtgt attattgcgc 293

cagagacgtg gacgactcct ccggagacga gcactacggc atggacgtct ggggccaggg 353
 cacaacagtg acagtgagca gcgctagcac aaaaggacca agcgtgtttc cactggcacc 413
 tagcagcaaa tccaccagcg gcggaacagc agccctcggg tgcctggtga aggattactt 473
 ccctgagcca gtcacagtgt cctggaactc cggagccctg acatccggcg tgcacacctt 533
 ccccgctgtg ctgcaatcca gcggactgta tagcctcagc tccgtcgtga cagtcccttc 593
 cagcagcctg ggcacacaga cttacatttg caacgtgaac caaaaacctt ccaacactaa 653
 ggtggacaaa aagggtggaac ccaaattcctg tgataagacc catacatgcc caccttgtcc 713
 cgctcctgag ctgctggggg gaccttccgt ctttctgttt cctccaaaac caaaagacac 773
 actcatgatc agccggaccc ccgaagtcac ctgtgtggtg gtggacgtca gccacgaaga 833
 tccagaggtc aagttcaatt ggtacgtgga tggagtggaa gtccacaacg caaaaaccaa 893
 acctagagaa gaacagtaca atagcacata cagggtggtg tccgtcctga cagtgtcca 953
 ccaggactgg ctcaatggca aagagtataa gtgcaagggtg agcaacaagg ccctgcctgc 1013
 accaattgag aaaacaatta gcaaggcaaa ggggcagcca cggaacccc aggtgtatac 1073
 cctgccccca agccgggatg aactgaccaa aaaccagggtc agcctgacat gcctggtgaa 1133
 aggggttttac ccaagcgata ttgccgtcga gtgggagagc aacggacagc cagaaaacaa 1193
 ttacaaaacc accccacctg tgctggactc cgatgggagc tttttcctgt acagcaagct 1253
 cacagtggac aagtccagat ggcaacaggg caacgtgttt tcctgctccg tgatgcacga 1313
 ggccctccac aaccactata caaaaagtc cctctccctc agcccaggaa agtga 1368

<210> 55

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein

<400> 55

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

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

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

Trp Ile Gly Ser Ile His Tyr Ser Gly Leu Thr Tyr Tyr Asn Pro Ser
 50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
 85 90 95

Cys Ala Arg Asp Val Asp Asp Ser Ser Gly Asp Glu His Tyr Gly Met
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
 115 120 125

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

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

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

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

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

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 245 250 255

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

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

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

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

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

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 370 375 380

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 56
 <211> 1368
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA

<220>
 <221> CDS
 <222> (1)..(3)
 <223> nnn=GAA or GAG

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> n is a, c, g, or t

<400> 56
 nnn gtccagctgc aggaatccgg acccggcctg gtgaagccta gccagaccct 53
 Xaa
 1

gagcctgacc tgtaccgtgt ccggcggaag catctattcc ggcgccctact actggtcctg 113

gattaggcag caccgccgca agggcctgga atggatcggc tccatccact acagcggcct 173

gacctattac aaccctctcc tgaagtccag ggtgaccatc agcgtcgaca caagcaagaa 233

ccagttctcc ctcaagctga gcagcgtgac cgccgccgac accgccgtgt attattgcgc 293

cagagacgtg gacgactcct ccggagacga gcactacggc atggacgtct ggggccaggg 353

cacaacagtg acagtgagca gcgctagcac aaaaggacca agcgtgtttc cactggcacc 413
 tagcagcaaa tccaccagcg gcggaacagc agccctcggg tgcctggtga aggattactt 473
 ccctgagcca gtcacagtgt cctggaactc cggagccctg acatccggcg tgcacacctt 533
 ccccgctgtg ctgcaatcca gcggactgta tagcctcagc tccgtcgtga cagtcccttc 593
 cagcagcctg ggcacacaga cttacatttg caacgtgaac cacaaacctt ccaacactaa 653
 ggtggacaaa aaggtggaac ccaaatacctg tgataagacc catacatgcc caccttgtcc 713
 cgctcctgag ctgctggggg gaccttccgt ctttctgttt cctccaaaac caaaagacac 773
 actcatgatc agccggaccc ccgaagtcac ctgtgtggtg gtggacgtca gccacgaaga 833
 tccagaggtc aagttcaatt ggtacgtgga tggagtggaa gtccacaacg caaaaaccaa 893
 acctagagaa gaacagtaca atagcacata cagggtggtg tccgtcctga cagtgtcca 953
 ccaggactgg ctcaatggca aagagtataa gtgcaagggtg agcaacaagg ccctgcctgc 1013
 accaattgag aaaacaatta gcaaggcaaa ggggcagcca cggaacccc aggtgtatac 1073
 cctgccccca agccgggatg aactgaccaa aaaccagggtc agcctgacat gcctggtgaa 1133
 agggttttac ccaagcgata ttgccgtcga gtgggagagc aacggacagc cagaaaacaa 1193
 ttacaaaacc accccacctg tgctggactc cgatgggagc tttttcctgt acagcaagct 1253
 cacagtggac aagtccagat ggcaacaggg caacgtgttt tcctgctccg tgatgcacga 1313
 ggccctccac aaccactata cacaaaagtc cctctccctc agcccaggaa agtga 1368

<210> 57
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein

<400> 57

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
 20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
 50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Met Ile Glu Tyr Phe Gln His Trp
 100 105 110

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

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

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

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

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

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

77
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
 210 215 220

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
 225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
 260 265 270

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

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

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

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

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

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

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

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

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

405 78 415

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

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

<210> 58
<211> 1344
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA

<220>
<221> CDS
<222> (1)..(3)
<223> nnn= CAG or CAA

<220>
<221> misc_feature
<222> (1)..(3)
<223> n is a, c, g, or t

<400> 58
nnn gtccagctgc aggagagcgg ccctggcctg gtgaagccta gcgagacact 53
Xaa
1

gtccctgacc tgcgccgtga gcggctacag catctccagc ggctatttct ggggatggat 113
cagacagccc cctggcaagg gcctggaatg gatcggttct atcctgcact ccggcgtgac 173
atactataac cctagcctga agagcagggg gaccatctcc gtggatacca gcaagaatca 233
gttcagcctg aagctcagca gcgtgaccgc cgccgatacc gctgtgtact actgcgccag 293
agacaggacc accgtctcca tgatcgagta cttccagcac tggggccaag gcaccctggg 353
caccgtgtcc tccgcctcca ccaagggccc tagcgtgttt cctctggccc cctgctccag 413
atccacaagc gagagcaccg ctgccctggg ctgtctggtc aaggactact tccccgagcc 473

cgtgacagtg tcctggaaca gcggcgccct gacaagcggc gtccatacat tccccgccgt 533
 gctgcagtcc agcggactgt atagcctgag ctccgtgggtg accgtgcctt ccagcagcct 593
 gggaaccaag acatatacct gcaacgtgga ccataagccc agcaacacaa aagtcgacaa 653
 gaggggtggag agcaagtacg gaccccccttg tcccccttgt cctgctcccg agttcctcgg 713
 cggacctagc gtgttcctgt ttcctcccaa gcccaaggat accctgatga tcagcaggac 773
 ccctgaggtc acctgcgtgg tggtcgacgt gtcccaggag gaccctgagg tccagtttaa 833
 ctggtacgtg gacggagtgg aggtgcacaa cgccaagacc aagcccagag aggagcagtt 893
 caattccacc tacagggtgg tgagcgtcct gaccgtgctg caccaggact ggctgaatgg 953
 aaaggagtac aaatgcaagg tctccaacaa gggcctccct agcagcatcg agaagaccat 1013
 ctccaaggcc aagggccagc ctagggagcc ccagggtgtac accctgcctc ctagccagga 1073
 ggaaatgacc aagaaccagg tgtccctgac atgcctgggtg aagggttct atcctagcga 1133
 catcgccgtg gagtgggaga gcaatggcca gcccgagaat aactacaaga ccaccccccc 1193
 tgtgctcgat agcgacggca gcttctttct gtacagcagg ctgaccgtgg acaagagcag 1253
 gtggcaagag ggcaacgtgt ttagctgctc cgatcatgcac gaggccctgc ataaccacta 1313
 caccacaaaaa tccctgtccc tgtccctggg c 1344

<210> 59
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein

<400> 59

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
 20 25 30

Tyr Phe Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 80 45

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Met Ile Glu Tyr Phe Gln His Trp
100 105 110

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

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

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

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

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

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

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

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro

225						230						81	235						240
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser				
				245					250					255					
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp				
			260				265				270								
Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn				
		275				280					285								
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val				
		290				295				300									
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu				
305					310					315									
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys				
			325				330						335						
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr				
		340				345						350							
Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr				
		355				360						365							
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu				
		370				375				380									
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu				
385					390					395									
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys				
			405				410						415						
Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu				
		420				425				430									

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

<210> 60
 <211> 1344
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA

<220>
 <221> CDS
 <222> (1)..(3)
 <223> nnn=GAA or GAG

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> n is a, c, g, or t

<400> 60
 nnn gtccagctgc aggagagcgg ccctggcctg gtgaagccta gcgagacact 53
 Xaa
 1

gtccctgacc tgcgccgtga gcggctacag catctccagc ggctatttct ggggatggat 113
 cagacagccc cctggcaagg gcctggaatg gatcggttct atcctgcact ccggcgtgac 173
 atactataac cctagcctga agagcagggt gaccatctcc gtggatacca gcaagaatca 233
 gttcagcctg aagctcagca gcgtgaccgc cgccgatacc gctgtgtact actgcgccag 293
 agacaggacc accgtctcca tgatcgagta cttccagcac tggggccaag gcaccctggt 353
 caccgtgtcc tccgcctcca ccaaggggccc tagcgtgttt cctctggccc cctgctccag 413
 atccacaagc gagagcaccg ctgccctggg ctgtctggtc aaggactact tccccgagcc 473
 cgtgacagtg tcctggaaca gcggcgccct gacaagcggc gtccatacat tccccgccgt 533
 gctgcagtcc agcggactgt atagcctgag ctccgtgggtg accgtgcctt ccagcagcct 593
 gggaaccaag acatatacct gcaacgtgga ccataagccc agcaacacaa aagtcgacaa 653

gaggggtggag agcaagtacg gaccccccttg tcccccttgt cctgctcccg agttcctcgg 713
 cggacctagc gtgttcctgt ttcctcccaa gccaaggat accctgatga tcagcaggac 773
 ccctgaggtc acctgcgtgg tggtcgacgt gtcccaggag gaccctgagg tccagtttaa 833
 ctggtacgtg gacggagtgg aggtgcacaa cgccaagacc aagcccagag aggagcagtt 893
 caattccacc tacagggtgg tgagcgtcct gaccgtgctg caccaggact ggctgaatgg 953
 aaaggagtac aaatgcaagg tctccaacaa gggcctccct agcagcatcg agaagaccat 1013
 ctccaaggcc aagggccagc ctagggagcc ccagggtgac accctgcctc ctagccagga 1073
 ggaaatgacc aagaaccagg tgtccctgac atgcctgggtg aagggttct atcctagcga 1133
 catcgccgtg gagtgggaga gcaatggcca gcccgagaat aactacaaga ccaccccccc 1193
 tgtgctcgat agcgacggca gcttctttct gtacagcagg ctgaccgtgg acaagagcag 1253
 gtggcaagag ggcaacgtgt ttagctgctc cgtcatgcac gaggccctgc ataaccacta 1313
 cacccaaaaaa tccctgtccc tgtccctggg c 1344

<210> 61
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein

<400> 61

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
 20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu

50

55

84

60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Leu Ile Glu Tyr Phe Gln His Trp
100 105 110

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

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

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

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

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

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

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

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
 260 265 270

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

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

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

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

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

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

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

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

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

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

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

<210> 62
 <211> 1344
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA

<220>
 <221> CDS
 <222> (1)..(3)
 <223> nnn= CAG or CAA

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> n is a, c, g, or t

<400> 62
 nnn gtccagctgc aggagagcgg ccctggactc gtgaagccct ccgaaaccct 53
 Xaa
 1

gagcctcaca tgcgccgtct ccggatacag catcagcagc ggatacttct ggggctggat 113
 cagacagccc cccggcaaag gcctggagtg gatcggttct attctccaca gcggcgtgac 173
 atactacaac ccctccctga agagcagggt gaccatcagc gtggacacct ccaagaacca 233
 gttttccctc aagctgagca gcgtgaccgc cgctgacaca gccgtgtatt actgcgccag 293
 ggacaggacc accgtgtccc tgattgagta cttccagcat tggggccagg gcacactggt 353
 gaccgtcagc agcgccagca ccaaggggccc ttccgtcttc cctctggccc cttgcagcag 413
 aagcacctcc gagtccacag ccgccctggg atgcctcgtg aaggattact tccccgagcc 473
 cgtcacagtc tcctggaact ccggcgctct gaccagcggg gtgcacacct tccccgccgt 533
 gctgcaaagc agcggcctgt acagcctgtc cagcgtggtc accgtgcctt cctccagcct 593
 gggcaccaag acctacacat gcaacgtgga ccacaagcct tccaacacca aggtggacaa 653
 gagagtggaa agcaagtacg gccccccctg ccccccttgt cctgcccccg agtttctggg 713
 aggaccctcc gtgttcctct ttctcccaa gcctaaggac accctgatga tctccaggac 773

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ccccgaagtg acctgcgtgg tcgtggacgt gtcccaggag gaccctgagg tgcagtttaa      833
ctggtacgtg gacggcgtgg aggtgcacaa cgccaagacc aagcccaggg aggagcagtt      893
caatagcacc tacagggtgg tgtccgtgct gaccgtgctg caccaggact ggctgaacgg      953
caaagagtac aagtgcaaag tcagcaacaa gggcctgccc tcctccatcg agaagaccat     1013
tagcaaggcc aagggccagc ctagggagcc tcaggtgtac accctgcccc ccagccagga     1073
ggagatgacc aagaaccagg tgtccctgac ctgcctggtc aagggatttt accccagcga     1133
catcgctgtg gaatgggaga gcaatggcca gcccgagaac aactacaaga ccaccctcc      1193
cgtgctcgat tccgacggca gctttttcct gtacagcagg ctgaccgtgg ataagagcag     1253
gtggcaggaa ggcaacgtgt tctcctgttc cgtgatgcat gaggccctgc acaaccacta     1313
cacacagaag agcctgtccc tgtccctggg c                                   1344

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<210> 63
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein

<400> 63

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
 20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
 50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Leu Ile Glu Tyr Phe Gln His Trp
 100 105 110

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

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

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

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

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

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

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

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
 225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
 260 265 270

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

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

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

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

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

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

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

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

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

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

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

<210> 64

<211> 1344

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA

<220>

<221> CDS

<222> (1)..(3)

<223> nnn=GAA or GAG

<220>

<221> misc_feature

<222> (1)..(3)

<223> n is a, c, g, or t

<400> 64

nnn gtccagctgc aggagagcgg ccctggactc gtgaagccct ccgaaaccct 53

Xaa

1

gagcctcaca tgcgccgtct ccggatacag catcagcagc ggatacttct ggggctggat 113

cagacagccc cccggcaaaag gcctggagtg gatcggttct attctccaca gcggcgtgac 173

atactacaac ccctccctga agagcagggt gaccatcagc gtggacacct ccaagaacca 233

gttttccctc aagctgagca gcgtgaccgc cgctgacaca gccgtgtatt actgcgccag 293

ggacaggacc accgtgtccc tgattgagta cttccagcat tggggccagg gcacactggt 353

gaccgtcagc agcgccagca ccaagggccc ttccgtcttc cctctggccc cttgcagcag 413

aagcacctcc gagtccacag ccgccctggg atgcctcgtg aaggattact tccccgagcc 473

cgtcacagtc tcctggaact ccggcgctct gaccagcggg gtgcacacct tccccgccgt 533

gctgcaaagc agcggcctgt acagcctgtc cagcgtggtc accgtgcctt cctccagcct 593

gggcaccaag acctacacat gcaacgtgga ccacaagcct tccaacacca aggtggacaa 653

gagagtggaa agcaagtacg gccccccctg ccccccttgt cctgcccccg agtttctggg 713

aggaccctcc gtgttcctct ttcctcccaa gcctaaggac accctgatga tctccaggac 773

ccccgaagtg acctgcgtgg tcgtggacgt gtcccaggag gaccctgagg tgcagtttaa 833

ctggtacgtg gacggcgtgg aggtgcacaa cgccaagacc aagcccaggg aggagcagtt 893

caatagcacc tacagggtgg tgtccgtgct gaccgtgctg caccaggact ggctgaacgg 953

caaagagtac aagtgcaaag tcagcaacaa gggcctgccc tcctccatcg agaagaccat 1013
 tagcaaggcc aagggccagc ctagggagcc tcaggtgtac accctgcccc ccagccagga 1073
 ggagatgacc aagaaccagg tgtccctgac ctgcctggtc aagggatttt accccagcga 1133
 catcgctgtg gaatgggaga gcaatggcca gcccgagaac aactacaaga ccaccctcc 1193
 cgtgctcgat tccgacggca gctttttcct gtacagcagg ctgaccgtgg ataagagcag 1253
 gtggcaggaa ggcaacgtgt tctcctgttc cgtgatgcat gaggccctgc acaaccacta 1313
 cacacagaag agcctgtccc tgtccctggg c 1344

<210> 65
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protein

<400> 65

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

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

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

Trp Ile Gly Ser Ile His Tyr Ser Gly Leu Thr Tyr Tyr Asn Pro Ser
 50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
 85 90 95

Cys Ala Arg Asp Val Asp Asp Ser Ser Gly Asp Glu His Tyr Gly Met
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
 115 120 125

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

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

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

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

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

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

Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu
 225 230 235 240

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

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

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
 290 295 300 93

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

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

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

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

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

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

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

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

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

Ser Leu Gly
 450

<210> 66
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>

<223> DNA

<220>

<221> CDS

<222> (1)..(3)

<223> nnn= CAG or CAA

<220>

<221> misc_feature

<222> (1)..(3)

<223> n is a, c, g, or t

<400> 66

nnn gtccagctgc aggaatccgg acccggcctg gtgaagccta gccagaccct 53

Xaa

1

gagcctgacc tgtaccgtgt ccggcgggaag catctattcc ggcgccctact actggtcctg 113

gattaggcag caccccggca agggcctgga atggatcggc tccatccact acagcggcct 173

gacctattac aaccctctcc tgaagtccag ggtgaccatc agcgtcgaca caagcaagaa 233

ccagttctcc ctcaagctga gcagcgtgac cgccgccgac accgccgtgt attattgcgc 293

cagagacgtg gacgactcct ccggagacga gcactacggc atggacgtct ggggccaggg 353

cacaacagtg acagtgagca gcgccagcac caaaggaccc tccgtcttcc ctctggcccc 413

ttgctccagg agcacaagcg aaagcacagc cgccctgggc tgcctgggtga aggactactt 473

tcccagagccc gtgaccgtga gctggaatag cggagccctc acctccggag tccacacatt 533

tcccgccgtc ctgcagagca gcggcctgta ctccctgagc tccgtgggtga ccgtgccttc 593

ctccagcctg ggcaccaaga cctacacctg caacgtggac cacaagccta gcaataccaa 653

ggtggacaag aggggtggaat ccaagtacgg ccccccttgc cctccttgtc ctgccccga 713

atttctgggc ggcccttccg tgttcctgtt ccctccaag cccaaggata ccctgatgat 773

cagcaggacc cctgagggtga cctgtgtggt ggtggacgtg agccaggagg accccgaggt 833

gcagttcaac tgggtacgtgg atggcgtgga agtgcacaat gccaaagaaa agcccaggga 893

ggagcagttc aatagcacct acagggtggt cagcgtgctc acagtgtctg accaggactg 953

95

gctgaacgga aaggagtaca agtgcaaagt gtccaacaag ggcctgccct cctccatcga 1013
aaagaccatc tccaaggcca aaggccagcc caggagagccc caagtgtata ccctcccccc 1073
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tcccagcgac atcgctgtgg agtgggagag caacggccaa cccgagaaca actataagac 1193
cacaccccc gtcctggact ccgatggctc cttcttcctg tacagcaggc tgaccgtcga 1253
caagtccagg tggcaggaag gaaacgtgtt ctcctgtagc gtcatgcacg aggccctgca 1313
caaccactat acccagaagt ccctgtccct ggcctgggc 1353

<210> 67
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein

<400> 67

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

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

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

Trp Ile Gly Ser Ile His Tyr Ser Gly Leu Thr Tyr Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Val Asp Asp Ser Ser Gly Asp Glu His Tyr Gly Met
100 105 96 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

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

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

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

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

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

Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu
225 230 235 240

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

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

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

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr

97

290

295

300

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

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

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

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

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

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

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

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

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

Ser Leu Gly
450

<210> 68

<211> 1353

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA

<220>

<221> CDS

<222> (1)..(3)

<223> nnn=GAA or GAG

<220>

<221> misc_feature

<222> (1)..(3)

<223> n is a, c, g, or t

<400> 68

nnn gtccagctgc aggaatccgg acccggcctg gtgaagccta gccagaccct 53

Xaa

1

gagcctgacc tgtaccgtgt ccggcgggaag catctattcc ggcgccctact actggtcctg 113

gattaggcag caccccggca agggcctgga atggatcggc tccatccact acagcggcct 173

gacctattac aaccctctcc tgaagtccag ggtgaccatc agcgtcgaca caagcaagaa 233

ccagttctcc ctcaagctga gcagcgtgac cgccgccgac accgccgtgt attattgcgc 293

cagagacgtg gacgactcct ccggagacga gcactacggc atggacgtct ggggccaggg 353

cacaacagtg acagtgagca gcgccagcac caaaggaccc tccgtcttcc ctctggcccc 413

ttgctccagg agcacaagcg aaagcacagc cgccctgggc tgcctgggtga aggactactt 473

tcccagagccc gtgaccgtga gctggaatag cggagccctc acctccggag tccacacatt 533

tcccgccgtc ctgcagagca gcggcctgta ctccctgagc tccgtgggtga ccgtgccttc 593

ctccagcctg ggcaccaaga cctacacctg caacgtggac cacaagccta gcaataccaa 653

ggtggacaag aggggtggaat ccaagtacgg ccccccttgc cctccttgct ctgccccga 713

atttctgggc ggcccttccg tgttcctggt ccctcccaag cccaaggata ccctgatgat 773

cagcaggacc cctgagggtga cctgtgtggt ggtggacgtg agccaggagg accccgaggt 833

gcagttcaac tggtagctgg atggcgtgga agtgcacaat gccaaagaaa agcccaggga 893

ggagcagttc aatagcacct acagggtggt cagcgtgctc acagtgtctgc accaggactg 953

gctgaacgga aaggagtaca agtgcaaagt gtccaacaag ggccctgccct cctccatcga 1013

aaagaccatc tccaaggcca aaggccagcc caggagagccc caagtgtata ccctcccccc 1073
 tagccaggag gaaatgacca aaaaccaggt ctccctgacc tgtctggtga agggcttcta 1133
 tcccagcgac atcgctgtgg agtgggagag caacggccaa cccgagaaca actataagac 1193
 cacaccccc gtcctggact ccgatggctc cttcttcctg tacagcaggc tgaccgtcga 1253
 caagtccagg tggcaggaag gaaacgtgtt ctcctgtagc gtcatgcacg aggccctgca 1313
 caaccactat acccagaagt ccctgtccct gagcctgggc 1353

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

<220>
 <223> Protein

<400> 69

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
 20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
 50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Met Ile Glu Tyr Phe Gln His Trp

100																105																110															
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro																																
		115						120												125																											
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr																																
		130						135												140																											
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr																																
		145						150												155																											
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro																																
								165												170																											
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr																																
								180												185																											
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn																																
								195												200																											
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser																																
								210												215																											
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu																																
								225												230																											
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu																																
								245												250																											
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser																																
								260												265																											
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu																																
								275												280																											
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr																																
								290												295																											
																				300																											

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

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

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

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

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

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

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

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

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

Ser Pro Gly
 450

<210> 70
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA

<220>
 <221> CDS
 <222> (1)..(3)
 <223> nnn= CAG or CAA

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> n is a, c, g, or t

<400> 70
 nnn gtccagctgc aggagagcgg ccctggcctg gtgaagccta gcgagacact 53
 Xaa
 1

 gtccctgacc tgcgccgtga gcggctacag catctccagc ggctatttct ggggatggat 113
 cagacagccc cctggcaagg gcctggaatg gatcggttct atcctgcact ccggcgtgac 173
 atactataac cctagcctga agagcagggt gaccatctcc gtggatacca gcaagaatca 233
 gttcagcctg aagctcagca gcgtgaccgc cgccgatacc gctgtgtact actgcgccag 293
 agacaggacc accgtctcca tgatcgagta cttccagcac tggggccaag gcaccctgggt 353
 caccgtgtcc tccgctagca caaaaggacc aagcgtgttt ccactggcac ctagcagcaa 413
 atccaccagc ggcggaacag cagccctcgg gtgcctgggtg aaggattact tccctgagcc 473
 agtcacagtg tcctggaact ccggagccct gacatccggc gtgcacacct tccccgctgt 533
 gctgcaatcc agcggactgt atagcctcag ctccgtcgtg acagtccctt ccagcagcct 593
 gggcacacag acttacatth gcaacgtgaa ccacaaacct tccaacacta aggtggacaa 653
 aaaggtggaa cccaaatcct gtgataagac ccatacatgc ccaccttgtc ccgctcctga 713
 gctgctgggg ggaccttccg tctttctgtt tcctccaaaa ccaaaagaca cactcatgat 773
 cagccggacc cccgaagtca cctgtgtggt ggtggacgtc agccacgaag atccagaggt 833
 caagttcaat tggtagctgg atggagtgga agtccacaac gcaaaaaacca aacctagaga 893
 agaacagtac aatagcacat acagggtggt gtccgtcctg acagtgtctc accaggactg 953
 gctcaatggc aaagagtata agtgcaaggt gagcaacaag gccctgcctg caccaattga 1013

Ala Arg Asp Arg Thr Thr Val Ser Met Ile Glu Tyr Phe Gln His Trp
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

105

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

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

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

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

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

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

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

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

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

Ser Pro Gly
450

<210> 72
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA

<220>

<221> CDS

<222> (1)..(3)

<223> nnn=GAA or GAG

<220>

<221> misc_feature

<222> (1)..(3)

<223> n is a, c, g, or t

<400> 72

nnn gtccagctgc aggagagcgg ccctggcctg gtgaagccta gcgagacact 53

Xaa

1

gtccctgacc tgcgccgtga gcggctacag catctccagc ggctatttct ggggatggat 113

cagacagccc cctggcaagg gcctggaatg gatcggttct atcctgcact ccggcgtgac 173

atactataac cctagcctga agagcagggt gaccatctcc gtggatacca gcaagaatca 233

gttcagcctg aagctcagca gcgtgaccgc cgccgatacc gctgtgtact actgcgccag 293

agacaggacc accgtctcca tgatcgagta cttccagcac tggggccaag gcaccctggt 353

caccgtgtcc tccgctagca caaaaggacc aagcgtgttt ccactggcac ctagcagcaa 413

atccaccagc ggcggaacag cagccctcgg gtgcctgggtg aaggattact tccctgagcc 473

agtcacagtg tcctggaact ccggagccct gacatccggc gtgcacacct tccccgctgt 533

gctgcaatcc agcggactgt atagcctcag ctccgtcgtg acagtccctt ccagcagcct 593

gggcacacag acttacattt gcaacgtgaa ccacaaacct tccaacacta aggtggacaa 653

aaaggtggaa cccaaatcct gtgataagac ccatacatgc ccaccttgtc ccgctcctga 713

gctgctgggg ggaccttccg tctttctgtt tcctccaaaa ccaaaagaca cactcatgat 773

cagccggacc cccgaagtca cctgtgtggt ggtggacgtc agccacgaag atccagaggt 833

caagttcaat tggtagctgg atggagtgga agtccacaac gcaaaaaacca aacctagaga 893

agaacagtac aatagcacat acagggtggt gtccgtcctg acagtgtctc accaggactg 953

gctcaatggc aaagagtata agtgcaaggt gagcaacaag gccctgcctg caccaattga 1013

gaaaacaatt agcaaggcaa aggggcagcc acgggaaccc caggtgtata ccctgcccc 1073

aagccgggat gaactgacca aaaaccaggt cagcctgaca tgcctggtga aagggtttta 1133
cccaagcgat attgccgtcg agtgggagag caacggacag ccagaaaaca attacaaaac 1193
caccacacct gtgctggact ccgatgggag ctttttcctg tacagcaagc tcacagtgga 1253
caagtccaga tggcaacagg gcaacgtgtt ttcctgctcc gtgatgcacg aggccctcca 1313
caaccactat acacaaaagt ccctctccct cagcccagga 1353

<210> 73
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein

<400> 73

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Leu Ile Glu Tyr Phe Gln His Trp
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

109
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305 310 315 320

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

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

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

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

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

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

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

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

Ser Pro Gly
450

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

<220>
<223> DNA

<220>

<221> CDS

<222> (1)..(3)

<223> nnn= CAG or CAA

<220>

<221> misc_feature

<222> (1)..(3)

<223> n is a, c, g, or t

<400> 74

nnn gtccagctgc aggagagcgg ccctggactc gtgaagccct ccgaaaccct 53

Xaa

1

gagcctcaca tgcgccgtct ccggatacag catcagcagc ggatacttct ggggctggat 113

cagacagccc cccggcaaag gcctggagtg gatcggttct attctccaca gcggcgtgac 173

atactacaac ccctccctga agagcagggt gaccatcagc gtggacacct ccaagaacca 233

gttttccctc aagctgagca gcgtgaccgc cgctgacaca gccgtgtatt actgcgccag 293

ggacaggacc accgtgtccc tgattgagta cttccagcat tggggccagg gcacactggt 353

gaccgtcagc agcgctagca caaaaggacc aagcgtgttt cactggcac ctagcagcaa 413

atccaccagc ggcggaacag cagccctcgg gtgcctgggtg aaggattact tccctgagcc 473

agtcacagtg tcctggaact ccggagccct gacatccggc gtgcacacct tccccgctgt 533

gctgcaatcc agcggactgt atagcctcag ctccgtcgtg acagtccctt ccagcagcct 593

gggcacacag acttacattt gcaacgtgaa ccacaaacct tccaacacta aggtggacaa 653

aaaggtggaa cccaaatcct gtgataagac ccatacatgc ccaccttgtc ccgctcctga 713

gctgctgggg ggaccttccg tctttctgtt tcctccaaaa ccaaaagaca cactcatgat 773

cagccggacc cccgaagtca cctgtgtggt ggtggacgtc agccacgaag atccagaggt 833

caagttcaat tggtagctgg atggagtgga agtccacaac gcaaaaacca aacctagaga 893

agaacagtac aatagcacat acagggtggt gtccgtcctg acagtgtctc accaggactg 953

gctcaatggc aaagagtata agtgcaaggt gagcaacaag gccctgcctg caccaattga 1013

gaaaacaatt agcaaggcaa aggggcagcc acgggaaccc caggtgtata ccctgcccc 1073

						111	
aagccgggat	gaactgacca	aaaaccaggt	cagcctgaca	tgcctgggtga	aaggggtttta		1133
cccaagcgat	attgccgtcg	agtgggagag	caacggacag	ccagaaaaca	attacaaaac		1193
caccccacct	gtgctggact	ccgatgggag	ctttttcctg	tacagcaagc	tcacagtgga		1253
caagtccaga	tggcaacagg	gcaacgtggt	ttcctgctcc	gtgatgcacg	aggccctcca		1313
caaccactat	acacaaaagt	ccctctccct	cagcccagga				1353

$\langle 210 \rangle$	75
$\langle 211 \rangle$	451
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial Sequence

<220>
<223> Protein

<400> 75

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile Ser Ser Gly
20 25 30

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

Ile Gly Ser Ile Leu His Ser Gly Val Thr Tyr Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Thr Thr Val Ser Leu Ile Glu Tyr Phe Gln His Trp
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn

		113	
305	310	315	320

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

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

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

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

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

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

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

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

Ser Pro Gly
450

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

<220>
<223> DNA

$\langle 220 \rangle$

<221> CDS
 <222> (1)..(3)
 <223> nnn=GAA or GAG

 <220>
 <221> misc_feature
 <222> (1)..(3)
 <223> n is a, c, g, or t

 <400> 76
 nnn gtccagctgc aggagagcgg ccctggactc gtgaagccct ccgaaaccct 53
 Xaa
 1

 gagcctcaca tgcgccgtct ccggatacag catcagcagc ggatacttct ggggctggat 113
 cagacagccc cccggcaaaag gcctggagtg gatcggttct attctccaca gcggcgtgac 173
 atactacaac ccctccctga agagcagggt gaccatcagc gtggacacct ccaagaacca 233
 gttttccctc aagctgagca gcgtgaccgc cgctgacaca gccgtgtatt actgcgccag 293
 ggacaggacc accgtgtccc tgattgagta cttccagcat tggggccagg gcacactggg 353
 gaccgtcagc agcgctagca caaaaggacc aagcgtgttt cactggcac ctagcagcaa 413
 atccaccagc ggcggaacag cagccctcgg gtgcctgggtg aaggattact tccctgagcc 473
 agtcacagtg tcctggaact ccggagccct gacatccggc gtgcacacct tccccgctgt 533
 gctgcaatcc agcggactgt atagcctcag ctccgtcgtg acagtccctt ccagcagcct 593
 gggcacacag acttacattt gcaacgtgaa ccacaaacct tccaacacta aggtggacaa 653
 aaaggtggaa cccaaatcct gtgataagac ccatacatgc ccaccttgtc ccgctcctga 713
 gctgctgggg ggaccttccg tctttctgtt tcctccaaaa ccaaaagaca cactcatgat 773
 cagccggacc cccgaagtca cctgtgtggg ggtggacgtc agccacgaag atccagaggt 833
 caagttcaat tggtagctgg atggagtggg agtcacacac gcaaaaacca aacctagaga 893
 agaacagtac aatagcacat acagggtggg gtccgtcctg acagtgtctc accaggactg 953
 gctcaatggc aaagagtata agtgcaagggt gagcaacaag gccctgcctg caccaattga 1013
 gaaaacaatt agcaaggcaa aggggcagcc acgggaaccc caggtgtata ccctgcccc 1073
 aagccgggat gaactgacca aaaaccagggt cagcctgaca tgcctgggtga aagggtttta 1133

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cccaagcgat attgccgtcg agtgggagag caacggacag ccagaaaaca attacaaaac      1193
cacccccacct gtgctggact ccgatgggag ctttttcctg tacagcaagc tcacagtgga      1253
caagtccaga tggcaacagg gcaacgtgtt ttcctgctcc gtgatgcacg aggccctcca      1313
caaccactat acacaaaagt ccctctccct cagcccagga                             1353

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<210> 77
<211> 454
<212> PRT
<213> Artificial Sequence

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<220>
<223> Protein

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<400> 77

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

```

```

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

```

```

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

```

```

Trp Ile Gly Ser Ile His Tyr Ser Gly Leu Thr Tyr Tyr Asn Pro Ser
50          55          60

```

```

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

```

```

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85          90          95

```

```

Cys Ala Arg Asp Val Asp Asp Ser Ser Gly Asp Glu His Tyr Gly Met
100         105         110

```

```

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr

```

115						120				116			125			
Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	
	130					135					140					
Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	
145					150					155					160	
Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	
				165					170					175		
Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	
			180					185					190			
Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	
		195					200					205				
Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	
	210					215					220					
Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
225					230					235					240	
Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	
				245					250					255		
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	
			260					265					270			
Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	
		275					280					285				
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	
	290					295					300					
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	
305					310					315					320	

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

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 370 375 380

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

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

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

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

Leu Ser Leu Ser Pro Gly
 450

<210> 78
 <211> 1362
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA

<220>
 <221> CDS

<222> (1)..(3)

<223> nnn= CAG or CAA

<220>

<221> misc_feature

<222> (1)..(3)

<223> n is a, c, g, or t

<400> 78

nnn gtccagctgc aggaatccgg acccggcctg gtgaagccta gccagaccct 53

Xaa

1

gagcctgacc tgtaccgtgt ccggcgggaag catctattcc ggcgccctact actggtcctg 113

gattaggcag caccgccgga agggcctgga atggatcggc tccatccact acagcggcct 173

gacctattac aaccctctcc tgaagtccag ggtgaccatc agcgtcgaca caagcaagaa 233

ccagttctcc ctcaagctga gcagcgtgac cgccgccgac accgccgtgt attattgcgc 293

cagagacgtg gacgactcct ccggagacga gcactacggc atggacgtct ggggccaggg 353

cacaacagtg acagtgagca gcgctagcac aaaaggacca agcgtgtttc cactggcacc 413

tagcagcaaa tccaccagcg gcggaacagc agccctcggg tgcctggtga aggattactt 473

ccctgagcca gtcacagtgt cctggaactc cggagccctg acatccggcg tgcacacctt 533

ccccgctgtg ctgcaatcca gcggactgta tagcctcagc tccgtcgtga cagtcccttc 593

cagcagcctg ggcacacaga cttacatttg caacgtgaac cacaaacctt ccaacactaa 653

ggtggacaaa aaggtggaac ccaaatcctg tgataagacc catacatgcc caccttgtcc 713

cgctcctgag ctgctggggg gaccttccgt ctttctgttt cctccaaaac caaaagacac 773

actcatgatc agccggaccc ccgaagtcac ctgtgtgggtg gtggacgtca gccacgaaga 833

tccagaggtc aagttcaatt ggtacgtgga tggagtggaa gtccacaacg caaaaaccaa 893

acctagagaa gaacagtaca atagcacata cagggtgggtg tccgtcctga cagtgtcca 953

ccaggactgg ctcaatggca aagagtataa gtgcaagggtg agcaacaagg ccctgcctgc 1013

accaattgag aaaacaatta gcaaggcaaa ggggcagcca cggaaccccc aggtgtatac 1073

cctgccccca agccgggatg aactgaccaa aaaccagggtc agcctgacat gcctggtgaa 1133

119						
agggtttttac	ccaagcgata	ttgccgtcga	gtggggagagc	aacggacagc	cagaaaaaaa	1193
ttacaaaacc	accccacctg	tgctggactc	cgatgggagc	tttttcctgt	acagcaagct	1253
cacagtggac	aagtccagat	ggcaacaggg	caacgtgttt	tcctgctccg	tgatgcacga	1313
ggccctccac	aaccactata	cacaaaagtc	cctctccctc	agcccagga		1362

$\langle 210 \rangle$	79
$\langle 211 \rangle$	454
$\langle 212 \rangle$	PRT
$\langle 213 \rangle$	Artificial Sequence

<220>
<223> Protein

<400> 79

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

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

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

Trp Ile Gly Ser Ile His Tyr Ser Gly Leu Thr Tyr Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Val Asp Asp Ser Ser Gly Asp Glu His Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
115 120 125

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

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

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

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

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

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 245 250 255

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

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

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

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

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

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

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 370 375 380

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

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

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

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

Leu Ser Leu Ser Pro Gly
 450

<210> 80
 <211> 1362
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA

<220>
 <221> CDS
 <222> (1)..(3)

<223> nnn=GAA or GAG

<220>

<221> misc_feature

<222> (1)..(3)

<223> n is a, c, g, or t

<400> 80

nnn gtccagctgc aggaatccgg acccggcctg gtgaagccta gccagaccct 53

Xaa

1

gagcctgacc tgtaccgtgt ccggcgggaag catctattcc ggcgcctact actggtcctg 113

gattaggcag caccgccgga agggcctgga atggatcggc tccatccact acagcggcct 173

gacctattac aaccctctcc tgaagtccag ggtgaccatc agcgtcgaca caagcaagaa 233

ccagttctcc ctcaagctga gcagcgtgac cgccgccgac accgccgtgt attattgcgc 293

cagagacgtg gacgactcct ccggagacga gcactacggc atggacgtct ggggccaggg 353

cacaacagtg acagtgagca gcgctagcac aaaaggacca agcgtgtttc cactggcacc 413

tagcagcaaa tccaccagcg gcggaacagc agccctcggg tgcctggtga aggattactt 473

ccctgagcca gtcacagtgt cctggaactc cggagccctg acatccggcg tgcacacctt 533

ccccgctgtg ctgcaatcca gcggactgta tagcctcagc tccgtcgtga cagtcccttc 593

cagcagcctg ggcacacaga cttacatttg caacgtgaac caaaaacctt ccaacactaa 653

ggtggacaaa aaggtggaac ccaaactctg tgataagacc catacatgcc caccttgtcc 713

cgctcctgag ctgctggggg gaccttccgt ctttctgttt cctccaaaac caaaagacac 773

actcatgatc agccggaccc ccgaagtcac ctgtgtgggtg gtggacgtca gccacgaaga 833

tccagaggtc aagttcaatt ggtacgtgga tggagtggaa gtccacaacg caaaaaccaa 893

acctagagaa gaacagtaca atagcacata cagggtgggtg tccgtcctga cagtgtcca 953

ccaggactgg ctcaatggca aagagtataa gtgcaagggtg agcaacaagg ccctgcctgc 1013

accaattgag aaaacaatta gcaaggcaaa ggggcagcca cggaaccccc aggtgtatac 1073

cctgccccca agccgggatg aactgaccaa aaaccagggtc agcctgacat gcctggtgaa 1133

agggttttac ccaagcgata ttgccgtcga gtgggagagc aacggacagc cagaaaacaa 1193

ttacaaaacc accccacctg tgctggactc cgatgggagc tttttcctgt acagcaagct 1253
cacagtggac aagtccagat ggcaacaggg caacgtgttt tcctgctccg tgatgcacga 1313
ggccctccac aaccactata cacaaaagtc cctctccctc agcccagga 1362

<210> 81
<211> 607
<212> PRT
<213> Homo sapiens
<400> 81

Glu Cys Val Thr Gln Leu Leu Lys Asp Thr Cys Phe Glu Gly Gly Asp
1 5 10 15

Ile Thr Thr Val Phe Thr Pro Ser Ala Lys Tyr Cys Gln Val Val Cys
20 25 30

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

Ser Glu Asp Pro Thr Arg Trp Phe Thr Cys Val Leu Lys Asp Ser Val
50 55 60

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

Ser Phe Lys Gln Cys Ser His Gln Ile Ser Ala Cys Asn Lys Asp Ile
85 90 95

Tyr Val Asp Leu Asp Met Lys Gly Ile Asn Tyr Asn Ser Ser Val Ala
100 105 110

Lys Ser Ala Gln Glu Cys Gln Glu Arg Cys Thr Asp Asp Val His Cys
115 120 125

His Phe Phe Thr Tyr Ala Thr Arg Gln Phe Pro Ser Leu Glu His Arg
130 135 140

Asn Ile Cys Leu Leu Lys His Thr Gln Thr Gly Thr Pro Thr Arg Ile
 145 150 155 160

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

Leu Ser Asn Leu Ala Cys Ile Arg Asp Ile Phe Pro Asn Thr Val Phe
 180 185 190

Ala Asp Ser Asn Ile Asp Ser Val Met Ala Pro Asp Ala Phe Val Cys
 195 200 205

Gly Arg Ile Cys Thr His His Pro Gly Cys Leu Phe Phe Thr Phe Phe
 210 215 220

Ser Gln Glu Trp Pro Lys Glu Ser Gln Arg Asn Leu Cys Leu Leu Lys
 225 230 235 240

Thr Ser Glu Ser Gly Leu Pro Ser Thr Arg Ile Lys Lys Ser Lys Ala
 245 250 255

Leu Ser Gly Phe Ser Leu Gln Ser Cys Arg His Ser Ile Pro Val Phe
 260 265 270

Cys His Ser Ser Phe Tyr His Asp Thr Asp Phe Leu Gly Glu Glu Leu
 275 280 285

Asp Ile Val Ala Ala Lys Ser His Glu Ala Cys Gln Lys Leu Cys Thr
 290 295 300

Asn Ala Val Arg Cys Gln Phe Phe Thr Tyr Thr Pro Ala Gln Ala Ser
 305 310 315 320

Cys Asn Glu Gly Lys Gly Lys Cys Tyr Leu Lys Leu Ser Ser Asn Gly
 325 330 335

Ser Pro Thr Lys Ile Leu His Gly Arg Gly Gly Ile Ser Gly Tyr Thr
 340 345 350

Leu Arg Leu Cys Lys Met Asp Asn Glu Cys Thr Thr Lys Ile Lys Pro
 355 360 365

Arg Ile Val Gly Gly Thr Ala Ser Val Arg Gly Glu Trp Pro Trp Gln
 370 375 380

Val Thr Leu His Thr Thr Ser Pro Thr Gln Arg His Leu Cys Gly Gly
 385 390 395 400

Ser Ile Ile Gly Asn Gln Trp Ile Leu Thr Ala Ala His Cys Phe Tyr
 405 410 415

Gly Val Glu Ser Pro Lys Ile Leu Arg Val Tyr Ser Gly Ile Leu Asn
 420 425 430

Gln Ser Glu Ile Lys Glu Asp Thr Ser Phe Phe Gly Val Gln Glu Ile
 435 440 445

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

Leu Leu Lys Leu Glu Thr Thr Val Asn Tyr Thr Asp Ser Gln Arg Pro
 465 470 475 480

Ile Cys Leu Pro Ser Lys Gly Asp Arg Asn Val Ile Tyr Thr Asp Cys
 485 490 495

Trp Val Thr Gly Trp Gly Tyr Arg Lys Leu Arg Asp Lys Ile Gln Asn
 500 505 510

Thr Leu Gln Lys Ala Lys Ile Pro Leu Val Thr Asn Glu Glu Cys Gln
 515 520 525

126
Lys Arg Tyr Arg Gly His Lys Ile Thr His Lys Met Ile Cys Ala Gly
530 535 540

Tyr Arg Glu Gly Gly Lys Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro
545 550 555 560

Leu Ser Cys Lys His Asn Glu Val Trp His Leu Val Gly Ile Thr Ser
565 570 575

Trp Gly Glu Gly Cys Ala Gln Arg Glu Arg Pro Gly Val Tyr Thr Asn
580 585 590

Val Val Glu Tyr Val Asp Trp Ile Leu Glu Lys Thr Gln Ala Val
595 600 605

<210> 82
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein

<400> 82

Asp Ile Phe Pro Asn Thr Val Phe
1 5

<210> 83
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein

<400> 83

Pro Ser Thr Arg Ile Lys Lys Ser Lys Ala Leu Ser Gly
1 5 10

<210> 84

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

<220>
 <223> anti-RSV Kappa Light Chain

<400> 84

Met Ala Pro Val Gln Leu Leu Gly Leu Leu Val Leu Phe Leu Pro Ala
 1 5 10 15

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

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

Gly Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
 50 55 60

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

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

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

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

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

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

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
165 170 175 128

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

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

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

Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 85
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-RSV IgG4 HC S228P

<400> 85

Met Ala Val Val Gln Leu Leu Gly Leu Leu Val Leu Phe Leu Pro Ala
1 5 10 15

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

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

Ser Thr Ser Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
50 55 60

Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr
65 70 75 80

Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys
 85 90 95

Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala
 100 105 110

Thr Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val
 115 120 125

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

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

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

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

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

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

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

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

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

130
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
275 280 285

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

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

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

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

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

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

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

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

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

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

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

Gly Lys

