

SEQUENCE LISTING

<110> CHIOME Bioscience Inc.

<120> Purification method of antibody composition

<130> G2920W0

<150> JP 2021-079977

<151> 2021-05-10

<160> 78

<170> PatentIn version 3.5

<210> 1

<211> 420

<212> DNA

<213> Artificial

<220>

<223> Recombinant DNA

<220>

<221> CDS

<222> (1).. (420)

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atg ggt tgg agc tgt atc atc ttc ttt ctg gta gca aca gct aca ggc	48
Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	

gtg cac tcc caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	

cct ggg gcc tca gtg aaa gtc tcc tgc aag gct tcc ggc tac aca ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	

act gat tat gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg	192
Thr Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
50 55 60	

gag tgg att gga gtt att agt act tac tat ggt aat aca aac tac aac	240
Glu Trp Ile Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn	
65 70 75 80	

cag aag ttt aag ggc aag gcc aca atg act gtc gac aca tcc acc agc	288
Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Thr Ser Thr Ser	

85	90	95	
aca gcc tat atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg			336
Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val			
100	105	110	
tat tac tgt gca aga gga gga ttg cga gag tat tac tat gct atg gac			384
Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp			
115	120	125	
tac tgg ggt caa gga acc atg gtc acc gtc tcc tca			420
Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser			
130	135	140	

<210> 2

<211> 140

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

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

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

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

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

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Thr Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

<210> 3
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<222> (1).. (363)

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
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tca gtg aaa gtc tcc tgc aag gct tcc ggc tac aca ttc act gat tat 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30
gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg gag tgg att 144
Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
gga gtt att agt act tac tat ggt aat aca aac tac aac cag aag ttt 192
Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe
50 55 60
aag ggc aag gcc aca atg act gtc gac aca tcc acc agc aca gcc tat 240
Lys Gly Lys Ala Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80
atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg tat tac tgt 288
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
gca aga gga gga ttg cga gag tat tac tat gct atg gac tac tgg ggt 336
Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly
100 105 110

caa gga acc atg gtc acc gtc tcc tca
 Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

363

<210> 4
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 <212> PRT
 <213> Artificial

<220>
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<400> 4

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

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

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

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

Lys Gly Lys Ala Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

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

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

Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 5
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 <212> DNA

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<222> (1)..(420)

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

gtg	cac	tcc	caa	gtc	cag	ctg	gtg	cag	tct	ggg	gct	gaa	gtg	aag	aag	96
Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
			20					25					30			

cct	ggg	gcc	tca	gtg	aaa	gtc	tcc	tgc	aag	gct	tcc	ggc	tac	aca	ttc	144
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
		35					40					45				

act	gat	tat	gct	atg	cac	tgg	gtg	cga	cag	gcc	cct	gga	caa	ggc	ctg	192
Thr	Asp	Tyr	Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
	50					55					60					

gag	tgg	att	gga	gtt	att	agt	act	tac	tat	ggc	aat	aca	aac	tac	aac	240
Glu	Trp	Ile	Gly	Val	Ile	Ser	Thr	Tyr	Tyr	Gly	Asn	Thr	Asn	Tyr	Asn	
65				70						75					80	

cag	aag	ttt	aag	ggc	cga	gcc	aca	atg	act	gtc	gac	aca	tcc	acc	agc	288
Gln	Lys	Phe	Lys	Gly	Arg	Ala	Thr	Met	Thr	Val	Asp	Thr	Ser	Thr	Ser	
			85						90					95		

aca	gcc	tat	atg	gaa	ctt	agg	agc	ttg	aga	tct	gac	gat	act	gcc	gtg	336
Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	
			100					105						110		

tat	tac	tgt	gca	aga	gga	gga	ttg	cga	gag	tat	tac	tat	gct	atg	gac	384
Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Leu	Arg	Glu	Tyr	Tyr	Tyr	Ala	Met	Asp	
		115					120						125			

tac	tgg	ggc	caa	gga	acc	atg	gtc	acc	gtc	tcc	tca					420
Tyr	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser					
		130					135				140					

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<213> Artificial

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<223> Synthetic Construct

<400> 6

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

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

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

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

Gln Lys Phe Lys Gly Arg Ala Thr Met Thr Val Asp Thr Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

<210> 7

<211> 363

<212> DNA

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<222> (1).. (363)

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caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag cct ggg gcc	48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala	
1 5 10 15	

tca gtg aaa gtc tcc tgc aag gct tcc ggc tac aca ttc act gat tat	96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr	
20 25 30	

gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg gag tgg att	144
Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile	
35 40 45	

gga gtt att agt act tac tat ggt aat aca aac tac aac cag aag ttt	192
Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe	
50 55 60	

aag ggc cga gcc aca atg act gtc gac aca tcc acc agc aca gcc tat	240
Lys Gly Arg Ala Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr	
65 70 75 80	

atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg tat tac tgt	288
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	

gca aga gga gga ttg cga gag tat tac tat gct atg gac tac tgg ggt	336
Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly	
100 105 110	

caa gga acc atg gtc acc gtc tcc tca	363
Gln Gly Thr Met Val Thr Val Ser Ser	
115 120	

<210> 8

<211> 121

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 8

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

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

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

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

Lys Gly Arg Ala Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 9
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<222> (1).. (399)

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Met Glu Ser Gln Thr Gln Val Leu Met Phe Leu Leu Leu Trp Val Ser
1 5 10 15

ggt gcc tgt gca gac att gtc atg aca cag tct cca gac tcc ctg gct 96
Gly Ala Cys Ala Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30

gtg tca ctg gga gag agg gcc act atc aac tgc aag tcc agt cag agc 144
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
35 40 45

ctt ctg aat agt agc aat caa aag aac tat ttg gcc tgg tac cag cag 192
Leu Leu Asn Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60

aaa cca gga cag cct cct aaa ctt ctg gtc tac ttt gca tcc act agg 240
Lys Pro Gly Gln Pro Pro Lys Leu Leu Val Tyr Phe Ala Ser Thr Arg
65 70 75 80

gaa tct ggg gtc cct gat cgc ttc agt ggc agt gga tct ggg aca gat 288
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

ttc act ctt acc atc agc agt ctg cag gct gaa gat gtg gca gtt tac 336
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
100 105 110

tac tgt cag caa cat tat agc act cct ccc aca ttc ggt cag ggg acc 384
Tyr Cys Gln Gln His Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr
115 120 125

aag ctg gag atc aaa 399
Lys Leu Glu Ile Lys
130

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Met Glu Ser Gln Thr Gln Val Leu Met Phe Leu Leu Leu Trp Val Ser
1 5 10 15

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

Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
35 40 45

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

Lys Pro Gly Gln Pro Pro Lys Leu Leu Val Tyr Phe Ala Ser Thr Arg
65 70 75 80

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

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

Tyr Cys Gln Gln His Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr
115 120 125

Lys Leu Glu Ile Lys
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<220>
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<222> (1).. (339)

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Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
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gag agg gcc act atc aac tgc aag tcc agt cag agc ctt ctg aat agt 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

agc aat caa aag aac tat ttg gcc tgg tac cag cag aaa cca gga cag 144
Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

cct cct aaa ctt ctg gtc tac ttt gca tcc act agg gaa tct ggg gtc	192
Pro Pro Lys Leu Leu Val Tyr Phe Ala Ser Thr Arg Glu Ser Gly Val	
50 55 60	

cct gat cgc ttc agt ggc agt gga tct ggg aca gat ttc act ctt acc	240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
65 70 75 80	

atc agc agt ctg cag gct gaa gat gtg gca gtt tac tac tgt cag caa	288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	
85 90 95	

cat tat agc act cct ccc aca ttc ggt cag ggg acc aag ctg gag atc	336
His Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile	
100 105 110	

aaa	339
Lys	

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 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 12

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

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

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

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

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

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

His Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 13
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<222> (1)..(420)

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Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15
gtg cac tcc caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag 96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30
cct ggg gcc tca gtg aaa gtc tcc tgc aag ggt tcc ggc tac aca ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe
35 40 45
act gat tat gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg 192
Thr Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60
gag tgg att gga gtt att agt act tac tat ggt aat aca aac tac aac 240
Glu Trp Ile Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn
65 70 75 80
cag aag ttt aag ggc aag gcc aca atg act gtc gac aca tcc acc agc 288
Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Thr Ser Thr Ser
85 90 95
aca gcc tat atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg 336

Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val		
			100					105					110				
tat	tac	tgt	gca	aga	gga	gga	ttg	cga	gag	tat	tac	tat	gct	atg	gac		384
Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Leu	Arg	Glu	Tyr	Tyr	Tyr	Ala	Met	Asp		
		115					120					125					
tac	tgg	ggt	caa	gga	acc	atg	gtc	acc	gtc	tcc	tca						420
Tyr	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser						
	130					135					140						

<210> 14
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 <223> Synthetic Construct

<400> 14

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

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

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

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

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

Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Met	Thr	Val	Asp	Thr	Ser	Thr	Ser
				85					90					95	

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

Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Leu	Arg	Glu	Tyr	Tyr	Tyr	Ala	Met	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115

120

125

Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 130 135 140

<210> 15
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 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

tca gtg aaa gtc tcc tgc aag ggt tcc ggc tac aca ttc act gat tat 96
 Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg gag tgg att 144
 Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

gga gtt att agt act tac tat ggt aat aca aac tac aac cag aag ttt 192
 Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

aag ggc aag gcc aca atg act gtc gac aca tcc acc agc aca gcc tat 240
 Lys Gly Lys Ala Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg tat tac tgt 288
 Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gca aga gga gga ttg cga gag tat tac tat gct atg gac tac tgg ggt 336
 Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly
 100 105 110

caa gga acc atg gtc acc gtc tcc tca 363
 Gln Gly Thr Met Val Thr Val Ser Ser

115

120

<210> 16
 <211> 121
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 16

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

Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

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

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

Lys Gly Lys Ala Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

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

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

Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 17
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 <212> DNA
 <213> Artificial

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<223> Recombinant DNA

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<221> CDS

<222> (1).. (420)

<400> 17

atg ggt tgg agc tgt atc atc ttc ttt ctg gta gca aca gct aca ggc	48
Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	

gtg cac tcc caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	

cct ggg gcc tca gtg aaa gtc tcc tgc aag gct tcc ggc tac aca ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	

act gat tat gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg	192
Thr Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
50 55 60	

gag tgg att gga gtt att agt act tac tat ggt aat aca aac tac aac	240
Glu Trp Ile Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn	
65 70 75 80	

cag aag ttt aag ggc aag gcc aca atg act gtc gac aaa tcc acc agc	288
Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser	
85 90 95	

aca gcc tat atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg	336
Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val	
100 105 110	

tat tac tgt gca aga gga gga ttg cga gag tat tac tat gct atg gac	384
Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp	
115 120 125	

tac tgg ggt caa gga acc atg gtc acc gtc tcc tca	420
Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser	
130 135 140	

<210> 18

<211> 140

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 18

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

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

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

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

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

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

<210> 19

<211> 363

<212> DNA

<213> Artificial

<220>

<223> Recombinant DNA

<220>

<221> CDS

<222> (1).. (363)

<400> 19

caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag cct ggg gcc	48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala	
1 5 10 15	

tca gtg aaa gtc tcc tgc aag gct tcc ggc tac aca ttc act gat tat	96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr	
20 25 30	

gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg gag tgg att	144
Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile	
35 40 45	

gga gtt att agt act tac tat ggt aat aca aac tac aac cag aag ttt	192
Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe	
50 55 60	

aag ggc aag gcc aca atg act gtc gac aaa tcc acc agc aca gcc tat	240
Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr	
65 70 75 80	

atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg tat tac tgt	288
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	

gca aga gga gga ttg cga gag tat tac tat gct atg gac tac tgg ggt	336
Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly	
100 105 110	

caa gga acc atg gtc acc gtc tcc tca	363
Gln Gly Thr Met Val Thr Val Ser Ser	
115 120	

<210> 20

<211> 121

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 20

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

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

20	25	30
Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile		
35	40	45
Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe		
50	55	60
Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr		
65	70	75
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys		
	85	90
Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly		
	100	105
Gln Gly Thr Met Val Thr Val Ser Ser		
	115	120

<210> 21
 <211> 420
 <212> DNA
 <213> Artificial

<220>
 <223> Recombinant DNA

<220>
 <221> CDS
 <222> (1).. (420)

<400> 21	
atg ggt tgg agc tgt atc atc ttc ttt ctg gta gca aca gct aca ggc	48
Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
gtg cac tcc caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	
cct ggg gcc tca gtg aaa gtc tcc tgc aag ggt tcc ggc tac aca ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe	

35						40						45						
act	gat	tat	gct	atg	cac	tgg	gtg	cga	cag	gcc	cct	gga	caa	ggc	ctg	192		
Thr	Asp	Tyr	Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu			
50					55					60								
gag	tgg	att	gga	gtt	att	agt	act	tac	tat	ggt	aat	aca	aac	tac	aac	240		
Glu	Trp	Ile	Gly	Val	Ile	Ser	Thr	Tyr	Tyr	Gly	Asn	Thr	Asn	Tyr	Asn			
65					70					75					80			
cag	aag	ttt	aag	ggc	aag	gcc	aca	atg	act	gtc	gac	aaa	tcc	acc	agc	288		
Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Met	Thr	Val	Asp	Lys	Ser	Thr	Ser			
85					90					95								
aca	gcc	tat	atg	gaa	ctt	agg	agc	ttg	aga	tct	gac	gat	act	gcc	gtg	336		
Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val			
100					105					110								
tat	tac	tgt	gca	aga	gga	gga	ttg	cga	gag	tat	tac	tat	gct	atg	gac	384		
Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Leu	Arg	Glu	Tyr	Tyr	Tyr	Ala	Met	Asp			
115					120					125								
tac	tgg	ggt	caa	gga	acc	atg	gtc	acc	gtc	tcc	tca					420		
Tyr	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser							
130					135					140								

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

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

<210> 23
<211> 363
<212> DNA
<213> Artificial

<220>
<223> Recombinant DNA

<220>
<221> CDS
<222> (1).. (363)

<400> 23

caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag cct ggg gcc 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

tca gtg aaa gtc tcc tgc aag ggt tcc ggc tac aca ttc act gat tat 96
Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg gag tgg att 144
Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

gga gtt att agt act tac tat ggt aat aca aac tac aac cag aag ttt 192
Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe
50 55 60

aag ggc aag gcc aca atg act gtc gac aaa tcc acc agc aca gcc tat 240
Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg tat tac tgt 288
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gca aga gga gga ttg cga gag tat tac tat gct atg gac tac tgg ggt 336
Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly
100 105 110

caa gga acc atg gtc acc gtc tcc tca 363
Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210>	24
<211>	121
<212>	PRT
<213>	Artificial

<220>
<223> Synthetic Construct

<400> 24

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

Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 25
<211> 420
<212> DNA
<213> Artificial

<220>
<223> Recombinant DNA

<220>
<221> CDS
<222> (1)..(420)

<400> 25
atg ggt tgg agc tgt atc atc ttc ttt ctg gta gca aca gct aca ggc 48
Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15
gtg cac tcc caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag 96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30
cct ggg gcc tca gtg aaa gtc tcc tgc aag ggt tcc ggc tac aca ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe
35 40 45
act gat tat gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg 192
Thr Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60
gag tgg att gga gtt att agt act tac tat ggt aat aca aac tac aac 240
Glu Trp Ile Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn
65 70 75 80
cag aag ttt aag ggc cga gcc aca atg act gtc gac aca tcc acc agc 288
Gln Lys Phe Lys Gly Arg Ala Thr Met Thr Val Asp Thr Ser Thr Ser
85 90 95
aca gcc tat atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg 336
Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

tat	tac	tgt	gca	aga	gga	gga	ttg	cga	gag	tat	tac	tat	gct	atg	gac	384
Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Leu	Arg	Glu	Tyr	Tyr	Tyr	Ala	Met	Asp	
		115					120					125				

tac	tgg	ggt	caa	gga	acc	atg	gtc	acc	gtc	tcc	tca	420
Tyr	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser	
	130					135					140	

<210> 26
 <211> 140
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 26

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

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

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

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

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

Gln	Lys	Phe	Lys	Gly	Arg	Ala	Thr	Met	Thr	Val	Asp	Thr	Ser	Thr	Ser
				85					90					95	

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

Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Leu	Arg	Glu	Tyr	Tyr	Tyr	Ala	Met	Asp
		115					120						125		

Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
130 135 140

<210> 27
<211> 363
<212> DNA
<213> Artificial

<220>
<223> Recombinant DNA

<220>
<221> CDS
<222> (1)..(363)

<400> 27
caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag cct ggg gcc 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
tca gtg aaa gtc tcc tgc aag ggt tcc ggc tac aca ttc act gat tat 96
Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30
gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg gag tgg att 144
Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
gga gtt att agt act tac tat ggt aat aca aac tac aac cag aag ttt 192
Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe
50 55 60
aag ggc cga gcc aca atg act gtc gac aca tcc acc agc aca gcc tat 240
Lys Gly Arg Ala Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80
atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg tat tac tgt 288
Met Glu Leu Arg Ser Leu Arg Ser Asp Thr Ala Val Tyr Tyr Cys
85 90 95
gca aga gga gga ttg cga gag tat tac tat gct atg gac tac tgg ggt 336
Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly
100 105 110
caa gga acc atg gtc acc gtc tcc tca 363
Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 28
<211> 121
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 28

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

Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

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

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

Lys Gly Arg Ala Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 29
<211> 420
<212> DNA
<213> Artificial

<220>
<223> Recombinant DNA

<220>

<221> CDS

<222> (1).. (420)

<400> 29

atg ggt tgg agc tgt atc atc ttc ttt ctg gta gca aca gct aca ggc 48

Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly

1 5 10 15

gtg cac tcc caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag 96

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys

20 25 30

cct ggg gcc tca gtg aaa gtc tcc tgc aag gct tcc ggc tac aca ttc 144

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

35 40 45

act gat tat gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg 192

Thr Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu

50 55 60

gag tgg att gga gtt att agt act tac tat ggt aat aca aac tac aac 240

Glu Trp Ile Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn

65 70 75 80

cag aag ttt aag ggc cga gcc aca atg act gtc gac aaa tcc acc agc 288

Gln Lys Phe Lys Gly Arg Ala Thr Met Thr Val Asp Lys Ser Thr Ser

85 90 95

aca gcc tat atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg 336

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val

100 105 110

tat tac tgt gca aga gga gga ttg cga gag tat tac tat gct atg gac 384

Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp

115 120 125

tac tgg ggt caa gga acc atg gtc acc gtc tcc tca 420

Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser

130 135 140

<210> 30

<211> 140

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 30

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

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

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

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

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

Gln Lys Phe Lys Gly Arg Ala Thr Met Thr Val Asp Lys Ser Thr Ser
 85 90 95

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

Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp
 115 120 125

Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 130 135 140

<210> 31
 <211> 363
 <212> DNA
 <213> Artificial

<220>
 <223> Recombinant DNA

<220>
 <221> CDS
 <222> (1).. (363)

<400> 31

caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag cct ggg gcc	48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala	
1 5 10 15	
tca gtg aaa gtc tcc tgc aag gct tcc ggc tac aca ttc act gat tat	96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr	
20 25 30	
gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg gag tgg att	144
Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile	
35 40 45	
gga gtt att agt act tac tat ggt aat aca aac tac aac cag aag ttt	192
Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe	
50 55 60	
aag ggc cga gcc aca atg act gtc gac aaa tcc acc agc aca gcc tat	240
Lys Gly Arg Ala Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr	
65 70 75 80	
atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg tat tac tgt	288
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gca aga gga gga ttg cga gag tat tac tat gct atg gac tac tgg ggt	336
Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly	
100 105 110	
caa gga acc atg gtc acc gtc tcc tca	363
Gln Gly Thr Met Val Thr Val Ser Ser	
115 120	

<210> 32
 <211> 121
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 32

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala	
1 5 10 15	
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr	
20 25 30	

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

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

Lys Gly Arg Ala Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

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

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

Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 33
 <211> 420
 <212> DNA
 <213> Artificial

<220>
 <223> Recombinant DNA

<220>
 <221> CDS
 <222> (1).. (420)

<400> 33
 atg ggt tgg agc tgt atc atc ttc ttt ctg gta gca aca gct aca ggc 48
 Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

gtg cac tcc caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag 96
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

cct ggg gcc tca gtg aaa gtc tcc tgc aag ggt tcc ggc tac aca ttc 144
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe
 35 40 45

act gat tat gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg 192

Thr	Asp	Tyr	Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
50						55					60					
gag tgg att gga gtt att agt act tac tat ggt aat aca aac tac aac																240
Glu	Trp	Ile	Gly	Val	Ile	Ser	Thr	Tyr	Tyr	Gly	Asn	Thr	Asn	Tyr	Asn	
65					70					75					80	
cag aag ttt aag ggc cga gcc aca atg act gtc gac aaa tcc acc agc																288
Gln	Lys	Phe	Lys	Gly	Arg	Ala	Thr	Met	Thr	Val	Asp	Lys	Ser	Thr	Ser	
				85					90					95		
aca gcc tat atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg																336
Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	
			100					105					110			
tat tac tgt gca aga gga gga ttg cga gag tat tac tat gct atg gac																384
Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Leu	Arg	Glu	Tyr	Tyr	Tyr	Ala	Met	Asp	
		115					120					125				
tac tgg ggt caa gga acc atg gtc acc gtc tcc tca																420
Tyr	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser					
	130					135					140					

<210> 34
 <211> 140
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 34

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

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

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

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

Glu	Trp	Ile	Gly	Val	Ile	Ser	Thr	Tyr	Tyr	Gly	Asn	Thr	Asn	Tyr	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65	70	75	80	
atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg tat tac tgt				288
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys				
	85	90	95	
gca aga gga gga ttg cga gag tat tac tat gct atg gac tac tgg ggt				336
Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly				
	100	105	110	
caa gga acc atg gtc acc gtc tcc tca				363
Gln Gly Thr Met Val Thr Val Ser Ser				
	115	120		
<210>	36			
<211>	121			
<212>	PRT			
<213>	Artificial			
<220>				
<223>	Synthetic Construct			
<400>	36			
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala				
1	5	10	15	
Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr				
	20	25	30	
Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile				
	35	40	45	
Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe				
	50	55	60	
Lys Gly Arg Ala Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr				
65	70	75	80	
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys				
	85	90	95	
Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly				
	100	105	110	

Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 37
 <211> 1413
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> antibody

<220>
 <221> CDS
 <222> (1)..(1413)

<400> 37
 atg ggt tgg agc tgt atc atc ttc ttt ctg gta gca aca gct aca ggc 48
 Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15
 gtg cac tcc caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag 96
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30
 cct ggg gcc tca gtg aaa gtc tcc tgc aag gct tcc ggc tac aca ttc 144
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 act gat tat gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg 192
 Thr Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60
 gag tgg att gga gtt att agt act tac tat ggt aat aca aac tac aac 240
 Glu Trp Ile Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn
 65 70 75 80
 cag aag ttt aag ggc aag gcc aca atg act gtc gac aca tcc acc agc 288
 Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Thr Ser Thr Ser
 85 90 95
 aca gcc tat atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg 336
 Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
 100 105 110
 tat tac tgt gca aga gga gga ttg cga gag tat tac tat gct atg gac 384
 Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp
 115 120 125

tac tgg ggt caa gga acc atg gtc acc gtc tcc tca gcc tcc acc aag Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys 130 135 140	432
ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly 145 150 155 160	480
ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro 165 170 175	528
gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr 180 185 190	576
ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val 195 200 205	624
gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn 210 215 220	672
gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro 225 230 235 240	720
aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu 245 250 255	768
ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp 260 265 270	816
acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp 275 280 285	864
gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly 290 295 300	912
gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn 305 310 315 320	960
agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp	1008

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

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

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

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

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Thr Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp
115 120 125

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Pro Gly Lys
465 470

<210> 39
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> antibody

<220>
<221> CDS
<222> (1)..(1356)

<400> 39
caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag cct ggg gcc 48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
tca gtg aaa gtc tcc tgc aag gct tcc ggc tac aca ttc act gat tat 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30
gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg gag tgg att 144
Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
gga gtt att agt act tac tat ggt aat aca aac tac aac cag aag ttt 192
Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe
50 55 60
aag ggc aag gcc aca atg act gtc gac aca tcc acc agc aca gcc tat 240
Lys Gly Lys Ala Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80
atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg tat tac tgt 288

Met	Glu	Leu	Arg	Ser	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
				85					90					95			
gca	aga	gga	gga	ttg	cga	gag	tat	tac	tat	gct	atg	gac	tac	tgg	ggt	336	
Ala	Arg	Gly	Gly	Leu	Arg	Glu	Tyr	Tyr	Tyr	Ala	Met	Asp	Tyr	Trp	Gly		
			100					105					110				
caa	gga	acc	atg	gtc	acc	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	384	
Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser		
		115					120					125					
gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	432	
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala		
		130				135					140						
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	480	
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val		
145					150					155					160		
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	528	
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala		
			165					170					175				
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	576	
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val		
			180					185					190				
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	624	
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His		
		195					200					205					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt	672	
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys		
	210					215				220							
gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	720	
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly		
225					230					235					240		
gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	768	
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met		
			245						250					255			
atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	816	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His		
			260					265					270				
gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	864	
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val		
		275					280					285					

cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac	912
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr	
290 295 300	
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc	960
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly	
305 310 315 320	
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc	1008
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile	
325 330 335	
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg	1056
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val	
340 345 350	
tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc	1104
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser	
355 360 365	
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag	1152
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu	
370 375 380	
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc	1200
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro	
385 390 395 400	
gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg	1248
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val	
405 410 415	
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg	1296
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met	
420 425 430	
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct	1344
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser	
435 440 445	
ccg ggt aaa tga	1356
Pro Gly Lys	
450	

<210> 40
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 40

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

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

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

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

Lys Gly Lys Ala Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
450

<210> 41
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> antibody

<220>
<221> CDS
<222> (1).. (1413)

<400> 41
atg ggt tgg agc tgt atc atc ttc ttt ctg gta gca aca gct aca ggc 48
Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15
gtg cac tcc caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag 96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30
cct ggg gcc tca gtg aaa gtc tcc tgc aag gct tcc ggc tac aca ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
act gat tat gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg 192
Thr Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60
gag tgg att gga gtt att agt act tac tat ggt aat aca aac tac aac 240
Glu Trp Ile Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn
65 70 75 80

cag aag ttt aag ggc cga gcc aca atg act gtc gac aca tcc acc agc Gln Lys Phe Lys Gly Arg Ala Thr Met Thr Val Asp Thr Ser Thr Ser 85 90 95	288
aca gcc tat atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val 100 105 110	336
tat tac tgt gca aga gga gga ttg cga gag tat tac tat gct atg gac Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp 115 120 125	384
tac tgg ggt caa gga acc atg gtc acc gtc tcc tca gcc tcc acc aag Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys 130 135 140	432
ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly 145 150 155 160	480
ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro 165 170 175	528
gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr 180 185 190	576
ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val 195 200 205	624
gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn 210 215 220	672
gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro 225 230 235 240	720
aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu 245 250 255	768
ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp 260 265 270	816
acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp 280 285 290 295 300	864

275	280	285	
gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc			912
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly			
290	295	300	
gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac			960
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn			
305	310	315	320
agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg			1008
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp			
325	330	335	
ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca			1056
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro			
340	345	350	
gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa			1104
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu			
355	360	365	
cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac			1152
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn			
370	375	380	
cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc			1200
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile			
385	390	395	400
gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc			1248
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr			
405	410	415	
acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag			1296
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys			
420	425	430	
ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc			1344
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys			
435	440	445	
tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc			1392
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu			
450	455	460	
tcc ctg tct ccg ggt aaa tga			1413
Ser Leu Ser Pro Gly Lys			
465	470		

<210> 42
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 42

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

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

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

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

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

Gln Lys Phe Lys Gly Arg Ala Thr Met Thr Val Asp Thr Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp
115 120 125

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Pro Gly Lys
 465 470

<210> 43
 <211> 1356
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> antibody

<220>
 <221> CDS
 <222> (1)..(1356)

<400> 43
 caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag cct ggg gcc 48
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

tca gtg aaa gtc tcc tgc aag gct tcc ggc tac aca ttc act gat tat 96
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg gag tgg att 144

Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile	
35 40 45	
gga gtt att agt act tac tat ggt aat aca aac tac aac cag aag ttt	192
Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe	
50 55 60	
aag ggc cga gcc aca atg act gtc gac aca tcc acc agc aca gcc tat	240
Lys Gly Arg Ala Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr	
65 70 75 80	
atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg tat tac tgt	288
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gca aga gga gga ttg cga gag tat tac tat gct atg gac tac tgg ggt	336
Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly	
100 105 110	
caa gga acc atg gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg	384
Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser	
115 120 125	
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg	432
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala	
130 135 140	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg	480
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val	
145 150 155 160	
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct	528
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala	
165 170 175	
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg	576
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val	
180 185 190	
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac	624
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His	
195 200 205	
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt	672
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys	
210 215 220	
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg	720
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly	
225 230 235 240	

gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 245 250 255	768
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His 260 265 270	816
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 275 280 285	864
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr 290 295 300	912
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 305 310 315 320	960
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 325 330 335	1008
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 340 345 350	1056
tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 355 360 365	1104
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 370 375 380	1152
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 385 390 395 400	1200
gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val 405 410 415	1248
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 420 425 430	1296
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 435 440 445	1344

ccg ggt aaa tga
Pro Gly Lys
450

1356

<210> 44
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 44

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

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

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

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

Lys Gly Arg Ala Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
 450

<210> 45
 <211> 1413
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> antibody

<220>
 <221> CDS
 <222> (1).. (1413)

<400> 45
 atg ggt tgg agc tgt atc atc ttc ttt ctg gta gca aca gct aca ggc 48
 Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15
 gtg cac tcc caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag 96
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

cct ggg gcc tca gtg aaa gtc tcc tgc aag ggt tcc ggc tac aca ttc Pro Gly Ala Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe 35 40 45	144
act gat tat gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg Thr Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu 50 55 60	192
gag tgg att gga gtt att agt act tac tat ggt aat aca aac tac aac Glu Trp Ile Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn 65 70 75 80	240
cag aag ttt aag ggc aag gcc aca atg act gtc gac aca tcc acc agc Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Thr Ser Thr Ser 85 90 95	288
aca gcc tat atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val 100 105 110	336
tat tac tgt gca aga gga gga ttg cga gag tat tac tat gct atg gac Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp 115 120 125	384
tac tgg ggt caa gga acc atg gtc acc gtc tcc tca gcc tcc acc aag Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys 130 135 140	432
ggc cca tog gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly 145 150 155 160	480
ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro 165 170 175	528
gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr 180 185 190	576
ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val 195 200 205	624
gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn 210 215 220	672
gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro 225 230 235 240	720

225	230	235	240	
aaa tct tgt gac Lys Ser Cys Asp	aaa act cac aca tgc Lys Thr His Thr Cys	cca ccg tgc cca gca cct Pro Pro Cys Pro Ala Pro	gaa Glu	768
	245	250	255	
ctc ctg ggg gga Leu Leu Gly Gly	ccg tca gtc ttc Pro Ser Val Phe	ctc ttc ccc cca Leu Phe Pro Pro	aaa ccc aag gac Lys Pro Lys Asp	816
	260	265	270	
acc ctc atg atc tcc Thr Leu Met Ile Ser	cgg acc cct gag gtc Arg Thr Pro Glu Val	aca tgc gtg gtg gtg Thr Cys Val Val Val	gac Asp	864
	275	280	285	
gtg agc cac gaa gac Val Ser His Glu Asp	cct gag gtc aag ttc Pro Glu Val Lys Phe	aac tgg tac gtg gac ggc Asn Trp Tyr Val Asp Gly		912
	290	295	300	
gtg gag gtg cat aat Val Glu Val His Asn	gcc aag aca aag ccg Ala Lys Thr Lys Pro	cgg gag gag cag tac aac Arg Glu Glu Gln Tyr Asn		960
	305	310	320	
agc acg tac cgt gtg Ser Thr Tyr Arg Val	gtc agc gtc ctc acc Ser Val Leu Thr Val	ctg cac cag gac tgg Leu His Gln Asp Trp		1008
	325	330	335	
ctg aat ggc aag gag Leu Asn Gly Lys Glu	tac aag tgc aag gtc Tyr Lys Cys Lys Val	tcc aac aaa gcc ctc cca Ser Asn Lys Ala Leu Pro		1056
	340	345	350	
gcc ccc atc gag aaa Ala Pro Ile Glu Lys	acc atc tcc aaa gcc Thr Ile Ser Lys Ala	aaa ggg cag ccc cga gaa Lys Gly Gln Pro Arg Glu		1104
	355	360	365	
cca cag gtg tac acc Pro Gln Val Tyr Thr	ctg ccc cca tcc cgg Leu Pro Pro Ser Arg	gat gag ctg acc aag aac Asp Glu Leu Thr Lys Asn		1152
	370	375	380	
cag gtc agc ctg acc Gln Val Ser Leu Thr	tgc ctg gtc aaa ggc Cys Leu Val Lys Gly	ttc tat ccc agc gac atc Phe Tyr Pro Ser Asp Ile		1200
	385	390	400	
gcc gtg gag tgg gag Ala Val Glu Trp Glu	agc aat ggg cag ccg Ser Asn Gly Gln Pro	gag aac aac tac aag acc Asn Asn Tyr Lys Thr		1248
	405	410	415	
acg cct ccc gtg ctg Thr Pro Pro Val Leu	gac tcc gac ggc tcc Asp Ser Asp Gly Ser	ttc ttc ctc tac agc aag Phe Phe Leu Tyr Ser Lys		1296
	420	425	430	
ctc acc gtg gac aag Leu Thr Tyr Ser Lys	agc agg tgg cag cag Arg Lys Thr Tyr Ser Lys	ggg aac gtc ttc tca tgc Gly Asn Glu Thr Tyr Ser		1344

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

tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc 1392
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 450 455 460

tcc ctg tct ccg ggt aaa tga 1413
 Ser Leu Ser Pro Gly Lys
 465 470

<210> 46
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 46

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

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

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

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

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

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Thr Ser Thr Ser
 85 90 95

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

Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Pro Gly Lys
465 470

<210> 47
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> antibody

<220>
<221> CDS

<222> (1).. (1356)

<400> 47

caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag cct ggg gcc	48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala	
1 5 10 15	

tca gtg aaa gtc tcc tgc aag ggt tcc ggc tac aca ttc act gat tat	96
Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr	
20 25 30	

gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg gag tgg att	144
Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile	
35 40 45	

gga gtt att agt act tac tat ggt aat aca aac tac aac cag aag ttt	192
Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe	
50 55 60	

aag ggc aag gcc aca atg act gtc gac aca tcc acc agc aca gcc tat	240
Lys Gly Lys Ala Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr	
65 70 75 80	

atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg tat tac tgt	288
Met Glu Leu Arg Ser Leu Arg Ser Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	

gca aga gga gga ttg cga gag tat tac tat gct atg gac tac tgg ggt	336
Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly	
100 105 110	

caa gga acc atg gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg	384
Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser	
115 120 125	

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg	432
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala	
130 135 140	

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg	480
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val	
145 150 155 160	

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct	528
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala	
165 170 175	

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg	576
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val	
180 185 190	

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 195 200 205	624
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 210 215 220	672
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly 225 230 235 240	720
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 245 250 255	768
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His 260 265 270	816
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 275 280 285	864
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr 290 295 300	912
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 305 310 315 320	960
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 325 330 335	1008
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 340 345 350	1056
tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 355 360 365	1104
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 370 375 380	1152
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 385 390 395 400	1200

gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	1248
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	
				405					410					415		

gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	1296
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	
			420					425						430		

cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	1344
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	
		435					440							445		

ccg	ggt	aaa	tga	1356
Pro	Gly	Lys		
	450			

<210> 48
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 48

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

Ser	Val	Lys	Val	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr
			20					25					30		

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

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

Lys	Gly	Lys	Ala	Thr	Met	Thr	Val	Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr
65					70					75				80	

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
 450

<210> 49
 <211> 1413
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> antibody

<220>

<221> CDS

<222> (1).. (1413)

<400> 49

atg ggt tgg agc tgt atc atc ttc ttt ctg gta gca aca gct aca ggc 48

Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly

1 5 10 15

gtg cac tcc caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag 96

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys

20 25 30

cct ggg gcc tca gtg aaa gtc tcc tgc aag ggt tcc ggc tac aca ttc 144

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

35 40 45

act gat tat gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg 192

Thr Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu

50 55 60

gag tgg att gga gtt att agt act tac tat ggt aat aca aac tac aac 240

Glu Trp Ile Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn

65 70 75 80

cag aag ttt aag ggc cga gcc aca atg act gtc gac aca tcc acc agc 288

Gln Lys Phe Lys Gly Arg Ala Thr Met Thr Val Asp Thr Ser Thr Ser

85 90 95

aca gcc tat atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg 336

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val

100 105 110

tat tac tgt gca aga gga gga ttg cga gag tat tac tat gct atg gac 384

Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp

115 120 125

tac tgg ggt caa gga acc atg gtc acc gtc tcc tca gcc tcc acc aag 432

Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys

130 135 140

ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg 480

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

145 150 155 160

ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg 528

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

165 170 175

gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc 576

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

180	185	190	
ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val			624
195	200	205	
gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn			672
210	215	220	
gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro			720
225	230	235	240
aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu			768
245	250	255	
ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp			816
260	265	270	
acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp			864
275	280	285	
gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly			912
290	295	300	
gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn			960
305	310	315	320
agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp			1008
325	330	335	
ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro			1056
340	345	350	
gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu			1104
355	360	365	
cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn			1152
370	375	380	
cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc			1200

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

gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc 1248
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 405 410 415

acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag 1296
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 420 425 430

ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc 1344
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 435 440 445

tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc 1392
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 450 455 460

tcc ctg tct ccg ggt aaa tga 1413
 Ser Leu Ser Pro Gly Lys
 465 470

<210> 50
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 50

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

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

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

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

Glu Trp Ile Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Pro Gly Lys
 465 470

<210> 51
 <211> 1356
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> antibody

<220>
 <221> CDS
 <222> (1)..(1356)

<400> 51
 caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag cct ggg gcc 48
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 tca gtg aaa gtc tcc tgc aag ggt tcc ggc tac aca ttc act gat tat 96
 Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30
 gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg gag tgg att 144
 Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 gga gtt att agt act tac tat ggt aat aca aac tac aac cag aag ttt 192
 Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe
 50 55 60
 aag ggc cga gcc aca atg act gtc gac aca tcc acc agc aca gcc tat 240
 Lys Gly Arg Ala Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg tat tac tgt 288
 Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gca aga gga gga ttg cga gag tat tac tat gct atg gac tac tgg ggt 336
 Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly
 100 105 110
 caa gga acc atg gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg 384
 Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg 432
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg	480
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val	
145 150 155 160	
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct	528
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala	
165 170 175	
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg	576
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val	
180 185 190	
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac	624
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His	
195 200 205	
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt	672
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys	
210 215 220	
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg	720
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly	
225 230 235 240	
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg	768
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met	
245 250 255	
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac	816
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His	
260 265 270	
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg	864
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val	
275 280 285	
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac	912
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr	
290 295 300	
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc	960
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly	
305 310 315 320	
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc	1008
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile	
325 330 335	
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg	1056
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val	
340 345 350	

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc	1104
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser	
355 360 365	

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag	1152
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu	
370 375 380	

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc	1200
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro	
385 390 395 400	

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg	1248
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val	
405 410 415	

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg	1296
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met	
420 425 430	

cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct	1344
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser	
435 440 445	

ccg ggt aaa tga	1356
Pro Gly Lys	
450	

<210> 52
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 52

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

Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

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

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

Lys Gly Arg Ala Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys

<210> 53
 <211> 1413
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> antibody

<220>
 <221> CDS
 <222> (1)..(1413)

<400> 53
 atg ggt tgg agc tgt atc atc ttc ttt ctg gta gca aca gct aca ggc 48
 Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

gtg cac tcc caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag 96
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

cct ggg gcc tca gtg aaa gtc tcc tgc aag gct tcc ggc tac aca ttc 144
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

act gat tat gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg 192
 Thr Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60

gag tgg att gga gtt att agt act tac tat ggt aat aca aac tac aac 240
 Glu Trp Ile Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn
 65 70 75 80

cag aag ttt aag ggc aag gcc aca atg act gtc gac aaa tcc acc agc 288
 Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser
 85 90 95

aca gcc tat atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg 336
 Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
 100 105 110

tat tac tgt gca aga gga gga ttg cga gag tat tac tat gct atg gac 384
 Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp
 115 120 125

tac tgg ggt caa gga acc atg gtc acc gtc tcc tca gcc tcc acc aag 432
 Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys

130	135	140	
ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg			480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly			
145	150	155	160
ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg			528
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro			
	165	170	175
gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc			576
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr			
	180	185	190
ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg			624
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val			
	195	200	205
gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac			672
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn			
	210	215	220
gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc			720
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro			
	225	230	235
aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa			768
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu			
	245	250	255
ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac			816
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp			
	260	265	270
acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac			864
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp			
	275	280	285
gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc			912
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly			
	290	295	300
gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac			960
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn			
	305	310	315
agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg			1008
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp			
	325	330	335
ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca			1056

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro	
340 345 350	
gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa	1104
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu	
355 360 365	
cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac	1152
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn	
370 375 380	
cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc	1200
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile	
385 390 395 400	
gcc gtg gag tgg gag agc aat ggg cag cgg gag aac aac tac aag acc	1248
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr	
405 410 415	
acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag	1296
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys	
420 425 430	
ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc	1344
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys	
435 440 445	
tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc	1392
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu	
450 455 460	
tcc ctg tct ccg ggt aaa tga	1413
Ser Leu Ser Pro Gly Lys	
465 470	

<210> 54
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 54

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

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Pro Gly Lys
 465 470

<210> 55
 <211> 1356
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> antibody

<220>
 <221> CDS
 <222> (1)..(1356)

<400> 55
 caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag cct ggg gcc 48
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 tca gtg aaa gtc tcc tgc aag gct tcc ggc tac aca ttc act gat tat 96
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30
 gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg gag tgg att 144
 Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 gga gtt att agt act tac tat ggt aat aca aac tac aac cag aag ttt 192
 Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe
 50 55 60
 aag ggc aag gcc aca atg act gtc gac aaa tcc acc agc aca gcc tat 240
 Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg tat tac tgt 288
 Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gca aga gga gga ttg cga gag tat tac tat gct atg gac tac tgg ggt Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly 100 105 110	336
caa gga acc atg gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 115 120 125	384
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 130 135 140	432
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 145 150 155 160	480
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 165 170 175	528
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 180 185 190	576
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 195 200 205	624
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 210 215 220	672
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly 225 230 235 240	720
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 245 250 255	768
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His 260 265 270	816
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 275 280 285	864
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr 290 295 300	912

cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc	960
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly	
305 310 315 320	
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc	1008
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile	
325 330 335	
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg	1056
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val	
340 345 350	
tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc	1104
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser	
355 360 365	
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag	1152
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu	
370 375 380	
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc	1200
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro	
385 390 395 400	
gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg	1248
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val	
405 410 415	
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg	1296
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met	
420 425 430	
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct	1344
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser	
435 440 445	
ccg ggt aaa tga	1356
Pro Gly Lys	
450	

<210> 56
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 56

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

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

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

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

Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

405

410

415

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

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

Pro Gly Lys
 450

<210> 57
 <211> 1413
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> antibody

<220>
 <221> CDS
 <222> (1).. (1413)

<400> 57
 atg ggt tgg agc tgt atc atc ttc ttt ctg gta gca aca gct aca ggc 48
 Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

gtg cac tcc caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag 96
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

cct ggg gcc tca gtg aaa gtc tcc tgc aag gct tcc ggc tac aca ttc 144
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

act gat tat gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg 192
 Thr Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60

gag tgg att gga gtt att agt act tac tat ggt aat aca aac tac aac 240
 Glu Trp Ile Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn
 65 70 75 80

cag aag ttt aag ggc cga gcc aca atg act gtc gac aaa tcc acc agc 288
 Gln Lys Phe Lys Gly Arg Ala Thr Met Thr Val Asp Lys Ser Thr Ser

85	90	95	
aca gcc tat atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val 100 105 110			336
tat tac tgt gca aga gga gga ttg cga gag tat tac tat gct atg gac Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp 115 120 125			384
tac tgg ggt caa gga acc atg gtc acc gtc tcc tca gcc tcc acc aag Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys 130 135 140			432
ggc cca tog gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly 145 150 155 160			480
ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro 165 170 175			528
gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr 180 185 190			576
ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val 195 200 205			624
gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn 210 215 220			672
gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro 225 230 235 240			720
aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu 245 250 255			768
ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp 260 265 270			816
acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp 275 280 285			864
gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc			912

Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly		
290						295					300						
gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	cgg	cgg	gag	gag	cag	tac	aac		960
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn		
305					310					315					320		
agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg		1008
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp		
				325					330					335			
ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca		1056
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro		
			340					345					350				
gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa		1104
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu		
		355					360					365					
cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac		1152
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn		
		370				375					380						
cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc		1200
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile		
385					390					395					400		
gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	cgg	gag	aac	aac	tac	aag	acc		1248
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr		
				405				410						415			
acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag		1296
Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys		
			420					425					430				
ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc		1344
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys		
		435					440					445					
tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc		1392
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu		
		450				455					460						
tcc	ctg	tct	ccg	ggt	aaa	tga											1413
Ser	Leu	Ser	Pro	Gly	Lys												
465					470												

<210> 58
 <211> 470
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 58

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

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

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

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

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

Gln Lys Phe Lys Gly Arg Ala Thr Met Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp
115 120 125

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Pro Gly Lys
 465 470

<210> 59
 <211> 1356
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> antibody

<220>
 <221> CDS
 <222> (1)..(1356)

<400> 59
 caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag cct ggg gcc 48
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

tca gtg aaa gtc tcc tgc aag gct tcc ggc tac aca ttc act gat tat 96
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg gag tgg att 144
 Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

gga gtt att agt act tac tat ggt aat aca aac tac aac cag aag ttt Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe 50 55 60	192
aag ggc cga gcc aca atg act gtc gac aaa tcc acc agc aca gcc tat Lys Gly Arg Ala Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr 65 70 75 80	240
atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg tat tac tgt Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys 85 90 95	288
gca aga gga gga ttg cga gag tat tac tat gct atg gac tac tgg ggt Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly 100 105 110	336
caa gga acc atg gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 115 120 125	384
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 130 135 140	432
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 145 150 155 160	480
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 165 170 175	528
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 180 185 190	576
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 195 200 205	624
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 210 215 220	672
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly 225 230 235 240	720
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 245 250 255	768

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His 260 265 270	816
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 275 280 285	864
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr 290 295 300	912
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 305 310 315 320	960
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 325 330 335	1008
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 340 345 350	1056
tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 355 360 365	1104
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 370 375 380	1152
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 385 390 395 400	1200
gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val 405 410 415	1248
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 420 425 430	1296
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 435 440 445	1344
ccg ggt aaa tga Pro Gly Lys	1356

450

<210> 60
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 60

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

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

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

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

Lys Gly Arg Ala Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

355 360 365
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Lys
 450

<210> 61
 <211> 1413
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> antibody

<220>
 <221> CDS
 <222> (1)..(1413)

<400> 61
 atg ggt tgg agc tgt atc atc ttc ttt ctg gta gca aca gct aca ggc 48
 Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15
 gtg cac tcc caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag 96
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30
 oct ggg gcc tca gtg aaa gtc tcc tgc aag ggt tcc ggc tac aca ttc 144
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe

35	40	45	
act gat tat gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg			192
Thr Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu			
50	55	60	
gag tgg att gga gtt att agt act tac tat ggt aat aca aac tac aac			240
Glu Trp Ile Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn			
65	70	75	80
cag aag ttt aag ggc aag gcc aca atg act gtc gac aaa tcc acc agc			288
Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser			
	85	90	95
aca gcc tat atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg			336
Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val			
	100	105	110
tat tac tgt gca aga gga gga ttg cga gag tat tac tat gct atg gac			384
Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp			
	115	120	125
tac tgg ggt caa gga acc atg gtc acc gtc tcc tca gcc tcc acc aag			432
Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys			
	130	135	140
ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg			480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly			
145	150	155	160
ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg			528
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro			
	165	170	175
gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc			576
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr			
	180	185	190
ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg			624
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val			
	195	200	205
gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac			672
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn			
	210	215	220
gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc			720
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro			
225	230	235	240
aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa			768

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu	
245 250 255	
ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac	816
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp	
260 265 270	
acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac	864
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp	
275 280 285	
gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc	912
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly	
290 295 300	
gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac	960
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn	
305 310 315 320	
agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg	1008
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp	
325 330 335	
ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca	1056
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro	
340 345 350	
gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa	1104
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu	
355 360 365	
cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac	1152
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn	
370 375 380	
cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc	1200
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile	
385 390 395 400	
gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc	1248
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr	
405 410 415	
acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag	1296
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys	
420 425 430	
ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc	1344
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys	
435 440 445	

tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc 1392
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 450 455 460

tcc ctg tct ccg ggt aaa tga 1413
 Ser Leu Ser Pro Gly Lys
 465 470

<210> 62
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 62

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

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

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

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

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

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser
 85 90 95

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

Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp
 115 120 125

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Pro Gly Lys
465 470

<210> 63
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> antibody

<220>
<221> CDS
<222> (1).. (1356)

<400> 63

caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag cct ggg gcc	48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala	
1 5 10 15	
tca gtg aaa gtc tcc tgc aag ggt tcc ggc tac aca ttc act gat tat	96
Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr	
20 25 30	
gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg gag tgg att	144
Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile	
35 40 45	
gga gtt att agt act tac tat ggt aat aca aac tac aac cag aag ttt	192
Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe	
50 55 60	
aag ggc aag gcc aca atg act gtc gac aaa tcc acc agc aca gcc tat	240
Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr	
65 70 75 80	
atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg tat tac tgt	288
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gca aga gga gga ttg cga gag tat tac tat gct atg gac tac tgg ggt	336
Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly	
100 105 110	
caa gga acc atg gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg	384
Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser	
115 120 125	
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg	432
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala	
130 135 140	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg	480
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val	
145 150 155 160	
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct	528
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala	
165 170 175	
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg	576
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val	
180 185 190	
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac	624
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His	
195 200 205	

aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 210 215 220	672
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly 225 230 235 240	720
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 245 250 255	768
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His 260 265 270	816
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 275 280 285	864
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr 290 295 300	912
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 305 310 315 320	960
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 325 330 335	1008
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 340 345 350	1056
tac acc ctg ccc cca tcc ccg gat gag ctg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 355 360 365	1104
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 370 375 380	1152
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 385 390 395 400	1200
gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val 1248	

405	410	415	
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg			1296
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met			
420	425	430	
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct			1344
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser			
435	440	445	
ccg ggt aaa tga			1356
Pro Gly Lys			
450			

<210> 64
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 64

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

Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

305		310		315		320
Lys Glu Tyr	Lys Cys Lys Val	Ser Asn Lys	Ala Leu Pro	Ala Pro Ile		
	325		330		335	
Glu Lys Thr	Ile Ser Lys Ala	Lys Gly Gln Pro	Arg Glu Pro	Gln Val		
	340		345		350	
Tyr Thr Leu	Pro Pro Ser Arg	Asp Glu Leu	Thr Lys Asn	Gln Val Ser		
	355		360		365	
Leu Thr Cys	Leu Val Lys Gly	Phe Tyr Pro	Ser Asp Ile	Ala Val Glu		
	370		375		380	
Trp Glu Ser	Asn Gly Gln Pro	Glu Asn Asn Tyr	Lys Thr Thr	Pro Pro		
	385		390		395	
Val Leu Asp	Ser Asp Gly Ser	Phe Phe Leu	Tyr Ser Lys	Leu Thr Val		
	405		410		415	
Asp Lys Ser	Arg Trp Gln Gln	Gly Asn Val Phe	Ser Cys Ser	Val Met		
	420		425		430	
His Glu Ala	Leu His Asn His	Tyr Thr Gln Lys	Ser Leu Ser	Leu Ser		
	435		440		445	
Pro Gly Lys						
	450					

<210> 65
 <211> 1413
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> antibody

<220>
 <221> CDS
 <222> (1)..(1413)

<400> 65
atg ggt tgg agc tgt atc atc ttc ttt ctg gta gca aca gct aca ggc 48
Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

gtg cac tcc caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag 96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gcc tca gtg aaa gtc tcc tgc aag ggt tcc ggc tac aca ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe
35 40 45

act gat tat gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg 192
Thr Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

gag tgg att gga gtt att agt act tac tat ggt aat aca aac tac aac 240
Glu Trp Ile Gly Val Ile Ser Thr Tyr Tyr Gly Asn Thr Asn Tyr Asn
65 70 75 80

cag aag ttt aag ggc cga gcc aca atg act gtc gac aaa tcc acc agc 288
Gln Lys Phe Lys Gly Arg Ala Thr Met Thr Val Asp Lys Ser Thr Ser
85 90 95

aca gcc tat atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg 336
Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100 105 110

tat tac tgt gca aga gga gga ttg cga gag tat tac tat gct atg gac 384
Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp
115 120 125

tac tgg ggt caa gga acc atg gtc acc gtc tcc tca gcc tcc acc aag 432
Tyr Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg 480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145 150 155 160

ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg 528
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165 170 175

gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc 576
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180 185 190

ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg 624

Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val		
	195						200					205					
gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac		672
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn		
	210					215					220						
gtg	aat	cac	aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc		720
Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro		
	225				230					235					240		
aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa		768
Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu		
				245					250					255			
ctc	ctg	ggg	gga	cgg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac		816
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp		
			260					265						270			
acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac		864
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp		
	275						280					285					
gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc		912
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly		
	290					295					300						
gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac		960
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn		
	305				310					315					320		
agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg		1008
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp		
				325					330					335			
ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca		1056
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro		
			340					345					350				
gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa		1104
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu		
		355					360					365					
cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac		1152
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn		
	370					375					380						
cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc		1200
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile		
	385				390					395					400		

gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc 1248
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 405 410 415

acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag 1296
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 420 425 430

ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc 1344
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 435 440 445

tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc 1392
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 450 455 460

tcc ctg tct ccg ggt aaa tga 1413
 Ser Leu Ser Pro Gly Lys
 465 470

<210> 66
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 66

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

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

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

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

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

Gln Lys Phe Lys Gly Arg Ala Thr Met Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp
115 120 125

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Pro Gly Lys
 465 470

<210> 67
 <211> 1356

<212> DNA
 <213> Artificial Sequence

<220>
 <223> antibody

<220>
 <221> CDS
 <222> (1)..(1356)

<400> 67
 caa gtc cag ctg gtg cag tct ggg gct gaa gtg aag aag cct ggg gcc 48
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 tca gtg aaa gtc tcc tgc aag ggt tcc ggc tac aca ttc act gat tat 96
 Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30
 gct atg cac tgg gtg cga cag gcc cct gga caa ggc ctg gag tgg att 144
 Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 gga gtt att agt act tac tat ggt aat aca aac tac aac cag aag ttt 192
 Gly Val Ile Ser Thr Tyr Gly Asn Thr Asn Tyr Asn Gln Lys Phe
 50 55 60
 aag ggc cga gcc aca atg act gtc gac aaa tcc acc agc aca gcc tat 240
 Lys Gly Arg Ala Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 atg gaa ctt agg agc ttg aga tct gac gat act gcc gtg tat tac tgt 288
 Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gca aga gga gga ttg cga gag tat tac tat gct atg gac tac tgg ggt 336
 Ala Arg Gly Gly Leu Arg Glu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly
 100 105 110
 caa gga acc atg gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg 384
 Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg 432
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140
 gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg 480
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 165 170 175	528
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 180 185 190	576
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 195 200 205	624
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 210 215 220	672
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly 225 230 235 240	720
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 245 250 255	768
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His 260 265 270	816
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 275 280 285	864
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr 290 295 300	912
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 305 310 315 320	960
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 325 330 335	1008
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 340 345 350	1056
tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser	1104

Lys Gly Arg Ala Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

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

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

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

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

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

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

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

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

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

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

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

<210> 69
 <211> 723
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> antibody

<220>
 <221> CDS
 <222> (1)..(723)

<400> 69
 atg gaa tca cag acc cag gtc ctc atg ttt ctt ctg ctc tgg gta tct 48
 Met Glu Ser Gln Thr Gln Val Leu Met Phe Leu Leu Leu Trp Val Ser
 1 5 10 15

ggt gcc tgt gca gac att gtc atg aca cag tct cca gac tcc ctg gct 96
 Gly Ala Cys Ala Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
 20 25 30

gtg tca ctg gga gag agg gcc act atc aac tgc aag tcc agt cag agc 144
 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
 35 40 45

ctt ctg aat agt agc aat caa aag aac tat ttg gcc tgg tac cag cag 192
 Leu Leu Asn Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
 50 55 60

aaa cca gga cag cct cct aaa ctt ctg gtc tac ttt gca tcc act agg 240
 Lys Pro Gly Gln Pro Pro Lys Leu Leu Val Tyr Phe Ala Ser Thr Arg
 65 70 75 80

gaa tct ggg gtc cct gat cgc ttc agt ggc agt gga tct ggg aca gat 288
 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 85 90 95

ttc act ctt acc atc agc agt ctg cag gct gaa gat gtg gca gtt tac 336
 Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
 100 105 110

tac tgt cag caa cat tat agc act cct ccc aca ttc ggt cag ggg acc 384
 Tyr Cys Gln Gln His Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr
 115 120 125

aag ctg gag atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc 432
 Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
 130 135 140

ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc 480

Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	
145					150					155					160	
ctg	ctg	aat	aac	tto	tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	528
Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	
				165					170					175		
gat	aac	gcc	ctc	caa	tcg	ggt	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	576
Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	
			180					185					190			
gac	agc	aag	gac	agc	acc	tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	624
Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	
		195					200					205				
aaa	gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	672
Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	
	210					215				220						
cag	ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	720
Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	
225					230					235					240	
tag																723

<210> 70
 <211> 240
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 70

Met	Glu	Ser	Gln	Thr	Gln	Val	Leu	Met	Phe	Leu	Leu	Leu	Trp	Val	Ser
1				5					10					15	

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

Val	Ser	Leu	Gly	Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser
		35					40					45			

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

Lys Pro Gly Gln Pro Pro Lys Leu Leu Val Tyr Phe Ala Ser Thr Arg
65 70 75 80

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

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

Tyr Cys Gln Gln His Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr
115 120 125

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

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

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

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

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

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
210 215 220

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235 240

<210> 71

<211> 663

<212> DNA

<213> Artificial Sequence

<220>

<223> antibody

<220>

<221> CDS

<222> (1)..(663)

<400> 71

gac att gtc atg aca cag tct cca gac tcc ctg gct gtg tca ctg gga	48
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
1 5 10 15	

gag agg gcc act atc aac tgc aag tcc agt cag agc ctt ctg aat agt	96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser	
20 25 30	

agc aat caa aag aac tat ttg gcc tgg tac cag cag aaa cca gga cag	144
Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
35 40 45	

cct cct aaa ctt ctg gtc tac ttt gca tcc act agg gaa tct ggg gtc	192
Pro Pro Lys Leu Leu Val Tyr Phe Ala Ser Thr Arg Glu Ser Gly Val	
50 55 60	

cct gat cgc ttc agt ggc agt gga tct ggg aca gat ttc act ctt acc	240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
65 70 75 80	

atc agc agt ctg cag gct gaa gat gtg gca gtt tac tac tgt cag caa	288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	
85 90 95	

cat tat agc act cct ccc aca ttc ggt cag ggg acc aag ctg gag atc	336
His Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile	
100 105 110	

aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat	384
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp	
115 120 125	

gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac	432
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn	
130 135 140	

ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc	480
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu	
145 150 155 160	

caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac	528
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp	
165 170 175	

agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac 576
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 180 185 190

gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc 624
 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 195 200 205

tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag 663
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215 220

<210> 72
 <211> 220
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 72

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

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

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

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

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

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95

His Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
 100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 130 135 140

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

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

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

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

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

<210> 73
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDRH1

<400> 73

Asp Tyr Ala Met His
 1 5

<210> 74
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDRH2

<400> 74

Val	Ile	Ser	Thr	Tyr	Tyr	Gly	Asn	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys
1				5					10					15	

Gly

<210> 75

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRH3

<400> 75

Gly	Gly	Leu	Arg	Glu	Tyr	Tyr	Tyr	Ala	Met	Asp	Tyr
1				5					10		

<210> 76

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRL1

<400> 76

Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Ser	Ser	Asn	Gln	Lys	Asn	Tyr	Leu
1				5					10					15	

Ala

<210> 77

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRL2

<400> 77

Phe Ala Ser Thr Arg Glu Ser
1 5

<210> 78

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRL3

<400> 78

Gln Gln His Tyr Ser Thr Pro Pro Thr
1 5