

SEQUENCE LISTING

<110> DAIICHI SANKYO COMPANY, LIMITED

<120> Anti-Siglec-15 antibodies

<130> DSPCT-FP1021

<150> JP 2009-94613

<151> 2009-04-09

<160> 106

<170> PatentIn version 3.4

<210> 1

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(987)

<223> Inventor: Hiruma, Yoshiharu; Tsuda, Eisuke

<223> Inventor: Takizawa, Takeshi; Nakayama, Makiko

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aca ggc tca ttt gtg aga act aaa ata gat act acg gag aac ttg ctc	96
Thr Gly Ser Phe Val Arg Thr Lys Ile Asp Thr Thr Glu Asn Leu Leu	
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aac aca gag gtg cac agc tcg cca gcg cag cgc tgg tcc atg cag gtg	144
Asn Thr Glu Val His Ser Ser Pro Ala Gln Arg Trp Ser Met Gln Val	
35 40 45	

cca ccc gag gtg agc gcg gag gca ggc gac gcg gca gtg ctg ccc tgc	192
Pro Pro Glu Val Ser Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys	
50 55 60	

acc ttc acg cac ccg cac cgc cac tac gac ggg ccg ctg acg gcc atc	240
Thr Phe Thr His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile	
65 70 75 80	

tgg cgc gcg ggc gag ccc tat gcg ggc ccg cag gtg ttc cgc tgc gct	288
Trp Arg Ala Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Ala	
85 90 95	

gcg gcg cgg ggc agc gag ctg tgc cag acg gcg ctg agc ctg cac ggc	336
Ala Ala Arg Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly	
100 105 110	

cgc ttc cgg ctg ctg ggc aac ccg cgc cgc aac gac ctg tcg ctg cgc	384
Arg Phe Arg Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg	
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Val Glu Arg Leu Ala Leu Ala Asp Asp Arg Arg Tyr Phe Cys Arg Val	
130 135 140	

gag ttc gcc ggc gac gtc cat gac cgc tac gag agc cgc cac ggc gtc	480
Glu Phe Ala Gly Asp Val His Asp Arg Tyr Glu Ser Arg His Gly Val	
145 150 155 160	

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Arg Leu His Val Thr 165 Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu 175	
ccc agt ccg gct cac gcc ttc cgc gcg ctc tgc act gcc gaa ggg gag	576
Pro Ser Pro Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu 180 185 190	
ccg ccg ccc gcc ctc gcc tgg tcc ggc ccg gcc ctg ggc aac agc ttg	624
Pro Pro Pro Ala Leu Ala Trp Ser Gly Pro Ala Leu Gly Asn Ser Leu 195 200 205	
gca gcc gtg cgg agc ccg cgt gag ggt cac ggc cac cta gtg acc gcc	672
Ala Ala Val Arg Ser Pro Arg Glu Gly His Gly His Leu Val Thr Ala 210 215 220	
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Asn Ser Leu Gly Arg Ser Glu Ala Ser Val Tyr Leu Phe Arg Phe His 245 250 255	
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Gly Ala Ser Gly Ala Ser Thr Val Ala Leu Leu Leu Gly Ala Leu Gly 260 265 270	
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Phe Lys Ala Leu Leu Leu Leu Gly Val Leu Ala Ala Arg Ala Ala Arg 275 280 285	
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Arg Arg Pro Glu His Leu Asp Thr Pro Asp Thr Pro Pro Arg Ser Gln 290 295 300	
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Asn Thr Glu Val His Ser Ser Pro Ala Gln Arg Trp Ser Met Gln Val
35 40 45

Pro Pro Glu Val Ser Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys
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 Val Glu Arg Leu Ala Leu Ala Asp Asp Arg Arg Tyr Phe Cys Arg Val
 130 135 140
 Glu Phe Ala Gly Asp Val His Asp Arg Tyr Glu Ser Arg His Gly Val
 145 150 155 160
 Arg Leu His Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu
 165 170 175
 Pro Ser Pro Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu
 180 185 190
 Pro Pro Pro Ala Leu Ala Trp Ser Gly Pro Ala Leu Gly Asn Ser Leu
 195 200 205
 Ala Ala Val Arg Ser Pro Arg Glu Gly His Gly His Leu Val Thr Ala
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 Glu Leu Pro Ala Leu Thr His Asp Gly Arg Tyr Thr Cys Thr Ala Ala
 225 230 235 240
 Asn Ser Leu Gly Arg Ser Glu Ala Ser Val Tyr Leu Phe Arg Phe His
 245 250 255
 Gly Ala Ser Gly Ala Ser Thr Val Ala Leu Leu Leu Gly Ala Leu Gly
 260 265 270
 Phe Lys Ala Leu Leu Leu Leu Gly Val Leu Ala Ala Arg Ala Ala Arg
 275 280 285
 Arg Arg Pro Glu His Leu Asp Thr Pro Asp Thr Pro Pro Arg Ser Gln
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atg gga tcc ctt gtg aaa act aga aga gac gct tcg ggg gat ctg ctc      96
Met Gly Ser Leu Val Lys Thr Arg Arg Asp Ala Ser Gly Asp Leu Leu
20 25 30

aac aca gag gcg cac agt gcc ccg gcg cag cgc tgg tcc atg cag gtg      144
Asn Thr Glu Ala His Ser Ala Pro Ala Gln Arg Trp Ser Met Gln Val
35 40 45

ccc gcg gag gtg aac gcg gag gct ggc gac gcg gcg gtg ctg ccc tgc      192
Pro Ala Glu Val Asn Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys
50 55 60

acc ttc acg cac ccg cac cgc cac tac gac ggg ccg ctg acg gcc atc      240
Thr Phe Thr His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile
65 70 75 80

tgg cgc tcg ggc gag ccg tac gcg ggc ccg cag gtg ttc cgc tgc acc      288
Trp Arg Ser Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Thr
85 90 95

gcg gcg ccg ggc agc gag ctg tgc cag acg gcg ctg agc ctg cac ggc      336
Ala Ala Pro Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly
100 105 110

cgc ttc cgc ctg ctg ggc aac ccg cgc cgc aac gac ctg tcc ctg cgc      384
Arg Phe Arg Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg
115 120 125

gtc gag cgc ctc gcc ctg gcg gac agc ggc cgc tac ttc tgc cgc gtg      432
Val Glu Arg Leu Ala Leu Ala Asp Ser Gly Arg Tyr Phe Cys Arg Val
130 135 140

gag ttc acc ggc gac gcc cac gat cgc tat gag agt cgc cat ggg gtc      480
Glu Phe Thr Gly Asp Ala His Asp Arg Tyr Glu Ser Arg His Gly Val
145 150 155 160

cgt ctg cgc gtg act gct gcg ccg ccg atc gtc aac atc tcg gtg ctg      528
Arg Leu Arg Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu
165 170 175

ccg ggc ccc gcg cac gcc ttc cgc gcg ctc tgc acc gcc gag ggg gag      576
Pro Gly Pro Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu
180 185 190

ccc ccg ccc gcc ctc gcc tgg tcg ggt ccc gcc cca ggc aac agc tcc      624
Pro Pro Pro Ala Leu Ala Trp Ser Gly Pro Ala Pro Gly Asn Ser Ser
195 200 205

gct gcc ctg cag ggc cag ggt cac ggc tac cag gtg acc gcc gag ttg      672
Ala Ala Leu Gln Gly Gln Gly His Gly Tyr Gln Val Thr Ala Glu Leu
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Pro Ala Leu Thr Arg Asp Gly Arg Tyr Thr Cys Thr Ala Ala Asn Ser
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 35 40 45

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

Trp Arg Ser Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Thr
 85 90 95

Ala Ala Pro Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly
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Arg Phe Arg Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg

115

120

125

Val Glu Arg Leu Ala Leu Ala Asp Ser Gly Arg Tyr Phe Cys Arg Val
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Glu Phe Thr Gly Asp Ala His Asp Arg Tyr Glu Ser Arg His Gly Val
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Arg Leu Arg Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu
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Pro Gly Pro Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu
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Pro Pro Pro Ala Leu Ala Trp Ser Gly Pro Ala Pro Gly Asn Ser Ser
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Ala Ala Leu Gln Gly Gln Gly His Gly Tyr Gln Val Thr Ala Glu Leu
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Pro Ala Leu Thr Arg Asp Gly Arg Tyr Thr Cys Thr Ala Ala Asn Ser
 225 230 235 240

Leu Gly Arg Ala Glu Ala Ser Val Tyr Leu Phe Arg Phe His Gly Ala
 245 250 255

Pro Gly Thr Ser Thr Leu Ala Leu Leu Leu Gly Ala Leu Gly Leu Lys
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Ala Leu Leu Leu Leu Gly Ile Leu Gly Ala Arg Ala Thr Arg Arg Arg
 275 280 285

Leu Asp His Leu Val Pro Gln Asp Thr Pro Pro Arg Ser Gln Ala Gln
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Glu Ser Asn Tyr Glu Asn Leu Ser Gln Met Ser Pro Pro Gly His Gln
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Met Gly Ser Leu Val Lys Thr Arg Arg Asp Ala Ser Gly Asp Leu Leu		
20 25 30		
aac aca gag gcg cac agt gcc ccg gcg cag cgc tgg tcc atg cag gtg		144
Asn Thr Glu Ala His Ser Ala Pro Ala Gln Arg Trp Ser Met Gln Val		
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ccc gcg gag gtg aac gcg gag gct ggc gac gcg gcg gtg ctg ccc tgc		192
Pro Ala Glu Val Asn Ala Glu Ala Gly Asp Ala Val Leu Pro Cys		
50 55 60		
acc ttc acg cac ccg cac cgc cac tac gac ggg ccg ctg acg gcc atc		240
Thr Phe Thr His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile		
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tgg cgc tcg ggc gag ccg tac gcg ggc ccg cag gtg ttc cgc tgc acc		288
Trp Arg Ser Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Thr		
85 90 95		
gcg gcg ccg ggc agc gag ctg tgc cag acg gcg ctg agc ctg cac ggc		336
Ala Ala Pro Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly		
100 105 110		
cgc ttc cgc ctg ctg ggc aac ccg cgc cgc aac gac ctg tcc ctg cgc		384
Arg Phe Arg Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg		
115 120 125		
gtc gag cgc ctc gcc ctg gcg gac agc ggc cgc tac ttc tgc cgc gtg		432
Val Glu Arg Leu Ala Leu Ala Asp Ser Gly Arg Tyr Phe Cys Arg Val		
130 135 140		
gag ttc acc ggc gac gcc cac gat cgc tat gag agt cgc cat ggg gtc		480
Glu Phe Thr Gly Asp Ala His Asp Arg Tyr Glu Ser Arg His Gly Val		
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cgt ctg cgc gtg act gct gcg ccg cgg atc gtc aac atc tcg gtg ctg		528
Arg Leu Arg Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu		
165 170 175		
ccg ggc ccc gcg cac gcc ttc cgc gcg ctc tgc acc gcc gag ggg gag		576
Pro Gly Pro Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu		
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ccc ccg ccc gcc ctc gcc tgg tcg ggt ccc gcc cca ggc aac agc tcc		624
Pro Pro Pro Ala Leu Ala Trp Ser Gly Pro Ala Pro Gly Asn Ser Ser		
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gct gcc ctg cag ggc cag ggt cac ggc tac cag gtg acc gcc gag ttg		672
Ala Ala Leu Gln Gly Gln Gly His Gly Tyr Gln Val Thr Ala Glu Leu		
210 215 220		
ccc gcg ctg acc cgc gac ggc cgc tac acg tgc acg gcg gcc aat agc		720
Pro Ala Leu Thr Arg Asp Gly Arg Tyr Thr Cys Thr Ala Ala Asn Ser		
225 230 235 240		
ctg ggc cgc gcc gag gcc agc gtc tac ctg ttc cgc ttc cac ggc gcc		768
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Pro Ala Glu Val Asn Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys
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Thr Phe Thr His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile
65 70 75 80

Trp Arg Ser Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Thr
85 90 95

Ala Ala Pro Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly
100 105 110

Arg Phe Arg Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg
115 120 125

Val Glu Arg Leu Ala Leu Ala Asp Ser Gly Arg Tyr Phe Cys Arg Val
130 135 140

Glu Phe Thr Gly Asp Ala His Asp Arg Tyr Glu Ser Arg His Gly Val
145 150 155 160

Arg Leu Arg Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu
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Pro Gly Pro Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu
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Pro Pro Pro Ala Leu Ala Trp Ser Gly Pro Ala Pro Gly Asn Ser Ser
195 200 205

Ala Ala Leu Gln Gly Gln Gly His Gly Tyr Gln Val Thr Ala Glu Leu
210 215 220

Pro Ala Leu Thr Arg Asp Gly Arg Tyr Thr Cys Thr Ala Ala Asn Ser
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Leu Gly Arg Ala Glu Ala Ser Val Tyr Leu Phe Arg Phe His Gly Ala
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Pro Gly

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Met	Gly	Ser	Leu	Val	Lys	Thr	Arg	Arg	Asp	Ala	Ser	Gly	Asp	Leu	Leu		
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Asn	Thr	Glu	Ala	His	Ser	Ala	Pro	Ala	Gln	Arg	Trp	Ser	Met	Gln	Val		
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Pro	Ala	Glu	Val	Asn	Ala	Glu	Ala	Gly	Asp	Ala	Ala	Val	Leu	Pro	Cys		
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acc	ttc	acg	cac	ccg	cac	cgc	cac	tac	gac	ggg	ccg	ctg	acg	gcc	atc		240
Thr	Phe	Thr	His	Pro	His	Arg	His	Tyr	Asp	Gly	Pro	Leu	Thr	Ala	Ile		
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tgg	cgc	tcg	ggc	gag	ccg	tac	gcg	ggc	ccg	cag	gtg	ttc	cgc	tgc	acc		288
Trp	Arg	Ser	Gly	Glu	Pro	Tyr	Ala	Gly	Pro	Gln	Val	Phe	Arg	Cys	Thr		
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gcg	gcg	ccg	ggc	agc	gag	ctg	tgc	cag	acg	gcg	ctg	agc	ctg	cac	ggc		336
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Glu	Phe	Thr	Gly	Asp	Ala	His	Asp	Arg	Tyr	Glu	Ser	Arg	His	Gly	Val		
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			165						170					175			
ccg	ggc	ccc	gcg	cac	gcc	ttc	cgc	gcg	ctc	tgc	acc	gcc	gag	ggg	gag		576
Pro	Gly	Pro	Ala	His	Ala	Phe	Arg	Ala	Leu	Cys	Thr	Ala	Glu	Gly	Glu		
			180					185					190				
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Pro	Pro	Pro	Ala	Leu	Ala	Trp	Ser	Gly	Pro	Ala	Pro	Gly	Asn	Ser	Ser		
		195					200					205					
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Ala	Ala	Leu	Gln	Gly	Gln	Gly	His	Gly	Tyr	Gln	Val	Thr	Ala	Glu	Leu		
	210					215					220						
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Pro	Ala	Leu	Thr	Arg	Asp	Gly	Arg	Tyr	Thr	Cys	Thr	Ala	Ala	Asn	Ser		
225					230					235					240		
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Leu	Gly	Arg	Ala	Glu	Ala	Ser	Val	Tyr	Leu	Phe	Arg	Phe	His	Gly	Ala		
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ccc gga gac cca gct ttc ttg tac aaa gtg gtt gat atc gaa ggt cgt 816
Pro Gly Asp Pro Ala Phe Leu Tyr Lys Val Val Asp Ile Glu Gly Arg
260 265 270

ggg ggt aag cct atc cct aac cct ctc ctc ggt ctc gat tct acg cgt 864
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acc ggt cat cat cac cat cac cat tga 891
Thr Gly His His His His His His
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20 25 30

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35 40 45

Pro Ala Glu Val Asn Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys
50 55 60

Thr Phe Thr His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile
65 70 75 80

Trp Arg Ser Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Thr
85 90 95

Ala Ala Pro Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly
100 105 110

Arg Phe Arg Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg
115 120 125

Val Glu Arg Leu Ala Leu Ala Asp Ser Gly Arg Tyr Phe Cys Arg Val
130 135 140

Glu Phe Thr Gly Asp Ala His Asp Arg Tyr Glu Ser Arg His Gly Val
145 150 155 160

Arg Leu Arg Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu
165 170 175

Pro Gly Pro Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu

180

185

190

Pro Pro Pro Ala Leu Ala Trp Ser Gly Pro Ala Pro Gly Asn Ser Ser
195 200 205

Ala Ala Leu Gln Gly Gln Gly His Gly Tyr Gln Val Thr Ala Glu Leu
210 215 220

Pro Ala Leu Thr Arg Asp Gly Arg Tyr Thr Cys Thr Ala Ala Asn Ser
225 230 235 240

Leu Gly Arg Ala Glu Ala Ser Val Tyr Leu Phe Arg Phe His Gly Ala
245 250 255

Pro Gly Asp Pro Ala Phe Leu Tyr Lys Val Val Asp Ile Glu Gly Arg
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Gly Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg
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Thr Gly His His His His His His
290 295

<210> 13

<211> 1512

<212> DNA

<213> Artificial sequence

<220>

<223> Fc-fused mouse Siglec-15 cDNA

<220>

<221> CDS

<222> (1)..(1512)

<400> 13

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1 5 10 15

atg gga tcc ctt gtg aaa act aga aga gac gct tcg ggg gat ctg ctc 96
Met Gly Ser Leu Val Lys Thr Arg Arg Asp Ala Ser Gly Asp Leu Leu
20 25 30

aac aca gag gcg cac agt gcc ccg gcg cag cgc tgg tcc atg cag gtg 144
Asn Thr Glu Ala His Ser Ala Pro Ala Gln Arg Trp Ser Met Gln Val
35 40 45

ccc gcg gag gtg aac gcg gag gct ggc gac gcg gcg gtg ctg ccc tgc 192
Pro Ala Glu Val Asn Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys
50 55 60

acc ttc acg cac ccg cac cgc cac tac gac ggg ccg ctg acg gcc atc 240
Thr Phe Thr His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile
65 70 75 80

tgg cgc tcg ggc gag ccg tac gcg ggc ccg cag gtg ttc cgc tgc acc 288
Trp Arg Ser Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Thr
85 90 95

gcg gcg ccg ggc agc gag ctg tgc cag acg gcg ctg agc ctg cac ggc Ala Ala Pro Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly 100 105 110	336
cgc ttc cgc ctg ctg ggc aac ccg cgc cgc aac gac ctg tcc ctg cgc Arg Phe Arg Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg 115 120 125	384
gtc gag cgc ctc gcc ctg gcg gac agc ggc cgc tac ttc tgc cgc gtg Val Glu Arg Leu Ala Leu Ala Asp Ser Gly Arg Tyr Phe Cys Arg Val 130 135 140	432
gag ttc acc ggc gac gcc cac gat cgc tat gag agt cgc cat ggg gtc Glu Phe Thr Gly Asp Ala His Asp Arg Tyr Glu Ser Arg His Gly Val 145 150 155 160	480
cgt ctg cgc gtg act gct gcg ccg cgg atc gtc aac atc tcg gtg ctg Arg Leu Arg Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu 165 170 175	528
ccg ggc ccc gcg cac gcc ttc cgc gcg ctc tgc acc gcc gag ggg gag Pro Gly Pro Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu 180 185 190	576
ccc ccg ccc gcc ctc gcc tgg tcg ggt ccc gcc cca ggc aac agc tcc Pro Pro Pro Ala Leu Ala Trp Ser Gly Pro Ala Pro Gly Asn Ser Ser 195 200 205	624
gct gcc ctg cag ggc cag ggt cac ggc tac cag gtg acc gcc gag ttg Ala Ala Leu Gln Gly Gln Gly His Gly Tyr Gln Val Thr Ala Glu Leu 210 215 220	672
ccc gcg ctg acc cgc gac ggc cgc tac acg tgc acg gcg gcc aat agc Pro Ala Leu Thr Arg Asp Gly Arg Tyr Thr Cys Thr Ala Ala Asn Ser 225 230 235 240	720
ctg ggc cgc gcc gag gcc agc gtc tac ctg ttc cgc ttc cac ggc gcc Leu Gly Arg Ala Glu Ala Ser Val Tyr Leu Phe Arg Phe His Gly Ala 245 250 255	768
ccc gga gac cca gct ttc ttg tac aaa gtg gtt gat atc cag gca gag Pro Gly Asp Pro Ala Phe Leu Tyr Lys Val Val Asp Ile Gln Ala Glu 260 265 270	816
ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro 275 280 285	864
gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Lys Pro Lys 290 295 300	912
gac acc ctc atg atc tcc ccg acc cct gag gtc aca tgc gtg gtg gtg Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val 305 310 315 320	960
gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp 325 330 335	1008
ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 340 345 350	1056
aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp 355 360 365	1104

tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc	1152
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu	
370 375 380	
cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga	1200
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg	
385 390 395 400	
gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag	1248
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys	
405 410 415	
aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac	1296
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp	
420 425 430	
atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag	1344
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys	
435 440 445	
acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tat agc	1392
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser	
450 455 460	
aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca	1440
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser	
465 470 475 480	
tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc	1488
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser	
485 490 495	
ctc tcc ctg tct ccg ggt aaa taa	1512
Leu Ser Leu Ser Pro Gly Lys	
500	

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 <223> Synthetic Construct

<400> 14

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Met Gly Ser Leu Val Lys Thr Arg Arg Asp Ala Ser Gly Asp Leu Leu
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35 40 45

Pro Ala Glu Val Asn Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys
50 55 60

Thr Phe Thr His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile
65 70 75 80

Trp Arg Ser Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Thr
 85 90 95
 Ala Ala Pro Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly
 100 105 110
 Arg Phe Arg Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg
 115 120 125
 Val Glu Arg Leu Ala Leu Ala Asp Ser Gly Arg Tyr Phe Cys Arg Val
 130 135 140
 Glu Phe Thr Gly Asp Ala His Asp Arg Tyr Glu Ser Arg His Gly Val
 145 150 155 160
 Arg Leu Arg Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu
 165 170 175
 Pro Gly Pro Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu
 180 185 190
 Pro Pro Pro Ala Leu Ala Trp Ser Gly Pro Ala Pro Gly Asn Ser Ser
 195 200 205
 Ala Ala Leu Gln Gly Gln Gly His Gly Tyr Gln Val Thr Ala Glu Leu
 210 215 220
 Pro Ala Leu Thr Arg Asp Gly Arg Tyr Thr Cys Thr Ala Ala Asn Ser
 225 230 235 240
 Leu Gly Arg Ala Glu Ala Ser Val Tyr Leu Phe Arg Phe His Gly Ala
 245 250 255
 Pro Gly Asp Pro Ala Phe Leu Tyr Lys Val Val Asp Ile Gln Ala Glu
 260 265 270
 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 275 280 285
 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 290 295 300
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 305 310 315 320
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 325 330 335
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 340 345 350

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
355 360 365

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
370 375 380

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
385 390 395 400

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
405 410 415

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

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
435 440 445

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
450 455 460

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
465 470 475 480

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
485 490 495

Leu Ser Leu Ser Pro Gly Lys
500

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<211> 780
<212> DNA
<213> Homo sapiens

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<222> (1)..(780)

<220>
<221> CDS
<222> (1)..(780)

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aca ggc tca ttt gtg aga act aaa ata gat act acg gag aac ttg ctc 96
Thr Gly Ser Phe Val Arg Thr Lys Ile Asp Thr Thr Glu Asn Leu Leu
20 25 30

aac aca gag gtg cac agc tcg cca gcg cag cgc tgg tcc atg cag gtg 144
Asn Thr Glu Val His Ser Ser Pro Ala Gln Arg Trp Ser Met Gln Val
35 40 45

cca ccc gag gtg agc gcg gag gca ggc gac gcg gca gtg ctg ccc tgc 192

Pro	Pro	Glu	Val	Ser	Ala	Glu	Ala	Gly	Asp	Ala	Ala	Val	Leu	Pro	Cys		
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Thr	Phe	Thr	His	Pro	His	Arg	His	Tyr	Asp	Gly	Pro	Leu	Thr	Ala	Ile	80	
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tgg	cgc	gcg	ggc	gag	ccc	tat	gcg	ggc	ccg	cag	gtg	ttc	cgc	tgc	gct	288	
Trp	Arg	Ala	Gly	Glu	Pro	Tyr	Ala	Gly	Pro	Gln	Val	Phe	Arg	Cys	Ala	95	
				85					90								
gcg	gcg	ccg	ggc	agc	gag	ctc	tgc	cag	acg	gcg	ctg	agc	ctg	cac	ggc	336	
Ala	Ala	Arg	Gly	Ser	Glu	Leu	Cys	Gln	Thr	Ala	Leu	Ser	Leu	His	Gly	110	
			100					105									
cgc	ttc	ccg	ctg	ctg	ggc	aac	ccg	cgc	cgc	aac	gac	ctc	tcg	ctg	cgc	384	
Arg	Phe	Arg	Leu	Leu	Gly	Asn	Pro	Arg	Arg	Asn	Asp	Leu	Ser	Leu	Arg	125	
			115				120										
gtc	gag	cgc	ctc	gcc	ctg	gct	gac	gac	cgc	cgc	tac	ttc	tgc	cgc	gtc	432	
Val	Glu	Arg	Leu	Ala	Leu	Ala	Asp	Asp	Arg	Arg	Tyr	Phe	Cys	Arg	Val	140	
	130					135											
gag	ttc	gcc	ggc	gac	gtc	cat	gac	cgc	tac	gag	agc	cgc	cac	ggc	gtc	480	
Glu	Phe	Ala	Gly	Asp	Val	His	Asp	Arg	Tyr	Glu	Ser	Arg	His	Gly	Val	160	
					150					155							
cgg	ctg	cac	gtg	aca	gcc	gcg	ccg	cgg	atc	gtc	aac	atc	tcg	gtg	ctg	528	
Arg	Leu	His	Val	Thr	Ala	Ala	Pro	Arg	Ile	Val	Asn	Ile	Ser	Val	Leu	175	
				165					170								
ccc	agt	ccg	gct	cac	gcc	ttc	cgc	gcg	ctc	tgc	act	gcc	gaa	ggg	gag	576	
Pro	Ser	Pro	Ala	His	Ala	Phe	Arg	Ala	Leu	Cys	Thr	Ala	Glu	Gly	Glu	190	
			180					185									
ccg	ccg	ccc	gcc	ctc	gcc	tgg	tcc	ggc	ccg	gcc	ctg	ggc	aac	agc	ttg	624	
Pro	Pro	Pro	Ala	Leu	Ala	Trp	Ser	Gly	Pro	Ala	Leu	Gly	Asn	Ser	Leu	205	
			195				200										
gca	gcc	gtg	cgg	agc	ccg	cgt	gag	ggc	cac	ggc	cac	cta	gtg	acc	gcc	672	
Ala	Ala	Val	Arg	Ser	Pro	Arg	Glu	Gly	His	Gly	His	Leu	Val	Thr	Ala	220	
						215											
gaa	ctg	ccc	gca	ctg	acc	cat	gac	ggc	cgc	tac	acg	tgt	acg	gcc	gcc	720	
Glu	Leu	Pro	Ala	Leu	Thr	His	Asp	Gly	Arg	Tyr	Thr	Cys	Thr	Ala	Ala	240	
					230					235							
aac	agc	ctg	ggc	cgc	tcc	gag	gcc	agc	gtc	tac	ctg	ttc	cgc	ttc	cat	768	
Asn	Ser	Leu	Gly	Arg	Ser	Glu	Ala	Ser	Val	Tyr	Leu	Phe	Arg	Phe	His	255	
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ggc	gcc	agc	ggg													780	
Gly	Ala	Ser	Gly													260	

<210> 16
 <211> 260
 <212> PRT
 <213> Homo sapiens

<400> 16

Met	Glu	Lys	Ser	Ile	Trp	Leu	Leu	Ala	Cys	Leu	Ala	Trp	Val	Leu	Pro
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Thr Gly Ser Phe Val Arg Thr Lys Ile Asp Thr Thr Glu Asn Leu Leu
 Page 17

20

25

30

Asn Thr Glu Val His Ser Ser Pro Ala Gln Arg Trp Ser Met Gln Val
 35 40 45

Pro Pro Glu Val Ser Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys
 50 55 60

Thr Phe Thr His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile
 65 70 75 80

Trp Arg Ala Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Ala
 85 90 95

Ala Ala Arg Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly
 100 105 110

Arg Phe Arg Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg
 115 120 125

Val Glu Arg Leu Ala Leu Ala Asp Asp Arg Arg Tyr Phe Cys Arg Val
 130 135 140

Glu Phe Ala Gly Asp Val His Asp Arg Tyr Glu Ser Arg His Gly Val
 145 150 155 160

Arg Leu His Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu
 165 170 175

Pro Ser Pro Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu
 180 185 190

Pro Pro Pro Ala Leu Ala Trp Ser Gly Pro Ala Leu Gly Asn Ser Leu
 195 200 205

Ala Ala Val Arg Ser Pro Arg Glu Gly His Gly His Leu Val Thr Ala
 210 215 220

Glu Leu Pro Ala Leu Thr His Asp Gly Arg Tyr Thr Cys Thr Ala Ala
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Gly Ala Ser Gly
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<211> 56

<212> DNA

<213> Artificial sequence

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<210> 18
 <211> 52
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer of soluble human Siglec-15 cDNA
 <400> 18
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<210> 19
 <211> 897
 <212> DNA
 <213> Artificial Sequence

<220>
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<220>
 <221> CDS
 <222> (1)..(897)

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aca ggc tca ttt gtg aga act aaa ata gat act acg gag aac ttg ctc 96
 Thr Gly Ser Phe Val Arg Thr Lys Ile Asp Thr Thr Glu Asn Leu Leu
 20 25 30

aac aca gag gtg cac agc tcg cca gcg cag cgc tgg tcc atg cag gtg 144
 Asn Thr Glu Val His Ser Ser Pro Ala Gln Arg Trp Ser Met Gln Val
 35 40 45

cca ccc gag gtg agc gcg gag gca ggc gac gcg gca gtg ctg ccc tgc 192
 Pro Pro Glu Val Ser Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys
 50 55 60

acc ttc acg cac ccg cac cgc cac tac gac ggg ccg ctg acg gcc atc 240
 Thr Phe Thr His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile
 65 70 75 80

tgg cgc gcg ggc gag ccc tat gcg ggc ccg cag gtg ttc cgc tgc gct 288
 Trp Arg Ala Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Ala
 85 90 95

gcg gcg cgg ggc agc gag ctc tgc cag acg gcg ctg agc ctg cac ggc 336
 Ala Ala Arg Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly
 100 105 110

cgc ttc cgg ctg ctg ggc aac ccg cgc cgc aac gac ctc tcg ctg cgc 384
 Arg Phe Arg Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg
 115 120 125

gtc gag cgc ctc gcc ctg gct gac gac cgc cgc tac ttc tgc cgc gtc 432
 Val Glu Arg Leu Ala Leu Ala Asp Asp Arg Arg Tyr Phe Cys Arg Val
 130 135 140

gag ttc gcc ggc gac gtc cat gac cgc tac gag agc cgc cac ggc gtc	480
Glu Phe Ala Gly Asp Val His Asp Arg Tyr Glu Ser Arg His Gly Val	
145 150 155 160	
cgg ctg cac gtg aca gcc gcg ccg cgg atc gtc aac atc tcg gtg ctg	528
Arg Leu His Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu	
165 170 175	
ccc agt ccg gct cac gcc ttc cgc gcg ctc tgc act gcc gaa ggg gag	576
Pro Ser Pro Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu	
180 185 190	
ccg ccg ccc gcc ctc gcc tgg tcc ggc ccg gcc ctg ggc aac agc ttg	624
Pro Pro Pro Ala Leu Ala Trp Ser Gly Pro Ala Leu Gly Asn Ser Leu	
195 200 205	
gca gcc gtg cgg agc ccg cgt gag ggt cac ggc cac cta gtg acc gcc	672
Ala Ala Val Arg Ser Pro Arg Glu Gly His Gly His Leu Val Thr Ala	
210 215 220	
gaa ctg ccc gca ctg acc cat gac ggc cgc tac acg tgt acg gcc gcc	720
Glu Leu Pro Ala Leu Thr His Asp Gly Arg Tyr Thr Cys Thr Ala Ala	
225 230 235 240	
aac agc ctg ggc cgc tcc gag gcc agc gtc tac ctg ttc cgc ttc cat	768
Asn Ser Leu Gly Arg Ser Glu Ala Ser Val Tyr Leu Phe Arg Phe His	
245 250 255	
ggc gcc agc ggg gac cca gct ttc ttg tac aaa gtg gtt gat atc gaa	816
Gly Ala Ser Gly Asp Pro Ala Phe Leu Tyr Lys Val Val Asp Ile Glu	
260 265 270	
ggt cgt ggg ggt aag cct atc cct aac cct ctc ctc ggt ctc gat tct	864
Gly Arg Gly Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser	
275 280 285	
acg cgt acc ggt cat cat cac cat cac cat tga	897
Thr Arg Thr Gly His His His His His His	
290 295	

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 <212> PRT
 <213> Artificial sequence

 <220>
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Asn Thr Glu Val His Ser Ser Pro Ala Gln Arg Trp Ser Met Gln Val	
35 40 45	
Pro Pro Glu Val Ser Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys	
50 55 60	

Thr Phe Thr His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile
 65 70 75 80
 Trp Arg Ala Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Ala
 85 90 95
 Ala Ala Arg Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly
 100 105 110
 Arg Phe Arg Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg
 115 120 125
 Val Glu Arg Leu Ala Leu Ala Asp Asp Arg Arg Tyr Phe Cys Arg Val
 130 135 140
 Glu Phe Ala Gly Asp Val His Asp Arg Tyr Glu Ser Arg His Gly Val
 145 150 155 160
 Arg Leu His Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu
 165 170 175
 Pro Ser Pro Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu
 180 185 190
 Pro Pro Pro Ala Leu Ala Trp Ser Gly Pro Ala Leu Gly Asn Ser Leu
 195 200 205
 Ala Ala Val Arg Ser Pro Arg Glu Gly His Gly His Leu Val Thr Ala
 210 215 220
 Glu Leu Pro Ala Leu Thr His Asp Gly Arg Tyr Thr Cys Thr Ala Ala
 225 230 235 240
 Asn Ser Leu Gly Arg Ser Glu Ala Ser Val Tyr Leu Phe Arg Phe His
 245 250 255
 Gly Ala Ser Gly Asp Pro Ala Phe Leu Tyr Lys Val Val Asp Ile Glu
 260 265 270
 Gly Arg Gly Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser
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 290 295

<210> 21
 <211> 1518
 <212> DNA
 <213> Artificial Sequence
 <220>
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<220>
 <221> CDS
 <222> (1)..(1518)

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aac aca gag gtg cac agc tcg cca gcg cag cgc tgg tcc atg cag gtg Asn Thr Glu Val His Ser Ser Pro Ala Gln Arg Trp Ser Met Gln Val 35 40 45	144
cca ccc gag gtg agc gcg gag gca ggc gac gcg gca gtg ctg ccc tgc Pro Pro Glu Val Ser Ala Glu Ala Gly Asp Ala Val Leu Pro Cys 50 55 60	192
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tgg cgc gcg ggc gag ccc tat gcg ggc ccg cag gtg ttc cgc tgc gct Trp Arg Ala Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Ala 85 90 95	288
gcg gcg cgg ggc agc gag ctc tgc cag acg gcg ctg agc ctg cac ggc Ala Ala Arg Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly 100 105 110	336
cgc ttc cgg ctg ctg ggc aac ccg cgc cgc aac gac ctc tcg ctg cgc Arg Phe Arg Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg 115 120 125	384
gtc gag cgc ctc gcc ctg gct gac gac cgc cgc tac ttc tgc cgc gtc Val Glu Arg Leu Ala Leu Ala Asp Asp Arg Arg Tyr Phe Cys Arg Val 130 135 140	432
gag ttc gcc ggc gac gtc cat gac cgc tac gag agc cgc cac ggc gtc Glu Phe Ala Gly Asp Val His Asp Arg Tyr Glu Ser Arg His Gly Val 145 150 155 160	480
cgg ctg cac gtg aca gcc gcg ccg cgg atc gtc aac atc tcg gtg ctg Arg Leu His Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu 165 170 175	528
ccc agt ccg gct cac gcc ttc cgc gcg ctc tgc act gcc gaa ggg gag Pro Ser Pro Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu 180 185 190	576
ccg ccg ccc gcc ctc gcc tgg tcc ggc ccg gcc ctg ggc aac agc ttg Pro Pro Pro Ala Leu Ala Trp Ser Gly Pro Ala Leu Gly Asn Ser Leu 195 200 205	624
gca gcc gtg cgg agc ccg cgt gag ggt cac ggc cac cta gtg acc gcc Ala Ala Val Arg Ser Pro Arg Glu Gly His Gly His Leu Val Thr Ala 210 215 220	672
gaa ctg ccc gca ctg acc cat gac ggc cgc tac acg tgt acg gcc gcc Glu Leu Pro Ala Leu Thr His Asp Gly Arg Tyr Thr Cys Thr Ala Ala 225 230 235 240	720
aac agc ctg ggc cgc tcc gag gcc agc gtc tac ctg ttc cgc ttc cat Asn Ser Leu Gly Arg Ser Glu Ala Ser Val Tyr Leu Phe Arg Phe His	768

245										250					255					
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Gly	Ala	Ser	Gly	Asp	Pro	Ala	Phe	Leu	Tyr	Lys	Val	Val	Asp	Ile	Gln					
			260					265					270							
gca	gag	ccc	aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	864				
Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro					
		275					280					285								
gca	cct	gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	912				
Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys					
	290					295					300									
ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	960				
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val					
305					310					315					320					
gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	1008				
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr					
				325					330					335						
gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	1056				
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu					
			340					345					350							
cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	1104				
Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His					
		355					360					365								
cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	1152				
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys					
	370					375					380									
gcc	ctc	cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	1200				
Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln					
385					390					395					400					
ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg	gag	gag	atg	1248				
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met					
				405					410					415						
acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	1296				
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro					
			420					425					430							
agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	1344				
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn					
		435					440					445								
tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	1392				
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu					
	450					455					460									
tat	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	1440				
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val					
465					470					475					480					
ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	1488				
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln					
				485					490					495						
aag	agc	ctc	tcc	ctg	tct	ccg	ggt	aaa	taa							1518				
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys												
			500					505												

<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 22

Met Glu Lys Ser Ile Trp Leu Leu Ala Cys Leu Ala Trp Val Leu Pro
1 5 10 15

Thr Gly Ser Phe Val Arg Thr Lys Ile Asp Thr Thr Glu Asn Leu Leu
20 25 30

Asn Thr Glu Val His Ser Ser Pro Ala Gln Arg Trp Ser Met Gln Val
35 40 45

Pro Pro Glu Val Ser Ala Glu Ala Gly Asp Ala Ala Val Leu Pro Cys
50 55 60

Thr Phe Thr His Pro His Arg His Tyr Asp Gly Pro Leu Thr Ala Ile
65 70 75 80

Trp Arg Ala Gly Glu Pro Tyr Ala Gly Pro Gln Val Phe Arg Cys Ala
85 90 95

Ala Ala Arg Gly Ser Glu Leu Cys Gln Thr Ala Leu Ser Leu His Gly
100 105 110

Arg Phe Arg Leu Leu Gly Asn Pro Arg Arg Asn Asp Leu Ser Leu Arg
115 120 125

Val Glu Arg Leu Ala Leu Ala Asp Asp Arg Arg Tyr Phe Cys Arg Val
130 135 140

Glu Phe Ala Gly Asp Val His Asp Arg Tyr Glu Ser Arg His Gly Val
145 150 155 160

Arg Leu His Val Thr Ala Ala Pro Arg Ile Val Asn Ile Ser Val Leu
165 170 175

Pro Ser Pro Ala His Ala Phe Arg Ala Leu Cys Thr Ala Glu Gly Glu
180 185 190

Pro Pro Pro Ala Leu Ala Trp Ser Gly Pro Ala Leu Gly Asn Ser Leu
195 200 205

Ala Ala Val Arg Ser Pro Arg Glu Gly His Gly His Leu Val Thr Ala
210 215 220

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

Asn Ser Leu Gly Arg Ser Glu Ala Ser Val Tyr Leu Phe Arg Phe His
 245 250 255
 Gly Ala Ser Gly Asp Pro Ala Phe Leu Tyr Lys Val Val Asp Ile Gln
 260 265 270
 Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 275 280 285
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 290 295 300
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 305 310 315 320
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 325 330 335
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 340 345 350
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 355 360 365
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 370 375 380
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 385 390 395 400
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 405 410 415
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 420 425 430
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 435 440 445
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 450 455 460
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 465 470 475 480
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 485 490 495
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 500 505

<210> 23
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer of heavy chain cDNA of rat #32A1 antibody

 <400> 23
 ggccgggtgg gctacgttgc aggtgacggt ctg 33

<210> 24
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer of light chain cDNA of rat #32A1 antibody

 <400> 24
 catgctgtac gtgctgtctt tgctgtcctg atcag 35

<210> 25
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequencing primer of heavy chain cDNA of rat #32A1 antibody

 <400> 25
 ctccagagtt ccaggtcacg gtgactggc 29

<210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequencing promoter of light chain cDNA of rat #32A1 antibody

 <400> 26
 tccagttgct aactgttccg 20

<210> 27
 <211> 501
 <212> DNA
 <213> Rattus norvegicus

<220>
 <221> CDA
 <222> (1)..(501)

<220>
 <221> CDS
 <222> (1)..(501)

<400> 27
 atg aag ttg tgg ttg agc tgg ata ttc ctt gtt gtt ctt ttc aaa ggt 48
 Met Lys Leu Trp Leu Ser Trp Ile Phe Leu Val Val Leu Phe Lys Gly
 1 5 10 15

gtg agg tgt gag gtg caa att ttg gag act gga gga ggc ttg gtg aag Val Arg Cys Glu Val Gln Ile Leu Glu Thr Gly Gly Gly Leu Val Lys 20 25 30	96
ccc ggt ggt tcc ctg aga ctg tct tgt gca acg tct gga ttc aat ttc Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Asn Phe 35 40 45	144
aat gat tat ttc atg aac tgg gtc cgt cag gct cca gaa aag ggg cta Asn Asp Tyr Phe Met Asn Trp Val Arg Gln Ala Pro Glu Lys Gly Leu 50 55 60	192
gag tgg gtt gct caa ata agg aac aaa att tat act tat gcc aca ttt Glu Trp Val Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe 65 70 75 80	240
tat gcg gag tct ttg gaa ggc aga gtc aca atc tca cga gac gat tcc Tyr Ala Glu Ser Leu Glu Gly Arg Val Thr Ile Ser Arg Asp Asp Ser 85 90 95	288
gaa agc agt gtc tac ctg caa gtg agc agt tta aga gct gaa gac act Glu Ser Ser Val Tyr Leu Gln Val Ser Ser Leu Arg Ala Glu Asp Thr 100 105 110	336
gcc att tat tac tgt aca aga tcc cta act ggg gga gac tac ttt gat Ala Ile Tyr Tyr Cys Thr Arg Ser Leu Thr Gly Gly Asp Tyr Phe Asp 115 120 125	384
tac tgg ggc caa gga gtc atg gtc aca gtc tcc tta gct gaa aca aca Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser Leu Ala Glu Thr Thr 130 135 140	432
gcc cca tct gtc tat cca ctg gct cct gga act gct ctc aaa agt aac Ala Pro Ser Val Tyr Pro Leu Ala Pro Gly Thr Ala Leu Lys Ser Asn 145 150 155 160	480
tcc atg gtg acc ctg gga tgc Ser Met Val Thr Leu Gly Cys 165	501

<210> 28
 <211> 167
 <212> PRT
 <213> Rattus norvegicus

<400> 28

Met Lys Leu Trp Leu Ser Trp Ile Phe Leu Val Val Leu Phe Lys Gly 1 5 10 15
Val Arg Cys Glu Val Gln Ile Leu Glu Thr Gly Gly Gly Leu Val Lys 20 25 30
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Asn Phe 35 40 45
Asn Asp Tyr Phe Met Asn Trp Val Arg Gln Ala Pro Glu Lys Gly Leu 50 55 60
Glu Trp Val Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe 65 70 75 80

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

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

Ala Ile Tyr Tyr Cys Thr Arg Ser Leu Thr Gly Gly Asp Tyr Phe Asp
115 120 125

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

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

Ser Met Val Thr Leu Gly Cys
165

<210> 29
<211> 417
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (1)..(417)

<400> 29	
atg gag aca gac aga ctc ctg cta tgg gca ctg ctg ctc tgg gtt cca	48
Met Glu Thr Asp Arg Leu Leu Leu Trp Ala Leu Leu Leu Trp Val Pro	
1 5 10 15	
ggc tcc act ggt gac att gtc ttg acc cag tct cct gct ttg gct gtg	96
Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Leu Ala Val	
20 25 30	
tct cta ggg cag agg gcc aca atc tcc tgt agg gcc agc caa agt gtc	144
Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val	
35 40 45	
act att tct gga tat agt ttt ata cac tgg tac caa cag aaa cca gga	192
Thr Ile Ser Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly	
50 55 60	
cag caa ccc aga ctc ctc atc tat cgt gca tcc aac cta gcc tct ggg	240
Gln Gln Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly	
65 70 75 80	
atc ccg gcc agg ttc agt ggc agt ggg tct ggg aca gac ttc acc ctc	288
Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu	
85 90 95	
acc atc aat cct gtg cag gct gat gat att gca acc tat ttc tgt cag	336
Thr Ile Asn Pro Val Gln Ala Asp Asp Ile Ala Thr Tyr Phe Cys Gln	
100 105 110	
cag agt agg aaa tct ccg tgg acg ttc gct gga ggc acc aag ctg gaa	384
Gln Ser Arg Lys Ser Pro Trp Thr Phe Ala Gly Gly Thr Lys Leu Glu	
115 120 125	
ttg aga cgg gct gat gct gca cca act gta tct	417

Leu Arg Arg Ala Asp Ala Ala Pro Thr Val Ser
130 135

<210> 30
<211> 139
<212> PRT
<213> Rattus norvegicus

<400> 30

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

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

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

Thr Ile Ser Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Gln Gln Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly
65 70 75 80

Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
85 90 95

Thr Ile Asn Pro Val Gln Ala Asp Asp Ile Ala Thr Tyr Phe Cys Gln
100 105 110

Gln Ser Arg Lys Ser Pro Trp Thr Phe Ala Gly Gly Thr Lys Leu Glu
115 120 125

Leu Arg Arg Ala Asp Ala Ala Pro Thr Val Ser
130 135

<210> 31
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer EFF1

<400> 31
ccacgcgcc tgtagcggcg cattaagc

28

<210> 32
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer EFsmaR

<400> 32

aaacccgga gctttttgca aaagcctagg

30

<210> 33
<211> 1704
<212> DNA
<213> Artificial Sequence

<220>
<223> Fragment B

<400> 33
ggtaccaccc aagctggcta ggtaagcttg ctagcgccac catggtgctg cagaccagc 60
tggtcatctc cctgctgctg tggatctccg gcgcataatg cgatatcgtg atgattaaac 120
gtacggtggc cgccccctcc gtgttcatct tccccccctc cgacgagcag ctgaagtccg 180
gcaccgcctc cgtggtgtgc ctgctgaata acttctaccc cagagaggcc aaggtgcagt 240
ggaaggtgga caacgccttg cagtccggga actcccagga gagcgtgacc gagcaggaca 300
gcaaggacag cacctacagc ctgagcagca ccctgaccct gagcaaagcc gactacgaga 360
agcacaaggt gtacgcctgc gaggtgaccc accagggcct gagctcccc gtcaccaaga 420
gcttcaacag gggggagtgt taggggccc tttaaacggg tggcatccct gtgaccctc 480
cccagtgcct ctcttgccc tggaagtgc cactccagtg cccaccagcc ttgtcctaata 540
aaaattaagt tgcatactt tgtctgacta ggtgtccttc tataatatta tggggtggag 600
gggggtggta tggagcaagg ggcaagtgg gaagacaacc tgtagggcct gcggggtcta 660
ttgggaacca agctggagt cagtggcaca atcttggctc actgcaatct ccgcctcctg 720
ggttcaagcg attctcctgc ctacgcctcc cgagttgttg ggattccagg catgcatgac 780
caggctcacc taatttttgt ttttttggtg gagacgggt ttcaccatat tggccaggct 840
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acaggcgtga accactgctc cacgcgcct gtacggcgc attaagcgc gcgggtgtgg 960
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tccctttagg gttccgattt agtgctttac ggcacctga ccccaaaaaa cttgattagg 1140
gtgatggtc acgtagtgg ccatcgccct gatagacggt ttttcgccct ttgacgttgg 1200
agtccacgtt ctttaatatg ggactcttgt tccaaactgg aacaacactc aaccctatct 1260
cggctctattc ttttgattta taagggattt tgccgatttc ggcctatttg ttaaaaaatg 1320
agctgattta acaaaaattt aacgcgaatt aattctgttg aatgtgtgtc agttagggtg 1380
tggaagtcc ccaggctccc cagcaggcag aagtatgcaa agcatgcatc tcaattagtc 1440
agcaaccagg tgtggaaagt ccccaggctc ccagcaggc agaagtatgc aaagcatgca 1500
tctcaattag tcagcaacca tagtcccgc cctaactccg cccatccccg ccctaactcc 1560
gccagttcc gccattctc cgcccatgg ctgactaatt ttttttattt atgcagaggc 1620
cgaggccgcc tctgcctctg agctattcca gaagtagtga ggaggctttt ttggaggcct 1680

aggctttttgc aaaaagctcc cggg

1704

<210> 34
<211> 1120
<212> DNA
<213> Artificial Sequence

<220>
<223> human IgG1 signal + human IgG1 constant

<400> 34
tgctagcgcc accatgaaac acctgtggtt cttcctcctg ctggtggcag ctcccagatg 60
ggtgctgagc caggtgcaat tgtgcaggcg gttagctcag cctccaccaa gggcccaagc 120
gtcttcccc tggcaccctc ctccaagagc acctctggcg gcacagccgc cctgggctgc 180
ctggtcaagg actacttccc cgaacccgtg accgtgagct ggaactcagg cgccctgacc 240
agcggcgtgc acaccttccc cgctgtcctg cagtcctcag gactctactc cctcagcagc 300
gtggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 360
aagcccagca acaccaaggt ggacaagaga gttgagccca aatcttgtga caaaactcac 420
acatgcccac cctgcccagc acctgaactc ctgggggggac cctcagtctt cctcttcccc 480
ccaaaacca aggacacct catgatctcc cggacccctg aggtcacatg cgtgggtggtg 540
gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 600
cataatgcca agacaaagcc ccgggaggag cagtacaaca gcacgtaccg ggtggtcagc 660
gtcctcaccg tcttgacca ggactggctg aatggcaagg agtacaagt caaggtctcc 720
aacaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg ccagccccgg 780
gaaccacagg tgtacacct gccccatcc cgggaggaga tgaccaagaa ccaggtcagc 840
ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagt ggagagcaat 900
ggccagcccg agaacaacta caagaccacc cctcccgtgc tggactccga cggctccttc 960
ttccttaca gcaagctcac cgtggacaag agcaggtggc agcagggcaa cgtcttctca 1020
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cccggcaaat gagatatcgg gcccgtttaa acgggtggca 1120

<210> 35
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer of heavy chain variable region cDNA of #32A1 antibody

<400> 35
aaagctgagc gaggtgcaaa ttttggagac tggaggaggc 40

<210> 36
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
 <223> PCR primer of heavy chain variable region cDNA of #32A1 antibody
 <400> 36
 aaagctgagc tgactgtgac catgactcct tggccccag 39

<210> 37
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequencing primer of heavy chain variable region cDNA of #32A1 antibody
 <400> 37
 taatacgact cactataggg 20

<210> 38
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer of light chain variable region cDNA of #32A1 antibody
 <400> 38
 aaacatatgg cgacattgtc ttgacccagt ctcctgcttt gg 42

<210> 39
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer of light chain variable region cDNA of #32A1 antibody
 <400> 39
 aaacgtacgt ctcaattcca gcttggtgcc tccagcg 37

<210> 40
 <211> 1413
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chimeric heavy chain of #32A1

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

<400> 40
 atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 1 5 10 15

gtg ctg agc gag gtg caa att ttg gag act gga gga ggc ttg gtg aag 96
 Val Leu Ser Glu Val Gln Ile Leu Glu Thr Gly Gly Gly Leu Val Lys
 20 25 30

ccc ggt ggt tcc ctg aga ctg tct tgt gca acg tct gga ttc aat ttc 144
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Asn Phe

35	40	45	
aat gat tat ttc atg aac tgg gtc cgt cag gct cca gaa aag ggg cta Asn Asp Tyr Phe Met Asn Trp Val Arg Gln Ala Pro Glu Lys Gly Leu 50 55 60			192
gag tgg gtt gct caa ata agg aac aaa att tat act tat gcc aca ttt Glu Trp Val Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe 65 70 75 80			240
tat gcg gag tct ttg gaa ggc aga gtc aca atc tca cga gac gat tcc Tyr Ala Glu Ser Leu Glu Gly Arg Val Thr Ile Ser Arg Asp Asp Ser 85 90 95			288
gaa agc agt gtc tac ctg caa gtg agc agt tta aga gct gaa gac act Glu Ser Ser Val Tyr Leu Gln Val Ser Ser Leu Arg Ala Glu Asp Thr 100 105 110			336
gcc att tat tac tgt aca aga tcc cta act ggg gga gac tac ttt gat Ala Ile Tyr Tyr Cys Thr Arg Ser Leu Thr Gly Gly Asp Tyr Phe Asp 115 120 125			384
tac tgg ggc caa gga gtc atg gtc aca gtc agc tca gcc tcc acc aag Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser Ser Ala Ser Thr Lys 130 135 140			432
ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly 145 150 160			480
ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro 165 170 175			528
gtg acc gtg agc 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 ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg Phe Pro Ala Val Leu Gln Ser 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 aga gtt gag ccc Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro 225 230 235 240			720
aaa tct tgt gac aaa act cac aca tgc cca ccc 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 ccc 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 ccc cgg gag gag cag tac aac Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn 305 310 315 320 325 330			960

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

<210> 41
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 41

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Glu Val Gln Ile Leu Glu Thr Gly Gly Gly Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Asn Phe
35 40 45

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

Glu Trp Val Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe
 65 70 75 80
 Tyr Ala Glu Ser Leu Glu Gly Arg Val Thr Ile Ser Arg Asp Asp Ser
 85 90 95
 Glu Ser Ser Val Tyr Leu Gln Val Ser Ser Leu Arg Ala Glu Asp Thr
 100 105 110
 Ala Ile Tyr Tyr Cys Thr Arg Ser Leu Thr Gly Gly Asp Tyr Phe Asp
 115 120 125
 Tyr Trp Gly Gln Gly Val 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 Arg 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 Glu Glu Met 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> 42
 <211> 714
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Chimeric light chain of #32A1

<220>
 <221> CDS
 <222> (1)..(714)

<400> 42		
atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc		48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser		
1 5 10 15		
ggc gca tat ggc gac att gtc ttg acc cag tct cct gct ttg gct gtg		96
Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Leu Ala Val		
20 25 30		
tct cta ggg cag agg gcc aca atc tcc tgt agg gcc agc caa agt gtc		144
Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val		
35 40 45		
act att tct gga tat agt ttt ata cac tgg tac caa cag aaa cca gga		192
Thr Ile Ser Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly		
50 55 60		
cag caa ccc aga ctc ctc atc tat cgt gca tcc aac cta gcc tct ggg		240

Gln	Gln	Pro	Arg	Leu	Leu	Ile	Tyr	Arg	Ala	Ser	Asn	Leu	Ala	Ser	Gly		
65					70					75					80		
atc	ccg	gcc	agg	ttc	agt	ggc	agt	ggg	tct	ggg	aca	gac	ttc	acc	ctc		288
Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu		
				85					90					95			
acc	atc	aat	cct	gtg	cag	gct	gat	gat	att	gca	acc	tat	ttc	tgt	cag		336
Thr	Ile	Asn	Pro	Val	Gln	Ala	Asp	Asp	Ile	Ala	Thr	Tyr	Phe	Cys	Gln		
			100					105					110				
cag	agt	agg	aaa	tct	ccg	tgg	acg	ttc	gct	gga	ggc	acc	aag	ctg	gaa		384
Gln	Ser	Arg	Lys	Ser	Pro	Trp	Thr	Phe	Ala	Gly	Gly	Thr	Lys	Leu	Glu		
			115				120					125					
ttg	aga	cgt	acg	gtg	gcc	gcc	ccc	tcc	gtg	ttc	atc	ttc	ccc	ccc	tcc		432
Leu	Arg	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser		
							135					140					
gac	gag	cag	ctg	aag	tcc	ggc	acc	gcc	tcc	gtg	gtg	tgc	ctg	ctg	aat		480
Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn		
					150					155					160		
aac	ttc	tac	ccc	aga	gag	gcc	aag	gtg	cag	tgg	aag	gtg	gac	aac	gcc		528
Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala		
				165					170					175			
ctg	cag	tcc	ggg	aac	tcc	cag	gag	agc	gtg	acc	gag	cag	gac	agc	aag		576
Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys		
				180				185					190				
gac	agc	acc	tac	agc	ctg	agc	agc	acc	ctg	acc	ctg	agc	aaa	gcc	gac		624
Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp		
							200					205					
tac	gag	aag	cac	aag	gtg	tac	gcc	tgc	gag	gtg	acc	cac	cag	ggc	ctg		672
Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu		
						215					220						
agc	tcc	ccc	gtc	acc	aag	agc	ttc	aac	agg	ggg	gag	tgt	tag				714
Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys					
					230					235							

<210> 43
 <211> 237
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 43

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

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

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

Thr	Ile	Ser	Gly	Tyr	Ser	Phe	Ile	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly		
	50					55					60						

Gln Gln Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly
65 70 75 80

Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
85 90 95

Thr Ile Asn Pro Val Gln Ala Asp Asp Ile Ala Thr Tyr Phe Cys Gln
100 105 110

Gln Ser Arg Lys Ser Pro Trp Thr Phe Ala Gly Gly Thr Lys Leu Glu
115 120 125

Leu Arg Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145 150 155 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
165 170 175

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

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

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
210 215 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 44
<211> 5
<212> PRT
<213> Rattus norvegicus

<400> 44

Asp Tyr Phe Met Asn
1 5

<210> 45
<211> 19
<212> PRT
<213> Rattus norvegicus

<400> 45

Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe Tyr Ala Glu Ser
1 5 10 15

Leu Glu Gly

<210> 46
<211> 10
<212> PRT
<213> Rattus norvegicus

<400> 46

Ser Leu Thr Gly Gly Asp Tyr Phe Asp Tyr
1 5 10

<210> 47
<211> 15
<212> PRT
<213> Rattus norvegicus

<400> 47

Arg Ala Ser Gln Ser Val Thr Ile Ser Gly Tyr Ser Phe Ile His
1 5 10 15

<210> 48
<211> 7
<212> PRT
<213> Rattus norvegicus

<400> 48

Arg Ala Ser Asn Leu Ala Ser
1 5

<210> 49
<211> 9
<212> PRT
<213> Rattus norvegicus

<400> 49

Gln Gln Ser Arg Lys Ser Pro Trp Thr
1 5

<210> 50
<211> 1410
<212> DNA
<213> Artificial sequence

<220>
<223> h#32A1-T1H

<220>
<221> CDS
<222> (1)..(1410)

<400> 50
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc gag gtg caa ctg gtg gag agc ggc ggc gga ctt gtg caa 96
Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln

20										25										30										
cct	ggc	ggc	tcc	ctg	aga	ctt	agc	tgt	gcc	gcc	tcc	ggc	ttc	aac	ttc	144														
Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asn	Phe															
		35					40					45																		
aac	gac	tac	ttc	atg	aac	tgg	gtg	aga	caa	gcc	cct	ggc	aag	ggc	ctg	192														
Asn	Asp	Tyr	Phe	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu															
	50					55					60																			
gag	tgg	gtg	gcc	caa	atc	aga	aac	aag	atc	tac	acc	tac	gcc	acc	ttc	240														
Glu	Trp	Val	Ala	Gln	Ile	Arg	Asn	Lys	Ile	Tyr	Thr	Tyr	Ala	Thr	Phe															
	65				70					75					80															
tac	gcc	gag	agc	ctt	gag	ggc	aga	ttc	acc	atc	tcc	aga	gac	aac	gcc	288														
Tyr	Ala	Glu	Ser	Leu	Glu	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala															
				85					90					95																
aag	aac	agc	ctg	tac	ctt	caa	atg	aac	tcc	ctg	aga	gcc	gag	gac	acc	336														
Lys	Asn	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr															
			100					105					110																	
gcc	gtg	tac	tac	tgt	gcc	aga	agc	ctt	acc	ggc	ggc	gac	tac	ttc	gac	384														
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Ser	Leu	Thr	Gly	Gly	Asp	Tyr	Phe	Asp															
		115					120					125																		
tac	tgg	ggc	caa	ggc	acc	ctg	gtg	acc	gtg	agc	tca	gcc	tcc	acc	aag	432														
Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys															
	130					135					140																			
ggc	cca	agc	gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggc	480														
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly															
					150					155					160															
ggc	aca	gcc	gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccc	528														
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro															
				165					170					175																
gtg	acc	gtg	agc	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	ccc	gct	gtc	ctg	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	aga	gtt	gag	ccc	720														
Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro															
	225				230					235				240																
aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	ccc	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	ccc	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 ccc 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 cgg 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 325 330 335			1008
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 340 345 350			1056
gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu 355 360 365			1104
cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn 370 375 380			1152
cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile 385 390 400			1200
gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag acc Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr 405 410 415			1248
acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys 420 425 430			1296
ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys 435 440 445			1344
tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc ctc Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu 450 455 460			1392
tcc ctg tct ccc ggc aaa Ser Leu Ser Pro Gly Lys 465 470			1410

<210> 51
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct
 <400> 51

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp 1 5 10 15
Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln 20 25 30
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe 35 40 45

Asn Asp Tyr Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60
 Glu Trp Val Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe
 65 70 75 80
 Tyr Ala Glu Ser Leu Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
 85 90 95
 Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 100 105 110
 Ala Val Tyr Tyr Cys Ala Arg Ser Leu Thr Gly Gly Asp Tyr Phe Asp
 115 120 125
 Tyr Trp Gly Gln Gly Thr Leu 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 Arg 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 Glu Glu Met 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> 52
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> h#32A1-T2H

<220>
 <221> CDS
 <222> (1)..(1410)

<400> 52		
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg		48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp		
1 5 10 15		
gtg ctg agc gag gtg caa ctg gtg gag agc ggc ggc gga ctg gtg caa		96
Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln		
20 25 30		
cct ggc ggc tcc ctg aga ctg agc tgt gcc gcc tcc ggc ttc aac ttc		144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe		
35 40 45		
aac gac tac ttc atg aac tgg gtg aga caa gcc cct gag aag ggc ctg		192

Asn	Asp	Tyr	Phe	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Glu	Lys	Gly	Leu		
50	50					55					60						
gag	tgg	gtg	gcc	caa	atc	aga	aac	aag	atc	tac	acc	tac	gcc	acc	ttc	240	
Glu	Trp	Val	Ala	Gln	Ile	Arg	Asn	Lys	Ile	Tyr	Thr	Tyr	Ala	Thr	Phe		
65					70				75						80		
tac	gcc	gag	agc	ctg	gag	ggc	aga	gtg	acc	atc	tcc	aga	gac	aac	gcc	288	
Tyr	Ala	Glu	Ser	Leu	Glu	Gly	Arg	Val	Thr	Ile	Ser	Arg	Asp	Asn	Ala		
				85					90					95			
aag	aac	agc	ctg	tac	ctg	caa	atg	tcc	tcc	ctg	aga	gcc	gag	gac	acc	336	
Lys	Asn	Ser	Leu	Tyr	Leu	Gln	Met	Ser	Ser	Leu	Arg	Ala	Glu	Asp	Thr		
			100					105					110				
gcc	gtg	tac	tac	tgt	gcc	aga	agc	ctg	acc	ggc	ggc	gac	tac	ttc	gac	384	
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Ser	Leu	Thr	Gly	Gly	Asp	Tyr	Phe	Asp		
		115					120					125					
tac	tgg	ggc	caa	ggc	acc	ctg	gtg	acc	gtg	agc	tca	gcc	tcc	acc	aag	432	
Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys		
	130					135					140						
ggc	cca	agc	gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggc	480	
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly		
145					150				155						160		
ggc	aca	gcc	gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccc	528	
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro		
				165					170					175			
gtg	acc	gtg	agc	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	ccc	gct	gtc	ctg	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	aga	gtt	gag	ccc	720	
Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro		
225					230				235					240			
aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	ccc	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	ccc	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	ccc	cgg	gag	gag	cag	tac	aac	960	
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn		
					310					315					320		
agc	acg	tac	cgg	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	ggc	cag	ccc	cgg	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	gag	gag	atg	acc	aag	aac	1152
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	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	ggc	cag	ccc	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		
acc	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	ggc	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	acc	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	ccc	ggc	aaa											1410
Ser	Leu	Ser	Pro	Gly	Lys											
	465				470											

<210> 53
 <211> 470
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic Construct

 <400> 53

Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp
1			5						10					15	
Val	Leu	Ser	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln
			20					25					30		
Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asn	Phe
		35					40					45			
Asn	Asp	Tyr	Phe	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Glu	Lys	Gly	Leu
	50					55					60				
Glu	Trp	Val	Ala	Gln	Ile	Arg	Asn	Lys	Ile	Tyr	Thr	Tyr	Ala	Thr	Phe
65					70					75					80

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

Lys Asn Ser Leu Tyr Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr
 100 105 110

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

Tyr Trp Gly Gln Gly Thr Leu 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 Arg 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 Glu Glu Met Thr Lys Asn
370 375 380

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

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> 54
<211> 1410
<212> DNA
<213> Artificial sequence

<220>
<223> h#32A1-T3H

<220>
<221> CDS
<222> (1)..(1410)

<400> 54
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc gag gtg cag atc gtg gag agc ggc ggc gga ctt gtg cag 96
Val Leu Ser Glu Val Gln Ile Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

cct ggc ggc tcc ctg aga ctt agc tgt gcc acc tcc ggc ttc aac ttc 144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Asn Phe
35 40 45

aac gac tac ttc atg aac tgg gtg aga cag gcc cct gag aag ggc ctg 192
Asn Asp Tyr Phe Met Asn Trp Val Arg Gln Ala Pro Glu Lys Gly Leu
50 55 60

gag tgg gtg gcc cag atc aga aac aag atc tac acc tac gcc acc ttc 240
Glu Trp Val Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe
65 70 75 80

tac Tyr	gcc Ala	gag Glu	agc Ser	ctt Leu 85	gag Glu	ggc Gly	aga Arg	gtg Val	acc Thr 90	atc Ile	tcc Ser	aga Arg	gac Asp 95	gac Asp 95	agc Ser	288
gag Glu	tcc Ser	agc Ser	gtg Val 100	tac Tyr	ctt Leu	cag Gln	atg Met	tcc Ser 105	agc Ser	ctg Leu	aga Arg	gcc Ala 110	gag Glu 110	gac Asp	acc Thr	336
gcc Ala	gtg Val	tac Tyr 115	tac Tyr	tgt Cys	acc Thr	aga Arg	agc Ser 120	ctt Leu	acc Thr	ggc Gly	ggc Gly	gac Asp 125	tac Tyr	ttc Phe	gac Asp	384
tac Tyr	tgg Trp 130	ggc Gly	cag Gln	ggc Gly	acc Thr	ctg Leu 135	gtg Val	acc Thr	gtg Val	agc Ser	tca Ser 140	gcc Ala	tcc Ser	acc Thr	aag Lys	432
ggc Gly 145	cca Pro	agc Ser	gtc Val	ttc Phe	ccc Pro 150	ctg Leu	gca Ala	ccc Pro	tcc Ser	tcc Ser 155	aag Lys	agc Ser	acc Thr	tct Ser	ggc Gly 160	480
ggc Gly	aca Thr	gcc Ala	gcc Ala	ctg Leu 165	ggc Gly	tgc Cys	ctg Leu	gtc Val	aag Lys 170	gac Asp	tac Tyr	ttc Phe	ccc Pro	gaa Glu 175	ccc Pro	528
gtg Val	acc Thr	gtg Val	agc Ser 180	tgg Trp	aac Asn	tca Ser	ggc Gly	gcc Ala 185	ctg Leu	acc Thr	agc Ser	ggc Gly	gtg Val 190	cac His	acc Thr	576
ttc Phe	ccc Pro	gct Ala 195	gtc Val	ctg Leu	cag Gln	tcc Ser	tca Ser 200	gga Gly	ctc Leu	tac Tyr	tcc Ser 205	ctc Leu 205	agc Ser	agc Ser	gtg Val	624
gtg Val 210	acc Thr	gtg Val	ccc Pro	tcc Ser	agc Ser	agc Ser 215	ttg Leu	ggc Gly	acc Thr	cag Gln	acc Thr 220	tac Tyr	atc Ile	tgc Cys	aac Asn	672
gtg Val 225	aat Asn	cac His	aag Lys	ccc Pro	agc Ser 230	aac Asn	acc Thr	aag Lys	gtg Val	gac Asp 235	aag Lys	aga Arg	gtt Val	gag Glu	ccc Pro 240	720
aaa Lys	tct Ser	tgt Cys	gac Asp	aaa Lys 245	act Thr	cac His	aca Thr	tgc Cys	cca Pro 250	ccc Pro	tgc Cys	cca Pro	gca Ala	cct Pro 255	gaa Glu	768
ctc Leu	ctg Leu	ggg Gly	gga Gly 260	ccc Pro	tca Ser	gtc Val	ttc Phe	ctc Leu 265	ttc Phe	ccc Pro	cca Pro	aaa Lys	ccc Pro 270	aag Lys	gac Asp	816
acc Thr	ctc Leu	atg Met 275	atc Ile	tcc Ser	cgg Arg	acc Thr	cct Pro 280	gag Glu	gtc Val	aca Thr	tgc Cys	gtg Val 285	gtg Val	gtg Val	gac Asp	864
gtg Val 290	agc Ser	cac His	gaa Glu	gac Asp	cct Pro	gag Glu 295	gtc Val	aag Lys	ttc Phe	aac Asn	tgg Trp 300	tac Tyr	gtg Val	gac Asp	ggc Gly	912
gtg Val 305	gag Glu	gtg Val	cat His	aat Asn	gcc Ala 310	aag Lys	aca Thr	aag Lys	ccc Pro	cgg Arg 315	gag Glu	gag Glu	cag Gln	tac Tyr	aac Asn 320	960
agc Ser	acg Thr	tac Tyr	cgg Arg	gtg Val 325	gtc Val	agc Ser	gtc Val	ctc Leu	acc Thr 330	gtc Val	ctg Leu	cac His	cag Gln	gac Asp 335	tgg Trp	1008
ctg Leu	aat Asn	ggc Gly	aag Lys 340	gag Glu	tac Tyr	aag Lys	tgc Cys	aag Lys 345	gtc Val	tcc Ser	aac Asn	aaa Lys	gcc Ala 350	ctc Leu	cca Pro	1056

gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggc	cag	ccc	cgg	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	gag	gag	atg	acc	aag	aac	1152
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	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	
					390					395					400	
gcc	gtg	gag	tgg	gag	agc	aat	ggc	cag	ccc	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		
acc	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	ggc	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	acc	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	ccc	ggc	aaa											1410
Ser	Leu	Ser	Pro	Gly	Lys											
					470											

<210> 55
 <211> 470
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic Construct

 <400> 55

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Glu Val Gln Ile Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Asn Phe
35 40 45

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

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

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

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

100										105										110									
Ala	Val	Tyr	Tyr	Cys	Thr	Arg	Ser	Leu	Thr	Gly	Gly	Asp	Tyr	Phe	Asp														
		115					120					125																	
Tyr	Trp	Gly	Gln	Gly	Thr	Leu	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	Arg	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	Glu	Glu	Met	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> 56
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> h#32A1-T5H

<220>
<221> CDS
<222> (1)..(1410)

<400> 56
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15
gtg ctg agc gag gtg cag gtg gtg gag agc ggc ggc gga ctt gtg cag 96
Val Leu Ser Glu Val Gln Val Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30
cct ggc ggc tcc ctg aga ctt agc tgt gcc acc tcc ggc ttc aac ttc 144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Asn Phe
35 40 45
aac gac tac ttc atg aac tgg gtg aga cag gcc cct ggc aag ggc ctg 192
Asn Asp Tyr Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60
gag tgg gtg gcc cag atc aga aac aag atc tac acc tac gcc acc ttc 240
Glu Trp Val Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe
65 70 75 80
tac gcc gag agc ctt gag ggc aga ttc acc atc tcc aga gac aac agc 288
Tyr Ala Glu Ser Leu Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
85 90 95
aag tcc acc gtg tac ctt cag atg aac tcc ctg aga gcc gag gac acc 336
Lys Ser Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

gcc	gtg	tac	tac	tgt	acc	aga	agc	ctt	acc	ggc	ggc	gac	tac	ttc	gac	384
Ala	Val	Tyr	Tyr	Cys	Thr	Arg	Ser	Leu	Thr	Gly	Gly	Asp	Tyr	Phe	Asp	
		115					120					125				
tac	tgg	ggc	cag	ggc	acc	ctg	gtg	acc	gtg	agc	tca	gcc	tcc	acc	aag	432
Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	
	130					135					140					
ggc	cca	agc	gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggc	480
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	
					150					155					160	
ggc	aca	gcc	gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccc	528
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	
				165					170					175		
gtg	acc	gtg	agc	tgg	aac	tca	ggc	ggc	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	ccc	gct	gtc	ctg	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	aga	gtt	gag	ccc	720
Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	
	225				230					235					240	
aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	ccc	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	ccc	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	ccc	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	cgg	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	ggc	cag	ccc	cgg	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	gag	gag	atg	acc	aag	aac	1152
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	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 ggc cag ccc 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	
acc 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 ggc 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 acc 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 ccc ggc aaa	1410
Ser Leu Ser Pro Gly Lys	
465 470	

<210> 57
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 57

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Glu Val Gln Val Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Asn Phe
35 40 45

Asn Asp Tyr Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

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

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

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

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

Tyr Trp Gly Gln Gly Thr Leu 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 Arg 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 Glu Glu Met 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> 58
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> h#32A1-T6H

<220>
<221> CDS
<222> (1)..(1410)

<400> 58
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc gag gtg cag gtg gtg gag agc ggc ggc gga ctt gtg cag 96
Val Leu Ser Glu Val Gln Val Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

cct ggc ggc tcc ctg aga ctt agc tgt gcc acc tcc ggc ttc aac ttc 144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Asn Phe
35 40 45

aac gac tac ttc atg aac tgg gtg aga cag gcc cct gag aag ggc ctg 192
Asn Asp Tyr Phe Met Asn Trp Val Arg Gln Ala Pro Glu Lys Gly Leu
50 55 60

gag tgg gtg gcc cag atc aga aac aag atc tac acc tac gcc acc ttc 240
Glu Trp Val Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe
65 70 75 80

tac gcc gag agc ctt gag ggc aga gtg acc atc tcc aga gac aac agc 288
Tyr Ala Glu Ser Leu Glu Gly Arg Val Thr Ile Ser Arg Asp Asn Ser
85 90 95

aag tcc acc gtg tac ctt cag atg tcc agc ctt aga gcc gag gac acc 336
Lys Ser Thr Val Tyr Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr
100 105 110

gcc gtg tac tac tgt acc aga agc ctt acc ggc ggc gac tac ttc gac 384
Ala Val Tyr Tyr Cys Thr Arg Ser Leu Thr Gly Gly Asp Tyr Phe Asp
115 120 125

tac tgg ggc cag ggc acc ctt gtg aca gtg agc tca gcc tcc acc aag 432
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys

130	135	140	
ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly 145 150 155 160	480		
ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro 165 170 175	528		
gtg acc gtg agc 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 ccc gct gtc ctg 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 aga gtt gag ccc Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro 225 230 235 240	720		
aaa tct tgt gac aaa act cac aca tgc cca ccc 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 ccc 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 ccc 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 cgg 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 325 330 335	1008		
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 340 345 350	1056		
gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu 355 360 365	1104		
cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn 370 375 380	1152		
cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile 385 390 395 400	1200		
gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag acc Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr 1248			

	405	410	415	
acc 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 ggc 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 acc 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 ccc ggc aaa				1410
Ser Leu Ser Pro Gly Lys	465	470		

<210> 59
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 59

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Glu Val Gln Val Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Asn Phe
35 40 45

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

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

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

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

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

Tyr Trp Gly Gln Gly Thr Leu 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 Arg 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 Glu Glu Met 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> 60
 <211> 714
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> h#32A1-T1L

<220>
 <221> CDS
 <222> (1)..(714)

<400> 60
 atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc 48
 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 1 5 10 15

ggc gca tat ggc gac atc gtg atg acc cag agc cct gac tcc ctt gcc 96
 Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
 20 25 30

gtg tcc ctg ggc gag aga gcc acc atc aac tgt aga gcc tcc cag agc 144
 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser
 35 40 45

gtg acc atc tcc ggc tac agc ttc atc cac tgg tac cag cag aag cct 192
 Val Thr Ile Ser Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro
 50 55 60

ggc cag cct cct aag ctt ctg atc tac aga gcc tcc aac ctt gcc agc 240
 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser
 65 70 75 80

ggc gtg cct gcc aga ttc tcc ggc agc ggc tcc ggc acc gac ttc acc 288
 Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 85 90 95

ctg acc atc agc tcc ctt cag gcc gag gac gtg gcc gtg tac tac tgt 336
 Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
 100 105 110

cag cag agc aga aag tcc cct tgg acc ttc ggc ggc ggc acc aag gtg 384
 Gln Gln Ser Arg Lys Ser Pro Trp Thr Phe Gly Gly Gly Thr Lys Val
 115 120 125

gag atc aag cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc 432
 Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
 130 135 140

tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg 480
 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
 145 150 155 160

aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac aac 528

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac agc 576
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190

aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa gcc 624
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205

gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag gcc 672
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt 714
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 61
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 61

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

Gly Ala Tyr Gly 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 Arg Ala Ser Gln Ser
35 40 45

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

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

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

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

Gln Gln Ser Arg Lys Ser Pro Trp Thr Phe Gly Gly Gly Thr Lys Val
115 120 125

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

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

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

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 62
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> h#32A1-T2L

<220>
<221> CDS
<222> (1)..(714)

<400> 62	
atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc	48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser	
1 5 10 15	
ggc gca tat ggc gac atc gtg atg acc cag agc cct gac tcc ctt gcc	96
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala	
20 25 30	
gtg tcc ctg ggc gag aga gcc acc atc agc tgt aga gcc tcc cag agc	144
Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser	
35 40 45	
gtg acc atc tcc ggc tac agc ttc atc cac tgg tac cag cag aag cct	192
Val Thr Ile Ser Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro	
50 55 60	
ggc cag cct cct aga ctt ctg atc tac aga gcc tcc aac ctt gcc agc	240
Gly Gln Pro Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser	
65 70 75 80	
ggc gtg cct gcc aga ttc tcc ggc agc ggc tcc ggc acc gac ttc acc	288
Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr	
85 90 95	
ctg acc atc agc tcc ctt cag gcc gag gac gtg gcc gtg tac ttc tgt	336
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys	
100 105 110	
cag cag agc aga aag tcc cct tgg acc ttc gcc ggc ggc acc aag gtg	384
Gln Gln Ser Arg Lys Ser Pro Trp Thr Phe Ala Gly Gly Thr Lys Val	
115 120 125	

gag atc aag cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc	432
Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro	
130 135 140	
tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg	480
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu	
145 150 155 160	
aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac aac	528
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn	
165 170 175	
gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac agc	576
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser	
180 185 190	
aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa gcc	624
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala	
195 200 205	
gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag gcc	672
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly	
210 215 220	
ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt	714
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
225 230 235	

<210> 63
 <211> 238
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 63

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

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

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

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

Gly Gln Pro Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser
65 70 75 80

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

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

Gln Gln Ser Arg Lys Ser Pro Trp Thr Phe Ala Gly Gly Thr Lys Val

115 120 125
 Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
 130 135 140
 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
 145 150 155 160
 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
 165 170 175
 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
 180 185 190
 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
 195 200 205
 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
 210 215 220
 Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 64
 <211> 714
 <212> DNA
 <213> Artificial sequence

<220>
 <223> h#32A1-T3L

<220>
 <221> CDS
 <222> (1)..(714)

<400> 64
 atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc 48
 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 1 5 10 15
 ggc gca tat ggc gac atc gtg ctt acc cag agc cct gac tcc ctt gcc 96
 Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala
 20 25 30
 gtg tcc ctg ggc gag aga gcc acc atc agc tgt aga gcc tcc cag agc 144
 Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser
 35 40 45
 gtg acc atc tcc ggc tac agc ttc atc cac tgg tac cag cag aag cct 192
 Val Thr Ile Ser Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro
 50 55 60
 ggc cag cag cct aga ctt ctg atc tac aga gcc tcc aac ctt gcc agc 240
 Gly Gln Gln Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser
 65 70 75 80
 ggc atc cct gcc aga ttc tcc ggc agc ggc tcc ggc acc gac ttc acc 288
 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 85 90 95

ctg acc atc agc tcc ctt cag gcc gag gac gtg gcc acc tac ttc tgt	336
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Thr Tyr Phe Cys	
100 105 110	
cag cag agc aga aag tcc cct tgg acc ttc gcc ggc ggc acc aag gtg	384
Gln Gln Ser Arg Lys Ser Pro Trp Thr Phe Ala Gly Gly Thr Lys Val	
115 120 125	
gag atc aag cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc	432
Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro	
130 135 140	
tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg	480
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu	
145 150 155 160	
aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac aac	528
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn	
165 170 175	
gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac agc	576
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser	
180 185 190	
aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa gcc	624
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala	
195 200 205	
gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag ggc	672
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly	
210 215 220	
ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt	714
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
225 230 235	

<210> 65
 <211> 238
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic Construct

<400> 65

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser	
1 5 10 15	
Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala	
20 25 30	
Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser	
35 40 45	
Val Thr Ile Ser Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro	
50 55 60	
Gly Gln Gln Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser	
65 70 75 80	

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

<210> 66
 <211> 711
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> h#32A1-T4L

<220>
 <221> CDS
 <222> (1)..(711)

<400> 66	
atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc	48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser	
1 5 10 15	
ggc gca tat ggc gac atc gtg ctt acc cag agc cct gcc ctt gcc gtg	96
Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Leu Ala Val	
20 25 30	
tcc ctg ggc gag aga gcc acc atc agc tgt aga gcc tcc cag agc gtg	144
Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val	
35 40 45	
acc atc tcc ggc tac agc ttc atc cac tgg tac cag cag aag cct ggc	192
Thr Ile Ser Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly	

50	55	60	
cag Gln 65	cag Gln 65	cct Pro 65	aga Arg 65
ctt Leu 70	ctg Leu 70	atc Ile 70	tac Tyr 70
aga Arg 75	gcc Ala 75	tcc Ser 75	aac Asn 75
ctt Leu 80	gcc Ala 80	agc Ser 80	ggc Gly 80
240			
atc Ile 85	cct Pro 85	gcc Ala 85	aga Arg 85
ttc Phe 85	tcc Ser 85	ggc Gly 85	agc Ser 85
ggc Gly 90	tcc Ser 90	ggc Gly 90	acc Thr 90
gac Asp 95	ttc Phe 95	acc Thr 95	ctg Leu 95
288			
acc Thr 100	atc Ile 100	agc Ser 100	tcc Ser 100
ctt Leu 105	cag Gln 105	gcc Ala 105	gag Glu 105
gac Asp 110	gtg Val 110	gcc Ala 110	acc Thr 110
ttc Phe 110	tgt Cys 110	cag Gln 110	
336			
cag Gln 115	agc Ser 115	aga Arg 115	aag Lys 115
tcc Ser 120	cct Pro 120	tggt Trp 120	acc Thr 120
ttc Phe 125	ggc Gly 125	ggc Gly 125	acc Thr 125
aag Lys 125	ctg Leu 125	gag Glu 125	
384			
atc Ile 130	aag Lys 130	cgt Arg 130	acg Thr 130
gtg Val 135	ggc Ala 135	ggc Ala 135	ccc Pro 135
tcc Ser 140	gtg Val 140	ttc Phe 140	atc Ile 140
ttc Phe 140	ccc Pro 140	ccc Pro 140	tcc Ser 140
432			
gac Asp 145	gag Glu 145	cag Gln 145	ctg Leu 145
aag Lys 150	tcc Ser 150	ggc Gly 150	acc Thr 150
ggc Gly 155	tcc Ser 155	gtg Val 155	gtg Val 155
tgc Cys 160	ctg Leu 160	ctg Leu 160	aat Asn 160
480			
aac Asn 165	ttc Phe 165	tac Tyr 165	ccc Pro 165
aga Arg 165	gag Glu 165	ggc Ala 165	aag Lys 165
gtg Val 170	cag Gln 170	tggt Trp 170	aag Lys 170
gtg Val 175	gac Asp 175	aac Asn 175	ggc Ala 175
528			
ctg Leu 180	cag Gln 180	tcc Ser 180	ggg Gly 180
aac Asn 185	tcc Ser 185	cag Gln 185	gag Glu 185
agc Ser 190	gtg Val 190	acc Thr 190	gag Glu 190
gac Asp 190	agc Ser 190	aaa Lys 190	ggc Ala 190
gag Ser 195	gac Asp 195	aac Asn 195	ggc Ala 195
576			
gac Asp 195	agc Ser 195	tac Tyr 195	agc Ser 195
ctg Leu 200	agc Ser 200	acc Thr 200	ctg Leu 200
acc Thr 205	ctg Leu 205	agc Ser 205	aaa Lys 205
ggc Ala 205	gac Asp 205	aac Asn 205	ggc Ala 205
624			
tac Tyr 210	gag Glu 210	aag Lys 210	cac His 210
gtg Val 215	tac Tyr 215	ggc Ala 215	tggt Cys 215
gtg Val 220	acc Thr 220	cac His 220	cag Gln 220
ggc Gly 220	ctg Leu 220		
672			
agc Ser 225	tcc Ser 225	ccc Pro 225	gtc Val 225
acc Thr 230	aag Lys 230	agc Ser 230	ttc Phe 230
aac Asn 235	agg Arg 235	ggg Gly 235	gag Glu 235
tgt Cys 235			
711			

<210> 67
 <211> 237
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 67

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

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

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

Thr Ile Ser Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Gln Gln Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly
65 70 75 80

Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
85 90 95

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

Gln Ser Arg Lys Ser Pro Trp Thr Phe Ala Gly Gly Thr Lys Leu Glu
115 120 125

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145 150 155 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
165 170 175

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

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

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
210 215 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 68
<211> 714
<212> DNA
<213> Artificial sequence

<220>
<223> h#32A1-T5L

<220>
<221> CDS
<222> (1)..(714)

<400> 68
atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggc gca tat ggc gac atc gtg ctt acc cag agc cct gac tcc ctt gcc 96
Page 67

Gly	Ala	Tyr	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala		
			20					25					30				
gtg	tcc	ctg	ggc	gag	aga	gcc	acc	atc	aac	tgt	aga	gcc	tcc	cag	agc		144
Val	Ser	Leu	Gly	Glu	Arg	Ala	Thr	Ile	Asn	Cys	Arg	Ala	Ser	Gln	Ser		
		35					40					45					
gtg	acc	atc	tcc	ggc	tac	agc	ttc	atc	cac	tgg	tac	cag	cag	aag	cct		192
Val	Thr	Ile	Ser	Gly	Tyr	Ser	Phe	Ile	His	Trp	Tyr	Gln	Gln	Lys	Pro		
	50					55					60						
ggc	cag	cct	cct	aag	ctt	ctg	atc	tac	aga	gcc	tcc	aac	ctt	gcc	agc		240
Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Arg	Ala	Ser	Asn	Leu	Ala	Ser		
	65				70				75					80			
ggc	atc	cct	gcc	aga	ttc	tcc	ggc	agc	ggc	tcc	ggc	acc	gac	ttc	acc		288
Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr		
			85					90					95				
ctg	acc	atc	agc	tcc	ctt	cag	gcc	gag	gac	gtg	gcc	acc	tac	tac	tgt		336
Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Thr	Tyr	Tyr	Cys		
			100					105					110				
cag	cag	agc	aga	aag	tcc	cct	tgg	acc	ttc	ggc	cag	ggc	acc	aag	gtg		384
Gln	Gln	Ser	Arg	Lys	Ser	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val		
		115					120					125					
gag	atc	aag	cgt	acg	gtg	gcc	gcc	ccc	tcc	gtg	ttc	atc	ttc	ccc	ccc		432
Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro		
	130					135					140						
tcc	gac	gag	cag	ctg	aag	tcc	ggc	acc	gcc	tcc	gtg	gtg	tgc	ctg	ctg		480
Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu		
	145				150					155				160			
aat	aac	ttc	tac	ccc	aga	gag	gcc	aag	gtg	cag	tgg	aag	gtg	gac	aac		528
Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn		
				165					170					175			
gcc	ctg	cag	tcc	ggg	aac	tcc	cag	gag	agc	gtg	acc	gag	cag	gac	agc		576
Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser		
			180					185					190				
aag	gac	agc	acc	tac	agc	ctg	agc	agc	acc	ctg	acc	ctg	agc	aaa	gcc		624
Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala		
		195					200					205					
gac	tac	gag	aag	cac	aag	gtg	tac	gcc	tgc	gag	gtg	acc	cac	cag	ggc		672
Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly		
	210					215					220						
ctg	agc	tcc	ccc	gtc	acc	aag	agc	ttc	aac	agg	ggg	gag	tgt				714
Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				
	225				230					235							

<210> 69
 <211> 238
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic Construct

 <400> 69

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

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

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

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

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

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

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

Gln Gln Ser Arg Lys Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val
115 120 125

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

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

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

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 70
<211> 714
<212> DNA
<213> Artificial sequence

<220>
<223> h#32A1-T6L

<220>

<221> CDS
 <222> (1)..(714)

<400> 70

atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc	48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser	
1 5 10 15	
ggc gca tat ggc gac atc gtg ctt acc cag agc cct gac tcc ctt gcc	96
Gly Ala Tyr Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala	
20 25 30	
gtg tcc ctg ggc gag aga gcc acc atc agc tgt aga gcc tcc cag agc	144
Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser	
35 40 45	
gtg acc atc tcc ggc tac agc ttc atc cac tgg tac cag cag aag cct	192
Val Thr Ile Ser Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro	
50 55 60	
ggc cag cct cct aga ctg ctg atc tac aga gcc tcc aac ctt gcc agc	240
Gly Gln Pro Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser	
65 70 75 80	
ggc atc cct gcc aga ttc tcc ggc agc ggc tcc ggc acc gac ttc acc	288
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr	
85 90 95	
ctg acc atc agc tcc ctt cag gcc gag gac gtg gcc acc tac ttc tgt	336
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Thr Tyr Phe Cys	
100 105 110	
cag cag agc aga aag tcc cct tgg acc ttc gcc ggc ggc acc aag gtg	384
Gln Gln Ser Arg Lys Ser Pro Trp Thr Phe Ala Gly Gly Thr Lys Val	
115 120 125	
gag atc aag cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc	432
Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro	
130 135 140	
tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg	480
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu	
145 150 155 160	
aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac aac	528
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn	
165 170 175	
gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac agc	576
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser	
180 185 190	
aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa gcc	624
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala	
195 200 205	
gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag ggc	672
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly	
210 215 220	
ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt	714
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
225 230 235	

<210> 71
 <211> 238
 <212> PRT

<213> Artificial sequence

<220>

<223> Synthetic Construct

<400> 71

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

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

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

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

Gly Gln Pro Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser
65 70 75 80

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

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

Gln Gln Ser Arg Lys Ser Pro Trp Thr Phe Ala Gly Gly Thr Lys Val
115 120 125

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

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

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

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 72

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

<220>
<223> h#32A1-T7H

<400> 72

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

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

Phe Met Asn Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val
35 40 45

Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe Tyr Ala Glu
50 55 60

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

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

Tyr Cys Ala Arg Ser Leu Thr Gly Gly Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
450

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

<220>
<223> h#32A1-T8H

<400> 73

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
Page 73

1	5	10	15
Ser	Leu	Arg	Leu
	20		
Ser	Cys	Ala	Ala
		25	
Ser	Gly	Phe	Asn
			30
Phe	Met	Asn	Trp
	35		
Val	Arg	Gln	Ala
		40	
Pro	Gly	Lys	Gly
			45
Leu	Glu	Trp	Val
Ala	Gln	Ile	Arg
	50		
Asn	Lys	Ile	Tyr
		55	
Thr	Tyr	Ala	Thr
			60
Phe	Tyr	Ala	Glu
Ser	Leu	Glu	Gly
	65		
Arg	Val	Thr	Ile
	70		
Ser	Arg	Asp	Asn
		75	
Ala	Lys	Asn	Ser
			80
Leu	Tyr	Leu	Gln
		85	
Met	Asn	Ser	Leu
Arg	Ala	Glu	Asp
	90		
Thr	Ala	Val	Tyr
			95
Tyr	Cys	Ala	Arg
		100	
Ser	Leu	Thr	Gly
			105
Asp	Tyr	Phe	Asp
			110
Tyr	Trp	Gly	
Gln	Gly	Thr	Leu
	115		
Val	Thr	Val	Ser
			120
Ser	Ala	Ser	Thr
			125
Lys	Gly	Pro	Ser
Val	Phe	Pro	Leu
	130		
Ala	Pro	Ser	Ser
		135	
Lys	Ser	Thr	Ser
			140
Gly	Gly	Thr	Ala
Ala	Leu	Gly	Cys
	145		
Leu	Val	Lys	Asp
	150		
Tyr	Phe	Pro	Glu
		155	
Pro	Val	Thr	Val
			160
Ser	Trp	Asn	Ser
		165	
Ala	Leu	Thr	Ser
			170
Gly	Val	His	Thr
			175
Phe	Pro	Ala	
Val	Leu	Gln	Ser
	180		
Ser	Ser	Gly	Leu
			185
Tyr	Ser	Leu	Ser
			190
Val	Thr	Val	
Pro	Ser	Ser	Leu
	195		
Gly	Thr	Gln	Thr
		200	
Tyr	Ile	Cys	Asn
			205
Val	Asn	Val	Asn
His			
Lys	Pro	Ser	Asn
	210		
Thr	Lys	Val	Asp
		215	
Lys	Arg	Val	Glu
			220
Pro	Lys	Ser	Cys
Asp	Lys	Thr	His
	225		
Thr	Cys	Pro	Pro
	230		
Cys	Pro	Ala	Pro
		235	
Glu	Leu	Leu	Gly
			240
Gly	Pro	Ser	Val
Phe	Leu	Phe	Pro
	245		
Pro	Pro	Lys	Pro
		250	
Lys	Asp	Thr	Leu
			255
Met			
Ile	Ser	Arg	Thr
		260	
Pro	Glu	Val	Thr
			265
Cys	Val	Val	Val
			270
Asp	Val	Ser	His
Glu	Asp	Pro	Glu
Val	Lys	Phe	Asn
Trp	Tyr	Val	Asp
Gly	Val	Glu	Val

275 280 285
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Lys
 450

<210> 74
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> h#32A1-T9H

<400> 74

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe Asn Asp Tyr
 20 25 30
 Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe Tyr Ala Glu
50 55 60

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

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

Tyr Cys Ala Arg Ser Leu Thr Gly Gly Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
450

<210> 75
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> h#32A1-T10H

<400> 75

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

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

Phe Met Asn Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val
35 40 45

Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe Tyr Ala Glu
50 55 60

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

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
Page 77

Tyr Cys Ala Arg Ser Leu Thr Gly Gly Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
Page 78

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> 76
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> h#32A1-T11H

<400> 76

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

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

Phe Met Asn Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val
35 40 45

Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe Tyr Ala Glu
50 55 60

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

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

Tyr Cys Ala Arg Ser Leu Thr Gly Gly Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
 210 215 220
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 225 230 235
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400

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

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

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

Pro Gly Lys
450

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

<220>
<223> h#32A1-T12H

<400> 77

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

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

Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe Tyr Ala Glu
50 55 60

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

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

Tyr Cys Ala Arg Ser Leu Thr Gly Gly Asp Tyr Phe Asp Tyr Trp Gly
100 105 110

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

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

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
Page 81

165

170

175

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
Page 82

435

440

445

Pro Gly Lys
450

<210> 78
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> h#32A1-T7L

<400> 78

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

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
50 55 60

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

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

Lys Ser Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 79
<211> 218
<212> PRT
<213> Artificial sequence

<220>
<223> h#32A1-T8L

<400> 79

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 Arg Ala Ser Gln Ser Val Thr Ile Ser
20 25 30

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

Lys Ser Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210

215

<210> 80
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> h#32A1-T9L

<400> 80

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 Arg Ala Ser Gln Ser Val Thr Ile Ser
 20 25 30

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
 50 55 60

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

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

Lys Ser Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105 110

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 81
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> h#32A1-T10L

<400> 81

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 Arg Ala Ser Gln Ser Val Thr Ile Ser
20 25 30

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
50 55 60

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

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

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

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 82

<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> h#32A1-T11L

<400> 82

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

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

Lys Ser Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 83
<211> 218
<212> PRT

<213> Artificial Sequence

<220>

<223> h#32A1-T12L

<400> 83

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

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
50 55 60

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

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

Lys Ser Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 84

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> h#32A1-T13L

<400> 84

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

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
50 55 60

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

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

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

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 85

<211> 218

<212> PRT

<213> Artificial sequence

<220>

<223> h#32A1-T14L

<400> 85

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 Arg Ala Ser Gln Ser Val Thr Ile Ser
20 25 30

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

Lys Ser Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 86

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> h#32A1-T15L

<400> 86

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 Arg Ala Ser Gln Ser Val Thr Ile Ser
20 25 30

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 87
<211> 218
<212> PRT
<213> Artificial sequence

<220>
<223> h#32A1-T16L

<400> 87

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
Page 91

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

<210> 88
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> h#32A1-T17L

<400> 88

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

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

Lys Ser Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 89
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> h#32A1-T18L

<400> 89

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 Ser Cys Arg Ala Ser Gln Ser Val Thr Ile Ser
Page 93

20

25

30

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

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

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

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

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

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175

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

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Val Pro Ala
50 55 60

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

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

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

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Thr Ile Ser
20 25 30

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
Page 95

35

40

45

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

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

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

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

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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<210> 92

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<400> 92

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

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Ile Pro Ala
50 55 60

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

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

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

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

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

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Ile Pro Ala
Page 97

50

55

60

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

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

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

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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<400> 94

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

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Ile Pro Ala
50 55 60

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

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

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

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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<400> 95

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

Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser Gly Ile Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
Page 99

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

Ser Leu Glu Pro Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Ser Arg
85 90 95

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

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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gtg ctg agc gaa gtc cag ctt gtg gaa agc gga ggg gga ctc gtt cag 96
Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
Page 101

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Asn	Asp	Tyr	Phe	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
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Tyr	Ala	Ala	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	
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Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Ser	Leu	Thr	Gly	Gly	Asp	Tyr	Phe	Asp	
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Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	
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Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	
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Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	
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Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	
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Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	
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Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	
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gga aag Gly Lys 465			1398

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 <400> 99

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Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe
35 40 45

Asn Asp Tyr Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

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

Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
85 90 95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
100 105 110

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

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

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
145 150 155 160

Ser 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 Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn
210 215 220

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

Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
275 280 285

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
305 310 315 320

Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys
325 330 335

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

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

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

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

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met
405 410 415

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
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Gly Lys
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20 25 30

cct ggc ggc tcc ctg aga ctt agc tgt gcc acc tcc ggc ttc aac ttc 144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Asn Phe
35 40 45

aac gac tac ttc atg aac tgg gtg aga cag gcc cct ggc aag ggc ctg 192
Page 105

Asn 50	Asp	Tyr	Phe	Met	Asn	Trp 55	Val	Arg	Gln	Ala	Pro 60	Gly	Lys	Gly	Leu	
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cct Pro	tcc Ser	gtg Val	ttc Phe 260	ctt Leu	ttc Phe	cct Pro	cct Pro	aag Lys 265	cct Pro	aag Lys	gac Asp	acc Thr	ctg Leu 270	atg Met	atc Ile	816
agc Ser	cgt Arg	acc Thr 275	cct Pro	gag Glu	gtg Val	acc Thr	tgt Cys 280	gtg Val	gtg Val	gtg Val	gac Asp	gtg Val 285	tcc Ser	cac His	gag Glu	864
gac Asp	cct Pro 290	gag Glu	gtg Val	cag Gln	ttc Phe	aac Asn 295	tgg Trp	tac Tyr	gtg Val	gac Asp	ggc Gly 300	gtg Val	gag Glu	gtg Val	cac His	912
aac Asn 305	gcc Ala	aag Lys	acc Thr	aag Lys	cct Pro 310	cgt Arg	gag Glu	gag Glu	caa Gln 315	ttc Phe	aac Asn	agc Ser	acc Thr	ttc Phe	cgt Arg 320	960
gtg	gtg	tcc	gtg	ctt	acc	gtg	gtg	cac	caa	gac	tgg	ctg	aac	ggc	aag	1008

Val	Val	Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	
				325					330					335		
gag	tac	aag	tgt	aag	gtg	agc	aac	aag	gga	ctt	cct	gcc	cct	atc	gag	1056
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	
			340					345					350			
aag	acc	atc	tcc	aag	acc	aag	ggc	caa	cct	cgt	gag	cct	caa	gtg	tac	1104
Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	
		355					360					365				
acc	ctt	cct	cct	agc	cgt	gag	gag	atg	acc	aag	aac	caa	gtg	tcc	ctt	1152
Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	
	370					375					380					
acc	tgt	ctg	gtg	aag	ggc	ttc	tac	cct	agc	gac	atc	gcc	gtg	gag	tgg	1200
Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	
	385				390					395					400	
gag	tcc	aac	gga	caa	cct	gag	aac	aac	tac	aag	acc	acc	cct	cct	atg	1248
Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	
				405					410					415		
ctt	gac	agc	gac	ggc	tcc	ttc	ttc	ctg	tac	agc	aag	ctg	acc	gtg	gac	1296
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	
			420					425					430			
aag	tcc	cgt	tgg	caa	caa	ggc	aac	gtg	ttc	agc	tgt	tcc	gtg	atg	cac	1344
Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	
		435					440					445				
gag	gcc	ctg	cac	aac	cac	tac	acc	caa	aag	agc	ctt	tcc	ctg	agc	cct	1392
Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	
	450					455					460					
gga	aag															1398
Gly	Lys															
465																

<210> 101
 <211> 466
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 101

Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp	
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Val	Leu	Ser	Glu	Val	Gln	Val	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	
			20					25					30			
Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Thr	Ser	Gly	Phe	Asn	Phe	
		35				40						45				
Asn	Asp	Tyr	Phe	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
	50					55					60					
Glu	Trp	Val	Ala	Gln	Ile	Arg	Asn	Lys	Ile	Tyr	Thr	Tyr	Ala	Thr	Phe	
65					70					75					80	

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

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

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

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

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
145 150 155 160

Ser 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 Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn
210 215 220

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

Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
275 280 285

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
305 310 315 320

Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys
325 330 335

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

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

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

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

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met
405 410 415

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

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

Gly Lys
465

<210> 102
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> h#32A1-L2-15

<220>
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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser	
1 5 10 15	
ggc gca tat ggc gaa att ctg atg acg cag agt cct gca act ctt agt	96
Gly Ala Tyr Gly Glu Ile Leu Met Thr Gln Ser Pro Ala Thr Leu Ser	
20 25 30	
ctg tca cct ggc gag aga gcc aca ctc agc tgc cga gcg tcc cag tcc	144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser	
35 40 45	
gtg acc att agc ggc tat tct ttt att cat tgg tat cag caa aag cct	192
Val Thr Ile Ser Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro	
50 55 60	
gga cag gcg cca agg ctg ctc att tac aga gca agc aac ctt gcc tct	240
Gly Gln Ala Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser	
65 70 75 80	

ggc att cca gca aga ttc agc ggg agc gga tca ggg aca gat ttc acc Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr	288
85 90 95	
ttg acc atc tcc tcc ctg gag ccg gag gat ttc gcg ttg tat tat tgt Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Leu Tyr Tyr Cys	336
100 105 110	
cag caa tct agg aag agt cca tgg aca ttt ggc cag ggc acc aaa gtg Gln Gln Ser Arg Lys Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val	384
115 120 125	
gag atc aag cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro	432
130 135 140	
tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu	480
145 150 155 160	
aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac aac Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn	528
165 170 175	
gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac agc Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser	576
180 185 190	
aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa gcc Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala	624
195 200 205	
gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag ggc Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly	672
210 215 220	
ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	714
225 230 235	

<210> 103
 <211> 238
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic Construct
 <400> 103

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

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

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

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

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser
Page 110

gtc act att agt gga tac tca ttt atc cat tgg tat caa cag aaa cca	192
Val Thr Ile Ser Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro	
50 55 60	
gga cag gcg cct cgg ctt ctg atc tac cgc gcc tca aac ctt gcc tct	240
Gly Gln Ala Pro Arg Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser	
65 70 75 80	
ggc atc ccc gcg agg ttc tct ggc tct ggc agc ggt acc gat ttt aca	288
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr	
85 90 95	
ctg act atc tca agc ctc gaa cct gaa gac ttc gca ctg tac ttt tgc	336
Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Leu Tyr Phe Cys	
100 105 110	
cag cag agc agg aag tcc ccc tgg act ttt gca cag gga acc aaa gtc	384
Gln Gln Ser Arg Lys Ser Pro Trp Thr Phe Ala Gln Gly Thr Lys Val	
115 120 125	
gaa atc aag cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc	432
Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro	
130 135 140	
tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg	480
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu	
145 150 155 160	
aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac aac	528
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn	
165 170 175	
gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac agc	576
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser	
180 185 190	
aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa gcc	624
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala	
195 200 205	
gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag ggc	672
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly	
210 215 220	
ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt	714
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
225 230 235	

<210> 105
 <211> 238
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> Synthetic Construct
 <400> 105

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

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
 35 40 45

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

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser
 65 70 75 80

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 85 90 95

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Leu Tyr Phe Cys
 100 105 110

Gln Gln Ser Arg Lys Ser Pro Trp Thr Phe Ala Gln Gly Thr Lys Val
 115 120 125

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
 130 135 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
 145 150 155 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
 165 170 175

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

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

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
 210 215 220

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 106

<211> 1111

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence coding signal peptide and constant region of human IgG2 heavy chain

<400> 106

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agatgggtgc tgagccaggt gcaattgtgc aggcggttag ctgagccagc accaagggcc 120

cttccgtggt ccctctggcc ccttgtagcc gttccaccag cgagtccaac gccgccttg 180

gctgtctggt gaaggactac ttccctgagc ctgtgaccgt gagctggaac tccggagccc	240
ttaccagcgg cgtgcacacc ttccctgccg tgctgcagtc cagcggcctt tactccctga	300
gctccgtggt gaccgtgcct agctccaact tcggcaccca aacctacacc tgtaacgtgg	360
accacaagcc tagcaacacc aaggtggaca agaccgtgga gcgtaagtgt tgtgtggagt	420
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ctaaggacac cctgatgac agccgtaccc ctgagggtgac ctgtgtgggtg gtggacgtgt	540
cccacgagga ccctgagggtg cagttcaact ggtacgtgga cggcgtggag gtgcacaacg	600
ccaagaccaa gcctcgtgag gagcaattca acagcacctt ccgtgtgggtg tccgtgctta	660
ccgtgggtgca ccaagactgg ctgaacggca aggagtacaa gtgtaagggtg agcaacaagg	720
gacttcctgc ccctatcgag aagaccatct ccaagaccaa gggccaacct cgtgagcctc	780
aagtgtacac ctttcctcct agccgtgagg agatgaccaa gaaccaagtg tcccttacct	840
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ctgagaacaa ctacaagacc acccctccta tgcttgacag cgacggctcc ttcttcctgt	960
acagcaagct gaccgtggac aagtcccgtt ggcaacaagg caacgtgttc agctgttccg	1020
tgatgcacga ggccctgcac aaccactaca cccaaaagag cctttccctg agccctggaa	1080
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