

SEQUENCE LISTING

<110> Astellas Pharma Inc.
 <120> Novel anti-human Ig-beta antibody
 <130> A15019A00
 <150> JP2014-160141
 <151> 2014-08-06
 <160> 15
 <170> PatentIn version 3.5
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 <211> 1350
 <212> DNA
 <213> Artificial Sequence
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 <223> H-chain of anti-human Ig-beta antibody

<220>
 <221> CDS
 <222> (1).. (1350)

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

acc	ctg	gtc	acc	gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tgc	gtc	ttc	384
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	
		115					120					125				
ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	432
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	
	130					135					140					
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Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	
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Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	
				165					170					175		
cag	tcc	tca	gga	ctc	tac	tcc	ctt	agt	agc	gtg	gtg	acc	gtg	ccc	tcc	576
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	
			180					185						190		
agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	624
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	
		195					200					205				
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Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	
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Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	
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gac	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	768
Asp	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	
				245					250					255		
cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	gac	gaa	gac	816
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Asp	Glu	Asp	
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Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	
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gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgt	gtg	912
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	
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gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	960
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	
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tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	tgg	cca	gcc	ccc	atc	gag	aaa	1008
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Trp	Pro	Ala	Pro	Ile	Glu	Lys	
				325					330					335		
acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	1056

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

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 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

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Ser	Val	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
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Ala	Gly	Ile	Trp	Ser	Gly	Gly	Ser	Ile	His	Tyr	Thr	Pro	Ala	Leu	Ser
	50					55					60				

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

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

Arg Tyr Asp Arg Tyr Glu Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

<210> 3
 <211> 657
 <212> DNA
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<220>
 <223> L-chain of anti-human Ig-beta antibody

<220>
 <221> CDS
 <222> (1).. (657)

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ggc gac tcc tac atg aac tgg tat cag cag aag ccc gcc aag gcc ccc Gly Asp Ser Tyr Met Asn Trp Tyr 40 Gln Gln Lys Pro 45 Gly Lys Ala Pro	144
aag ctg ctg atc tac gcc gcc tcc aac ctg gaa tcc gcc gtg ccc tcc Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Val Pro Ser	192
aga ttc tcc gcc tcc gcc tct ggc acc gac ttc acc ctg acc atc tcc Arg Phe Ser Gly Ser 70 Gly Ser Gly Thr Asp Phe 75 Thr Leu Thr Ile Ser 80	240
agc ctg cag ccc gag gac ttc gcc acc tac tac tgc cag cag tcc aac Ser Leu Gln Pro 85 Glu Asp Phe Ala Thr 90 Tyr Tyr Cys Gln Gln 95 Ser Asn	288
gag gac ccc ctg acc ttc gcc cag gcc acc aag gtg gaa atc aag cgt Glu Asp Pro 100 Leu Thr Phe Gly Gln 105 Gly Thr Lys Val Glu Ile 110 Lys Arg	336
acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln	384
ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat Leu Lys Ser Gly Thr Ala Ser 135 Val Val Cys Leu 140 Asn Asn Phe Tyr	432
ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg Pro Arg Glu Ala Lys 150 Val Gln Trp Lys Val 155 Asp Asn Ala Leu Gln Ser 160	480
ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc Gly Asn Ser Gln 165 Glu Ser Val Thr Glu Gln 170 Asp Ser Lys Asp Ser Thr 175	528
tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa Tyr Ser Leu Ser 180 Ser Thr Leu Thr 185 Leu Ser Lys Ala Asp Tyr Glu Lys 190	576
cac aaa gtc tac gcc tgc gaa gtc acc cat cag gcc ctg agc tcg ccc His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu 205 Ser Ser Pro 210	624
gtc aca aag agc ttc aac agg gga gag tgt tag Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	657

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Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
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Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Val Pro Ser
 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 Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
 85 90 95

Glu Asp Pro Leu 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
 210 215

<210> 5
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> H-chain of anti-human Ig-beta antibody

<220>
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 <222> (1).. (1350)

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

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

355	360	365	
tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu 370 375 380			1152
agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu 385 390 395 400			1200
gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys 405 410 415			1248
agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu 420 425 430			1296
gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly 435 440 445			1344
aaa tga Lys			1350

<210> 6
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<220>
 <223> Synthetic Construct

<400> 6

Gln Val Gln Met Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Ser Tyr
 20 25 30

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

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

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

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

Arg Tyr Asp Arg Tyr Glu Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu

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

Lys

<210> 7
 <211> 657
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> L-chain of anti-human Ig-beta antibody

<220>
 <221> CDS
 <222> (1).. (657)

<400>	7														
gac	atc	cag	ctg	acc	cag	tcc	ccc	tcc	agc	ctg	tcc	gcc	tct	gtg	ggc
Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	

48

gac aga gtg acc atc aca tgc aag gcc tcc cag tcc gtg gac tac gac Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp	96
ggc gac tcc tac atg aac tgg tat cag cag aag ccc ggc aag gcc ccc Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro	144
aag ctg ctg atc tac gcc gcc tcc aac ctg gaa tcc ggc gtg ccc tcc Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Val Pro Ser	192
aga ttc tcc ggc tcc ggc tct ggc acc gac ttc acc ttc acc atc tcc Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser	240
agc ctg cag ccc gag gat atc gcc acc tac tac tgc cag cag tcc aac Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ser Asn	288
gag gac ccc ctg acc ttc ggc cag ggc acc aag gtg gaa atc aag cgt Glu Asp Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg	336
acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln	384
ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr	432
ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser	480
ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr	528
tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys	576
cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro	624
gtc aca aag agc ttc aac agg gga gag tgt tag Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	657

<210> 8
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 8

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

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

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

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

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

Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
85 90 95

Glu Asp Pro Leu 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
 210 215

<210> 9
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> H-chain of anti-human Ig-beta antibody

<220>
 <221> CDS
 <222> (1).. (1350)

<400> 9
 gaa gtg cag ctg gtg gag tcc ggg gga ggt ctg gtg cag ccc ggg ggt 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tct ctg cgt ctg tct tgt gcc gtg tct ggg ttt agt ctg tcc agc tat 96
 Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Leu Ser Ser Tyr
 20 25 30
 agt gtg cac tgg ttc cga aag gct ccc ggc aaa gga ctg gag tgg ctg 144
 Ser Val His Trp Phe Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45
 ggc gga atc tgg tca ggg ggt tcc att cat tat acc cct gca ctg tct 192
 Gly Gly Ile Trp Ser Gly Gly Ser Ile His Tyr Thr Pro Ala Leu Ser
 50 55 60
 agt aga ctg aca gtg agc cgc gac atc tct aag aac aca gtc tac ctg 240
 Ser Arg Leu Thr Val Ser Arg Asp Ile Ser Lys Asn Thr Val Tyr Leu
 65 70 75 80
 cag atg aat agc ctg agg gcc gag gat acc gct gtc tac tat tgc gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 aga tac gac cgg tat gaa act tac gcc atg gat tac tgg ggc cag ggc 336
 Arg Tyr Asp Arg Tyr Glu Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 100 105 110
 acc ctg gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc 384
 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125
 ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg 432
 Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140
 ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg 480
 Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp

145	150	155	160	
aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu	165	170	175	528
cag tcc tca gga ctc tac tcc ctt agt agc gtg gtg acc gtg ccc tcc Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser	180	185	190	576
agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro	195	200	205	624
agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt gac aaa Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys	210	215	220	672
act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro	225	230	235	720
gac gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc Asp Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser	245	250	255	768
cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc gac gaa gac Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Asp Glu Asp	260	265	270	816
cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn	275	280	285	864
gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val	290	295	300	912
gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu	305	310	315	960
tac aag tgc aag gtc tcc aac aaa gcc tgg cca gcc ccc atc gag aaa Tyr Lys Cys Lys Val Ser Asn Lys Ala Trp Pro Ala Pro Ile Glu Lys	325	330	335	1008
acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr	340	345	350	1056
ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr	355	360	365	1104
tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu	370	375	380	1152

agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg	1200
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu	
385 390 395 400	
gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag	1248
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys	
405 410 415	
agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag	1296
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu	
420 425 430	
gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt	1344
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly	
435 440 445	
aaa tga	1350
Lys	

<210> 10
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 10

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 Val Ser Gly Phe Ser Leu Ser Ser Tyr
20 25 30

Ser Val His Trp Phe Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

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

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

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

Arg Tyr Asp Arg Tyr Glu Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly

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

Gly	Asp	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro		
		35					40					45					
aag	ctg	ctg	atc	tac	gcc	gcc	tcc	aac	ctg	gaa	tcc	ggc	gtg	ccc	tcc		192
Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Val	Pro	Ser		
		50				55					60						
aga	ttc	toc	ggc	tcc	ggc	tct	ggc	acc	gac	ttc	acc	ctg	acc	atc	tcc		240
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser		
					70					75					80		
agc	ctg	cag	ccc	gag	gac	ttc	gcc	acc	tac	tac	tgc	cag	cag	tcc	aac		288
Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Asn		
				85					90					95			
gag	gac	ccc	ctg	acc	ttc	ggc	cag	ggc	acc	aag	gtg	gaa	atc	aag	cgt		336
Glu	Asp	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg		
			100					105					110				
acg	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	cgc	cca	tct	gat	gag	cag		384
Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln		
		115					120					125					
ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	ctg	aat	aac	ttc	tat		432
Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr		
		130				135					140						
ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	aac	gcc	ctc	caa	tcg		480
Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser		
		145			150				155						160		
ggt	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	agc	aag	gac	agc	acc		528
Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr		
				165					170					175			
tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	gca	gac	tac	gag	aaa		576
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys		
			180					185					190				
cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	ggc	ctg	agc	tcg	ccc		624
His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro		
		195					200					205					
gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag							657
Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys								
		210				215											

<210> 12
 <211> 218
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic Construct

 <400> 12

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

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

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

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Val Pro Ser
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 Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
85 90 95

Glu Asp Pro Leu 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
210 215

<210> 13
 <211> 450
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human Ig-beta-Flag fusion gene

<220>
 <221> CDS
 <222> (1)..(447)

<400> 13
 gcc aga tgc gag gac cgg tac cgg aat ccc aaa ggt agt gct tgt tcg 48
 Ala Arg Ser Glu Asp Arg Tyr Arg Asn Pro Lys Gly Ser Ala Cys Ser
 1 5 10 15
 cgg atc tgg cag agc cca cgt ttc ata gcc agg aaa cgg ggc ttc acg 96
 Arg Ile Trp Gln Ser Pro Arg Phe Ile Ala Arg Lys Arg Gly Phe Thr
 20 25 30
 gtg aaa atg cac tgc tac atg aac agc gcc tcc ggc aat gtg agc tgg 144
 Val Lys Met His Cys Tyr Met Asn Ser Ala Ser Gly Asn Val Ser Trp
 35 40 45
 ctc tgg aag cag gag atg gac gag aat ccc cag cag ctg aag ctg gaa 192
 Leu Trp Lys Gln Glu Met Asp Glu Asn Pro Gln Gln Leu Lys Leu Glu
 50 55 60
 aag ggc cgc atg gaa gag tcc cag aac gaa tct ctc gcc acc ctc acc 240
 Lys Gly Arg Met Glu Glu Ser Gln Asn Glu Ser Leu Ala Thr Leu Thr
 65 70 75 80
 atc caa ggc atc cgg ttt gag gac aat ggc atc tac ttc tgt cag cag 288
 Ile Gln Gly Ile Arg Phe Glu Asp Asn Gly Ile Tyr Phe Cys Gln Gln
 85 90 95
 aag tgc aac aac acc tcg gag gtc tac cag ggc tgc ggc aca gag ctg 336
 Lys Cys Asn Asn Thr Ser Glu Val Tyr Gln Gly Cys Gly Thr Glu Leu
 100 105 110
 cga gtc atg gga ttc agc acc ttg gca cag ctg aag cag agg aac acg 384
 Arg Val Met Gly Phe Ser Thr Leu Ala Gln Leu Lys Gln Arg Asn Thr
 115 120 125
 ctg aag gat tgc tca gca gac ctg gtt ccg cgc gga tcc gac tac aag 432
 Leu Lys Asp Ser Ser Ala Asp Leu Val Pro Arg Gly Ser Asp Tyr Lys
 130 135 140
 gac gat gac gat aaa tga 450
 Asp Asp Asp Asp Lys
 145

<210> 14
 <211> 453

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Monkey Ig-beta-Flag fusion gene

<220>
 <221> CDS
 <222> (1).. (450)

<400> 14
 gcc aaa tca gag gac ctg tac ccg aat ccc aaa ggt agt gct tgt tct 48
 Ala Lys Ser Glu Asp Leu Tyr Pro Asn Pro Lys Gly Ser Ala Cys Ser
 1 5 10 15
 cgg atc tgg cag agc cca cgt ttc ata gcc agg aaa cgg ggc ttc acg 96
 Arg Ile Trp Gln Ser Pro Arg Phe Ile Ala Arg Lys Arg Gly Phe Thr
 20 25 30
 gtg aaa atg cac tgc tac gtg acc aac agc acc ttc agc atc gtg agc 144
 Val Lys Met His Cys Tyr Val Thr Asn Ser Thr Phe Ser Ile Val Ser
 35 40 45
 tgg ctc cgg aag cgg gag acg gac aag gag ccc caa cag gtg aac ctg 192
 Trp Leu Arg Lys Arg Glu Thr Asp Lys Glu Pro Gln Gln Val Asn Leu
 50 55 60
 gag cag ggc cac atg cat cag acc caa aac agc tct gtc acc acc ctc 240
 Glu Gln Gly His Met His Gln Thr Gln Asn Ser Ser Val Thr Thr Leu
 65 70 75 80
 atc atc caa gac atc cgg ttt gag gac aac ggc atc tac ttc tgt cag 288
 Ile Ile Gln Asp Ile Arg Phe Glu Asp Asn Gly Ile Tyr Phe Cys Gln
 85 90 95
 cag gag tgc agc aag acc tcg gag gtc tac cgg ggc tgc ggc acg gag 336
 Gln Glu Cys Ser Lys Thr Ser Glu Val Tyr Arg Gly Cys Gly Thr Glu
 100 105 110
 ctg cga gtc atg ggg ttc agc acc ttg gca cag ctg aag cag agg aac 384
 Leu Arg Val Met Gly Phe Ser Thr Leu Ala Gln Leu Lys Gln Arg Asn
 115 120 125
 acg ctg aag gat tcg tca gca gac ctg gtt ccg cgc gga tcc gac tac 432
 Thr Leu Lys Asp Ser Ser Ala Asp Leu Val Pro Arg Gly Ser Asp Tyr
 130 135 140
 aag gac gat gac gat aaa tga 453
 Lys Asp Asp Asp Asp Lys
 145 150

<210> 15
 <211> 1350
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> H-chain of anti-human Ig-beta antibody

<220>
 <221> CDS
 <222> (1)..(1350)

<400> 15		
gag gtg cag atg gtg gaa tcc ggc gga ggc ctg gtg cag cct ggc ggc		48
Glu Val Gln Met Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly		
1 5 10 15		
tct ctg aga ctg tcc tgc gcc gtg tcc ggc ttc agc ctg tcc tcc tac		96
Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Leu Ser Ser Tyr		
20 25 30		
tcc gtg cac tgg gtc cga cag gcc cct ggc aag gga ctg gaa tgg gtg		144
Ser Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val		
35 40 45		
gcc ggc att tgg agc ggc ggc tcc atc cac tac acc cct gcc ctg tcc		192
Ala Gly Ile Trp Ser Gly Gly Ser Ile His Tyr Thr Pro Ala Leu Ser		
50 55 60		
tcc cgg ttc acc gtg tcc cgg gac gac tcc aag aac acc gtg tac ctg		240
Ser Arg Phe Thr Val Ser Arg Asp Asp Ser Lys Asn Thr Val Tyr Leu		
65 70 75 80		
cag atg aac tcc ctg cgg gcc gag gac acc gcc gtg tac tac tgc gcc		288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala		
85 90 95		
cgc tac gac aga tac gag aca tac gcc atg gac tac tgg ggc cag ggc		336
Arg Tyr Asp Arg Tyr Glu Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly		
100 105 110		
acc ctg gtg aca gtg tcc tcc gcc tcc acc aag ggc ccc tcc gtg ttc		384
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe		
115 120 125		
cct ctg gcc ccc tcc agc aag tcc acc tct ggc ggc acc gct gcc ctg		432
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu		
130 135 140		
ggc tgc ctg gtg aaa gac tac ttc ccc gag ccc gtg acc gtg tcc tgg		480
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp		
145 150 155 160		
aac tct ggc gcc ctg acc tcc ggc gtg cac acc ttc cct gcc gtg ctg		528
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu		
165 170 175		
cag tcc tcc ggc ctg tac tcc ctg tcc agc gtg gtg acc gtg ccc tcc		576
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser		
180 185 190		

agc tct ctg ggc acc cag acc tac atc tgc aac gtg aac cac aag ccc Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro 195 200 205	624
tcc aac acc aag gtg gac aag aag gtg gaa ccc aag tcc tgc gac aag Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys 210 215 220	672
acc cac acc tgt ccc cct tgc cct gcc cct gag ctg ctg ggc gga ccc Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro 225 230 235 240	720
gat gtg ttt ctg ttc ccc cca aag ccc aag gac acc ctg atg atc tcc Asp Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser 245 250 255	768
cgg acc ccc gaa gtg acc tgc gtg gtg gtg gac gtg tcc gac gag gac Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Asp Glu Asp 260 265 270	816
cct gaa gtg aag ttc aat tgg tac gtg gac ggc gtg gaa gtg cac aac Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn 275 280 285	864
gcc aag acc aag ccc aga gag gaa cag tac aac tcc acc tac cgg gtg Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val 290 295 300	912
gtg tcc gtg ctg acc gtg ctg cac cag gac tgg ctg aac ggc aaa gaa Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu 305 310 315 320	960
tac aag tgc aag gtt tcc aac aag gcc tgg cct gcc ccc atc gaa aag Tyr Lys Cys Lys Val Ser Asn Lys Ala Trp Pro Ala Pro Ile Glu Lys 325 330 335	1008
acc atc tcc aag gcc aag ggc cag ccc cgc gag ccc cag gtg tac acc Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr 340 345 350	1056
ctg ccc cct agc cgg gac gag ctg acc aag aac cag gtg tcc ctg acc Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr 355 360 365	1104
tgt ctg gtg aaa ggc ttc tac ccc tcc gat atc gcc gtg gaa tgg gag Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu 370 375 380	1152
tcc aac ggc cag ccc gag aac aac tac aag acc acc ccc cct gtg ctg Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu 385 390 395 400	1200
gac tcc gac ggc tca ttc ttc ctg tac tcc aag ctg acc gtg gac aag Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys 405 410 415	1248

tcc	cgg	tgg	cag	cag	ggc	aac	gtg	ttc	tcc	tgc	tcc	gtg	atg	cac	gag	1296
Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	
			420					425					430			
gcc	ctg	cac	aat	cac	tac	acc	cag	aag	tcc	ctg	tcc	ctg	agc	ccc	ggc	1344
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	
			435				440					445				
aag	tga															1350
Lys																